Plant Health Australia
Coordinator of government-industry partnerships for plant biosecurity

Helping protect plant industries and the environment from plant pests through:

- Partnerships
- Emergency response
- Preparedness
- Surveillance
- Diagnostics
- Research & development

Please drop by to see us at stand 1&2 at the APPS 2019 conference or visit planhealthaustralia.com.au
NSW DPI’s Plant Biosecurity Research and Diagnostics section enhances productivity of NSW primary producers with research and diagnostics services to detect and manage pests and diseases and provide surveillance against biosecurity threats.
## Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Welcome Message</td>
<td>7</td>
</tr>
<tr>
<td>Welcome to Melbourne</td>
<td>9</td>
</tr>
<tr>
<td>Conference Organising Committee</td>
<td>11</td>
</tr>
<tr>
<td>Acknowledgments</td>
<td>11</td>
</tr>
<tr>
<td>Our Sponsors</td>
<td>13</td>
</tr>
<tr>
<td>Sponsor Biographies</td>
<td>14</td>
</tr>
<tr>
<td>Exhibitor Biographies</td>
<td>16</td>
</tr>
<tr>
<td>Exhibition Floorplan</td>
<td>18</td>
</tr>
<tr>
<td>Delegate Information</td>
<td>19</td>
</tr>
<tr>
<td>Social Program</td>
<td>22</td>
</tr>
<tr>
<td>Presidents Message</td>
<td>23</td>
</tr>
<tr>
<td>APPS Foundation Members</td>
<td>24</td>
</tr>
<tr>
<td>McAlpine Lecture</td>
<td>25</td>
</tr>
<tr>
<td>APPS 2019 Awards</td>
<td>27</td>
</tr>
<tr>
<td>APPS 2019 Bursary Recipients</td>
<td>30</td>
</tr>
<tr>
<td>Plenary Speakers</td>
<td>31</td>
</tr>
<tr>
<td>Program</td>
<td></td>
</tr>
<tr>
<td>Tuesday 26 November</td>
<td>34</td>
</tr>
<tr>
<td>Wednesday 27 November</td>
<td>38</td>
</tr>
<tr>
<td>Thursday 28 November</td>
<td>42</td>
</tr>
<tr>
<td>Posters</td>
<td>46</td>
</tr>
<tr>
<td>Field Tours</td>
<td>59</td>
</tr>
<tr>
<td>Workshops</td>
<td>60</td>
</tr>
<tr>
<td>Maps &amp; Floor Plans</td>
<td>64</td>
</tr>
<tr>
<td>Abstract Review Sub-Committee</td>
<td>66</td>
</tr>
<tr>
<td>Abstracts Book</td>
<td>67</td>
</tr>
</tbody>
</table>
Our services have been operating for over 100 years. Our specialist entomologists, plant pathologists and virologists are experts in the identification of plant pests and diseases.

Diagnostics

We use traditional morphological techniques, molecular diagnostics, ELISA and electron microscopy to identify the following:

- insects, mites and other invertebrates
- bacteria and phytoplasmas
- fungi, fungal-like organisms and nematodes
- viruses and viroids

Agdia distributorship

Biosecurity Tasmania is the sole Australian Distributor for Agdia Inc., a world leader in the provision of plant diagnostic testing kits for both laboratory and field use.

www.Agdia.com

Other activities

- Advice, training and support for biosecurity policy and emergencies.
- Compilation of official pest records to facilitate trade.
- Monitoring and surveillance.

Our commitment to quality assurance

- Our state-wide laboratories operate under a quality management system.
- Our TASAG ELISA and Pathogen Testing Service is accredited by the National Association of Testing Authorities (NATA).
- We undertake annual proficiency testing in the Australian National Quality Assurance Program (ANQAP).
- Our laboratories are approved for working with pests of biosecurity significance and are inclusive of a BC2 rated laboratory.
- Our staff are members of the National Plant Biosecurity Diagnostic Network (NPBDN) and represent Tasmania on Plant Health Australia’s Subcommittee on Plant Health Diagnostics (SPHD).

Services offered by the Plant Diagnostic Services attract a fee. However, there is no fee to identify a plant pest or disease that is suspected of being an invasive or biosecurity pest.

Contact:
T: 03 6165 3777
E: plantdiagnosticservices@dpipwe.tas.gov.au

Have you spotted anything unusual lately in your plants?

EXOTIC PLANT PEST HOTLINE 1800 084 881
On behalf of the Victorian branch of the Australasian Plant Pathology Society (APPS), we welcome you to our 22nd Biennial Conference at the Melbourne Convention and Exhibition Centre (MCEC) in Melbourne, Australia from 25 – 28th November 2019. This conference will be the climax of the APPS 50th birthday celebrations, where we celebrate our “Strong Foundations and highlight the latest advances in plant pathology that will lead to “Future Innovations”.

Excellent scientific presentations by local and international speakers will be the backbone of our meeting, supported by engaging field tours and workshops allowing conference participants to experience plant pathology up close and to visit key agricultural sites in the areas surrounding Melbourne.

There will be plenty of opportunities for networking with colleagues and mentoring of students at our social functions, and our 50th birthday conference dinner. The city of Melbourne has much to offer you and accompanying family members, so why not make it a family trip?

We look forward to welcoming you to Melbourne for APPS2019. More than ever ‘Plant health is still earth’s wealth’!
Back to our roots—growing our future

The Queensland Government, through the Department of Agriculture and Fisheries, has a proud history of improving and protecting plant production across agricultural and forestry industries, through the delivery of biosecurity services, and plant pathology research, development and extension.

Through multidisciplinary teams located in regional facilities across Queensland, we continue to work in partnership with industry to deliver practical outcomes.

**Biosecurity services**
- Strategies to identify, prioritise and prevent plant biosecurity threats
- Preparedness to respond to plant pest and disease incursions
- Plant pest control, containment and eradication programs
- Surveillance and diagnostic services for plant pests and diseases
- Activities that protect plant production and market access for our agricultural industries and our environment, economy and lifestyle

**Research, development and extension**
- Improved understanding of plant diseases
- Solutions to minimise economic impacts of plant diseases on crops and natural systems
- Diagnostic services for growers and industry
- Advice on all aspects of plant pathology to growers, industry and biosecurity agencies
- Diagnostic tools to assist biosecurity preparedness and surveillance

Learn more about our past, present and future work by listening to our conference presentations and visiting us at exhibition booth 6.

13 25 23
daf.qld.gov.au
@QldAgriculture @BiosecurityQld

*Congratulations to the Australasian Plant Pathology Society on its 50-year anniversary*
Welcome to Melbourne

MESSAGE FROM THE LORD MAYOR OF MELBOURNE

Welcome to Melbourne for the Australasian Plant Pathology Society Conference 2019. The City of Melbourne is a proud supporter of this significant conference that will help deliver resilience and sustainability for our green ecosystem.

Throughout Australia, Melbourne has long been known as the garden city with an eclectic mix of exotic plants and Australian natives, thanks to our large network of extraordinary parks and gardens.

Laid out by some of Melbourne’s earliest European settlers these historic gardens, including the Fitzroy, Flagstaff and Carlton Gardens, and the beautiful Royal Botanic Gardens, are home to mature examples of numerous European species, carefully maintained in their Victorian landscape settings.

Nearby, our beloved boulevards are lined with a parade of English elm trees, providing a vivid juxtaposition to our native landscapes and local street trees. City of Melbourne is committed to increasing our tree canopy cover to 40 per cent. To reach this, we plant at least 3,000 trees a year. These new trees will include natives such as lemon scented gums and iron barks, increasing the diversity of our stock. Meanwhile, beyond the city’s fringe, lie our vital market gardens and the thousands of hectares of farmland that contribute to our state’s thriving agricultural industry.

All these plants and crops, both native and exotic, can be threatened by disease and climate change, which has put many of our plant species, particularly our treasured elm trees, under great stress.

This is why we are delighted that scientists, researchers and academics from across the globe, have gathered here in Melbourne to share their specialist knowledge on plant pathology; contributing to local expertise, future innovation and expanding our standing as a Knowledge City.

I hope you find some time to roam around our vibrant city and beyond while you are here. You will discover Melbourne easy to explore by foot or by tram, with hidden shops and cafes dotted through-out our extensive network of cobblestone laneways.

The world-class Melbourne Convention and Exhibition Centre is situated right next to the Yarra River – a culturally significant meeting place for our Aboriginal community – and just minutes from the heart of the city.

Congratulations also to the Australasian Plant Pathology Society on 50 years of work dedicated to increasing our understanding of plant health. This is a vital field and we are indebted to those who do so much to protect our plants and our planet, both now and into the future.

Sally Capp
Lord Mayor
Grains research delivering value to growers

- Grains research focused on crop production, soil science and nutrition, disease, pest and weed management, and genetic improvement.

- Our plant pathology research is targeted at finding solutions to cropping system challenges faced by Western Australian grain growers.
Our Organising Committee

The APPS acknowledges the substantial commitment made by members of the Scientific Program Committee:

Chair: A/Prof Jacqueline Edwards
Secretary: Dr Helen Hayden
Members: Dr Candace Elliott, Dr Ross Mann, Dr Rachel Mann, A/Prof Kim Plummer, Prof Peter Solomon, Prof Paul Taylor, Dr Tonya Wiechel

APPS also acknowledges and thanks Caroline Donald, A/Prof Alex Indrum and Prof David Cahill for their assistance to the committee.
The Department of Agriculture’s Plant Innovation Centre (PIC) at the Mickleham Post-Entry Quarantine (PEQ) facility improves the nation’s capacity for addressing current and future plant biosecurity risks.

PIC@PEQ helps strengthen our biosecurity system to safeguard our environment and $60 billion agriculture industries from biosecurity risks.

The PIC@PEQ team conduct a range of projects focused on improving Australia’s plant biosecurity measures into the future by collaborating with stakeholders to address operational issues.

We also actively engage with the scientific research community and develop relationships with the education sector.
Our Sponsors

The Conference acknowledges the support of our sponsors:

Platinum Partner

Gold Partner

Australian Government
Department of Agriculture

Silver Partner

Bronze Partner

Conference Supporting Organisation Partner

Developing Countries Conference Bursary

Session Partner

Keynote Sponsors

Note Pad and Pen Partner

Conference Supporter

Exhibitors
Plant Health Australia

Plant Health Australia (PHA) is the national coordinator of the government–industry partnership for plant biosecurity. PHA drives action to improve policy, practice and performance of the plant biosecurity system to benefit plant industries and the environment.

PHA is funded by member subscriptions from all Australian governments and 39 plant industries, and is also commissioned to undertake plant pest risk mitigation projects.

PHA works to
- strengthen partnerships
- enhance the operation and integrity of the Emergency Plant Pest Response Deed
- develop pest management and preparedness programs
- facilitate nationally coordinated surveillance programs
- strengthen the diagnostic system
- coordinate the planning and implementation of plant biosecurity RD&E.

Visit www.planthealthaustralia.com.au

GRDC

The Grains Research and Development Corporation (GRDC) supports the grains industry through investing in research, development and extension (RD&E) to create enduring profitability for Australian growers.

The GRDC invests over $170 million in around 730 RD&E initiatives to create enduring profitability for Australian grain growers across a broad range of research. The GRDC’s investments deliver results and aim to continually break new ground for growers.

Visit www.grdc.com.au

Plant Biosecurity

The Foundation invests in science and capacity building that will assist in safeguarding Australia, its plant industries, environment and regional communities through enhanced plant biosecurity.

Elizabeth Macarthur Agriculture Institute

NSW DPI’s Plant Biosecurity Research and Diagnostics section enhances the productivity of NSW primary producers with research and diagnostics services to detect and manage pests and diseases and provide surveillance against biosecurity threats. With premier biosecurity and research facilities and world recognised research scientists, we are resourced to collaborate and deliver across the plant industries. We aspire to become the provider of choice for research and diagnostics for high impact existing and emerging pests and diseases of plants.
Dept of Primary Industries & Regional Development

The Department of Primary Industries and Regional Development, Western Australia (WA) works in partnership with industry, government and community stakeholders to protect, grow and innovate in our primary industries and regions.

The department’s grains research is targeted at finding solutions to cropping system challenges faced by WA grain growers and focuses on:

- disease, pest and weed management
- crop production
- soil science and nutrition
- genetic improvement.

The Crop Pathology team undertakes both foliar and root disease research with a focus on epidemiology, disease modelling, risk forecasting and integrated management.

To find out more visit dpird.wa.gov.au

Biosecurity Tasmania

Biosecurity Tasmania’s Plant Diagnostic Services provide authoritative identification and advisory services for plant pests and diseases. Our skilled diagnosticians use morphology, molecular, ELISA and electron microscopy to identify a wide range of plant pests in support of Tasmania’s unique agricultural advantage.

Plant and Food Research

At Plant & Food Research, we believe science can create a better world. That by working together, we can create the world’s most sustainable food production systems, improving the way we grow, fish, harvest and share food to deliver a smart green future.
Exhibitors

Plant Health Australia
Booth Numbers: 01 & 02
Contact Name: Greg Fraser
Phone Number: +61 2 215 7700
Email: admin@phau.com.au
Web Address: www.planthealthaustralia.com.au
Address: Level 1, 1 Phipps Close, Deakin ACT 2600, Australia
Facebook: n/a
Twitter: @planthealthaust
LinkedIn: https://www.linkedin.com/company/plant-health-australia

GeneWorks Pty Ltd
Booth Number: 03
Contact Name: Sean McDonald
Phone Number: +61 438 801 099
Email: customerservice@geneworks.com.au
Web Address: www.geneworks.com.au
Address: Head Office - 28 Dalgleish Street, Thebarton SA 5031, Australia
Twitter: www.twitter.com/GeneworksAus
LinkedIn: www.linkedin.com/company/Geneworks

BGI
Booth Number: 04
Contact Name: Stephanie Sun
Phone Number: +61 7 3362 0475
Email: bgi-australia@genomics.cn
Web Address: www.bgi-australia.com.au
Address: L6, CBCRC Building, 300 Herston Road, Herston, QLD 4006, Australia
Facebook: BGI Genomics
Twitter: @BGI_Genomics
LinkedIn: @BGI Genomics

Agdia, Inc.
Booth Number: 05
Contact Name: David Rambow
Phone Number: (574) 264-2014
Email: drambow@agdia.com
Web Address: www.agdia.com
Address: 52642 Co Rd 1, Elkhart, IN 46514, USA
Facebook: https://www.facebook.com/AgdiaInc/
Twitter: @AgdiaInc
LinkedIn: https://www.linkedin.com/company/agdia-inc/

Queensland Government
Booth Number: 06
Contact Name: Tony Cooke
Phone Number: +61 413 491 729
Email: tony.cooke@daf.qld.gov.au
Web Address: daf.qld.gov.au
Address: Ecosciences Precinct, 41 Boggo Road, Dutton Park, QLD 4102, Australia
Facebook: Queensland agriculture /QldAgriculture/
Biosecurity Queensland /biosecurityqld/
Twitter: @QldAgriculture
@BiosecurityQld
LinkedIn: Queensland Agriculture
https://www.linkedin.com/showcase/queensland-agriculture/
Biosecurity Queensland https://www.linkedin.com/showcase/biosecurity-queensland/

Leica Microsystems
Booth Number: 07
Contact Name: Ann Wu
Phone Number: +61 408 178 529
Email: ann.wu@leica-microsystems.com
Web Address: https://www.leica-microsystems.com/
Address: Suite 2, Level 3, Building A, 11 Talavera Road, Macquarie Park, NSW 2113, Australia
Facebook: https://www.facebook.com/LeicaMicrosystems/?ref=ts
Twitter: https://twitter.com/leicamicro?lang=en
LinkedIn: https://www.linkedin.com/company/leica-microsystems/?originalSubdomain=au
Department of Agriculture
Booth Numbers: 09 & 10
Contact Name: Adrian Dinsdale
Phone Number: +61 421 237 569
Email: Adrian.dinsdale@agriculture.gov.au
Address: 18 Marcus Clarke Street, Canberra, ACT 2601, Australia
Facebook: https://www.facebook.com/australianbiosec/
Twitter: @DeptAgNews
LinkedIn: n/a

Australian Plant Pathology Herbaria
Table Top Number: 01
Contact Name: Jordan Bailey
Phone Number: +61 43 861 8745
Email: jordan.bailey@dpi.nsw.gov.au
Address: 1447 Forest Rd, Orange, NSW
Facebook: n/a
Twitter: @DrJordanBailey
LinkedIn: n/a
Delegate information

**Venue**
Melbourne Convention and Exhibition Centre  
1 Convention Centre Place  
South Wharf, 3006  
Victoria, Australia

**Registration Desk**
The registration desk is located in the Foyer of Level 1 at the Melbourne Convention and Exhibition Centre. Please visit the registration desk to pick up your name badge and conference materials. The registration desk will be open at the following times.
- Tuesday 07:00 – 17:15
- Wednesday 08:00 – 17:00
- Thursday 08:00 – 17:00

**Accessibility**
We strive to provide inclusive, safe access for all visitors to the Conference. All buildings and car parks at the venue are wheelchair accessible. If you’d like to hire a wheelchair from the venue, please call the Melbourne Convention and Exhibition Centre Customer Service team on (+61 3) 9235 8000.

**Facilities for People with Sensory Impairment**
Braille is provided on all room door signage and fixed directional signage throughout the venue. MCEC is guide dog friendly and welcomes any registered assistance dogs into all areas of the building.

Additionally, most meeting rooms within the Centre are equipped with TTA Hearing Assisted telephones, and other hearing assisted devices are available to hire.

**Car Park**
Melbourne Convention and Exhibition Centre has a car park located within the Exhibition Centre (open 24/7).

Additionally, there are secure car parks located in and around South Wharf including, South Wharf Retails Car Park, Siddeley Street Carpark and Montague Street Carpark.

**Transport**
Getting around Melbourne using public transport is easy. At https://www.ptv.vic.gov.au/ you’ll find timetables, maps and destinations, plus everything you need to know about catching a bus, train or tram. There is also information about night services and safety and security.

The closest tram stop is ‘#124A Casino/MCEC/Clarendon Street’, serviced by the 12, 96 and 109 trams. All three of these trams travel north into the Melbourne CBD and run through the Free Tram Zone, or south towards Port Melbourne and St Kilda.

A Myki card, available at shops, is required to travel on public transport or outside the Melbourne Free Tram Zone. Find further information at: https://www.ptv.vic.gov.au

**Taxis**
For guests arriving or departing the Centre, two taxi ranks are nearby – at Crown Casino on Clarendon Street, and at DFO South Wharf on Convention Centre Place.

**Emergency Details**
In any emergency please notify telephone 000 for Ambulance, Fire Service or Police.

**First Aid**
In any medical emergency notify your event security or first aid provider immediately. You can also report first aid/medical incidents to the Security Control Centre by calling 6666 from an internal phone.

**Security**
Please ensure that you take all items of value with you at all times when leaving a room. Do not leave bags or laptops unattended.

**Wi-Fi**
Free Wi-Fi is available throughout the Melbourne Convention and Exhibition Centre.

To connect:
1. Select the ‘M Connect’ Wireless Service
2. Open your preferred internet browser (such as Safari or Google Chrome)
3. The M Connect log in page will appear – read and agree to the Terms and Conditions
4. Click the ‘CONNECT NOW’ button and browse away

**App**
To Download
1. Search in your device app store for: World Leading Conferences
2. Download the World Leading Conferences App
3. Enter Access Code: APPS2019
Delegate information

Please see the friendly team at the registration desk if you need any assistance using the app.

Cloak Room and Luggage Storage
Visit the Customer Service desk at either Convention Centre Place or Clarendon Street entrances for storage facilities.

Parents Rooms
Located in both the Convention and Exhibition Centres the Parents’ Rooms offer a comfortable and private space for parents and children.

Location within Exhibition Centre: by Clarendon Street entry
Location within Convention Centre: by Convention Centre Place entry

Disclaimer of Liability
The Organising Committee will not accept liability for damages of any nature sustained by participants or their accompanying persons or loss of or damage to their personal property as a result of the meeting or related events.

Lost and Found
Any found item may be turned into the Registration Desk. Enquiries about lost items can be directed there.

Smoking
Smoking is not permitted indoors at the Melbourne Convention and Exhibition Centre. Smokers must remain at least 4m from any doorway when smoking. Fines can be imposed for smoking in prohibited places.

Catering
Morning tea, lunch and afternoon tea will be available during the Conference in the Exhibition area and are included in your registration fee. For break times please refer to the program.

Please speak to a catering staff member if you have dietary requirements.

Conference Sessions
Plenary Sessions will be located in Meeting Room 105/106 and concurrent sessions will run in Rooms 101 – 106 on Level 1

Exhibition
The Conference Exhibition will be located in the Level 1 foyer within the Convention Centre and will be open at the following times:

Tuesday 10:00 – 18:30
Wednesday 08:00 – 17:00
Thursday 08:00 – 17:00
**Program**

Every endeavour has been made to produce an accurate program. If you are presenting at the Conference, please confirm your presentation times as detailed within this program. Please note the Organising Committee reserves the right to change the Conference program at any time without notice.

**Speakers**

Please ensure that you are available in your presentation room at least 15 minutes prior to the start of the session to meet with the Session Chair. Speakers are requested to report to the Speaker Preparation Room at least 2 hours before their scheduled presentation with their presentation on a USB to allow sufficient time to upload and check their audio-visual presentations with the attending technician.

Speakers’ Preparation Room is in Speakers Room 101.

**Abstracts**

Abstracts for plenary, concurrent and poster sessions are available to view in your conference app and included in this book from pages 67 onwards.

**Digital Devices**

We encourage delegates to use digital devices throughout the conference to access the conference app and tweet. Please use #APPS2019 to share your experiences at the Conference.

As a courtesy to speakers and your fellow delegates, please set all of your devices to silent whilst in sessions.

Please also respect the wishes of any presenter who requests that their slides/posters not be photographed and or shared on social media.

**Photography**

By attending this event and/or associated events as part of APPS 2019, you consent to being filmed or photographed.

Any photography, filming, recording or reproduction in any medium without the express consent of the Conference is strictly prohibited. Exceptions to this policy include non-flash photography for personal use or use on social media is permitted if not disruptive.

**Media**

Please note that specialist media may be present at the Conference.

**Mobile phones**

Delegates are asked to switch off their mobile phones or set them to silent when attending sessions.

**Name Badges**

For security purposes, delegates, speakers and exhibitors are asked to wear their name badges to all sessions.

Entrance into sessions is restricted to registered delegates only. If you misplace your name badge, please see staff at the registration desk to arrange a replacement.

**Charging Stations**

There are various charging stations located throughout the Melbourne Convention and Exhibition Centre.

**Duplication/recording**

Unauthorised photography, audio taping, video recording or digital taping or any other form of duplication is prohibited in the Conference sessions.
Social Program

**Welcome Reception**
Venue: Showtime Events Centre, South Wharf Promenade  
Date: Monday 25 November 2019  
Time: 6:00pm – 8:00pm  
Dress code: Smart Casual  
Cost: Free to attend for all delegates with a full registration  

**How to get to the Welcome Reception:**
Walk from MCEC (5 minutes – 450m): Exit the Convention Centre on the side closest to the water, walk past Goldfields Café and Bar and turn right onto Rona Walk, turn left onto South Wharf Promenade and the venue will be on your left hand side after approximately 2 minutes.

Walk from Novotel Melbourne South Wharf (3 minutes – 290m): Walk along Rona Walk towards South Wharf Promenade, turn left onto South Wharf Promenade and the venue will be on your left hand side after approximately 2 minutes.

---

**50th Anniversary Gala Dinner**
Venue: Mural Hall, 314/336 Bourke Street, Melbourne  
Date: Wednesday 27 November 2019  
Time: 7:00pm  
Dress code: Cocktail/ Smart Casual  
Cost: Free to attend for all delegates with a full registration  

**How to get to the Gala Dinner:**
Walk (23 minutes): Along Yarra Promenade, across Queens Bridge Street, right onto Flinders Street and then left along Elizabeth Street until you reach Little Bourke Street, turn right and the entry is just off Postal Lane to your left.

Tram (12 minutes): Get the route 96 tram from Casino/MCEC/Clarendon Street and ride 6 stops to Elizabeth St/Bourke St and then simply walk 100m to the Mural Hall entry on Postal Lane, off Little Bourke Street:
This conference, the 22nd biennial conference of the Australasian Plant Pathology Society, is an auspicious conference as it marks and celebrates the 50th birthday of our society. Over 50 years our society, and its members, have made a substantial and significant contribution to the science of plant pathology, which like most science in this part of the world, has punched well above its weight. It is an appropriate time to reflect upon the efforts of our foundation members and thank them for their forethought in establishing our society.

I hope that you thoroughly enjoy this meeting, learn many new things, establish new collaborations and head back to the lab bench and field reinvigorated, and especially celebrate this half century of great plant pathology. Of course, 50 is only half the job, now is the time to push on even harder to the century mark.

Dr Brett Summerell  
President, Australasian Plant Pathology Society.
The list below includes all who joined when the Society was founded in 1969

Aberdeen, JEC
Alcock, K
Alcorn, J
Allen, RN
Arnold, JR
Arvier, AC
Atchison, BA
Ballantyne, BJ
Banyer, RJ
Barkley, P
Behncken, GM
Bertus, AL
Bevege, DI
Bird, AF
Bowyer, JW
Brown, BN
Brown, JF
Brown, RH
Bumbieris, M
Burgess, LW
Burnett, RM
Burnett, WM
Carter, MV
Chambers, SC
Chivers, GA
Clare, BG
Close, RC
Colbran, RC

Conroy, RJ
Cruickshank, IAM
Da Costa, EW
Darling, DD
Dodman, RL
Doepel, RF
Egan, BT
Evans, G
Finlay, JR
Fish, S
Fisher, JM

Howles, R
Hughes, CG
Hughes, IK
Hutchinson, PB
Janes, BS
Johnstone, GR
Jones, LC
Kable, PF
Keane, PJ
Kerr, A
Kile, GA
Kochman, JK
Kuiper, J
Langdon, RFN
Latch, GCM
Layton, AW
Lim, W-C
Lloyd, AB
MacNish, GC

Morschel, JRG
Munro, D
Murray, GM
Stubbs, LL
Summers, LA
Sutton, J
Talbot, PHB
Taylor, RH
Teakle, DS
Thistlethwayte, B
Titez, JF
Trimboli, D
Truman, RA
Tugwell, BL
Van Velsen, RJ
Wade, GC
Walker, J
Wallace, HR
Warcup, JH
Wauchope, DG
Weste, GM
White, NH
Wicks, TJ
Wildermuth, GB
Willetts, HJ
Williams, PG
Wong, AL
The Daniel McAlpine Memorial Lecture

The invitation to present the Daniel McAlpine lecture to the Biennial Conference of the Australasian Plant Pathology Society is extended to an eminent scientist in recognition of their significant contribution to Australasian Plant Pathology.

The lecture commemorates the life and work of Daniel McAlpine and his contribution to the science of plant pathology. He was born in Scotland, and arrived in Australia in 1884 at the age of 35. He had already received considerable training in biology, and became a lecturer at the University of Melbourne. Six years later he became a vegetable pathologist in the Department of Agriculture. At the time, plant pathology and plant breeding were facing the challenge of coping with stem rust epidemics, so McAlpine, together with Farrer became involved. Over the next 26 years McAlpine published 226 papers, a monograph on rusts (1906), and books on the smuts (1910), and on the diseases of citrus (1889), stone fruit (1902), and potatoes (1911) (Ron Close 1996).

Considered as the “Father of Australasian Plant Pathology”, McAlpine’s most notable contributions were to study wheat rust following the 1889 epidemic, to classify and describe Australian smuts, and to recognise Ophiobolus graminis (now Gaeumannomyces graminis) as the cause of wheat take-all. He also collaborated with Farrer on resistance to rust in wheat. It has been written that he did a difficult pioneering job pushing down deeply the roots of plants pathology in his adopted country and preparing the way for Australian plant pathologists of the future (Stanislaus Fish 1976, John Randles 1994).

The 2019 McAlpine Lecture

The McAlpine Lecture will be delivered by:

Professor Eileen Scott
University of Adelaide

Grapevine Powdery Mildew: From Fundamental Plant Pathology to New and Future Vineyard Technologies

Eileen Scott is Professor of Plant Pathology in the School of Agriculture, Food and Wine at the Waite Campus, University of Adelaide. She completed a BSc with honours in microbiology at the University of Edinburgh and PhD in plant pathology at the University of Cambridge. She joined the University of Adelaide in 1987, where she teaches plant pathology and conducts research on fungal and bacterial diseases, mainly of horticultural species, canola and pulse crops. Prof Scott’s research group has comprised postdoctoral scientists, postgraduate and honours students investigating pathogen detection, biology, epidemiology and disease management. Grapevine powdery mildew and trunk diseases have been the main research focus for the last 25 years.

The supervision, mentoring and sponsorship of students and early career researchers has long been a passion. To date, Prof Scott has supervised/co-supervised 39 PhD, 15 Masters and 31 honours students to successful completion, as well as supervising 13 postdoctoral researchers. She is proud to have continuing collaborations with numerous graduates from her group.

Prof Scott has been a member of APPS since 1987. She served as Executive Secretary (1997-99) and President (2013-15) and was awarded Fellow of the Society in 2011, the citation for which included teaching and supervision.
### Previous McAlpine Lecturers

<table>
<thead>
<tr>
<th>Year</th>
<th>Lecturer</th>
<th>Institution</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>1976</td>
<td>Dr Lilian Fraser</td>
<td>Department of Agriculture, NSW</td>
<td>Diseases of citrus trees in Australia – the first hundred years</td>
</tr>
<tr>
<td>1978</td>
<td>Dr David Griffin</td>
<td>Australian National University, ACT</td>
<td>Looking Ahead</td>
</tr>
<tr>
<td>1980</td>
<td>Mr John Walker</td>
<td>Department of Agriculture, NSW</td>
<td>Taxonomy, Specimens &amp; Plant Diseases</td>
</tr>
<tr>
<td>1982</td>
<td>Professor Richard Matthews</td>
<td>The University of Auckland, NZ</td>
<td>Relationships between Plant Pathology and Molecular Biology</td>
</tr>
<tr>
<td>1984</td>
<td>Professor Bob McIntosh &amp; Dr Colin Wellings</td>
<td>University of Sydney, NSW &amp; Department of Agriculture, NSW</td>
<td>Wheat Rust Resistance: The continuing Challenge</td>
</tr>
<tr>
<td>1986</td>
<td>Dr Allen Kerr</td>
<td>Waite Agriculture Research Institute, SA</td>
<td>Agrobacterium: Pathogen, genetic engineer and biological control agent</td>
</tr>
<tr>
<td>1989</td>
<td>Dr Albert Rovira</td>
<td>CSIRO Division of Soils, SA</td>
<td>Ecology, epidemiology, and control of take-all, Rhizoctonia and cereal cyst nematode in wheat</td>
</tr>
<tr>
<td>1991</td>
<td>Mr John Walker</td>
<td>Department of Agriculture, NSW</td>
<td>Plants, diseases and pathologists in Australasia – a personal view</td>
</tr>
<tr>
<td>1993</td>
<td>Dr John Randles</td>
<td>University of Adelaide, SA</td>
<td>Plant viruses, viroids and virologists of Australasia</td>
</tr>
<tr>
<td>1995</td>
<td>Dr Ron Close</td>
<td>Lincoln University, NZ</td>
<td>The ever changing challenges of plant pathology</td>
</tr>
<tr>
<td>1997</td>
<td>Professor John Irwin</td>
<td>CRC Tropical Plant Pathology, QLD</td>
<td>Biology and management of Phytophthora spp. attacking field crops in Australia</td>
</tr>
<tr>
<td>1999</td>
<td>Dr Dorothy Shaw</td>
<td>Department of Primary Industries, QLD</td>
<td>Bees and Fungi with special reference to certain plant pathogens</td>
</tr>
<tr>
<td>2001</td>
<td>Dr Alan Dubé</td>
<td>South Australian Research and Development Institute, SA</td>
<td>Long term careers in plant pathology</td>
</tr>
<tr>
<td>2003</td>
<td>Dr Mike Wingfield</td>
<td>University of Pretoria, South Africa</td>
<td>Increasing threat of diseases to exotic plantation forests in the Southern Hemisphere</td>
</tr>
<tr>
<td>2005</td>
<td>Dr Gretta Weste</td>
<td>University of Melbourne, VIC</td>
<td>A long and varied fungal foray</td>
</tr>
<tr>
<td>2007</td>
<td>Dr Graham Stirling</td>
<td>Biological Crop Protection, QLD</td>
<td>The impact of farming systems on soil biology and soil-borne diseases</td>
</tr>
<tr>
<td>2009</td>
<td>Associate Professor Philip Keane</td>
<td>La Trobe University, VIC</td>
<td>‘Lessons from the tropics’ An ongoing journey of discovery</td>
</tr>
<tr>
<td>2011</td>
<td>Honorary Professor Lester Burgess</td>
<td>University of Sydney, NSW</td>
<td>A love affair with Fusarium</td>
</tr>
<tr>
<td>2013</td>
<td>Dr Shaun Pennycook</td>
<td>Manaaki Whenua Landcare Research</td>
<td>Fungal Names in Flux</td>
</tr>
<tr>
<td>2015</td>
<td>Professor Giles Hardy</td>
<td>Murdoch University, WA</td>
<td>From ‘then to now’ – Phytophthora science and management in Western Australia</td>
</tr>
<tr>
<td>2017</td>
<td>Professor Barbara Howlett</td>
<td>The University of Melbourne</td>
<td>A ‘genome to paddock’ approach to control plant disease</td>
</tr>
</tbody>
</table>
Fellows of the Australasian Plant Pathology Society

The Fellow award honours the scientific achievements of members who have made substantial original contributions in one or more areas of plant pathology as demonstrated by their peer reviewed publications.

Fellows

PROF ELIZABETH AITKEN

Elizabeth (Liz) has been an active member of APPS and took a lead in the scientific program for the 2017 conference. Her publication record is outstanding and reflects a wide diversity of research interests throughout her career. The major areas of Liz’s research have included a sustained contribution to our understanding of a range of important diseases, especially the Fusaria in tropical plants such as banana and ginger, but also in cropping systems such as sunflower and wheat. Liz has been active in the genetics of plant-pathogen interactions, molecular aspects of pathogenicity and the development and application of disease diagnostics. Her commitment to student training, both at undergraduate and graduate levels, and her collaborative approach to multi-disciplinary research have been outstanding features over her career.

DR ANGUS CARNEGIE

Angus has contributed substantially to forest plant pathology in Australia, and in particular to forest biosecurity, pathogen detection, surveillance, impact assessment and disease management. The overarching theme of his work has emphasised productivity while enhancing sustainability of forest ecosystems. He has played a leading role in shaping biosecurity strategy and policy in Australia, and in particular during the incursion of myrtle rust from 2010. Angus has an excellent publication record, including significant reviews on the status of forest health in Australia, and takes various leadership roles including the current Chair of the Forest Health and Biosecurity Sub-committee.

PROF ANDRÉ DRENTH

André’s contributions to tropical plant pathology have resulted in a substantial publication record, and his undoubted reputation both in Australia and across a great range of international project engagements. As a teacher and mentor, André has contributed significantly to the development of a new generation of plant pathologists while also serving as editor to a range of highly esteemed international journals. His research interests have been broad and innovative as he developed a specialist reputation in the Phytophthora pathogen and is a recognised national and international authority on diseases of macadamia and banana.

PROF ROBERT PARK

Robert has developed an outstanding publication record, and has established a widely recognised national and international reputation in cereal rust pathology. His professional awards have included the Friendship Award of China, the Borlaug Global Rust Initiative Gene Stewardship Award, Fellow of the Australian Academy of Technological Sciences and Engineering, Fellow of the Royal Society of NSW, Clarke Medal, Fulbright Senior Scholar, and NSW Science and Engineering Award for Excellence in Biological Sciences. Robert has contributed in various roles in APPS, including current Vice-President, and continues to serve as editor to several national and international journals. He has had sustained success in developing graduate student programs that have trained many of the current cereal pathologists operating in various capacities across the globe.

PROF TERRY PRICE

Terry has made a significant contribution to the discipline of plant pathology through an outstanding career in teaching in Australia and PNG. His strong publication record with students and collaborators has reflected a wide range of interests, including diseases of ornamental, vegetable, fruit and pasture crops, and with an emphasis on applied research leading to practical outcomes for industry. He has been a long term and active member of APPS, serving the Society in various capacities including Regional Councillor, Executive Secretary, and as a member of national and international organising committees.

ASSOCIATE PROF JOHN THOMAS

John has had an outstanding career in plant pathology, with a specific international reputation in virology. His crop specialities have been broad ranging in tropical agriculture, with particular emphasis on geminiviruses affecting banana. His role in the containment of these significant plant pathogens has been a continuing effort in germplasm conservation and leading the international response to this effort through his role as Co-convener of the International Network for Improvement of Banana & Plantain. John led the citrus canker diagnostic response in Queensland in 2004 and continues to be engaged in international virology projects throughout South East Asia and Africa.

MR JOHN WALKER

John’s career has been devoted to the systematics of fungal pathogen identification. He established the
NSW Plant Disease Herbarium, and was instrumental in securing the long term protection for this invaluable biosecurity resource under the Agricultural Scientific Collections Act 1983 of the New South Wales parliament. His taxonomic work has been wide ranging, while also developing a long term reputation in the rust and smut diseases. His break through taxonomic work on the take-all pathogen had wide ranging international implications for the biology and management of this intractable cereal root disease. John was a founding member of APPS and the Australian Mycological Society, has been Daniel McAlpine lecturer on two occasions, and was the first Australian to hold office as Vice President of the British Mycological Society.

Lester Burgess Award
The Lester Burgess award recognises members who have made exceptional contributions in the fields of diagnostics and extension, or research communication over a significant period of their career. An award can be made to an individual or group (team). While a significant publication record is desirable the primary focus of the award is on contributions to the diagnosis of plant diseases, extension to clients in field crops, horticultural industries, forestry, natural ecosystems, and amenity plants, or research communication to clients and the general community.

Lester Burgess Award, Research Communication
DR GORDON MURRAY
Gordon’s career as a regional plant pathologist serving the cropping regions of southern NSW led him into a range of research and advisory roles in crop protection. His fundamental research on take-all and stripe rust in wheat led to the development of predictive models that were implemented by the industry to assist in decision support for disease control. The latter was particularly valued during recurring epidemics of stripe rust in the early/mid 2000s. Gordon was also instrumental, both nationally and internationally, in developing protocols for exotic incursions of Karnal bunt. His economic appraisal of the current and potential losses for cereal diseases across Australia was widely sought by industry at every level, and was acclaimed internationally for its scope, method and outcomes.

Lester Burgess Award, Diagnostics and Extension
DR NERIDA DONOVAN
Nerida has devoted her career to the diseases of citrus in NSW, Australia and internationally. Her research, diagnostic and germplasm assessment roles have been integrated in such a way that the industry has highly valued the contributions made by Nerida and her team. Their role in containing outbreaks of citrus canker is widely acknowledged. The maintenance and disease free status of the National Citrus Repository over decades of dedicated work has been an invaluable contribution to the sustained viability of the industry. Nerida, in recognition of her status as an international authority on citrus greening, canker and a range of viroid diseases, is currently Chair-Elect of the International Organisation of Citrus Virologists.

MS KATHY GRICE
Kathy has enjoyed a long and distinguished career as a diagnostician, extension practitioner and researcher across a range of crops in tropical Queensland, but her most significant contribution has been to the banana industry. Kathy and her team were instrumental in providing crucial diagnostic support (described by some as ‘round the clock’) during the successful black Sigatoka eradication campaign in 2001-2005 - the first successful eradication of this disease from a commercial growing region anywhere in the world. Kathy has had significant involvement and leadership in response to new banana pathogen incursions, development of a new technique for monitoring fungicide resistance in yellow Sigatoka, authored several diagnostic manuals and has regularly contributed to the scientific literature. Kathy is highly valued by the Australian Banana Growers Council and her professional colleagues.

MR MARK WHATTAM
Mark has developed a long and distinguished career in plant pathology and biosecurity. He has been an innovator in researching and deploying new approaches to post-entry quarantine and pathogen testing. He was the driving force behind the launch of the Plant Innovation Centre at the Department of Agriculture, a new and dedicated R&D group that he single-handedly established and now leads. Mark’s reputation within the industries served specifically by the needs for efficient and secure plant introduction is outstanding, and the large number of industry awards he has received bear testimony to his technical knowledge and leadership. Mark has also been an active member of APPS with roles.
including treasurer, co-editor of APP and involvement in organising national and regional meetings.

**Allen Kerr Post Graduate Prize**

This award is in recognition of the outstanding contribution made by Allen Kerr AO to the field of plant pathology. The Allen Kerr Postgraduate Prize is awarded by the Society for the best piece of original research relevant to Australasia by a postgraduate student in the field of plant pathology. The prize is awarded on the basis of publication in refereed journals. In 2019 the Committee has awarded the Allen Kerr Prize to joint winners.

**DR REBECCA ROACH**

Rebecca Roach was awarded PhD by La Trobe University for her research titled “Identification and classification of Xanthomonas spp. causing bacterial leaf spot on capsicum, chilli and tomato in Australia”. Her published work has made internationally significant contributions to the understanding of bacterial leaf spot (BLS) -causing Xanthomonas species in Australia and their significance in a global context. Prior to this study, the causal organisms of this disease in Australia were classified under obsolete taxonomy as Xanthomonas campestris pv. vesicatoria, with little understanding of the genetic capacity of the pathogen despite the frequency and severity of this disease. Rebecca described the identity and diversity of pathogens causing BLS in Australian capsicum, chilli and tomato production and the genetic variability that significantly impacts disease epidemiology. The understanding of pathogenicity, copper tolerance and genetic diversity in Australian Xanthomonas populations derived from her published work has placed a firm foundation for disease control strategies used by industry.

**DR NGA THI TRAN**

Nga Tran was awarded PhD by the University of Queensland for her research titled “Biology and epidemiology of citrus black spot (Phylllosticta citricarpa) in Australia”. Her research spanned classical and molecular plant pathology and lead to a developed understanding of the nature and role of ascospores in disease epidemiology. Breakthrough opportunities came as she developed for the first time an in vitro methodology for producing ascospores. This allowed the elucidation of the role of ascospores in disease, and the use of genetic markers to unequivocally demonstrate the occurrence of meiosis during the mating process. Nga demonstrated that spermatia play a key role in sexual reproduction of P. citricarpa, thereby confirming for the first time the hypothesis of Temple Kiely in 1948. Nga combined laboratory studies with extensive field trials which demonstrated that conidia are very important in the disease cycle and thereby disproved a popular belief that ascospores were the only major source of infections in the field.

**APPS Awards Sub Committee, 2019**

Colin Wellings (Chair)
Mike Pearson
Eileen Scott
Matthew Laurence
Rachel Mann
16th October 2019
APPS 2019 Bursary Recipients

**APPS-funded bursaries:**

This year the society is pleased to be supporting many students and early career researchers to attend the APPS2019 Conference. Following our biggest response to a call for student bursaries we welcome the below successful applicants

<table>
<thead>
<tr>
<th>Region</th>
<th>Awardee</th>
</tr>
</thead>
<tbody>
<tr>
<td>Australian Capital Territory</td>
<td>Pravin Khamblkar</td>
</tr>
<tr>
<td>Australian Capital Territory</td>
<td>Bayantes Dagvadorj</td>
</tr>
<tr>
<td>Australian Capital Territory</td>
<td>Haochen Wei</td>
</tr>
<tr>
<td>Bangladesh</td>
<td>Md. Abdullahil Baki Bhuiyan</td>
</tr>
<tr>
<td>India</td>
<td>Himadi Kaushik</td>
</tr>
<tr>
<td>New South Wales</td>
<td>Belinda Fabian</td>
</tr>
<tr>
<td>New South Wales</td>
<td>Michael Norman</td>
</tr>
<tr>
<td>New South Wales</td>
<td>Ganja Singh Rai</td>
</tr>
<tr>
<td>North Island, New Zealand</td>
<td>Toan Hong</td>
</tr>
<tr>
<td>North Island, New Zealand</td>
<td>Shweta Shinde</td>
</tr>
<tr>
<td>North Island, New Zealand</td>
<td>Toni Darling</td>
</tr>
<tr>
<td>North Island, New Zealand</td>
<td>Lee Rabbidge</td>
</tr>
<tr>
<td>North Island, New Zealand</td>
<td>Roshni Rohra</td>
</tr>
<tr>
<td>North Island, New Zealand</td>
<td>Tianyi Tang</td>
</tr>
<tr>
<td>Pakistan</td>
<td>Waqas Raza</td>
</tr>
<tr>
<td>Queensland</td>
<td>Henry Birt</td>
</tr>
<tr>
<td>Queensland</td>
<td>Sari Nurulita</td>
</tr>
<tr>
<td>Queensland</td>
<td>Moham Cassim Mohamed</td>
</tr>
<tr>
<td>Queensland</td>
<td>Zakeel</td>
</tr>
<tr>
<td>Queensland</td>
<td>Kandeeparoopan Prasannath</td>
</tr>
<tr>
<td>South Australia</td>
<td>Jade Rose</td>
</tr>
<tr>
<td>South Australia</td>
<td>Ismail Ismail</td>
</tr>
<tr>
<td>South Island, New Zealand</td>
<td>Luciano Nunes Leite</td>
</tr>
<tr>
<td>South Island, New Zealand</td>
<td>Noureddine Besselma</td>
</tr>
<tr>
<td>South Island, New Zealand</td>
<td>Caitlin Henderson</td>
</tr>
<tr>
<td>South Island, New Zealand</td>
<td>Lay Lay Nwe</td>
</tr>
<tr>
<td>Tasmania</td>
<td>Dharushana</td>
</tr>
<tr>
<td>Tasmania</td>
<td>Thanabalasingam</td>
</tr>
<tr>
<td>Tasmania</td>
<td>Yichen Kang</td>
</tr>
<tr>
<td>Victoria</td>
<td>Yee Lin Tai</td>
</tr>
<tr>
<td>Victoria</td>
<td>Prakash VR Nair</td>
</tr>
<tr>
<td>Victoria</td>
<td>Cordelia Dravitzki</td>
</tr>
<tr>
<td>Victoria</td>
<td>Amy Longmuir</td>
</tr>
<tr>
<td>Victoria</td>
<td>Linda Brain</td>
</tr>
<tr>
<td>Victoria</td>
<td>Anjali Zaveri</td>
</tr>
<tr>
<td>Victoria</td>
<td>Hayley Wilson</td>
</tr>
<tr>
<td>Victoria</td>
<td>Donovan Garcia Ceron</td>
</tr>
<tr>
<td>Western Australia</td>
<td>Virginia Mwape</td>
</tr>
</tbody>
</table>

**Australian Centre for International Agricultural Research (ACIAR) Developing Nation Recipients**

Dr Asma Akbar. Associate Scientist, Crop Diseases Research Institute Pakistan

Mr Beyene Bitew Eshete. PhD Candidate, Debre Birhan Agricultural Research Centre, Ethiopia

Ms Tonusree Roy. Research Associate, Wheat and Maize Research Institute, Bangladesh

Ms Subeksha Shrestha. Assistant Professor, Himalayan College of Agricultural Sciences and Technology, Nepal

Ms Yewubdar Shewaye Ishetu. Associate Researcher, Debre Ziet Agricultural Research Centre, Ethiopia

**Australian Nurserymen’s Fruit Improvement Company (ANFIC) Developing Nation Bursary Recipient**

Ms Marilyn Apa. Plant Protection Officer, National Agriculture Quarantine & Inspection Authority, Papua New Guinea

**Crawford Fund Recipients**

Dr Mark Balendres. Head of Plant Pathology Laboratory, Institute of Plant Breeding, University of the Philippines, Los Banos, Philippines

Dr Ratchadawan Cheewangkoon. Lecturer, Department of Plant Protection, Chiang Mai University, Thailand

Dr Andi Nasruddin. Lecturer, Department of Plant Pest & Diseases, Universitas Hasanuddin, Makassar, Indonesia

Dr Arif Wibowo. Lecturer, Department of Plant Protection Faculty of Agriculture, Universitas Gadjah Mada, Yogyakarta, Indonesia

Mrs Vinh Thi Dau. Plant Pathologist, Nghe An Plan Protection Sub-department, Vietnam

The APPS funded conference registration for ten international bursary delegates to support their attendance at the meeting. APPS 2019 was able to bring these developing nation delegates to the Conference thanks to our Sponsors:

![Sponsors Logos]

30
Plenary Speakers

Professor Carolee T Bull
Penn State University

Professor Carolee T. Bull, serves as the Head of the Department of Plant Pathology and Environmental Microbiology, Director of the Penn State Microbiome Centre which she established, and as a Professor of Plant Pathology and Systematic Bacteriology at Penn State University. Her research focuses on translational taxonomy using taxonomic inquiry to develop management strategies for diseases of mushrooms and plants. She serves as the convener of the ISPP Committee on the Taxonomy of Plant Pathogenic Bacteria and as the Secretary of the Judicial Commission of the Interinstitutional Committee on the Systematics of Prokaryotes. Prof Bull is a committed mentor and has received numerous awards for mentoring including the Secretary's Honor Award (the highest award for service to the nation in agriculture) from the US Secretary of Agriculture in 2014. Prof Bull received a BS in Botany from Ohio University in 1985, an MS in Plant Pathology from Washington State University in 1987, and a PhD in Plant Pathology from Oregon State University in 1992. She continued her work as an NSF Postdoctoral Fellow at the Swiss Federal Institute of Technology in Zurich and the University of Lausanne before beginning her 20-year career with the USDA Agricultural Research Service.

Doctor Thierry Candresse
INRA

Dr Thierry Candresse is a senior scientist working for INRA, the French National Institute for Agricultural Research (INRA). He is the Team leader for Plant Virology and the Director of the Fruit Biology and Pathology joint Laboratory (UMR 1332 BFP) between INRA and the University of Bordeaux. While he has broad interest in molecular plant virology, including plant-virus interactions, his current research focuses on the development and use of novel approaches for plant virus detection and characterization, with applications in aetiology, in diagnostics and in plant virus ecology through metagenomics. Following an initial training in crop protection as an agricultural engineer from the Institut National Agronomique Paris-Grignon, he obtained his PhD in the enzymology of plant virus replication from the University of Bordeaux 2 in 1984. Before joining INRA, he continued his work as a post-doctoral fellow at USDA-ARS in Beltsville (USA) studying viroids with Dr. T.O. Diener. From an initial emphasis in fruit tree virology, his research activities have extended gradually to a broader range of viruses and crops involving a range of collaborative efforts.

Professor Roger Innes
IUB Electron Microscopy Centre

Roger Innes holds the Class of 1954 Professorship in Biology at Indiana University-Bloomington, and currently directs IUB’s Electron Microscopy Centre. He received his Ph.D. in Molecular, Cellular and Developmental Biology at the University of Colorado-Boulder, and completed Post-doctoral research at the University of California-Berkeley. He is an elected fellow of the American Association for the Advancement of Science and the American Academy of Microbiology. Prof Innes’ research focuses on the immune system in plants, with a particular interest in how plants detect pathogens and how detection is translated into an active immune response. His group was among the first to identify and clone plant disease resistance genes using the model plant Arabidopsis thaliana. In a second area of research, the Innes laboratory has been investigating intracellular and intercellular signalling and cell biology of the plant immune system, including analysis of endomembrane trafficking in plant cells and production of extracellular vesicles.

Professor Hailing Jin
University of California

Dr Hailing Jin is a Professor and Cy Mouradick Endowed Chair in the Department of Microbiology & Plant Pathology, University of California, Riverside, USA. Her lab studies small RNA and epigenetic regulation of plant immunity and pathogen virulence, with an overall goal to develop effective and environmentally friendly strategies to control plant diseases and to ensure sufficient food production. Her lab discovered cross-kingdom RNAi and small RNA trafficking between plant and fungal pathogens. They also discovered that fungal cells can take up RNAs from the environment, which makes it possible to develop eco-friendly RNA-based new generation of fungicides. Prof. Jin’s lab also study the function
of infection-induced small RNAs and RNA silencing machinery in plant immunity against bacterial and fungal pathogens. Prof. Jin received her BS degree in Genetics from Wuhan University in 1991 and PhD in Molecular Genetics, from the Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences in 1996. She conducted postdoctoral work at the John Innes Centre and University of California, Berkeley. She joined the faculty of Department of Plant Pathology and Microbiology at the University of California, Riverside in 2004.

**Professor Sophien Kamoun**
The Sainsbury Laboratory

The EMBO Keynote Lecture

Sophien Kamoun grew up in Tunisia where he developed a passion and curiosity about nature. He studied genetics in Paris and Davis, California, before working in Wageningen, Ohio and Norwich, where he is currently a Senior Scientist at The Sainsbury Laboratory and Professor of Biology at The University of East Anglia. He is known for his seminal contributions to our understanding of plant diseases and plant immunity.

Professor Kamoun pioneered genomics and molecular biology methods to reveal fundamental insights into the biology and evolution of eukaryotic plant pathogens. He discovered virulence effector families from pathogenic oomycetes and fungi, and showed how they can modulate plant immunity. He demonstrated how antagonistic coevolution with host plants has impacted the architecture of pathogen genomes, accelerated the evolution of effector genes, and drove the emergence of immune receptors networks. His inventive work in plant pathology has resulted in new approaches to mitigate some of the world’s most serious crop diseases.

Professor Kamoun has received many awards and recognitions, notably the Kuwait Prize and The Linnean Medal.

**Professor Jan E. Leach**
Colorado State University

Jan Leach is a plant pathologist who studies the molecular basis of plant disease susceptibility and resistance and how these responses are influenced by interactions within the phytobiome. Prof Leach is the current President of the International Society of Plant Pathology. She is a Fellow and a past President of the American Phytopathological Society (APS). She served on the APS Public Policy Board for 16 years, leading advocacy efforts such as the Phytobiomes Initiative, a systems-level approach to improving crop productivity. Prof Leach is a Fellow of the American Association for the Advancement of Science (AAAS) and a Fellow of the American Academy of Microbiology. She is a member of the Board on Agriculture and Natural Resources of the US National Academy of Sciences, and a Non-Resident Fellow of the Noble Research Foundation Institute.

**Professor Neena Mitter**
University of Queensland

Prof Neena Mitter, Director, Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation, the University of Queensland, is one of Queensland’s leading biotechnologists, having been involved in molecular biology and biotechnology in Australia and India for over 20 years. She is internationally recognised for her leadership in innovative, cross-functional research and exceptional industry engagement to address global challenges of agriculture and food security. She leads an impactful research group to deliver global innovations, namely ‘DsRNA based BioClay spray for crop protection’, ‘Single dose- shelf stable Nanovaccines for animal health’ and ‘Clonal propagation of avocado using plant stem cells’. These are ground breaking platform technologies impacting agricultural production, environmental sustainability and socio-economic dynamics of farming community. With increased scrutiny on use of chemicals as crop and animal disease control agents; Prof Mitter is focussed is on developing clean technologies for the agriculture of tomorrow.
Mrs Lois Ransom PSM  
Department of Agriculture

Lois Ransom is an Assistant Secretary in the Australian Government Department of Agriculture and Water Resources. Mrs Ransom is the immediate past Chair of the Commission on Phytosanitary Measures of the International Plant Protection Convention (IPPC) and has held executive roles in both the IPPC and the Pacific Plant Protection Organisation.

A plant pathologist by training and practice, Mrs Ransom worked for the Tasmanian Government before moving to the Australian Government in Canberra, where she has held a number of senior biosecurity positions, including in plant import operations, international mail and pest risk analysis. She was Australia’s Chief Plant Protection Officer (CPPO) for eight years. In a two year project with the New Zealand Ministry for Primary Industries, she assisted the development of the Government Industry Agreement for Biosecurity Readiness and Response (GIA) and established the independent GIA Secretariat. She has also chaired a number of national policy committees including the Plant Health Committee, the Biosecurity Emergency Preparedness Working Group and has participated in many plant pest incursion responses.

Mrs Ransom was Australia’s Agriculture Counsellor in Tokyo from 2000 to 2003. She was awarded the Public Service Medal, which is an award in the Orders of Australia, in 2019 for services to biosecurity.

Professor George Sundin  
Michigan State University

George W. Sundin is a Professor and Extension Specialist in the Department of Plant, Soil, and Microbial Sciences at Michigan State University. He joined the faculty in 2002 with a research emphasis in phytobacteriology and with extension responsibilities in tree fruit disease management. His current research centres on the Erwinia amylovora fire blight pathosystem with projects ranging from developing improved chemical and biological approaches for fire blight management to basic studies of pathogen-host interactions. Ongoing projects in the lab include studies of the role of cyclic di-GMP and small RNAs in the regulation of virulence (type III secretion system, exopolysaccharide production, biofilm development, and motility) in E. amylovora, functional analysis of E. amylovora type III effectors, and development and use of virulence inhibitors for bacterial disease management. These are long-term research efforts that engage multiple graduate students and involve collaborators at other institutions. The work is challenging and exciting, and links with field research and apple growers keep these projects directed towards finding solutions to the fire blight problem.
07:00  Registration opens

08:30 - 09:00  Welcome to country  
Conference opening address  
Keynote Address  
Lois Ransom and Robyn Cleland (Acting) Australian Chief Plant Protection Officer, Department of Agriculture

09:00 - 09:30  Presidential address  
Brett Summerroll

09:30 - 10:30  The EMBIO Keynote Lecture  
The edge of tomorrow—Plant health in the 21st century  
Sophien Kamoun

10:30 - 11:00  Morning Tea

11:00 - 11:15  #29  
Viral suppressors of RNA silencing in grapevine leafroll-associated virus 3  
Waqas Ahmad

11:15 - 11:30  #4  
Saving an iconic forest species: can knowledge of molecular plant-pathogen interactions help in the fight against Kauri dieback?  
Rosie E. Bradshaw

11:30 - 11:45  #49  
Characterisation of chitin synthases from Fusarium graminearum  
Linda Brain

11:45 - 12:00  #168  
Pro-domain inclusion for efficient expression and purification of fungal effectors facilitating structural, biochemical and functional studies  
Megan Outram

12:00 - 12:15  #59  
Interaction of a plant virus protein with the scaffolding Cajal body protein coflin facilitates salicylic acid-mediated plant defence responses  
Michael Taliansky

12:15 - 12:30  #67  
A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle  
Kar-Chun Tan

12:30 - 13:15  Lunch
**Program**

**Tuesday 26 November**

<table>
<thead>
<tr>
<th>Concurrent Session 2 - 13:15 - 14:45</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Room 106</strong></td>
</tr>
<tr>
<td>Session Name</td>
</tr>
<tr>
<td><strong>Session Chair</strong></td>
</tr>
<tr>
<td>Don Gardiner</td>
</tr>
<tr>
<td>13:15 - 13:30</td>
</tr>
<tr>
<td>Stefan Kusch</td>
</tr>
<tr>
<td>#58</td>
</tr>
<tr>
<td>Mohamed Khan</td>
</tr>
<tr>
<td>13:30 - 13:45</td>
</tr>
<tr>
<td>Meredith McNeil</td>
</tr>
<tr>
<td>#125</td>
</tr>
<tr>
<td>Ravijit Khangura</td>
</tr>
<tr>
<td>13:45 - 14:00</td>
</tr>
<tr>
<td>Kim Plummer</td>
</tr>
<tr>
<td>#376</td>
</tr>
<tr>
<td>Robert Magarey</td>
</tr>
<tr>
<td>14:00 - 14:15</td>
</tr>
<tr>
<td>Barry William Schroeter</td>
</tr>
<tr>
<td>#207</td>
</tr>
<tr>
<td>Robin MacDiarmid</td>
</tr>
<tr>
<td>14:15 - 14:30</td>
</tr>
<tr>
<td>Jana Sperschneider</td>
</tr>
<tr>
<td>#146</td>
</tr>
<tr>
<td>Merran Neilsen</td>
</tr>
<tr>
<td>14:30 - 14:45</td>
</tr>
<tr>
<td>Haochen Wei</td>
</tr>
<tr>
<td>#16</td>
</tr>
<tr>
<td>Anthony Pattison</td>
</tr>
<tr>
<td>14:45 - 15:15</td>
</tr>
<tr>
<td>15:15 - 16:15</td>
</tr>
<tr>
<td>Extracellular vesicles as key mediators of plant-microbe interactions</td>
</tr>
<tr>
<td>Roger Innes</td>
</tr>
<tr>
<td>16:15 - 17:15</td>
</tr>
<tr>
<td>Cross-Kingdom RNAi between plants and fungal pathogens</td>
</tr>
<tr>
<td>Hailing Jin</td>
</tr>
<tr>
<td>17:15 - 18:15</td>
</tr>
</tbody>
</table>
Program

Wednesday 27 November

08:00 - 09:00
Registration opens

08:30 - 09:30
Daniel McAlpine Lecture
Grapevine powdery mildew: from fundamental plant pathology to new and future vineyard technologies
Eileen Scott

09:30 - 10:30
Plenary 4
A biosecurity perspective of high-throughput sequencing for virus detection and diagnosis
Thierry Candresse

10:30 - 11:00
Morning Tea

11:00 - 12:30
Concurrent Session 3 - 11:00 - 12:30

<table>
<thead>
<tr>
<th>Room 106</th>
<th>Room 105</th>
<th>Room 104</th>
<th>Room 103</th>
<th>Room 101 &amp; 102</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathogenomics 2</td>
<td>Agrichemicals and Managing Chemical Resistance 2</td>
<td>Monitoring and Diagnostics 2</td>
<td>New &amp; Emerging Diseases</td>
<td>Soilborne Diseases and Pests 2</td>
</tr>
<tr>
<td>Session Chair</td>
<td>Co-Chair</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Peter Solomon</td>
<td>Meredith McNeill</td>
<td>Tony Replinski</td>
<td>Karen Barry</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Reynolds Darma</td>
</tr>
<tr>
<td>11:00 - 11:15</td>
<td>#64</td>
<td>Transectome analysis of the Rhynchosporium commute infecting barley leaf to discover novel virulence factors of R. commute</td>
<td>#271</td>
<td>Control of foliar bacterial diseases: alternatives to copper</td>
</tr>
<tr>
<td>11:15 - 11:30</td>
<td>#167</td>
<td>Whole genome sequencing of putative somatic hybrids between formae speciales of Puccinia graminis</td>
<td>#344</td>
<td>Interspecies hybridisation and recombination events lead to the emergence of fungicide resistant clonal populations in Pynophthora teres f. maculata</td>
</tr>
<tr>
<td>11:30 - 11:45</td>
<td>#203</td>
<td>Pan-genome and phylogeographic analysis of wheat-infecting Parastagonospora nodorum</td>
<td>#345</td>
<td>Functional characterization of a putative histone acetyltransferase (PhESA1) gene to investigate its potential as a new fungicide target</td>
</tr>
<tr>
<td>11:45 - 12:00</td>
<td>#261</td>
<td>Genome-wide association mapping analysis to identify genomic regions associated with virulence in Pynophthora teres f. teres</td>
<td>#89</td>
<td>Blackleg in Australia: resistance groups, fungicide resistance and upper canopy infection</td>
</tr>
<tr>
<td>12:00 - 12:15</td>
<td>#267</td>
<td>Identification of candidate virulence genes from the apple pathogen Neorontecta alitssima</td>
<td>#160</td>
<td>Spatial and temporal distribution of copper-resistant strains of Pseudomonas syringae pv. actinidiae in a kiwifruit orchard and their control using copper</td>
</tr>
<tr>
<td>12:15 - 12:30</td>
<td>#240</td>
<td>Small RNA profiling of Sclerotinia sclerotiorum while infecting Brassica napus</td>
<td>#272</td>
<td>Widespread resistance to SDHI fungicides in New Zealand populations of the barley pathogen Ramularia collo-cygni</td>
</tr>
<tr>
<td>12:30 - 13:15</td>
<td>Lunch</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13:15 - 14:00</td>
<td>Poster Session 2</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Concurrent Session 4 - 14:00 - 15:30

Room 106  Room 105  Room 104  Room 103  Room 101 & 102

Session Name  Plant-Microbe Interactions 2  Resistance Breeding and Management  Taxonomy & Phylogeny  Disease Surveys and Monitoring 1  Agricultural Microbiomes

Session Chair  Candace Elliott  Andrea Matthews  Jason Sheedy  Tom May  Narelle Nancarrow  Helen Hayden

Co-Chair  Andrea Matthews  Virginia Mwape  Reannon Smith  Sophia Callaghan  Jatinder Kaur

14:00 - 14:15 #257
Towards an understanding of virulence mechanisms in the necrotrophic fungal phytopathogen Neonectria ditissima, the causal agent of European canker of apple
Joanna Bowen

14:15 - 14:30 #48
Isolation and characterization of extracellular vesicles from Fusarium graminearum and Fusarium oxysporum f. sp. vasinfectum
Donovan Garcia Ceron

14:30 - 14:45 #118
Host susceptibility factor, MLO, supports fungal symbiosis and pathogenesis
Catherine Jacott

14:45 - 15:00 #405
Fol SIX6: a semi-specific necrosis-inducing protein
Pravin Khambalkar

15:00 - 15:15 #62
Dissecting the dual functionality of the Tox3 effector protein from the wheat pathogen Parastagonospora nodorum
Peter Solomon

15:15 - 15:30 #202
The flax-rust effector AvrM14 is a nudix hydrolyse with mRNA decapping activity
Simon Williams

15:30 - 16:00 Afternoon Tea

16:00 - 17:00 Plenary 5
Pursuing durable, broad-spectrum disease resistance in plants
Jan Leach

17:00 – 18:00 APPS AG

19:00 - 22:00 APPS 50th Anniversary Gala Dinner
### Thursday 28 November

#### 08:00 - 08:30
Registration opens

#### 08:30 - 09:30
Plenary 6
Genetic dissection of the *Erwinia amylovora* disease cycle
George Sundin

#### 09:30 - 10:30
Plenary 7
Translational taxonomy: balancing utilitarian and theoretical taxonomies of plant pathogenic bacteria
Carollee Bull

#### 10:30 - 11:00
Morning Tea

#### 11:00 - 12:00
Plenary 8
Sustainable crop protection: BioClay technology to deliver RNAi
Neena Mitter

#### 12:00 - 12:30
Poster Session 3

#### 12:30 - 13:15
Lunch

<table>
<thead>
<tr>
<th>Session Name</th>
<th>Concurrent Session 5 - 13:15 - 14:45</th>
<th>Room 106</th>
<th>Room 105</th>
<th>Room 104</th>
<th>Room 103</th>
<th>Room 101 &amp; 102</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Host Resistance and Breeding</td>
<td>Biocontrol</td>
<td>Lines of Defence - the Biosecurity Continuum</td>
<td>Disease Surveys and Monitoring 2</td>
<td>Forest and Tree Crop Diseases</td>
<td></td>
</tr>
<tr>
<td>Session Chair Co-Chair</td>
<td>Peter Dracatos</td>
<td>Tamaya Peressini</td>
<td>Louise Thatcher</td>
<td>Anne Sawyer</td>
<td>Mark Whattam</td>
<td>Ji Xuemei</td>
</tr>
<tr>
<td>13:15 - 13:30</td>
<td>#26 Genome-wide association mapping for adult plant resistance to powdery mildew in common wheat</td>
<td>Yichen Kang</td>
<td>#233 Integrated use of <em>Aureobasidium pullulans</em> strain CG163 and acibenzolar-S-methyl for management of bacterial canker in kiwifruit</td>
<td>Huub de Jong</td>
<td>#241 Grapevine red blotch surveillance in New Zealand: Working in partnership to detect an unwanted pathogen</td>
<td>#195 Tung yellow virus in winter canola crops in Victoria; prevalence and incidence over multiple years</td>
</tr>
<tr>
<td></td>
<td>#347 Profiling volatile organic compounds produced by <em>Bacillus</em> species with biocontrol properties against <em>Leptosphaeria maculans</em></td>
<td>Nural Hidayah</td>
<td>#102 The ever increasing spread of tropical plant pathogens</td>
<td>Andre Drenth</td>
<td>#132 Investigating the impact of huanglongbing in Lao PDR</td>
<td>Nerida Donovan</td>
</tr>
<tr>
<td></td>
<td>#115 Harnessing genetics, genomics and pan-genomics to understand cyst nematode resistance in wheat and barley</td>
<td>Diane Mather</td>
<td>#347 Profiling volatile organic compounds produced by <em>Bacillus</em> species with biocontrol properties against <em>Leptosphaeria maculans</em></td>
<td>Sana Hanif</td>
<td>#191 Filling in the gaps: Preparing Australia for the arrival of a new biosecurity threat</td>
<td>Craig Elliott</td>
</tr>
<tr>
<td></td>
<td>#60 Investigating the genetics underpinning adult plant resistance (APR) to tan spot (<em>Pyrenophora nodorum</em>) in wheat (<em>Tritium aestivum</em>).</td>
<td>Tamaya Peressini</td>
<td>#137 Investigation of <em>Actinobacteria</em> as biocontrol candidates against necrotrophic fungal pathogens</td>
<td>Karinathia Belt</td>
<td>#389 Improving biosecurity outcomes through the establishment of a plant pest surveillance network in Australian botanic gardens</td>
<td>David Gale</td>
</tr>
<tr>
<td></td>
<td>#183 Fine mapping towards cloning of barley leaf rust resistance gene Rph5.e</td>
<td>Chris Rothwell</td>
<td>#221 Plant defense-bioreporters and combined microbial omics approaches facilitates the discovery of new <em>Actinobacteria</em> biofungicide candidates</td>
<td>Louise Thatcher</td>
<td>#336 Virus diseases of watermelon in southern Lao PDR and associated challenges for training on integrated disease management</td>
<td>Nicholas Pain</td>
</tr>
<tr>
<td></td>
<td>#131 Characterisation of genes involved in the sensitivity of barley to <em>Pyrenophora teres f. teres</em> toxins</td>
<td>Abolfazl Sarpeleh</td>
<td>#248 Clarifying the taxonomy of a fungus being investigated as a potential biocontrol agent for an invasive plant of beaches in Australia</td>
<td>Isabel Zeil-Rolfe</td>
<td>#184 Using honey bees for plant virus surveillance</td>
<td>John Roberts</td>
</tr>
<tr>
<td></td>
<td>#185 Industry-wide survey of diseases in Australian almond orchards</td>
<td>Tonya Wiechel</td>
<td>#181 <em>Phytophthora palmivora</em>: Potential threat to <em>Elaeis guineensis</em> Jacq and the ensued mitigation measures</td>
<td>Shamala Sundram</td>
<td>#205</td>
<td></td>
</tr>
</tbody>
</table>

---

**SPONSORED BY**

- **AFLA Australia**
- **Plant Health Australia**
- **Enactus**
- **University of Melbourne**

---

**Room Locations**

- **Room 101 & 102**
- **Room 103**
- **Room 104**
- **Room 105**
- **Room 106**
### Program: Thursday 28 November

#### 14:45 - 15:15 Afternoon Tea

#### 15:15 - 16:45 Concurrent Session 65 - 15:15 - 16:45

<table>
<thead>
<tr>
<th>Room 105</th>
<th>Room 104</th>
<th>Room 103</th>
<th>Room 101 &amp; 102</th>
</tr>
</thead>
<tbody>
<tr>
<td>Molecular Biology of Vector-Borne Diseases</td>
<td>New Technologies and Novel Methods for Disease Control</td>
<td>Epidemiology and Modelling</td>
<td>Evolution &amp; Diversity</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Session Name</th>
<th>Session Chair</th>
<th>Co-Chair</th>
<th>Session Time</th>
<th>Title and Abstract</th>
</tr>
</thead>
<tbody>
<tr>
<td>Molecular Biology of Vector-Borne Diseases</td>
<td>Cherie Gambley</td>
<td>Jacqui Morris</td>
<td>15:15 - 15:30</td>
<td>Genome-based phylogeny of phytoplasmas in coconut and banana Lilia Carvalhais</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#304 Optimisation of cold plasma to manage Fusarium species in postharvest wheat grain Kirsty Bayliss</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#95 Dispersal patterns of grapevine trunk disease pathogen spores in Australian vineyards Regina Baaijens</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#283 Phytogenetic relationship between the Australian Fusarium oxysporum isolates and resolving the species complex using the multispecies coalescent model Saidi Achari</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#152 How phytoplasmas modulate plant architecture and promote their own spread via insect vectors Hogenhout Lab</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#414 Selection of highly specific aptamers to detect Fusarium graminearum and Fusarium pseudograminearum Nitin Mantri</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#80 Decision apps for managing disease in canola, wheat and mungbean Art Diggle</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#43 A story of an evolving crop pathogen - population structure and evolution of pathogenicity in the Australian Ascochyta rabiei Ido Barr</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#396 Dancing with the stars: Botrytis cinerea and a novel, mechanically transmitted DNA mycovirus that it hosts mutually regulate each other’s replication rates Robin MacDiarmid</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#235 Exploring the interactions between bacterial endophytes and trunk disease pathogens of grapevine Jennifer Niem</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#101 Modelling long-distance dispersal of wheat rusts: towards early warning systems Christopher Gilligan</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#357 Characterisation of Candidatus Liberibacter brunswickensis, a novel candidate Liberibacter species identified in Australia Jacqueline Morris</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#124 Using microwave radiation to destroy macroconidia of the cereal pathogen Fusarium pseudograminearum: a hot solution? Toni Petronaitis</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#174 Diversity and economic impact of bacterial soft rot pathogens (Pectobacterium spp. and Dickeya spp.) on potato production in the Columbia Basin, USA Hannah Rivedal</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#120 What can we learn from population genomics studies of Curtobacterium flaccumfaciens pv. flaccumfaciens, the cause of tan spot on mungbean? Niloofar Vaghefi</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#333 High throughput detection of Australian pea seed-borne mosaic virus populations and its molecular properties Solomon Maina</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#101 Exploring the interactions between bacterial endophytes and trunk disease pathogens of grapevine Jennifer Niem</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#357 An archaeological contribution to 40+ years investigation into a ‘new’ disease of Australian grapes Peter A Magarey</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#318 Elucidation of diversity of barley yellow mosaic virus by RNA-seq analysis Youko Oono</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#358 Characterisation of Candidatus Liberibacter brunswickensis, a novel candidate Liberibacter species identified in Australia Jacqueline Morris</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#124 Using microwave radiation to destroy macroconidia of the cereal pathogen Fusarium pseudograminearum: a hot solution? Toni Petronaitis</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#174 Diversity and economic impact of bacterial soft rot pathogens (Pectobacterium spp. and Dickeya spp.) on potato production in the Columbia Basin, USA Hannah Rivedal</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#120 What can we learn from population genomics studies of Curtobacterium flaccumfaciens pv. flaccumfaciens, the cause of tan spot on mungbean? Niloofar Vaghefi</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#31 Grapevine leafroll-associated virus 3: symptoms, suppression and seasonal movement Roshni Rohra</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#166 RNA sprays to combat plant pathogenic fungi Anne Sawyer</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#252 Epidemiological characterisation of pasture dieback in eastern Australia Anthony Yong</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>#285 Genotypic characterization of Phytophthora infestans isolates from Indonesia Phillip Wharton</td>
</tr>
</tbody>
</table>

#### Closing ceremony

---

**Room 106**

**Session Chair**

| Cherie Gambley | Jacqui Morris | Victor Galea | Aurelia Quade | Robert Park | Ruvini Lelwala |

| Co-Chair | Jennifer Niem | Ruvini Lelwala | Aurelia Quade | Robert Park | Victor Galea |

**Session Name**

| Molecular Biology of Vector-Borne Diseases | New Technologies and Novel Methods for Disease Control | Epidemiology and Modelling | Evolution & Diversity |

**Session Name**


**Session Chair**

| Cherie Gambley | Jacqui Morris | Victor Galea | Aurelia Quade | Robert Park | Ruvini Lelwala |

| Co-Chair | Jennifer Niem | Ruvini Lelwala | Aurelia Quade | Robert Park | Victor Galea |

**Session Time**

| 15:15 - 15:30 | 15:30 - 15:45 | 15:45 - 16:00 | 16:00 - 16:15 | 16:15 - 16:30 | 16:30 - 16:45 | 16:45 - 17:00 |

**Session Name**

| Genome-based phylogeny of phytoplasmas in coconut and banana Lilia Carvalhais | How phytoplasmas modulate plant architecture and promote their own spread via insect vectors Hogenhout Lab | Dancing with the stars: Botrytis cinerea and a novel, mechanically transmitted DNA mycovirus that it hosts mutually regulate each other’s replication rates Robin MacDiarmid | High throughput detection of Australian pea seed-borne mosaic virus populations and its molecular properties Solomon Maina | Characterisation of Candidatus Liberibacter brunswickensis, a novel candidate Liberibacter species identified in Australia Jacqueline Morris | Grapevine leafroll-associated virus 3: symptoms, suppression and seasonal movement Roshni Rohra | Closing ceremony |
Poster Session 1

Agrichemicals & Managing Chemical Resistance 1

P031 – Evaluation of fungicide soil drench treatments to manage black root rot disease in avocado seedlings
Akila Devi Prabhakaran

P032 – Developing a fungicide efficacy baseline for Venturia inaequalis in Western Australia.
Andrew Taylor

P033 – Assessment of fungicide resistance in Botrytis cinerea from cherry fruit
Elaine Tai

P034 – Fluxapyroxad (Sercadis® Fungicide) activity on apple scab (Venturia inaequalis), powdery mildew (Podosphaera leucotricha), alternaria leaf blotch (Alternaria mali) in apple (Malus domestica) in Australia
Marco Montagna

P035 – Mefentrifluconazole (Belanty® Fungicide) activity on apple scab (Venturia inaequalis), powdery mildew (Podosphaera leucotricha), alternaria leaf blotch (Alternaria mali) in apple (Malus domestica) in Australia
Marco Montagna

P036 – The activity of mefentrifluconazole (Belanty® Fungicide) on powdery mildew (Uncinula necator) in grape (Vitis vinifera L.) in Australia
Marco Montagna

P037 – Pyraclostrobin+fluxapyroxad (Merivon® Fungicide): a new dual mode of action fungicide for the control of husk spot (Pseudocercospora macadamiae) in macadamia (Macadamia integrifolia) in Australia
Marco Montagna

Community & Industry Engagement

P038 – Festival of Plant Health 2020: a road map to promote the International Year
Andrea Masino

P039 – iMapPESTS: aiming for the sky in cross-industry plant pest surveillance initiative
Shakira Johnson

Foliar & Postharvest Diseases

P060 – Diaporthe spp.: pathogen or saprophyte of persimmon?
Cathryn Todd

P061 – Reaction of different species of Fabaceae and Solanaceae to three Cucumber mosaic virus isolates
Mohammad Aftab

P062 – Geographical distribution of two turf grass pathogens, Wongia griffinii and W. garrettii, in Australia
Percy Wong

P063 – Comparison of aggressive and non-aggressive Ascochyta lentis isolates on lentil cultivar PBA Hurricane XT.
Jade Rose

P064 – Effects of grapevine trunk disease on wine composition
Rebecca Woolley

P065 – New pathogens on leafy vegetable for the ready-to-eat sector
Andrea Masino

P066 – A review of Red Rot of sugarcane in Pakistan
Waqas Arshad

P067 – The impact of the outbreak of tomatoes disease Tuta Absoluta in Nigeria
Michael Oke
P068 – Identification of the powdery mildew species infecting mungbean in Australian paddocks
Lisa Kelly

Innovations in Detection & Diagnosis

P019 – Detection platforms of various crop plant fungal diseases using next generation molecular tools
Gopal Venkatesh Babu

P020 – Detection and quantification of plant pathogens using droplet digital PCR
Mark Andersen

P021 – Early disease detection using hyperspectral sensors
Ayalsew Zerihun

Integrated Disease Management

P069 – Seed Potato Certification: An important role
Nigel S. Crump

P070 – Effects of light spectra on growth and defence in potted Actinidia chinensis var. deliciosa ‘Hayward’ kiwifruit plants
Tony Reglinski

P071 – Effect of fungicides and variety resistance on the suppression of Fusarium head blight and Deoxynivalenol
LeAnn Lux

P072 – The use of totally impermeable film with fumigants improves control of charcoal rot of strawberry
Apollo Gomez

P073 – Effect of in-furrow phosphorus and zinc on Fusarium crown rot of hard red and soft white winter wheats in Oregon, USA
Duncan Kroese

P074 – A brief historical review of fifty-year’s progress in South Australian management of grapevine downy mildew - once the major foliage disease in Australian viticulture.
Peter A Magarey

P075 – A screening technique for alternative management options of Thielaviopsis musarum
Peter Trevorrow

Monitoring and Diagnostics 1

P023 – Rapid detection of Claviceps purpurea and quarantined Claviceps humidiphila by real-time PCR
Jana Monk

P024 – Development of loop-mediated isothermal amplification assay for the detection of seedborne fungal pathogen, Sarocladium oryzae causing sheath rot of rice
MK Prasannakumar

P025 – Citrus black spot: Sex, lies and milenex tape
Nga T Tran

P026 – Molecular diagnosis of Ascochyta spp. causing Ascochyta blight in Faba bean, Lentil and Vetch targeting the mitochondrial genome
Winnie Liu Heang

P027 – Evaluation of different diagnostic methods for grapevine fungal trunk disease
Rebecca Woolley
Poster Session 1

P028 – Development of a multiplex-PCR approach for the accurate and rapid detection of Gnomoniopsis smithogilvyi in Castanea sativa (Mill.)
Matias Silva-Campos

P029 – NARH: confirmed as a robust isolation medium for Phytophthora species
Suchana Rani Sarker

P030 – Protecting the Australian capsicum industry from incursions of exotic Colletotrichum pathogens
Awalikara De Silva

**Pathogenomics 1**

P021 – Genome sequencing of Ascochyta Blight pathogen of field pea (P. pinodes, P. pinodella and P. koolunga) using long-read sequencing technology
Yvonne Ogaji

P022 – Analysis of microRNA targets at different developmental stages of root-knot nematode (Meloidogyne incognita) genes regulated by the Zn2Cys6 binuclear cluster transcription factor Pf2
Soyoung Park

P076 – Transcriptomic analysis at different developmental stages of root-knot nematode (Meloidogyne incognita)
Bum-Soo Hahn

P077 – Endogenous viral elements in Macadamia genome and its putative role in abnormal vertical growth
Mohamed Cassim Mohamed Zakeel

P078 – Relative pathogenicity and molecular analysis of Sporisorium scitamineum isolates from Australia
Nurul Hidayah

**Plant-Microbe Interactions 1**

P001 – Functional characterisation of the necrotrophic effector ToxA from wheat pathogen Parastagonospora nodorum
Bayantes Dagvadorj

P002 – Secretome profiling analysis of Pyrenophora tritici-repentis genes regulated by the Zn2Cys6 binuclear cluster transcription factor Pt12
Pao Theen See

P003 – Cell death-inducing activity of a conserved family of small secreted proteins from Ciborinia camelliae, Botrytis cinerea and Sclerotinia sclerotiorum
Hannah McCarthy

P004 – Characterization of Brassicaceae smut fungal effectors responsible for plant infection
Summia Gul

P005 – The necrotrophic effector SnTox1 of Parastagonospora nodorum harbours a promoter variant associated with gene repression
Evan John

P006 – Using Agrobacterium-mediated GFP transformation of Fusarium oxysporum to study the infection process of pathogenic and non-pathogenic Fusaria on ginger (Zingiber officinale Roscoe) rhizomes
Andrea Matthews

P007 – Structural prediction of ToxA-like and MAX effector proteins using threading and comparative modelling methods
Lina Rozano

P042 – Opportunities through the Agricultural Microbiomes Research Coordination Network
JP Dundore-Arias
Soilborne Diseases & Pests 1

P010 – An overview of site-specific nematode management in Louisiana cotton
Manjula Kularathna

P011 – The effect of *Verticillium dahliae* to cause Potato Early Dying syndrome in Victoria, Australia
Prakash Nair

P012 – Surprises inside: Cereal cyst nematodes induce striking changes in root vascular anatomy
Diane Mather

P008 – Modelling *Pratylenchus thornei* field populations over multiple soil depth intervals and trials to rank wheat genotypes for resistance in the northern Australian grains region
Bethany Rognoni

P009 – Impact of deep soil amelioration treatments on *Rhizoctonia solani* and root lesion nematodes
Daniel Huberli

P040 – Wheat root histopathology and defensive biochemistry against root-lesion nematode *Pratylenchus thornei*
Md Motiur Rahaman

Surveillance and Incursion Response

P013 – An overview of banana bunchy top virus (BBTV) in South Africa
Anna Jooste

P014 – Phylogenetic analysis of *Cryphonectria parasitica* (Chestnut blight) incursion in NE Victoria
Jatinder Kaur

P015 – Occurrence of Banana Wilt Associated Phytoplasma
Cecilia O’Dwyer

P016 – Biosecurity Pest Surveillance in Queensland
Christine Horlock

P018 – Surveillance of bacterial pathogens associated with blackleg symptoms in certified seed potatoes crops in South Eastern Australia
Nellie A. Malseed
**Agrichemicals & Managing Chemical Resistance 2**

P010 – Barley Disease Cohort Project: a co-innovation approach to managing fungicide resistance  
L Lorenzo Covarelli

P011 – Evaluation of fungicide timing and efficacy for management of Phoma black stem in Sunflower in the USA  
Bryan Hansen

P012 – Blast in northern Queensland: not so nice for rice!  
Nirodha Weeraratne

P013 – Variability in fungicide sensitivity in the *Pyrenophora teres* f. *maculata* population in South-eastern Australia  
Hayley Wilson

P014 – Determination of fungicide efficacy for management of rust of field pea in North Dakota, U.S.A.  
Jessica Halvorson

P015 – Using fungicide mixtures with multi-site fungicides for managing resistance of *Cercospora beticola* in sugar beet  
Mohamed Khan

P009 – In vitro inhibitory activity of different selenium compounds towards a *Fusarium proliferatum* strain isolated from rice  
Lorenzo Covarelli

**Agricultural Microbiomes**

P001 – How does peanut crop rotation influence plant health?  
Asfakun Siddika

P003 – Impacts of cropping sequences on rhizosphere microbiome and root disease in sugarcane  
Paul Harvey

P004 – Symbionts of the tomato potato psyllid  
Rebekah Frampton

P005 – Effects of host plant on the endosymbionts in *Bemisia tabaci*  
Fang-Yu Hu

P006 – Acid soils in Pacific Northwest, USA wheat production and impacts on the soil microbiome  
Duncan Kroese

P007 – Blueberry Replant Decline: An inheritance worth avoiding.  
Michael Norman

P008 – Grapevines (*Vitis vinifera* L.) contain diverse communities of culturable fungi that differ between organic and standard management systems in New Zealand  
Noureddine Besselma

P053 – Occurrence of seed-borne pathogens in wheat grains across the Western Australian Wheatbelt  
Lorenzo Covarelli

**Disease Surveys and Monitoring 1**

P054 – Are groundcover and native plants potential reservoirs of pathogens within vineyards?  
Kar Mun Chooi

P055 – Surveillance of Potato Spindle Tuber Viroid (PSTVd) in Certified Seed Potato Crops in South Eastern Australia  
Nigel S. Crump

P056 – A spore trapping network for the early detection of potato pathogens in the USA  
Phillip Wharton
P057 – Molecular screening of Banana tissue culture plantlets for major viruses infecting banana in and around Bengaluru
S Basavaraj

P058 – Epidemiology of cereal viruses in southern Hungary
András Takács

P059 – Incidence of *Puccinia punctiformis* within and between populations of *Cirsium arvense* in New Zealand
Caitlin Henderson

P060 – Diseases of Roselle and Implications for Small-holder Farmers
Nicholas Pain

P061 – Can bacterial plant pathogens be written off from grain discolorations observed on rice in northern Queensland?
Peter Buyoyu

P062 – Area wide management of bacterial and viral pathogens in the vegetable industry
Shannon Mulholland

**Monitoring and Diagnostics 2**

P063 – The development of loop mediated isothermal amplification (LAMP) diagnostic assays for the detection of Deformed wing virus and Sacbrood virus in bees
Linda Zheng

P064 – Microscopic examination of *Ralstonia pseudosolanacearum* and *R. solanacearum* colonies and the response of tomato breeding lines to bacterial wilt caused by the two species
Mark Angelo Balendres

P065 – Isothermal detection of the *Dickeya* genus and *Clavibacter michiganensis* subsp. *sepedonicus*, prominent potato tuber pathogens
Bryant Davenport

P066 – Identification and detection of soft rot of carrot caused by *Klebsiella variicola* - a new pathogen on carrot
K Nandini

P067 – Population analysis and subgroup diagnosis of Lettuce necrotic yellows virus in New Zealand
Toni Darling

P068 – Rapid detection of Sweet Potato Virus G using novel LAMP detection technology
Winnie Maso

**New & Emerging Diseases**

P069 – Revisiting tomato pith necrosis: a new *Pseudomonas* species associated with the disease
Merje Toome-Heller

P070 – Chocolate streak disease of tomatoes in Australia is caused by a unique strain of *Fusarium oxysporum*
Sophia Callaghan

P071 – First report of *Phytophthora capsici* as a causal pathogen of blight disease of chilli (*Capsicum annuum* L.) in Bhutan
Ganja Singh Rai

P072 – Is Sugarcane an alternative host of Panama Disease?
Wayne O’Neill

P073 – Differences in the acquisition of *Candidatus Liberibacter solanacearum* by two New Zealand tomato potato psyllid genotypes
Gabrielle Drayton
P074 – Calonectria quinqueseptata associated with a leaf spot disease of Macadamia integrifolia in the Laos PDR
Lester Burgess

P075 – First report of mango stem-end rot, caused by Lasiodiplodia theobromae, in the Lao PDR
Lester Burgess

Pathogenomics 2

P021 – Implementing molecular techniques develops our understanding of a devastating bacterial disease of mungbean, halo blight
Thomas Noble

P022 – Using genome-wide screening to identify genes important for bacterial colonisation of plant surfaces
Belinda Fabian

P023 – Adaptation in a near-clonal pathogen, Dothistroma septosporum, over 50 years in New Zealand pine forests Rosie E. Bradshaw

P076 – A high-quality reference genome for the plant pathogen, Phytophthora cinnamomi
Amy Longmuir

P077 – Genome-wide association study to identify genomic regions associated with virulence in Pyrenophora teres f. maculata
Rudrakshi Sharma

P078 – Multi-domain interactions between Fusarium oxysporum and the banana microbiome
Henry W.G. Birt

Plant-Microbe Interactions 2

P016 – Identification and characterization of the interactions between the key plant protein RIN4 and the plant exocyst subunit Exo70B1 protein in kiwifruit using yeast two-hybrid system
Wei Cui

P017 – Initial characterisation of extracellular vesicles from the fungal wheat pathogen Zymoseptoria tritici
Erin Hill

P018 – A polyethylene glycol-mediated protoplast transformation system for the Basal Stem Rot causal fungus, Ganoderma boninense
Fook Hwa Lim

P019 – Fusaristatin production negatively contributes to the aggressiveness of the crown rot pathogen Fusarium pseudograminearum
Mohammed Khudhair

P020 – Fungal effectors and their potential role in infection
Cordelia Dravitzki

Resistance Breeding and Management

P031 – Comparison of measurement methods for determining Macrophomina phaseolina isolate aggressiveness
Dante Adorada

P032 – Mapping of quantitative trait loci for seedling and adult plant resistance to Blumeria graminis f. sp. tritici in wheat
Hossein Golzar

P033 – Mapping of quantitative trait loci for seedling and adult plant resistance to nodorum blotch in wheat
Hossein Golzar
P034 – Incidence of and resistance to *Heterodera avenae* and *H. filipjevi* in cereal production regions of Idaho in the United States  
*Juliet Marshall*

P035 – Screening of a macadamia breeding population for resistance to husk spot  
*Jasmine Nunn*

P036 – Field evaluation of Cavendish somaclones and mutants for Fusarium wilt race 4 resistance and agronomic performance in northern Mozambique  
*Sheryl Bothma*

P037 – Iranian landrace wheats are a valuable source of dual resistance to the root-lesion nematodes *Pratylenchus neglectus* and *P. thornei*  
*Jason Sheedy*

P038 – Visual scores and normalised difference vegetation index can be used to screen wheat cultivars for tolerance to *Pratylenchus thornei*  
*Neil Robinson*

P039 – Storage requirements of *Puccinia sorghi* urediniospores  
*Aurelie Quade*

P040 – Development and assessment of genetic stocks with four genes for yellow spot resistance  
*Dorthe Jorgensen*

P041 – Phenotypic evaluation of Sclerotinia sclerotiorum resistance in wild Cicer germplasm under greenhouse conditions  
*Virginia Mwape*

P042 – Monitoring virulence of the *Pyrenophora teres* f. *maculata* pathogen population on barley to aid breeding for host plant resistance  
*Jennifer Cutajar*

P043 – The impact of waterlogging tolerance on Phytophthora root rot resistance in chickpea  
*Nicole Dron*

P044 – Variations in macadamia varietal susceptibility to *Phytophthora multivora* and *P. cinnamomi*  
*Olumide Jeff-Ego*

P045 – Field Screening of Resistance to *Didymella arachidicola* in peanuts (*Arachis hypogaea*)  
*Shona Wood*

P046 – Management of Carlavirus in beans through varietal tolerance  
*Visnja Steele*

**Soilborne Diseases & Pests 2**

P047 – Fungal pathogens threatening quinoa (*Chenopodium quinoa* Willd.) cultivations in central Italy  
*Lorenzo Covarelli*

P048 – Assessing the efficacy of pot bioassays to indicate soil microbial changes related to suppression of banana Fusarium wilt  
*Hazel Gaza*

P049 – *Fusarium pseudograminearum* and *F. culmorum* in cereal stubble after harvest.  
*Margaret Evans*

P050 – Identification of alternative hosts in the management of *Fusarium oxysporum* f.sp. *cubense* Tropical Race 4 in the Northern Territory  
*Sharl Mintoff*
P051 – Pathogenicity and aggressiveness of Macrophomina phaseolina isolates to strawberry (Fragaria x ananassa)  
Apollo Gomez  
P052 – Infected strawberry crop debris is a source of inoculum for charcoal rot disease  
Apollo Gomez  

**Taxonomy & Phylogeny**  
P024 – Re-inventory of *Fusarium* species in the Victorian Plant Pathology Herbarium (VPRI)  
Jacky Edwards  
P025 – Secondary metabolite clusters distinguish different species of *Teratosphaeria* pathogens  
Janneke Aylward  
P026 – Phylogeny of *Fusarium* associated with *Euwallacea*-vectored branch dieback of avocado and other woody tree hosts in Australia  
Louisamarie Parkinson  
P027 – Morpho-molecular characterization and control of *Guignardia bidwellii* causing leaf spot of jackfruit  
Md. Abdullahil Baki Bhuiyan  
P028 – *Phytophthora* diagnoses and species associated with plant health in Victoria  
Ramez Aldaoud  
P029 – Identification of the *Colletotrichum* spp. causing anthracnose diseases of citrus in Australia  
Weixia Wang  
P030 – Four New *Pythium* Species of Clade B from Rice Paddy Fields  
Reza Mostowfizadeh-Ghalamfarsa
**Biocontrol**

P031 – Shelf life study of *Trichoderma* species and their efficacy to control root and basal stem rot disease on mandarin
Agnes Simamora

P063 – Management of Sheath blight disease utilizing Tricho-compost
Shireen Quazi

P064 – A robust quantitative approach using SPME-GC-MS, identified the volatilome of the biocontrol agent, *Aureobasidium pullulans*
Sashika Yalage Don

P065 – Using indigenous *Trichoderma* as a potential biocontrol of Fusarium Wilt (*Fusarium oxysporum* f.sp. *cubense*) in Australian banana cropping systems.
David East

P066 – The potential of *Aureobasidium pullulans* to inhibit or protect grapevines against *Eutypa lata*: *in silico*, *in vitro* and *in planta* analyses
Tianyi Tang

P067 – Arbuscular mycorrhizal fungi drive nodulation by rhizobia and yield of mungbean despite infestation with *Pratylenchus thornei*
Elaine Tabah

P068 – Modes of competition between bacterial pathogens during plant co-colonization
Hanareia Ehau-Taumaunu

P069 – Identification of novel fungal endophytes with bioactivity against *Neonectria ditissima*, the causal agent of European canker of apple
Lay Lay New

P070 – Bacteriophage-mediated control of *Pseudomonas syringae pv. actinidiae* on kiwifruit plants
Shea Addison

P071 – Green Fluorescent Protein transformation sheds more light on a widespread mycoparasitic interaction
Levente Kiss

**Disease Surveys and Monitoring 2**

P033 – Are pathogens responsible for dark staining of pistachio shells?
Belinda Rawnsley

P034 – Survey of banana leaf diseases in Southern Lao PDR
Jay Anderson

P035 – Hidden pathogens in soybean seed detected in the United States and Europe
Kristina Petrovic

P036 – Green leafhoppers population as a vector of Tungro virus
Arif Muazam

**Epidemiology and Modelling**

P018 – Suitability of New Zealand regions for the establishment of *Xylella fastidiosa* based on a temperature cut-off model.
Virginia Marroni

P019 – Yield losses associated with Turnip yellows virus infection in field peas and lentils
Narelle Nancarrow

P020 – Yield losses associated with Barley yellow dwarf virus in wheat and barley
Narelle Nancarrow
Poster Session 3

P021 – Leaf spot a possible source of inoculum of dry flower disease in macadamia in Australia
Kandeeparoopan Prasannath

P022 – Application of predicted weather data to forecast possible occurrence of bacterial grain rot of rice prior to grain infection
Hyo-suk Kim

P023 – Methods to standardise the severity of Botryosphaeriaceae infections in experimental grapevine plant materials
Regina Baaijens

P024 – Validation of weather based paddy blast disease forecasting model
Kuri Sharanaappa

P025 – The association of ice nucleating bacteria and frost damage in the Western Australian (WA) broadacre cropping region
Bec Swift

P037 – Epidemiology of Pyrenophora tritici repentis and Parastagonospora nodorum coinfection of wheat with contrasting host resistance profiles
Ayalsew Zerihun

Evolution & Diversity

P072 – Linking the present to the past: genome sequencing delineates persistent isolates of the skeleton weed biocontrol agent Puccinia chondrillina in Australia
Gavin Hunter

P073 – Genetic characterisation of South African Pyrenophora teres isolates using DArTseq™
Buddhika Dahanayaka

P074 – Determining Peronospora somniferi genotype diversity and its potential impact on management of systemic downy mildew of opium poppy
Dharushana Thanabalasingam

P075 – Contrasting genetic diversity and structure among Malagasy Ralstonia pseudosolanacearum phytype I populations inferred by a novel Multilocus Variable Number of Tandem Repeat Analysis scheme.
Hasina Ny Aina Rasoamanana

P076 – Horizontal gene transfer has boundaries: site saturation restricts the movement of an Integrative and Conjugative Element in plant pathogenic ‘Erwinias’
Luciano Nunes-Leite

P077 – Is Pseudomonas syringae pv. actinidiae (Psa) adapting to kiwifruit?
Saadiah Arshed

P078 – Molecular and phenotypic characterization of Xanthomonas oryzae pv. oryzae races from Bangladesh
Mohammad Islam

Forest and Tree Crop Diseases

P026 – Investigating the potential role of ring nematodes (Mesocriconema xenoplax) in predisposing plum trees to bacterial canker infection
Teresa Coutinho

P027 – Pathogens and diseases identified in Australian almond orchards
Simone Kreidl

P028 – Needle in a haystack – searching for evidence of symbiosis between Rhizopus stolonifer and a bacterium in the almond hull rot pathosystem
Anjali Zaveri

P029 – Pathogenicity and new records of exotic blue stain fungi on Pinus in Australia
Angus Carnegie
P030 – Where does Austropuccinia psidii have sex?
Alistair McTaggart

Host Resistance & Breeding
P015 – Ascochyta blight resistance in faba bean: marker development and fine mapping
Levina Pieter

P016 – Identification of quantitative trait loci and candidate genes associated with Ascochyta blight resistance in the interspecific RIL population
Rama Harinath Reddy Dadu

P017 – Nuclear fibrillarin and coilin are negative regulators of potato plant resistance to biotic and abiotic stresses mediated by salicylic acid
Natalia Kalinina

Lines of Defence - the Biosecurity Continuum
P010 – Systems approach risk framework for biosecurity pests: Plant pathogen case study
Kate Fiedler

P011 – Post Entry Quarantine, Mickleham – protecting Australia’s plant health.
Julie Pattemore

P012 – Tobamovirus infected tomato and capsicum seed shipments to Australia.
David Lovelock

P013 – Assessing testing efficiencies using pospiviroid prevalences in tomato and capsicum seed lots
David Dall

P014 – PIC@PEQ - a collaborative biosecurity concept between government, industry and academia
Adrian Dinsdale

P007 – Phytophthora: a scourge of vegetable, fruit, and field crops in southern Lao PDR – biosecurity issues.
Lester Burgess

P008 – Colletotrichum: A Headache for Australian Biosecurity
Vera Andjic

P009 – An emerging biosecurity risk: Tomato brown rugose fruit virus
Neil Grant

Molecular Biology of Vector-Borne Diseases
P004 – Mitogen-activated protein kinase phosphatase 1 reduces the replication efficiency of Bamboo mosaic virus in Nicotiana benthamiana
Menghsiao Meng

P005 – Molecular responses of Nicotiana glutinosa to infection with lettuce necrotic yellows virus subgroups
Shweta Shinde

P006 – Status of papaya phytoplasma diseases in far north Queensland
Nandita Pathania

New Technologies and Novel Methods for Disease Control
P001 – Effect(s) of compost tea on plant growth promotion and antifungal activity
Sang-mi Yu

P003 – ZnO nanoparticles can be used to manage white mold of french bean
Himadri Kaushik
ASDS2020
Protecting the roots of plant health
Hilton Cairns, 24 - 27th November 2020

Save the Date

Email: asds@yrd.com.au
to be added to the mailing list
Grampians grain pathology pre-conference field tour

Date: 24-25 November 2019 (2 days)
Location: Horsham area
Cost: $450 (includes transport, all meals and accommodation on night of 24 November)

Summary: Visit the field crops pathology research facility located at Horsham in the heart of Victoria’s wheat belt. This tour will showcase world renowned research into the management of fungal, bacterial, viral and nematode diseases of grain crops including cereals, pulses and canola. Research areas incorporate an integrated management approach that includes breeding, fungicides and cultural controls. The tour will also visit Agriculture Victoria’s world class Plant Phenomics facility featuring a fully automated robotic phenotyping system and the Australian Grains Genebank which holds approximately 300 million seeds, protecting precious genetic material for future generations.

The tour will depart from Melbourne at 8am and includes a social dinner with an overnight stay in Horsham, returning to Melbourne the following afternoon. On the way, you will enjoy the spectacular scenery of the Grampians National Park, visit a local winery and make a stop at a local farm.

Convenors: Narelle Nancarrow (Molecular Epidemiologist) narelle.nancarrow@ecodev.vic.gov.au, Ph: (03) 4344 3114), Mark McLean (Research Scientist-Plant Pathology) and Pragya Kant (Research Scientist-Molecular Plant Breeding), Agriculture Victoria (Department of Jobs, Precincts and Regions), Grains Innovation Park, 110 Natimuk Road, Horsham, VIC 3400

Potato Toolangi tour

Date: 29th November 2019
Location: Toolangi Research station 1015 Myers Creek Road Toolangi
Cost: $125 (Transport, Lunch included)

Summary: A workshop on key potato diseases aimed to promote discussion surrounding the latest knowledge and research outcomes. Discussion on key challenges including biosecurity preparedness, diagnostics and disease management. Delegates are invited to present papers at this workshop to be held at Toolangi Research Station in the Yarra Valley

Convenors: Dr Nigel Crump, General Manager and Principal Scientist, 1015 Myers Creek Road, Toolangi Vic 3777, Telephone +61 3 5962 0000, Fax +61 3 5962 9045, Mobile 0408 592 051
Workshops

**Agricultural Microbiomes: Promise, Practices, and Partnerships**

Date: 25th November 2019 – full day  
Time: 8:30 – 4:30  
Location: Victoria A, AgriBio, La Trobe University, 5 Ring Rd, Bundoora, Melbourne  
Cost: $130

**Summary:** Following on from the Agricultural Microbiome workshop run by Prof Linda Kinkel and Dr JP Dundore-Arias at the 2018 International Congress of Plant Pathology in Boston, USA, this event will be the first ever Agricultural Microbiome workshop held in Australia.

The one-day workshop will feature keynote presentations, lightening talks and small-group sessions. The program will cater for those interested in learning about agricultural microbiomes, new to the research and those actively working in the field. The focus of the talks and discussion sessions will be: a) the current status of agricultural microbiome research; b) progress in agricultural microbiome databases, metadata and technical information; c) identifying gaps in technical, analytical and education resources; d) developing, leveraging and coordinating collaborative efforts to advance agricultural microbiome science through training, databases, community building, platform development etc and e) developing draft strategies for advancing agricultural microbiome research and applications.

**Special guest presenters:** Prof Susanne Schmidt, School of Agriculture and Food Sciences, University of Queensland, Brisbane, and Dr Gupta Vadakattu, CSIRO Adelaide and Assoc Professor in the Faculty of Health Sciences, Flinders University, Adelaide.

**Convenors:** The workshop will be facilitated by international microbiome specialists and plant pathologists Prof Linda Kinkel (University of Minnesota) and Dr JP Dundore-Arias (University of Minnesota) and Australian microbiome specialists, microbial ecologists Assoc Prof Pauline Mele (Agriculture Victoria & La Trobe University) and Dr Helen Hayden (Agriculture Victoria).

Prof Kinkel and Dr. Dundore-Arias are leaders in the U.S. National Science Foundation-funded Agricultural Microbiomes Research Coordination Network which aims to develop an international network of microbiome research and researchers through workshops, training, and sponsored sessions at scientific meetings. Prof Kinkel also serves as Associate Editor-in-Chief for the Phytobiomes Journal.

**4th Australian Pathogen Bioinformatic Symposium (APBS) 2019**

Date: 25th November 2019 – full day  
Time: 9:30- 16:30  
Location: Victoria B, AgriBio, La Trobe University, 5 Ring Rd, Bundoora, Melbourne  
Cost: $100

**Summary:** In recent years, the study of the interactions between pathogens and their hosts has heavily relied on genomics, transcriptomics, proteomics and metabolomics. This has led to increased use of bioinformatics and the emergence of bioinformatics as a major sub-discipline of plant pathology. The Australian Pathogen Bioinformatics Symposium is a series of research seminars broadly covering all aspects of bioinformatics and computational biology that derive from or enable plant pathology studies, including but not limited to: software/algorithm development, curation of scientific databases, pathogen genome surveys, comparative genomics, quantitative transcriptomics and proteomics, analysis of effectors and defensins, structural biology, phylogeography and predictive biology. Previous meetings have also been open to and have featured presentations from researchers not directly working in the field of plant pathology, but with interests in other interactions (e.g. animal pathogens, endophytes) with which useful comparisons can be made.

**Convenors:** James Hane Senior Research Fellow Centre for Crop & Disease Management James.Hane@curtin.edu.au (08) 9266 1726

**Plant Pathology in Perennial Cropping Systems**

Date: 25th November 2019 – full day  
Time: 9:30 – 16:30  
Location: Old Arts 156, University of Melbourne Parkville  
Cost: $100

**Summary:** This symposium provides a collaborative platform for in-depth discussions on the current trends, experimental design, methodologies & challenges facing plant pathologists working with perennial crops. All presentations will provide key information on ‘how to’ and demonstrate successful outcomes. The symposium includes focused sessions on disease cycle & epidemiology; diagnostics of new or unknown diseases;
host and pesticide resistance; applications of digital
technology in disease control.

Participants are encouraged to make oral or poster
presentations. Those who wish to be selected for oral
presentation are encouraged to submit an abstract (100
words) to the convenor at the latest by 30 September
2019.

Convenors: Associate Professor Femi Akinsanmi - The
University of Queensland, Centre for Horticultural
Science; o.akinsanmi@uq.edu.au

Grapevine viruses: identification, symptoms
and management

Date: 25th November 2019 – full day
Time: 9:00 – 17:00
Location: Agriculture Victoria Attwood
Cost: $100

Summary: The one day workshop will comprise
presentations and discussion by researchers, viticulturists
and biosecurity practitioners. The aim is to gain and
promote understanding of the viruses of grapevines in
Australasia. Key objectives include promoting awareness
on: methods used for virus detection; symptoms with
which they are associated; effective management
method; and effective communication with the
viticultural community on virus management.

Outcomes of the workshop are increased knowledge
and capability in Australia and New Zealand, more
effective application of science research to in-vineyard
management and improved future interactions
on potential projects. Topics within the workshop
include: impacts of viruses; virus and vector detection;
surveillance and biosecurity; and communication of virus
management (relevant for those in the board room,
nursery, vineyard, and laboratory)

Convenors: Sophie Badland (Sophie.Badland@nzwine.
com), Inca Pearce (inca@vinehealth.com.au), Sharon
Harvey (sharon.harvey@wineaustralia.com), Fiona
Constable (Fiona.Constable@ecodev.vic.gov.au), Will
Kerner (Will.Kerner@bri.co.nz), Karmun Chooi Karmun
(Chooi@plantandfood.co.nz), Robin MacDiarmid (Robin.
MacDiarmid@plantandfood.co.nz), Lisa Ward (Lisa.
Ward@mpi.govt.nz)

Fusarium biosecurity RD&E workshop

Date: 25th November 2019 – full day
Time: 9:00 – 17:00
Location: Old Arts 129, University of Melbourne
Parkville
Cost: $20

Plant Health Australia is supporting this Workshop by
subsidising some of the cost for delegates participating.
Please note that the subsidised amount has already been
reduced from the cost.

Summary: Fusarium is a genus with many pathogenic
species affecting numerous different plant hosts,
including agricultural crops. With diseases such as
soybean sudden death syndrome, pitch pine canker
and Panama disease of banana, Fusarium is of plant
biosecurity concern.

Due to the large host range of the genus, all of the
plant Rural Research and Development Corporations
represent crops affected by Fusarium. Because of this,
there is much investment in crop specific RD&E. This
workshop aims to bring together researchers and
research funders to discuss the current Fusarium research
occurring in Australia and where synergies could be
made. The workshop will also highlight capacity, platform
technology opportunities and research gaps than need
to be filled and potential future directions of RD&E
on the genus. The workshop is being run on behalf
of the National Plant Biosecurity RD&E Strategy and
recommendations will be taken to government and to
research funders.

Convenors: Dr Edward Liew, Manager Plant Pathology,
Science and Conservation, Senior Research Scientist,
Botanic Gardens & Centennial Parklands, Sydney; Dr
Victoria Ludowici, Biosecurity Planning Coordinator,
Plant Health Australia, Canberra; Dr Rod Turner, General
Manager Preparedness and RD&E, Plant Health Australia,
Canberra; Dr Brett Summerell, Director, Research and
Chief Botanist, Botanic Gardens & Centennial Parklands,
Sydney
Innovations in tools and approaches for effective and durable biocontrol

Date: 25th November 2019
Time: 9:00-13:00
Location: Old Arts 124, University of Melbourne Parkville
Cost: $ 75

Summary: Management options for many crop diseases are limited due to the lack of host resistance, ineffective and/or harmful chemical controls, or persistence of the pathogens in crop residues. The loss of some chemical controls owing to increasing regulation or increased incidence of resistance in pathogen or pest populations due to chemical overuse necessitates the need for alternate or auxiliary controls.

Green agribiologicals such as biocontrols and biologics (the bioactive compounds) are of increasing interest, with the caveat that these microbes/compounds need to be competitive against or at least comparable to chemical alternatives. The effectiveness and durability of biocontrols and biologics are key factors to their commercial delivery/success and end-user uptake.

This workshop aims to bring together fresh ideas in the biocontrol space including new tools and approaches for both investigation and delivery of biocontrol solutions for effective disease management, and to support a new and growing molecular-informatics biocontrol community. The workshop delivery format will be two keynote speakers followed by a series of lightning talks with preference for early career scientists.

Keynote speakers:
Marc Bardin, Director Plant Pathology research unit, INRA, PACA, France
Scott Paton, Research and Development, Nufarm Australia

Convenors: Dr Louise Thatcher, Senior Research Scientist, CSIRO, Agriculture and Food, Floreat, WA; Dr Katherine Zulak, Research Fellow, Centre for Crop and Disease Management, Curtin University, School of Molecular and Life Sciences, Kent Street, Bentley, Perth, WA.

Colletotrichum taxonomy and impact on Biosecurity

Date: 25th November 2019
Time: 13:30 – 17:00
Location: Old Arts 124, University of Melbourne Parkville
Cost: $ 75

Summary: Colletotrichum is a genus of major plant pathogens causing anthracnose diseases in many plant crops worldwide. The genus comprises a highly diverse group of pathogens that infect a wide range of plant hosts. This workshop will provide a series of papers on the latest taxonomy of Colletotrichum and discuss the implications for plant biosecurity and integrated disease management. There will be a focus on the Colletotrichum species causing anthracnose in a range of crops in Asia and Australasia. Of particular interest will be how the taxonomy of Colletotrichum pathogens influences risk management decisions in trade and border protection.

Convenors: Prof Paul Taylor, Faculty of Veterinary and Agricultural Sciences, The University of Melbourne.

Reproducible Reports and Research Using R

Date: 25th November 2019 – half day
Time: 13:30 – 16:30
Location: Old Arts 204, University of Melbourne Parkville
Cost: $75

Summary: As scientists, we often read about or hear about reproducible research, but we may not be sure where to start or how we can make our research reproducible. Sharing code, scripts and data that make up your analysis with others such that they are able to easily reproduce your results can make it easy to obtain feedback and improve the quality of your work.

There are an overwhelming number of modern approaches, and online platforms, which can be used to make research reproducible. This workshop will introduce participants to ways that R and related tools, such as RMarkdown, can be used in creating reproducible research outputs. These outputs could be internal reports that are generated at the click of a button and each time the data are updated; detailed research compendia to supplement your latest research manuscript sharing the code, data and analysis; or even the research manuscript itself! This workshop will help
you improve your workflow in RStudio by using projects and keyboard shortcuts; managing figures and tables, which dynamically update; managing references and in-text citations; creating bibliographies and modifying bibliography styles. Participants will gain hands-on experience generating Microsoft Word, PDF, Markdown and HTML document outputs and become familiar using RMarkdown for reproducible research. Basic familiarity with R and RStudio is required.

**Convenors:** Dr Adam H Sparks, Associate Professor, University of Southern Queensland, Toowoomba, Qld; Dr Nicholas Tierney, Research Fellow, Monash University, Melbourne, Vic; Dr Paul Melloy, Research Fellow, University of Southern Queensland, Toowoomba, Qld; Dr Nirodha Weeraratne, Postdoctoral Research Fellow, University of Southern Queensland, Toowoomba, Qld.

---

**How to Be Your Own Best Mentor**

**Date:** 29th November 2019 – half day

**Time:** 9:30 -13:00

**Location:** Louis Pasteur, AgriBio, La Trobe University, 5 Ring Rd, Bundoora, Melbourne

**Cost:** $75

**Summary:** The “own best mentor” workshop is targeted at students, postdocs and early career faculty, though well-established faculty have also benefited from the workshop. It is a three-hour interactive workshop with introspective work, breakout sessions and group discussions. In the workshop we will discuss how to define and then teach yourself the knowledge and skills you need to be successful in your career. Each participant should bring writing tools (paper and pencil), their agenda (the tool used to keep your to do list), an open mind and willingness to participate.

The workshop is divided into three parts:

- **Part 1:** Define the skills on which you are evaluated.
- **Part 2:** Make an honest self-evaluation of yourself and learn to make time to benchmark.
- **Part 3:** Define ways to get the skills or demonstrate the skills that you have defined as weak.

**Convenor:** Carolee T. Bull, Professor and Head, Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University

---

**Molecular-Plant microbe interactions session - joint with Australian Society of Plant Scientists at AgriBio**

**Date:** 29th November 2019 – half day

**Time:** 9:00 – 12:00

**Location:** Szental Lecture Theatre La Trobe University, Bundoora, Melbourne

**Convenors:** Associate Professor Kim Plummer, La Trobe University, Melbourne, Vic (in collaboration with ASPS session organisers, Prof Peter Solomon, ANU, and Prof Marilyn Anderson, LTU).

**Cost:** $75 (or $100 as a bundle with the dsRNA applications for disease control afternoon workshop session)

**Summary:** Molecular-Plant microbe interactions session - joint session with ASPS at AgriBio. https://www.asps.org.au/combio/asps-2019

**Special guest presenters:** Dr Simon Williams ANU; Dr Carl Mesarich Massey Uni, NZ

**Molecular-Plant microbe interactions session - joint with Australian Society of Plant Scientists at AgriBio**

**Date:** 29th November 2019 – half day

**Time:** 9:00 – 12:00

**Location:** Szental Lecture Theatre La Trobe University, Bundoora, Melbourne

**Convenors:** Associate Professor Kim Plummer, La Trobe University, Melbourne, Vic (in collaboration with ASPS session organisers, Prof Peter Solomon, ANU, and Prof Marilyn Anderson, LTU).

**Cost:** $75 (or $100 as a bundle with the ASPS morning workshop session)

**Summary:** Recent breakthroughs that have led to increased understanding of the involvement of dsRNA in plant-microbe interactions have led to the development of multiple technologies that rely on gene silencing to achieve pathogen control. This workshop will bring together researchers with an interest in developing these technologies for plant protection.

**Special guest presenters:** Prof. Hailing Jin, University California Riverside; Prof. Neena Mitter QAAFI, The University of Queensland; Prof. Jennifer Ann Harikrishna and Prof Rofina Yasmin Othman, Institute of Biological Sciences, Faculty of Science, University of Malaya.

**Convenor:** Associate Professor Kim Plummer, La Trobe University, Melbourne, Vic.
Flooded with natural light, this space can be tailored to a range of events from dinners to exhibitions. It can be used for daily catering, pre-dinner drinks or as a space for registration desks and exhibition booths.

Your guests will have a seamless event experience, with direct access to the five-star Pan Pacific Melbourne via a private internal walkway.

MEETING SPACES
Available in small, medium and large, our spacious meeting rooms are ideal for business meetings, boardroom functions, seminars or dinners. If you’d like to utilise more space for registration or catering purposes, the outside foyer is available for use, as well as adjacent rooms that can be seamlessly connected to create even more room for your guests.

### CAPACITIES FLOOR AREA DIMENSIONS

<table>
<thead>
<tr>
<th>DESCRIPTION</th>
<th>THEATRE CLASS</th>
<th>ROOM</th>
<th>COCKTAIL</th>
<th>BANQUET</th>
<th>CABARET</th>
<th>BOARD</th>
<th>MEETING SPACES</th>
</tr>
</thead>
<tbody>
<tr>
<td>ROOM AREA</td>
<td>(M²)</td>
<td>(FT²)</td>
<td>(M)</td>
<td>(M)</td>
<td>(M)</td>
<td>(M)</td>
<td>(M)</td>
</tr>
<tr>
<td>LENGTH</td>
<td>WIDTH</td>
<td>HEIGHT</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>101 Small</td>
<td>70</td>
<td>27</td>
<td>60</td>
<td>30</td>
<td>24</td>
<td>18</td>
<td>21</td>
</tr>
<tr>
<td>102 Small</td>
<td>70</td>
<td>27</td>
<td>60</td>
<td>30</td>
<td>24</td>
<td>18</td>
<td>21</td>
</tr>
<tr>
<td>103 Medium</td>
<td>132</td>
<td>63</td>
<td>116</td>
<td>60</td>
<td>48</td>
<td>36</td>
<td>36</td>
</tr>
<tr>
<td>104 Medium</td>
<td>132</td>
<td>63</td>
<td>116</td>
<td>60</td>
<td>48</td>
<td>36</td>
<td>36</td>
</tr>
<tr>
<td>105 Large</td>
<td>234</td>
<td>96</td>
<td>196</td>
<td>120</td>
<td>96</td>
<td>42</td>
<td>51</td>
</tr>
<tr>
<td>106 Large</td>
<td>234</td>
<td>96</td>
<td>196</td>
<td>120</td>
<td>96</td>
<td>42</td>
<td>51</td>
</tr>
<tr>
<td>107 Small</td>
<td>60</td>
<td>27</td>
<td>63</td>
<td>30</td>
<td>24</td>
<td>20</td>
<td>16</td>
</tr>
<tr>
<td>108 Small</td>
<td>60</td>
<td>27</td>
<td>63</td>
<td>30</td>
<td>24</td>
<td>20</td>
<td>16</td>
</tr>
<tr>
<td>109 Large</td>
<td>234</td>
<td>96</td>
<td>196</td>
<td>120</td>
<td>96</td>
<td>42</td>
<td>51</td>
</tr>
<tr>
<td>110 Large</td>
<td>234</td>
<td>96</td>
<td>196</td>
<td>120</td>
<td>96</td>
<td>42</td>
<td>51</td>
</tr>
<tr>
<td>109 &amp; 110</td>
<td>468</td>
<td>192</td>
<td>394</td>
<td>280</td>
<td>224</td>
<td>-</td>
<td>485</td>
</tr>
<tr>
<td>111 Small</td>
<td>70</td>
<td>27</td>
<td>60</td>
<td>30</td>
<td>24</td>
<td>18</td>
<td>21</td>
</tr>
<tr>
<td>112 Small</td>
<td>70</td>
<td>27</td>
<td>60</td>
<td>30</td>
<td>24</td>
<td>18</td>
<td>21</td>
</tr>
<tr>
<td>111 &amp; 112</td>
<td>140</td>
<td>72</td>
<td>120</td>
<td>70</td>
<td>56</td>
<td>-</td>
<td>147</td>
</tr>
</tbody>
</table>

### MCEC First Floor

- **Link through to Pan Pacific**: A designated entrance point for guests to access the Pan Pacific Melbourne from the MCEC.

- **PLENARY**: The main presentation area for large audiences.
- **BACK OF HOUSE**: Areas behind the scenes where technical and service teams operate.
- **MEETING ROOMS**: Rooms available for small to medium-sized business meetings.
- **ORGANISERS' OFFICES**: Spaces designated for event coordinators and planners.
- **LINK TO PAN PACIFIC**: Access points for guests to move between the MCEC and Pan Pacific.
- **SPEAKER PREPARATION ROOM**: Rooms set aside for speakers to prepare their presentations.
- **WINNERS**: Visual indicators for windows and natural light sources.
### Abstract Review Sub-Committee

<table>
<thead>
<tr>
<th>Member Name</th>
<th>Position</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/Prof Jacqueline Edwards</td>
<td>Chair of Committee</td>
</tr>
<tr>
<td>Dr Angus Carnegie</td>
<td></td>
</tr>
<tr>
<td>Dr Nigel Crump</td>
<td></td>
</tr>
<tr>
<td>Dr Peter Dracatos</td>
<td></td>
</tr>
<tr>
<td>Dr Candace Elliott</td>
<td></td>
</tr>
<tr>
<td>Dr Rebekah Frampton</td>
<td></td>
</tr>
<tr>
<td>Prof Victor Galea</td>
<td></td>
</tr>
<tr>
<td>Dr Cherie Gambley</td>
<td></td>
</tr>
<tr>
<td>Dr Don Gardiner</td>
<td></td>
</tr>
<tr>
<td>Dr Helen Hayden</td>
<td></td>
</tr>
<tr>
<td>Dr Juliane Henderson</td>
<td></td>
</tr>
<tr>
<td>Ms Monica Kehoe</td>
<td></td>
</tr>
<tr>
<td>Dr Alistair McTaggart</td>
<td></td>
</tr>
<tr>
<td>Dr Rachel Mann</td>
<td></td>
</tr>
<tr>
<td>Dr Ross Mann</td>
<td></td>
</tr>
<tr>
<td>Dr Tom May</td>
<td></td>
</tr>
<tr>
<td>Dr Carl Mesarich</td>
<td></td>
</tr>
<tr>
<td>Ms Narelle Nancarrow</td>
<td></td>
</tr>
<tr>
<td>Dr Kirsty Owen</td>
<td></td>
</tr>
<tr>
<td>Prof Robert Park</td>
<td></td>
</tr>
<tr>
<td>Dr Suzy Perry</td>
<td></td>
</tr>
<tr>
<td>Assoc. Prof Kim Plummer</td>
<td></td>
</tr>
<tr>
<td>Dr Tony Reglinski</td>
<td></td>
</tr>
<tr>
<td>Prof Eileen Scott</td>
<td></td>
</tr>
<tr>
<td>Mr Jason Sheedy</td>
<td></td>
</tr>
<tr>
<td>Prof Peter Solomon</td>
<td></td>
</tr>
<tr>
<td>Prof Paul Taylor</td>
<td></td>
</tr>
<tr>
<td>Dr Robert Tegg</td>
<td></td>
</tr>
<tr>
<td>Dr Len Tesoriero</td>
<td></td>
</tr>
<tr>
<td>Dr Louise Thatcher</td>
<td></td>
</tr>
<tr>
<td>Mr Mark Whattam</td>
<td></td>
</tr>
<tr>
<td>Dr Tonya Wiechel</td>
<td></td>
</tr>
</tbody>
</table>
Opening Keynote Address

Ms Lois Ransom
Australian Government Department of Agriculture and Water Resources, Canberra, Australia

The International Plant Protection Convention (IPPC) is an international treaty that aims to prevent the international movement of plant pests. It provides a framework to harmonise regulation and phytosanitary operations to achieve the global safe trade of plants and plant products, as well as the ships, containers and packaging that can carry plant pests around the world. The Commission on Phytosanitary Measures directs the implementation of the Convention by the 183 countries that have signed it. An IPPC Strategic Framework has been developed that will direct global actions for the next 10 years to more rapidly detect and respond to new and emerging pests, facilitate safe trade through harmonisation of measures, build the capacity of countries to implement and benefit from the Convention, direct global plant health research and reduce pests moving with non-regulated goods, with travellers and through e-commerce. The United Nations has proclaimed 2020 as the International Year of Plant Health (IYPH). This global initiative will highlight the importance of plant health to enhance food security, protect the environment and biodiversity, and boost economic development, protect human health and reduce poverty. IYPH 2020 is an opportunity to raise awareness of the fundamental role that plants play in supporting life on earth and the imperative for healthy plants. All countries and regions are mobilising to focus their plant-based industries, regulators, researchers and plant health professional on activities that will achieve this outcome – ideally as a starting point for ongoing investment in people, processes and infrastructure to safeguard and optimise plant health into the future.
Communicating the science of Plant Pathology in a “fake news” world

Dr Brett Summerell
Australian Institution of Botanical Science, Royal Botanic Gardens and Domain Trust, Sydney, Australia

We live in an age where the community is more and more ignorant of the importance of plants to their existence, are less connected with agriculture, horticulture and nature, and are sceptical of scientific findings and suspicious of the intentions of scientists. The impacts of climate change, agreed by 97% of scientists, are dismissed by an influential component of the community and they are fearful of the impacts of modern technologies such as genetically modified organisms and gene editing. All of these factors have the potential to have a significant impact on plant pathology as the diseases that we work on are likely become more common and more impactful as the climate changes. Additionally, the need to feed more and more people as the global population grows will be a pressing concern that is likely to be partially answered by increased effectiveness of disease management that currently limit productivity. The impact of invasive diseases on the environment presents an overwhelming challenge that will inevitably require innovative approaches and developing technologies. Within this context it is critical that we continue to strive to communicate to and engage with the community at large about the importance of our science, the potential it has to answer these challenges and their co-operation in preventing new incursions and problems. In this presentation I will highlight examples of the importance (and frustrations) of communicating our science, discuss the pros and cons of social media engagement, and highlight the benefits that can be gained using examples from my 35 years as a plant pathologist in a public facing scientific organisation.
The edge of tomorrow—Plant health in the 21st century

Prof Sophien Kamoun
The Sainsbury Laboratory, Norwich Research Park, Norwich, United Kingdom.

Infectious plant diseases cause havoc to world agriculture and threaten to slow laudable efforts to launch a second green revolution to meet the food security needs of a booming world population. Filamentous pathogens such as the rice blast fungus, wheat stripe and stem rust, the Irish potato famine pathogen, and many others continue to trigger recurrent epidemics with far reaching consequences. In this talk, I will discuss how it is possible to perform cutting-edge research and significantly advance knowledge on economically important pathosystems, particularly in the post-genomics era. I will focus on the blast fungus Magnaporthe oryzae, a devastating cereal killer that infects the crops wheat, barley and rice, which are staple food for a majority of the world population. I will discuss our personal experience with the appearance in Bangladesh of wheat blast and stress the importance of open-science platforms and crowdsourced community responses in tackling emerging plant diseases. Also, together with several collaborators, we gained an unprecedented level of detail of the molecular interactions that define host-pathogen recognitions by solving the crystal structures of effectors of the blast fungus in complex with plant proteins and reconstructing the evolutionary history of these molecular interactions. Our aim is to build on these discoveries to drive both basic and applied plant pathology. We have started to develop a thorough understanding of the biophysical properties of pathogen effector binding to host proteins and their consequences on pathogenesis and immunity. Such knowledge, along with related mechanistic and evolutionary studies, will guide the retooling of the plant immune system towards resistance to diseases. Ultimately, we will deliver traits and non-transgenic cultivars for breeding disease resistance in crops.
Fungicide resistance characterised across six chemical classes in a Botrytis cinerea population from Australian vineyards

Mr Lincoln Harper¹, Curtin University Barbara Hall², Mrs Suzanne McKay¹, Mr Scott Paton¹, Mr Richard Oliver¹, Mr Francisco Lopez-Ruiz¹
¹Curtin University, Perth, Australia, ²SARDI, Adelaide, Australia, ³Nufarm, Kwinana Beach, Australia

Botrytis cinerea, the causative agent of Botrytis bunch rot, is one of the most economically significant diseases of grapevines worldwide. The use of fungicides to control B. cinerea is an integral part of disease management in grapevines. Fungicide resistance in B. cinerea for all current single-site fungicides is geographically widespread. In Australia, little is known about the fungicide sensitivity status of B. cinerea populations. In this study, 735 B. cinerea isolates were collected during the 2013 – 2016 growing seasons from vineyards across Western Australia, South Australia, Victoria, Tasmania, New South Wales and Queensland. A subset (n = 53) of these isolates were tested against six fungicides from different single-site mode of actions (azoxystrobin, boscalid, fenhexamid, iprodione, pyrimethanil and tebuconazole). From this subset, EC50 values were established and the genotype of target site genes (Cytb, SdhB, Erg27, Bos1, Pos5 and Cyp51) was determined by Sanger sequencing. Analysis of target site genes revealed several different mutations associated with fungicide resistance for all modes of action. All the mutations found had been previously described except for P357S in Cyp51. Using this data, discriminatory doses for the six fungicides were established and used to screen the remaining population. Overall, resistance frequencies for azoxystrobin, boscalid, fenhexamid, iprodione, pyrimethanil and tebuconazole ranged from 0.4 – 11.7%. Resistance was identified across a combination of five out of the six fungicides tested in the states of WA, SA, VIC and NSW, and for two fungicides (boscalid, iprodione) in Tasmania. No resistance was found in Queensland. An in-field diagnostic method using a loop-mediated isothermal amplification (LAMP) system has been developed for the rapid monitoring of iprodione resistance. These results have provided valuable information on the resistance status of B. cinerea in Australian vineyards, and could assist in improving resistance management strategies.

Microfluidic lab-on-chip for high-throughput fungicide screening against Alternaria spp

Dr Sehrish Iftikhar¹, Dr Aurélie Vigne¹, Dr Julia Sepulveda¹, Dr Guilhem Velvé Casquillas¹
¹Elvesys — Microfluidics innovation center, 83 Avenue Philippe-Auguste 75011, Paris, France

Fungicide development and screening is stuck in an innovation gap, in which it incurs staggering expenses and takes many years to get a fungicide to market. The conventional agar plates and high-density well plates techniques are time consuming and laborious. The present proposal is conceptualized to bridge the gap for high throughput (HT) screening of fungicides effectively, by designing the novel lab-on-chip device. Surveys were carried out to collect infected samples from potato-growing regions of France. The lesions were cut off from infected samples, disinfected and placed on potato dextrose agar medium at 22°C. The obtained isolates were purified by monospore culture. The lab-on-chip device consisted of two layers: a polydimethylsiloxane (PDMS) layer and a glass cover slip. The PDMS layer was fabricated using soft lithography of a master mold created with a 120 μm-thick layer of SU-8 photoresist. The glass cover slip was cleaned with nitrogen gas and coated with positive photoresist primer S1813 for 60 sec and soft baked at 95°C for 1 min. For the individual conidial seeding of Alternaria alternata, conidia were encapsulated in the droplets. Potato dextrose broth (PDB) was also seeded as nutrient medium. On-chip fungicide screening assay was carried out by injecting the fungicide with desired concentration and mixing with the PDB in mixing chamber. The mixture was then introduced to encapsulated conidia. When all the channels were filled, the microfluidic platforms were incubated at 25±1°C and stimulation was started. The relative germination of conidia and sensitivity were evaluated. We have established a simple microfluidic lab-on-chip to perform HT fungicide screening into droplets which creates a uniquely accurate method for observing the biological responses.
**Powdery mildew and fungicide resistance: evaluation of in-vivo and in-planta bioassays**

**Dr Ismail Ismail**, Dr Suzanne McKay, Mrs Barbara Hall, Mr Lincoln Harper, Dr Fran Lopez-Ruiz

1South Australian Research and Development Institute, Urrbrae, Australia, 2Centre for Crop and Disease Management, Curtin University, Perth, Australia

Fungicide resistance in *Erysiphe necator*, the cause of powdery mildew of grapevines, is a significant issue for one of the most economically important diseases in Australian vineyards. The Demethylation Inhibitor fungicides (DMIs) are an important component of the powdery mildew management program, however, recent research revealed the presence of Y136F, the mutation associated with resistance, is widespread in Australian vineyards. A laboratory-based test, the heterologous yeast expression system (HYES), was used to better understand the variability among the DMI fungicides when exposed to *E. necator* with Y136F present. HYES results showed that the resistance factors (RF) varied from 1 (most effective) to 7.5 (least effective) for the six DMI fungicides. To validate these results *in-planta*, detached leaf and potted plant bio-assays were carried out. Plant material was sprayed with the various fungicides at either 1/10 or 1/100 label rate, and inoculated before or after application with spore suspensions of *E. necator* containing varying ratios of wild type:Y136F. The most consistent results with the best relationship to the laboratory HYES tests were achieved with 1/10 label rate applied before inoculation, with the lowest disease severity (0%) with difenoconazole with a RF of 1 and the highest (57%) with triadimenol with a RF of 7.5. Detached leaf assays enabled a higher level of replication, however the leaf tissue did not always survive for the length of the test and also greater variability was observed. The bioassays using small potted vines resulted in greater consistency than the detached leaf bio-assays, however the number of replicates was lower due to space requirements and it was often difficult to obtain enough inoculum for good levels of infection. Several techniques have been trialled and work is continuing to develop a more effective *in-planta* test system using small plants in closed containers.

**Meta-analysis of fungicide application trials for the management of powdery mildew in mungbean**

**Dr Paul Melloy**, Assoc Prof Emerson Del Ponte, Mr Charles Gray, Assoc Prof Adam Sparks

1University Of Southern Queensland, Toowoomba, Australia, 2Universidade Federal de Viçosa, Viçosa, Brazil, 3La Trobe University, Melbourne, Australia

Current commercially available mungbean varieties lack adequate powdery mildew (*Podosphaera xanthii*) resistance to protect crop yields in the presence of high disease pressure. Growers therefore manage severe epidemics by applying fungicide and sowing early in the growing season to avoid the cooler temperatures, which are associated with powdery mildew infestations. Since 2001 twenty-four field trials have assessed the timing and frequency of fungicide application on powdery mildew disease incidence and mungbean yield in the northern grains region. Results from these trials have advised the best practice for managing the disease is through a fungicide application at first sign of disease followed by a second spray two weeks later if necessary. However, the outcomes of these trials have occasionally lacked certainty when analysed in isolation. This meta-analysis aims to use the combined power of multiple studies to increase certainty for the ideal fungicide spray window for minimising yield loss due to powdery mildew and maximise disease control. This meta-analysis also associates environmental variables to the first sighting of disease that can be used to inform agronomists and growers when to begin scouting their crop for the first signs of powdery mildew. The outcomes of this research can be used to refine decision support system tools like PowderyMildewMBM to boost accuracy and add functionality such as disease alerts.
Evaluating effects of acibenzolar-S-methyl in *Actinidia chinensis var. chinensis* ‘Zesy002’ kiwifruit

**Dr Tony Reglinski**, Dr Janine Cooney¹, Dr Tony McGhie¹, Dr Daryl Rowan¹, Ms Helen Boldingh¹, Dr Joel Vanneste¹, Ms Trisha Pereira¹, Mr Joseph Taylor¹

¹The New Zealand Institute For Plant & Food Research, Hamilton, New Zealand

Actigard® (acibenzolar-S-methyl [ASM], Syngenta) is used to control bacterial canker in *Actinidia chinensis* var. *chinensis* ‘Zesy002’ kiwifruit caused by *Pseudomonas syringae pv. actinidiae* (Psa biovar 3). ASM operates as a functional mimic of salicylic acid (SA) by activating SA-mediated defences and so enhancing the resistance response to pathogen attack. In potted kiwifruit plants, spray application of ASM, 14 days before inoculation with Psa, resulted in an enhanced resistance against both leaf and stem necrosis. ASM was effective across a broad concentration range (0.02 to 0.6 g/L) and exhibited a dose-dependent efficacy. ASM was equally effective against Psa when applied as a root drench or a foliar spray. Repeat sprays with ASM at 7, 14 and 21 days before inoculation with Psa resulted in growth retardation that was consistent with there being a trade-off between growth and defence. Phytohormones play a central role in regulation of plant defence and growth. The concentration of SA in leaf tissue was lower in ASM-treated leaves than in controls, whereas concentrations of salicylic acid glycoside (SAG), abscisic acid (ABA), and jasmonic acid (JA) depended upon leaf maturity and were not affected by ASM. Secondary metabolite profiles were affected by ASM, with several molecular features that differed between ASM-treated and control leaves in potted plants. Phytohormonal and metabolic responses identified under controlled conditions were not replicated in the orchard trials. However, the defence genes, PR1 and β-1,3-glucosidase, were upregulated in ASM-treated vines and are promising markers of induced resistance in the orchard. Fruit growth in ASM-treated vines tended to lag behind that of control vines but average fruit weights were not significantly different at harvest. Studies are ongoing to investigate potential cumulative effects of elicitor treatment.

Digital PCR improves detection and quantification of fungicide resistance in *Blumeria graminis* f. sp. *hordei*

**Dr Katherine G. Zulak**, Ms Belinda A. Cox, Dr Madeline A. Tucker, Prof Richard P. Oliver¹, Dr Francisco J. Lopez-Ruiz¹

¹Centre for Crop and Disease Management (CCDM), School of Molecular and Life Sciences, Curtin University, Bentley, Australia

Fungicide resistance has become a global issue in both clinics and in agriculture. Demethylase inhibitor (DMI) fungicides are extensively used to treat both human and plant fungal pathogens and thus resistance has become particularly problematic for this group of fungicides. In Western Australia in particular, DMI resistance of barley powdery mildew (Bgh; *Blumeria graminis* f. sp. *hordei*) has reached epidemic proportions, replacing wild type sensitive strains in only four seasons, and resulting in significant yield losses due to field control failure. DMI resistance is caused primarily by two point mutations in the target gene Cyp51. The first mutation (Y136F) leads to only a small shift in DMI sensitivity, however the second mutation (S509T) results in a large sensitivity shift with fungicide tebuconazole being the most compromised. In order to prevent the rapid spread of resistance, early detection and rapid accurate quantification is required so that spray regimes can be adjusted. To address this challenge, we have developed a digital PCR (dPCR) assay to detect and quantify these mutations in field samples of Bgh-infected barley as low as 0.2% in both genomic DNA and field samples. Combining our dPCR assay with a network of baiting trials across the country, we detected and quantified DMI-resistant Bgh in the Eastern states of Australia for the first time. This illustrates the power of an early warning system for the management of fungicide resistance.
Crop disease information and support at your fingertips

Mrs Kellyanne Harris^1
^1Agriculture Victoria, Bendigo, Australia

Despite living in the age of information, having so much to do and so little time presents new challenges every day. This presentation will demonstrate a number of initiatives aimed at helping growers and agronomists to report pests and diseases as well as providing them access up-to-date and trusted information on emerging crop disease issues during the season to assist with making informed decision making and provide trusted information to clients. The presentation will highlight the importance of early detection of exotic pests and diseases and provide agronomists with avenues to submit surveillance easily whilst in the field as well as being able to connect with crop disease experts. The presentation will focus on the following initiatives, which are supported by Agriculture Victoria, NSW DPI and the GRDC. GRDC Communities - Field Crop Diseases is comprised of crop disease experts from across the country, which deliver timely information about emerging crop disease issues and how best to combat them. Information is provided in real time, by webinar, Twitter, Facebook, Podcast and website. An Ask an Expert functionality enables agronomists and growers to ask a question of our national teams of experts at any time. GRDC GrowNotes™ Alert is a free system that delivers relevant warnings direct to mobile phones and email providing an increased level of awareness that can help growers protect their crops and maximise yield. GRDC GrowNotes™ Alert system is two-way, allowing growers and industry to upload photos on the spot, and feed relevant and immediate information back to our extensive range of pest and disease experts. CropSafe is Victoria’s ‘eyes in the field’ surveillance program to increase the identification and reporting of plant pests and diseases by agronomists. CropSafe is delivered in collaboration with a number of major agribusiness companies and a network of private providers across Victoria.

Indigenous responses to native plant species impacted on by the arrival of new diseases

Mr Alby Marsh^1, Dr Nick Waipara^2, Mr Hone Ropata^2
^1Plant and Food Research, New Zealand, Palmerston North, New Zealand, ^2Plant and Food Research, New Zealand, Mt Albert, New Zealand

Myrtle rust, caused by the pathogen Austropuccinia psidii is a recent arrival to New Zealand and is one disease impacting on indigenous species around the Pacific. Originally from Central and South America (Glen et al. 2007), it has been moving steadily around the world infecting Hawaii in April 2005, Australia and New Caledonia in 2016 and New Zealand in May 2017. In New Zealand, Myrtle rust infects tree species that the indigenous Māori peoples consider important cultural treasures (Ropata 2017). New Zealand myrtaceae have many traditional Māori uses ranging from medicine, construction and food, having significant cultural value (Teulon et al. 2016). Māori now consider these plants taonga (treasured entities). Taonga include tangible things such as land, waters, plants, wildlife and cultural works, and intangible things such as language, identity and culture, including Mātauranga Māori (Traditional Māori knowledge). Indigenous worldviews and concerns around the impacts of myrtle rust are currently underrepresented in literature. Apart from a short paragraph on the threat to Hawai‘ian indigenous culture Loope (2010), there is no other literature citations on the impact of P. psidii to Australian Aboriginal or other Pacific Island communities and culture. This work is important to both the indigenous and scientific communities interested in learning from one another through the sharing of knowledge, both traditional and modern.
Participatory development of a transport risk model for the movement of bulk citrus among state interior HLB quarantine zones in California

Dr Neil McRoberts¹, Sara Garcia Figuera¹
¹University Of California, Davis, Davis, United States

To slow the spread of citrus huanglongbing (HLB), the California citrus industry has taken several actions in collaboration with state and federal regulatory agencies. Experience of the disease in Florida showed that bacteriliferous psyllids can be moved with bulk fruit loads on trailers; transportation corridors can thus be a pathway for HLB dispersal. Because of this, California was divided into seven regional quarantine zones, making use of natural topographical barriers to psyllid dispersal where possible. Movement of bulk citrus between any two zones is prohibited unless it complies with uniform risk mitigation requirements. Since the quarantine regulation was implemented in January 2018, some actors within the citrus industry have asked for more flexible mitigation requirements and an evidence-based assessment of risk. To address this request, we developed a model using a participatory research approach and based on the international framework for plant pest risk analysis. It provides a qualitative estimation of the risk. Risk factors are assigned an ordinal qualitative rating through expert opinion and available data. The model is built as a tree in which the combination of ratings for risk factors on each node of the tree is computed using the software DEXi, generating a risk matrix with zones of origin (harvest) as columns and zones of destination (packing) as rows. Individual members of a working group comprising growers, scientists and regulatory officials built their own risk models in a process facilitated by us. The group then used facilitated discussion to reach consensus on a single unified risk model. At the end of the process they were shown the estimated risk levels for fruit transport for every model, including the consensus. The model was accepted as the approved framework for future discussions by the joint industry/regulatory agency working group to review any proposed changes to quarantine regulations.

Diagnostic and surveillance networking is key to biosecurity success

Dr Natalie O’Donnell¹, Dr Sharyn Taylor¹, Dr Stephen Dibley¹
¹Plant Health Australia, Deakin, Australia

Australia has a long-established biosecurity system that has kept Australia free from many pests and diseases that have significant agricultural, environmental and economic impacts on other countries. Changes in agricultural practices, trade and people movement mean the Australian biosecurity system must evolve to remain current. People, infrastructure, standards and tools to deliver plant biosecurity surveillance and diagnostic services now and into the future are all crucial to the system. The National Plant Biosecurity Diagnostic Network (NPBDN) and Plant Surveillance Network Australasia Pacific (PSNAP) were established in 2010 and 2019, respectively, to promote and improve connections between practitioners and improve Australia’s biosecurity capability. These networks aim to: 1) improve technical skills – build capacity and capability amongst the plant pest surveillance and diagnostic communities; 2) facilitate connections – create linkages between individuals and those requiring use of the services, technology and information; and 3) share knowledge and experiences – sharing tools and resources developed across the networks that will assist increase efficiency and consistency of outcomes. The networks connect people who are integral to the plant biosecurity diagnostic and surveillance systems across Australia, New Zealand and neighbouring countries. Members of these networks come together regularly at the Annual Diagnosticians’ Workshop and Annual Surveillance Workshop, to build connections, initiate projects, share knowledge and experiences, together with undertaking professional development workshops on core skills to support their work. This paper will present information on opportunities and activities for NPBDN members to engage in identification workshops, spend time in other laboratories or programs through Diagnostic Residentials, and verify their diagnostic skills through the proficiency testing program. Similar activities are expected to be delivered through PSNAP in the coming years.
An indigenous response to the management of myrtle rust (Austropuccinia psidii) threatening susceptible taonga (treasured) Myrtaceae plants in New Zealand

Amanda Black\(^1\), Alby Marsh\(^1\), Waitangi Wood\(^1\), Melanie Mark-Shadbolt\(^1\), Tame Malcolm\(^1\), Hone Ropata\(^1\), Nick Waipara\(^1\)

\(^1\)Te Tira Whakamātaki (Maori Biosecurity Network), New Zealand

The incursion of the myrtle rust disease (Austropuccinia psidii) was officially confirmed on 3 May 2017 at a plant nursery located in Kerikeri, North Island, New Zealand. Since then the presence of myrtle rust has now been detected throughout New Zealand. It has been detected on a range of exotic and native endemic Myrtaceae species including: ramarama (Lophomyrtus bullata), pohutukawa (Metrosideros excelsa), manuka (Leptospermum scoparium), crimson rata (Metrosideros carmine) and swamp maire (Syzygium maire). Many of these species are iconic to the Indigenous Māori and have historical significance, being taonga (treasures). Since the incursions, Te Tira Whakamātaki (National Māori Biosecurity Network), have been engaging and informing Māori communities throughout New Zealand about the potential impacts of myrtle rust via a series of regional meetings (hui), training workshops (wānanga), social media as well as undertaking research related to the cultural and other impacts of myrtle rust on Māori communities. Feedback from these meetings and social media has strongly highlighted the desires of Māori communities to be active participants in decision-making and response plans for the management of myrtle rust as well as other pests and diseases. Recognition of the many traditional and contemporary approaches to help protect and conserve the many vulnerable taonga myrtle plants was also highlighted. In this presentation, we describe the journey of an Indigenous community approach to a modern biosecurity incursion and how indigenous knowledge and practices have also been proposed to enhance and improve the long term management of the disease in New Zealand.

Indigenous approaches in forest management and biosecurity in response to kauri dieback (Phytophthora agathicidicida) in Aotearoa New Zealand

Dr Nick Waipara\(^1\), Dr Amanda Black\(^1\)

\(^1\)Te Tira Whakamātaki (Maori Biosecurity Network), New Zealand

In Aotearoa New Zealand, Māori have had an increasingly important leadership and role in environmental management, including protection of our taonga (treasured) biological heritage from biosecurity risks and threats from incursions of pests and diseases. The need for indigenous led approaches to biosecurity and forest conservation, has become critical to ensuring the long-term health and resilience of many taonga species and forest ecosystems such as those found in New Zealand’s kauri forests. Kauri (Agathis australis) are an ancient tree rākau now reduced to a fragment of their pre-colonial habitat and threatened with extinction from an introduced virulent plant pathogen (Phytophthora agathicidicida) known as kauri dieback. In 2007 kauri dieback was declared a pest of national priority (an ‘Unwanted Organism’) after it was discovered to be infected areas of kauri forest including many stands within the Waitākere forest. In 2008, a conventional disease management programme was implemented to mitigate the spread and impacts of the disease. However by 2016, it was determined these biosecurity measures were failing to arrest the accelerating spread of the pathogen and a projection of localised extinctions of kauri being predicted within many kauri stands such as Te Waonui a Tiriwa – Waitākere ngahere, the Waitākere kauri ecosystem. The Waitākere forest is the spiritual heartland of mana whenua iwi (tribe) Te Kawerau a Maki. In 2017 in response Te Kawerau a Maki placed a rāhui over their kauri ngahere to lead and manage a forest in crisis and stop the ongoing human assisted spread of the disease. This leadership by mana whenua was supported by West Auckland community and conservation groups and resulted in local agencies formally closing public kauri reserves in many other regions of New Zealand. This paper will outline the critical role of mātauranga (knowledge) and kaupapa Māori approaches specifically rāhui is essential to save and protect kauri for all in Aotearoa.
Mating types of *Teratosphaeria* leaf and stem pathogens of plantation-grown *Eucalyptus*

**Dr Janneke Aylward**1,2, Ms Minette Havenga1,2, Prof Brenda Wingfield1, Prof Francois Roets2, Prof Leanne Dreyer3, Prof Michael Wingfield1

1Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Hatfield, South Africa, 2Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa, 3Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa

The asexual states of the important *Eucalyptus* pathogens *Teratosphaeria destructans*, *T. gauchensis* and *T. zuluensis*, are commonly observed in diseased *Eucalyptus* plantations but their sexual states have never been seen. All three species are believed to have been introduced into these environments with infected host germplasm where they damage non-native *Eucalyptus* spp. in plantations. Population genetic diversity appears to be low to moderate for all three species and some studies have suggested that recombination may be occurring. The aim of this study was to characterise the mating type (MAT) loci of *T. destructans*, *T. gauchensis* and *T. zuluensis* using their whole genome sequences and to evaluate the presence of mating types in diseased plantations. Only the MAT1-1 or MAT1-2 idiomorph were found in individual genomes of the three species. They, consequently, have a heterothallic (out-crossing) mating system. The idiomorph sequences of the three species were subsequently used to develop degenerate primer sets that amplify conserved regions of the MAT1-1-1 and MAT1-2-1 genes, and therefore identify mating type. With only one exception in the case of *T. destructans* in South Africa where only MAT1-2 isolates were identified, both mating types occurred in the studied populations. Where opposite idiomorphs of *T. destructans* and *T. zuluensis*, co-occurred, one mating type was dominant. Such skewed mating type ratios would limit the potential for recombination in these species. In contrast, for two populations of *T. gauchensis*, mating types occurred in similar proportions. The genetic and genotypic diversity of *T. gauchensis* was however, lower than in the other species and the even mating type ratio may be a result of multiple introductions of both mating types. Overall, recombination does not appear to play a prominent role in the life cycle of these important *Eucalyptus* pathogens.

Evidence for transmission of *Cercospora beticola* on table beet seed

**Dr Noel Knight**1, Miss Lori Koenick1, Dr Sandeep Sharma1, Dr Sarah Pethybridge1

1Cornell AgriTech, Geneva, USA

*Cercospora beticola* is an important pathogen of table beet (*Beta vulgaris* subsp. *vulgaris*), causing Cercospora leaf spot. Inoculum sources include contaminated plant debris and alternative hosts however, seed contamination has been suggested in studies examining *C. beticola* population genetics in New York. A *C. beticola*-specific quantitative PCR assay was used to assess the presence of pathogen DNA in 12 table beet seed lots, with DNA of *C. beticola* detected in four seed lots. Agar plate tests and BIO-PCR confirmed the viability of the pathogen however, competitive growth of other microbes and low incidence of infested seed limited the frequency and sensitivity of detection. Further investigation of *C. beticola*-infested seed lots indicated the ability of seedborne *C. beticola* to cause Cercospora leaf spot on plants grown from infested seed. Detection of viable inoculum on table beet seed demonstrates the potential for pathogen dispersal and disease initiation via infested seed, and provides valuable insight into the epidemiology of Cercospora leaf spot.
Atypical sexual reproduction of *Colletotrichum tanaceti*

**Ms Ruvini Lelwala**, Dr Pasi Korhonen*, Dr Neil Young*, Dr Jason Scott*, Dr Peter Ades*, Prof Robin Gasser*, Prof Paul Taylor*

*1University of Melbourne, Parkville, Australia, 2Tasmanian Institute of Agriculture, Burnie, Australia*

*Colletotrichum* is an ascomycete fungal genus with a complex sexual reproduction strategy. *Colletotrichum tanaceti* is a foliar fungal pathogen of the commercially cultivated pyrethrum (*Tanacetum cinerariifolium*) in Australia. Although *C. tanaceti* has a known sexual stage, the molecular basis of sexual reproduction in *C. tanaceti* is unknown. Classical mating experiments confirmed the self-sterility of *C. tanaceti* and revealed that the mating strategy of this species departed from a typical unilocus bi-allelic system, by having more than two mating specificities. A second locus determining fertility, potentially polygenic was hypothesized to regulate mating in *C. tanaceti* together with the mate recognition locus. The atypical nature of the mating system was further supported by in-silico analyses conducted using the whole genome sequences of sexually compatible strains (BRIP57314 and BRIP57315) of *C. tanaceti*. The mating type MAT locus and homologs of other genes known to be involved in mating in fungi were identified from the genomes of both the sexually compatible strains of *C. tanaceti* contained only the MAT1-2-1 idiomorph. No trace of MAT1-1-1 gene was found, consistent with previous reports on other *Colletotrichum* species. Comparison of the MAT region of *C. tanaceti* with other *Colletotrichum* species revealed the conserved nature of the flanking region and the diverse nature of the idiomorphic region. The homologs of the α-factor pheromone precursor and both of the pheromone receptors were present in both genomes of a sexually compatible cross. Comparative genomics revealed polymorphism in the pheromone precursor duo within different *Colletotrichum* spp. Hence, the pheromone/precursor system which is independent of the MAT1-1-1 is hypothesized to regulate the mate recognition in *Colletotrichum*. Orthology to functionally validate mating genes suggested potential functions of the mating genes in *C. tanaceti*. Future sequencing and reverse genetics studies can be used to validate these hypotheses.

Introduction of a leaf-smut fungus for biological control of the environmental weed wandering trad in Australia

**Dr Louise Morin**, Mr John Lester*, Dr Ben Gooden*

*1CSIRO Health & Biosecurity, Canberra, Australia*

The leaf-smut fungus *Kordyana brasiliensis* (ex. Brazil) was approved for release in Australia in December 2018 for the biological control of the environmental weed wandering trad (*Tradescantia fluminensis*). Wandering trad is a long-lived perennial, prostrate herb that originates from South America. It is most common and invasive in the coastal regions of NSW, Victoria and south-east Queensland. It forms dense mats that smoother vegetation and kill seedlings, leading to a major decrease in species richness and abundance of native plants. A risk analysis based on a series of tests to explore the host-range of the fungus was performed to support the application for release submitted to the relevant authorities. The selection of plant taxa for testing was based on recent molecular phylogenies of the family Commelinaceae, to which wandering trad belongs. Results demonstrated that *K. brasiliensis* is highly host specific. The fungus successfully developed and produced lesions solely on wandering trad. Only five of the taxa tested developed a few small flecks, either water-soaked in appearance or necrotic, following inoculation with *K. brasiliensis*: the native *Aneilema acuminatum*, *Commelina aff. diffusa*, *Pollia macrophylla* and *Pollia crispata*, and the introduced *Tradescantia* sp. (Giant leaf). All other non-target plant taxa did not develop any visible symptoms. Release techniques appropriate for this particular fungus were developed and the fungus was first released in the Dandenong Ranges, Victoria during winter 2019, in partnership with the local community. Our longer-term goal is to release the fungus more broadly across the entire range of wandering trad in Australia, subject to available resources.
Production of fumonisins by *Aspergillus* species in Australian vineyards

**Mrs Dilhani Perera**1,2, Dr Paul Prenzler2, Dr Sandra Savocchia1,2, Dr Christopher Steel1,2

1National Wine and Grape Industry Centre, Wagga Wagga, Australia, 2School of Agriculture and Wine Sciences, Charles Sturt University, Wagga Wagga, Australia

Fumonisins are a group of carcinogenic compounds primarily produced by some *Fusarium* species. Recently, fumonisins were reported from *Aspergillus* isolates associated with vineyards overseas. Thirty-six *Aspergillus* isolates collected from seven vineyards in New South Wales and a vineyard in South Australia were identified using species-specific PCR primers and assessed for fumonisins in laboratory media. The effect of water activity (aw) (0.92, 0.95 and 0.98) and temperature (20°C, 25°C, 30°C and 35°C) on growth rate and the production of fumonisins was studied for three *Aspergillus* isolates in synthetic grape juice medium (SGJM). Liquid chromatography-tandem mass spectrometry was used to determine fumonisins in all the experimental samples. Six *Aspergillus* isolates produced fumonisins (FB2 & FB4), vis. three *A. welwitschiae* and three *A. niger* isolates. These isolates produced between 0.7 to 25 mg/kg and 0.4 to 13.5 mg/kg of fumonisins in Czapek Yeast Extract Agar with 5% NaCl and SGJM, respectively. For both species, maximum growth occurred at aw 0.98 and 35°C. The optimum temperature for fumonisin production was 20–25°C and little was produced above 25°C. Fumonisin production was greatest at aw 0.98 and less was produced at aw 0.95. This is the first report of fumonisin producing *Aspergillus* isolates and *A. welwitschiae* in Australian vineyards. These data may be useful in evaluating the risk of fumonisin occurrence in Australian grapes and grape-products and the development of predictive models of fungal growth and fumonisin contamination of grapes.

Biology and epidemiology of smut (*Ustilago cynodontis*) in couch grass

**Dr Nga Tran**1, Dr Alistair McTaggart1, Prof André Drenth1, Prof Roger Shivas1, Dr Don Loch1, Assoc Prof Andrew Geering1

1Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Australia, 2School of Agriculture and Food Sciences, The University of Queensland, St Lucia, Australia

Couch smut, caused by *Ustilago cynodontis* (Basidiomycota), is a common disease of couch grass (*Cynodon dactylon*). The disease causes economic losses to the turf industry as the rate of stolon extension is reduced by up to 50%. Infected turf is less tolerant of trampling and has slower rates of recovery. High disease incidence is also associated with increased wastage during cutting and rolling, as the turf roll frequently breaks at points of infection, presumably due to the shorter and weaker stolons. There are no effective disease management strategies due to limited understanding of the pathogen biology and disease epidemiology. The aims of the research were to investigate (i) the environmental conditions that affect growth of the pathogen *U. cynodontis*, (ii) mode of infection, and (iii) disease management strategies. Through *in vitro* germination assays, the optimal temperature for germination of teliospores of *U. cynodontis* was 27°C; there was no germination either below 7°C or above 37°C. We developed a nested PCR assay that targeted the internal transcribed spacer (ITS) region, which allowed detection of the fungus, even in the absence of disease symptoms. Results showed that the fungus moved systemically within the plant and latently infected all organs, including flowers, leaves, stolons, rhizomes and roots. In a glasshouse trial, we identified systemic fungicides that may reduce disease incidence. Further experiments are underway to screen couch cultivars for resistance to couch smut. Knowledge obtained from this study will provide a better understanding of the disease system and more effective management of the disease to reduce its impacts.
PathogenFinder – a tool to fast track plant viruses and viroids quarantine testing at the border

Assoc Prof Roberto Barrero1, Ms Joanne Mackie2, Mr Desmond Schmidt1, Dr Adrian Dinsdale2, Dr Lia Liefting3, Dr Julie Pattemore3, Dr Fiona Constable3, Dr Penny Measham5, Dr Brendan Rodoni4, Dr Lisa Ward2, Mr Mark Whattam2

1Queensland University of Technology, Brisbane, Australia, 2Department of Agriculture, Mickleham, Australia, 3Ministry for Primary Industries, Wellington, New Zealand, 4Agriculture Victoria, AgriBio, La Trobe University, Melbourne, Australia, 5Hort Innovation, Bowen Hills, Australia

Rapid and safe access to new plant genetic stocks is crucial for primary industries to remain profitable and internationally competitive when accessing high-value markets. Australia and New Zealand are at the forefront of biosecurity worldwide owing to their rigorous post entry quarantine (PEQ) scrutiny of imported plants. While the existing biosecurity system adequately safeguards plant industries, it can also cause prolonged delays, which limit the ability of plant industries to adapt quickly to new global market demands. Existing quarantine processes for detecting exotic plant viruses and viroids are laborious, resource intensive and time consuming, and often result in delays of more than two years while mandatory testing is completed. Based on our previous proof of concept, the virus surveillance and diagnosis (VSD) web-based toolkit will be optimised and compared to existing PEQ protocols with the objective of integrating it into our new portable and platform independent PathogenFinder standalone tool. PathogenFinder will enable fast and safe routine screening of imported plants for exotic viruses and viroids. PathogenFinder uses a small RNA sequencing (small RNA-Seq) approach to assess and diagnose the presence of all known viruses and viroids in a single assay. Over 100 samples representing 29 plant species including major horticultural crops such as citrus, grapevine, strawberry, raspberry and potato were tested using PathogenFinder in comparison with existing and current PEQ protocols. Testing results showed that there was a strong correlation between the current PEQ protocols and the PathogenFinder method with regards to the detection of viruses in these samples. We envisage that high throughput sequencing technology will significantly reduce PEQ screening costs and quarantine lead-in times thereby assisting plant industries’ competitiveness and profitability to access markets benefiting the broader community.

Specific and sensitive electrochemical detection of Botrytis spp. in temperate legume crops

Mrs Marzia Bilkiss1,2, Dr Muhammad J.A. Shiddiky1,3, Mr Mostafa Kamal Masud3,4, Dr Prabhakaran Sambasivam1,3, Dr Ido Bar1,3, Dr Jeremy Brownlie1,2, Dr Rebecca Ford1,2

1School of Environment and Science, Griffith University, Nathan, Brisbane, Australia, 2Environmental Future Research Institute, Griffith University, Nathan, Brisbane, Australia, 3Queensland Micro & Nanotechnology Centre, Griffith University, Nathan, Brisbane, Australia, 4Australian Institute for Bioengineering and Nanotechnology, University of Queensland, Brisbane, Australia

Botrytis grey mould (BGM), caused by Botrytis cinerea and Botrytis fabae, separately or within a complex, substantially reduces grain legume yield during environmentally conducive seasons. Greater success in application of Integrated Disease Management approaches to reduce loss would result from fast, accurate and cost-effective diagnosis and quantification of the causal pathogen(s). The existing immunogenic and molecular probe-type diagnostic methods are based on whole genome sequencing, PCR amplification or antibodies, are time consuming and offer varying levels of specificity and/or sensitivity. As an alternative, we have developed a portable diagnostic assay comprising species-specific molecular biosensors for detection and quantification of the mycelium and spore-derived nucleic acid of both of the target pathogens. For this, two sets of species-specific primers for Botrytis cinerea and Botrytis fabae were designed. Initially, probe sensitivities were determined (100 fg/µl; ~2 genome copies/µl) in pure fungal backgrounds using multiplexed quantitative PCR. During further validation, quantitative PCR detected 100 spores on artificially infected legume leaves. Simultaneously an electro-catalytic assay was developed for both target fungal DNA using functionalised magnetic nanoparticles. This was extremely sensitive, able to detect a single spore within a raw total plant nucleic acid extract background. We believe that the translation of this technology to the field will enable quantitative assessment of pathogen load for future accurate decision support of informed BGM management.
**Enhanced disease detection using proximal sensing and machine learning**

**Dr Kar Mun Chooi**, Dr Gareth N. Hill, Mr Kai S.J. Lewis, Dr Harris Lin, Dr Mark A. Whitty, Mr Mark Wohlers

*1The New Zealand Institute for Plant & Food Research Limited, Auckland, New Zealand, 2School of Mechanical and Manufacturing Engineering, UNSW Sydney, Australia*

Grapevine leafroll disease (GLD) is a widespread viral disease that can lead to reduced vine vigour and longevity, and reduced fruit yield and quality that, in turn, affect wine quality. The current management strategies rely on the identification of infected grapevines in-field to ensure the source of disease inoculum can be removed. The detection of the disease is currently based on visual identification of foliar symptoms for red berry cultivars, which is time consuming and can be unreliable because of the lack of experience of the assessor and other factors such as nutrient deficiencies. With no known visual symptoms for white berry cultivars, laboratory-based testing is time-consuming and also expensive.

This research has collected data over 3 years from an established GLD field-trial block that consists of four cultivars with disease status of each grapevine known through conventional testing. Three proximal imaging methods were used: standard RGB, multispectral, and hyperspectral. Over 2000 images of diseased and healthy leaves from multiple seasons have been processed through machine learning training and validation workflows. The best model resulted in over 84% accuracy for GLD detection in red berry cultivars based on the known infection status (Sensitivity/true-positive rate = 78%, Specificity/true-negative rate = 94%), and 98% GLD detection against the infection status assessments made by an experienced GLD assessor. Ongoing research looks to use the established workflows and co-innovate with growers to understand how the technology can be implemented and integrated into day-to-day operations. This will ensure effective adoption of this novel proximal sensing technology, which offers new opportunities in enhanced crop protection against diseases and whole vineyard/orchard management with accurate, automated, cost-effective and sustainable methods.

**Improving and developing diagnostics for high throughput identification of viruses**

**Dr Paul Campbell**, **Dr Fiona Filardo**, Dr Murray Sharman

*1Queensland Department Of Agriculture, Dutton Park, Australia*

Assays for high throughput screening of crops and weeds for virus monitoring and management need to be quick, easy, and ideally, low cost. Current methods include the use of tissue blot immuno assays (TBIA), where plant stems are blotted onto a nitrocellulose membrane and screened with available antibodies against a range of viruses. TBIA are fast and cheap, but are limited by antibody availability and specificity. One approach we recently used to increase TBIA specificity, was to generate an antibody against the polerovirus soybean dwarf virus (SbDV) via protein expression. The coat protein of SbDV was cloned into an expression vector, expressed, purified, and used to generate a specific SbDV antibody. The generated antibody shows good specificity and sensitivity of SbDV positive isolates in TBIA. This method can used to generate antibodies for specific viruses where there are currently no antibodies available or they are hard to purify, such as poleroviruses. Another and more novel high throughput approach we are developing is the tissue blot hybridization chain reaction (TB-HCR). Similar to TBIA, plant stems are blotted onto a membrane. However, TB-HCR involves using specific probes that can be designed to bind to either a family or group of viruses or specific viruses. During the assay, one probe or a number of different probes can be used for screening at the same time. Following probe binding, labelled small DNA hairpins are added and bind to initiator sequences on the probe causing a cascading unfolding and hybridisation of the hairpins (hybridisation chain reaction). Current advances in the development of this technique in the identification of viruses in pulse crops will be discussed.
New achievements for diagnostics of banana streak virus

Ms Ha Ngo¹, Ms Kathy Crew², Ms Megan Vance¹, Mr John Thomas¹, Mr Son Nguyen³, Ms Tania Duarte³, Mr Lachlan Coin³, Mr Andrew Geering¹
¹Queensland Alliance for Agriculture and Food Innovation, The University Of Queensland, Brisbane, Australia, ²Department of Agriculture and Fisheries, Brisbane, Dutton Park, Australia, ³Institute for Molecular Bioscience, The University of Queensland, St Lucia, Australia

Banana streak virus (BSV) remains one of the most challenging viral pathogens of banana to detect and most diagnostic assays rely on serological methods. The BSV capsid protein contains an N-terminal, intrinsically disordered (NID) domain that is surface-exposed on the virion and likely is multifunctional and plays important roles in viral replication and transmission. The immunodominant continuous epitopes on the virion are also located in the NID domain, and therefore this domain is of great interest from a diagnostics perspective. Using chemically synthesized peptides to mimic the continuous epitopes of five BSV species including Banana streak Mysore virus (BSMYV), Banana streak Obino I’Ewai virus (BSOLV), Banana streak Imo’v’ virus (BSIMV), Banana streak Goldfinger virus (BSGFV) and Banana streak Cavendish virus (BSCAV), antisera have been raised in rabbits, and shown specificity to each virus species and sensitivity in a range of assay formats such as Western Blot, enzyme-linked immunosorbent assay (ELISA), immunosorbent electron microscopy and immunocapture PCR. This work confirmed the applicability of synthesis epitopes/peptides to produce antipeptide antibodies for BSV diagnostics when the native protein is absent. The Oxford MinION Nanopore sequencing system is a promising new technology for point-of-care diagnostics. We have successfully used this system and generated long reads with greater than 99% accuracy, allowing accurate and sensitive detection of BSV. The long reads allow episomal from endogenous sequences to be differentiated.

High-throughput sequencing for Xylella fastidiosa surveillance: evaluation and optimization of pipelines for data acquisition and analysis

Dr Luciano Rigano¹, Dr Chandan Pal¹, Mr Robert Taylor¹, Dr Brett Alexander¹
¹Plant Health and Environment Laboratory, Ministry for Primary Industries, Auckland, New Zealand

*Xylella fastidiosa* is a xylem-limited bacterium that is causing a devastating impact worldwide on a wide range of important plant species. *X. fastidiosa* is native to the Americas, but is spreading rapidly around the world due to globalized trade. This microorganism is not present in New Zealand, but is a major biosecurity concern to New Zealand’s horticultural and conservation sectors. MPI’s Plant Health and Environment Laboratory (PHEL), as New Zealand’s plant pest reference laboratory, is responsible for the identification and verification of all suspected exotic, new, and emerging pathogens affecting plants and the environment. PHEL has an ongoing readiness programme to ensure that the latest diagnostic technologies are available for early and accurate detection of unwanted organisms. Real-time PCR is the method of choice for routine *X. fastidiosa* detection, due to its sensitivity and specificity, however it has been challenging to develop reliable real-time PCR assays that can enable subspecies and sequence-type level identification. In this work, we employed different high-throughput sequencing (HTS) approaches and downstream bioinformatic analyses to assess the diagnostic specificity, sensitivity, and in-depth information on strains obtained from a set of *Xylella*-infected *Vitis* and *Quercus* samples. We evaluated a number of 16S metabarcoding and shotgun metagenomic data analysis pipelines, including de novo assembly/query against reference databases, reference-assisted mapping, and metagenomic multilocus sequence typing, and identified potential advantages and disadvantages of each approach. Overall, our results indicate that HTS technology could be used as a modern diagnostic tool in detecting, characterizing and obtaining sequence-type level information of *X. fastidiosa* directly from infected plant material.
Viral suppressors of RNA silencing in grapevine leafroll-associated virus 3

Mr Waqas Ahmad1,2, Dr Heiko Ziebell3, Dr Karmun Chooi1, Dr Robin MacDiarmid1,2
1The New Zealand Institute for Plant and Food Research Ltd, Auckland, New Zealand, 2School of Biological Sciences, The University of Auckland, Auckland, New Zealand, 3Institute for Epidemiology and Pathogen Diagnostics, Julius Kühn-Institut, Messeweg, Braunschweig, Germany

Grapevine leafroll-associated virus 3 (GLRaV-3) is the main causative agent of grapevine leafroll disease (GLD). To date, GLD management and associated research has mainly focused on the use of control rather than protection measures. We have a lofty goal of identifying mild strains of the virus for use in cross-protection against severe strains of GLRaV-3. To achieve this, we aim to identify virus strains with low suppression of RNA-silencing activity, yet the proteins that encode this have not yet been identified for GLRaV-3. Plants have an RNAi mechanism to inhibit viral spread, locally and systemically. However, viruses have evolved in parallel to counteract this activity in plants via a variety of mechanisms, including suppressors of RNA silencing (VSR) that inhibit the plant RNAi defence mechanism at one or more points. Only one VSR, p19.7 protein, has been identified for GLRaV-3, yet similar viruses have at least three VSR proteins. This study aims to identify all VSRs encoded by GLRaV-3. We have developed a step-wise system for identifying weak through to strong VSRs using a range of RNAi inducers in wild type or the traditionally used 16C Nicotiana benthamiana line which constitutively expresses the Aequorea victoria green fluorescent protein (GFP). Using this system, we have identified at least three new-to-science VSRs encoded by GLRaV-3, based on preliminary data showing silencing of the GFP reporter. These include a moderate, and two strong VSRs. The real-time RT-qPCR analysis currently in progress will be presented, along with the fluorescence data. With the focus on identification and characterization of VSRs in terms of their activity and strength, results from this study are expected to add to the understanding of GLRaV-3’s pathogenicity, and to support the identification of mild strains of the virus to protect grapevines and consequently high-quality wine production.
In New Zealand, the existence of the iconic and culturally important kauri tree (*Agathis australis*) is under threat from *Phytophthora agathidicida*, a root-infecting oomycete pathogen. A screening programme in progress at Scion (New Zealand Forest Research Institute) suggests that tolerance to *P. agathidicida* is present in natural kauri populations. In order to gauge the extent to which such tolerance might be durable over time in the forest, many questions need to be answered about the plant, the pathogen and the environment, and how these factors interact to determine the disease status. The aim of our study is to explore the molecular basis of interactions between *P. agathidicida* and kauri, by first identifying pathogen molecules that are required for virulence or for triggering host defence. The *P. agathidicida* genome was screened for RxLR effector genes which are known to be important in the virulence of other *Phytophthora* pathogens. The functions of a core set of 75 RxLR effectors were first assessed using a high-throughput model system involving transient *Agrobacterium* transformation of *Nicotiana* spp. Eight of these RxLR proteins induced cell death, suggesting a hypersensitive plant defence response. One of these, PaRxLR24, is an orthologue of the well-characterised Avh238 of *P. sojae* and was highly expressed in kauri tissue. Furthermore, the cell death elicited by PaRxLR24 was suppressed by another *P. agathidicida* effector, PaRxLR40, suggesting an interacting network of pathogen molecules. Using an RNAi hairpin library we aimed to identify NB-LRR receptor(s) in *N. benthamiana* that specifically recognize PaRxLR24. In future we hope to screen RxLR proteins in kauri tissue to determine if they trigger or suppress cell death responses in the natural host and to identify host targets that will help us determine the genetic basis of resistance in this very important gymnosperm species.
Characterisation of chitin synthases from *Fusarium graminearum*

**Ms Linda Brain**, Dr Mark Bleackley, Prof Marilyn Anderson, Prof Vincent Bulone

1 La Trobe University, Bundoora, Australia, 2 University of Adelaide, Adelaide, Australia

*Fusarium graminearum* (Fg) is a devastating agricultural pathogen that causes significant losses to cereal crops worldwide. These losses are due to its negative impact on grain yield, as well as its adverse effect on grain quality through the production of carcinogenic mycotoxins. Chemical fungicides are currently used to control this pathogen, but resistance is now common globally, which is limiting their sustainable use. Thus, there is an urgent need for new fungicides with different mechanisms of action. Chitin synthases (CHS) are excellent targets for new antifungal drugs, because chitin is essential to the integrity of the fungal cell wall, and thus the survival and virulence of fungal cells. Furthermore, this polysaccharide is not made by plants or mammals, and thus this target is specific for fungi. No CHS inhibitors have been successfully developed for the control of human or agricultural fungal pathogens. One reason for this is the paucity of biochemical information on these important enzymes, because they are embedded in the plasma membrane and cannot be purified in the quantities needed for biochemical analysis. This is further complicated by the presence of several CHS genes in each fungal species. The aim of this study is to identify the full complement of CHS in Fg, and to recombinantly express these CHS in yeast for biochemical characterisation. Eight potential CHS genes were identified in Fg using a combination of bioinformatics, functional complementation and microscopy. Two of these genes complemented a chs double knockout in *S. cerevisiae* and were taken forward for biochemical characterisation. The FgCHS3b and FgCHS4 proteins were successfully expressed as C-terminal GFP-tagged fusions; a challenging prerequisite for enabling purification and biochemical characterisation of these Fg CHS enzymes for the first time.

Pro-domain inclusion for efficient expression and purification of fungal effectors facilitating structural, biochemical and functional studies

**Mrs Megan Outram**, Mr Daniel Yu, Mr Yi-Chang Sung, Prof Peter Solomon, Prof Bostjan Kobe, Dr Simon Williams

1 Australian National University, Canberra, Australia, 2 University of Queensland, Brisbane, Australia

Effectors are key virulence factors for fungal plant pathogens; however, our understanding of their biological functions is largely unknown. Often, effector proteins lack sequence identity to proteins of known function, or functional domains, making it impossible to infer function on sequence alone. Structural biology and protein biochemistry are important techniques for unravelling the biological functions of these proteins, yet these research approaches are generally underpinned by the requirement of high yields of functional, and pure protein. Here we report our experiences expressing the cysteine-rich effector Tox3 from *Parastagonospora nodorum*, the causal agent of Septoria nodorum blotch on wheat. We have shown that Tox3 encodes an N-terminal pro-domain that is required to produce the effector recombinantly in the *E. coli* strain Shuffle®. However, this domain inhibits downstream processes, including protein crystallisation. We report a novel approach for overcoming this requirement by incorporating specific cleavage of the recombinant protein using the protease Kex2, which we believe represents the natural processing of this protein. This work culminated in the structure determination of Tox3 by X-ray crystallography. A subsequent bioinformatics search led to the identification of a number of other fungal effectors from important plant pathogens that possibly contain Kex2-cleavable pro-domains. We have subsequently applied this strategy to several other fungal effectors, and shown that it is more broadly applicable, providing a useful tool for other researchers working toward understanding effector function. The wider implications of this work, with a focus on the role of pro-domains and their importance in the maturation of effectors from multiple fungal plant pathogens, will also be presented.
Interaction of a plant virus protein with the scaffolding Cajal body protein coilin facilitates salicylic acid-mediated plant defence responses

Prof Michael Taliansky1,2, Dr Jane Shaw1, Ms Antonida Makhotenko1,3, Dr Svetlana Makarova1,3, Dr Andrew Love1, Dr Stuart MacFarlane1, Prof Natalia Kalinina1,3
1Pushchino Branch, Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry of the RAS, Pushchino, Russia, 2James Hutton Institute, Dundee, UK, 3Lomonosov Moscow State University, Moscow, Russia

In addition to well-known roles in RNA metabolism, the nucleolus and Cajal bodies (CBs), both located within the nucleus, are involved in plant responses to biotic and abiotic stress. Previously we showed that plants in which expression of the signature (scaffolding) CB protein coilin is down-regulated are more susceptible to certain viruses including tobacco rattle virus (TRV), suggesting a role of coilin in antiviral defence. Experiments with coilin-deficient plants and the deletion mutant of the TRV 16K protein showed that both 16K and coilin are required for restriction of systemic TRV infection. The potential mechanisms of coilin-mediated antiviral defence were elucidated via experiments involving co-immunoprecipitation, Far-Western blot analysis, use of NahG transgenic plants deficient in salicylic acid (SA) accumulation, measurement of endogenous SA levels and assessment of SA-responsive gene expression. We have shown that the TRV 16K protein interacts with and relocates coilin to the nucleolus. These events are accompanied by activation of SA-responsive gene expression and restriction of TRV systemic infection. In contrast, viral systemic spread was enhanced in NahG plants. Our findings suggest that coilin is an activator of a hitherto unrecognised mechanism of plant defence, involving the interaction of the TRV 16K protein with coilin, which is associated with coilin redistribution to the nucleolus and subsequent activation of SA-dependent defence pathways. Mechanistic implications of these results for defining and manipulating host systems involved in controlling responses to other biotic and abiotic stresses will be presented.

A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle

Mr Darcy Jones1, Ms Kasia Rybak1, Mr Evan John1, Dr Huyen Phan1, Prof Karam Singh1,2, Dr Shao-Yu Lin3, Prof Peter Solomon3, Prof Richard Oliver1, Dr Kar-Chun Tan1
1Curtin University, Perth, Australia, 2CSIRO, Perth, Australia, 3ANU, Canberra, Australia

The fungus *Parastagonospora nodorum* causes septoria nodorum blotch (SNB) of wheat. SNB is largely dictated by interactions between necrotrophic effectors (NEs) and host dominant susceptibility genes. Three of the best characterised NE-sensitivity gene interactions are *SnToxA-Tsn1, SnTox1-Snn1* and *SnTox3-Snn3*. *SnToxA* and *SnTox3* are positively regulated by a Zn2Cys6 transcription factor, PnPf2. Mutants deleted in *PnPf2* lost the ability to infect *Tsn1* and *Snn3* wheat lines, but remained infectious on hosts carrying *Snn1*. RNAseq was used to compare the transcriptomes of the *P. nodorum* wildtype (SN15) and a *PnPf2*-deficient strain (*pf2-69*) to further identify other targets of PnPf2 regulation. Gene ontology enrichment analysis of the differentially expressed (DE) genes revealed that genes associated with plant cell wall degradation and proteolysis were enriched in down-regulated DE gene sets in *pf2-69* compared to SN15. In contrast, genes associated with redox control, nutrient and ion transport were up-regulated in the mutant. Further analysis of the DE gene set revealed that PnPf2 positively regulates twelve genes that encode effector-like proteins. Furthermore, several putative TF binding motifs were enriched in the promoter region of DE genes. One of these corresponded to a putative Zn2Cys6 binding site, and was present in *SnToxA* and *SnTox3* promoters. Functional characterisation indicates that PnPf2 does not interact with this motif. Instead, PnPf2 may exert its regulatory function on *SnToxA* and *SnTox3* through other downstream TFs uncovered in this study. Functional analysis of several PnPf2-regulated TFs revealed critical roles in virulence and asexual reproduction. We concluded that in addition to modulating effector gene expression, PnPf2 may play a broader role in establishment of a necrotrophic lifestyle by orchestrating the expression of genes associated with plant cell wall degradation and nutrient assimilation.
Options for Managing *Rhizoctonia solani* in Sugar Beet

**Prof Mohamed Khan**

1North Dakota State University & University Of Minnesota, Fargo, United States

Rhizoctonia root rot, caused by *Rhizoctonia solani* Kühn, is currently the most devastating soil borne disease of sugar beet (*Beta vulgaris* L.) in North Dakota and Minnesota. In the bi-state area, *R. solani* causes damping off, root and crown rot of sugar beet. *R. solani* survives as thickened hyphae and sclerotia in organic material and is endemic in soils where sugar beet is grown. Crop rotations of three or more years with small grains planted before sugar beet is recommended to reduce disease incidence. In fields with a history of high disease severity, growers may plant varieties that are more tolerant but with lower yield potential compared to more susceptible varieties. Research was conducted in Minnesota and North Dakota, USA, to evaluate the efficacy of fungicides for controlling *R. solani* in sugar beet. Research showed that azoxystrobin when used alone, and when mixed with starter fertilizer and applied in-furrow at planting provided effective control against *R. solani*. Research also showed that penthiopyrad seed treatment provided effective early season control but required a post application of azoxystrobin to provide acceptable season long control against *R. solani*. Research indicated that fungicides applied after planting need to get into the soil close to the sugar beet roots to provide effective protection.

Can Sclerotinia stem rot be controlled by using cultural practices alone in canola?

**Dr Ravjit Khangura**, Mr Mehreteaab Aberra, Mr Stuart Vincent

1Department Of Primary Industries And Regional Development, South Perth, Australia

Sclerotinia stem rot (SSR) caused by *Sclerotinia sclerotiorum* is the second most important disease of canola (*Brassica napus*) in Australia. Due to lack of genetic resistance in the current Australian commercial varieties, management of SSR relies heavily on the use of fungicides and some cultural practices. Field trials were conducted for three years to evaluate the effectiveness of various cultural practices, such as wide row spacing (44 cm) and low plant densities (15 plants/m²) in conjunction with fungicide on the incidence of SSR and yield of canola in the northern agricultural region of Western Australia. Each trial was sown with two varieties (either a hybrid and an open-pollinated or two hybrid varieties with different maturities) with and without fungicide application. The fungicide Prosaro® (450 ml/ha) was applied at 30% bloom as per label recommendations. Disease incidence (DI) was recorded at the end of the season close to physiological maturity. Analysis of DI data indicated that the main effects of fungicide and variety were significant (*p*<0.05), however, row spacing and plant density were not significant. Likewise, the main effect of fungicide, variety and plant density was significant (*p*<0.05) on yield but an effect of row spacing was not significant. Averaged across row spacing and plant density, the fungicide application at 30% bloom resulted in over 50% reduction in disease incidence and increased canola yield by 9%. Trial results revealed that neither wide row spacing nor low plant densities were effective on their own in reducing DI of SSR and improving canola yield. Fungicide intervention was still required to ameliorate losses from SSR, particularly under conditions highly conducive for SSR development.
The potential and progress toward eradication of Fiji leaf gall from Australia

Dr Robert Magarey¹, Dr Nicole Thompson²
¹Sugar Research Australia, Tully, Australia, ²Sugar Research Australia, Woodford, Australia

Fiji leaf gall is a viral disease likely to have arisen in Papua New Guinea, where it is still commonly seen in indigenous garden sugarcanes (*Saccharum officinarum*). It is characterised by leaf galls on the back of affected leaves, the distortion and limited growth of shoots and severe stunting of individual plants. The disease has been a major consideration for the Australian sugarcane industry, causing several significant epidemics over the last 100 years, most notably in Bundaberg in the 1970-1990 period. The virus is transmitted in Australia by the planthopper *Perkinsiella saccharicida*, a common inhabitant of commercial canes. Apart from causing direct yield losses, appropriate management leads to further indirect losses from the discard of high-yielding, but susceptible, commercial cultivars within the plant improvement selection program. Selection of parents with adequate resistance also limits the use of high-yielding parental germplasm – another potential productivity loss. With the implementation of key management strategies, the sugarcane industry has been able to limit, then reduce the incidence of the disease through the cropping of resistant varieties, the selection of disease-free plant sources, the termination of heavily-diseased crops and thorough inspection of nursery material. The industry is now in a position to consider progressive eradication of the disease from different cropping regions. Routine plant source inspections have led to the accumulation of large amounts of crop data by Cane Productivity Service (CPS) groups; these have been used to model the probability of disease presence in regions where it has not been seen for over 20 years. A paper has been written to suggest ‘area freedom’ in the central (Mackay) region of Queensland. Strategies are in place to eradicate the disease in the other regions where it has been observed. This could be the third major disease eradicated from the Australian sugarcane industry.

The New Zealand Winegrowers Grafted Grapevine Standard: ensuring high quality planting material to the New Zealand wine industry

Dr Edwin Massey¹, Dr Robin MacDiarmid²
¹New Zealand Winegrowers, Blenheim, New Zealand, ²Plant & Food Research, Kerikeri, New Zealand

The New Zealand Winegrowers Grafted Grapevine Standard (GGS), established in 2006, is an industry owned grapevine certification scheme that applies to nursery-produced grafted grapevines. The GGS relies on nurseries producing grafted grapevines that comply with specific certification requirements. Certification is issued by independent auditors following an audit of the production process. Certified vines can be confirmed as true to type, have a very low incidence of grapevine leafroll-associated virus 3 (GLRaV-3), and have specific physical specifications. In addition, certified vines are purchased with the knowledge that the producing nurseries have taken steps to minimize the potential spread of fungi that cause grapevine trunk disease. GLRaV-3 is one of the most economically important and widespread disease agents affecting wine production in New Zealand. This presentation examines the impact that GGS has had on reducing the spread of GLRaV-3 and other viruses through the nursery pathway to the New Zealand vineyard commercial estate. We also explore how, throughout its 13-year lifespan, a technical review group made up of nursery representatives, industry representatives and independent researchers has helped to ensure that the GGS meets the quality requirements of the industry without making nursery production overly onerous and costly. Based on this analysis, the presentation makes recommendations for other countries looking to establish similar schemes to improve the quality of nursery-produced material.
Improved management options for Cucumber green mottle mosaic virus

Dr David Lovelock, Dr Fiona Constable, Dr Brenda Coutts, Dr Mary Finlay-Doney, Mr Denis Persley, Dr Merran Neilsen, Dr Paul Campbell, Dr Craig Webster, Ms Vicki Simlesa, Dr Sharl Mintoff, Ms Nadine Kurz, Dr Lucy Tran-Nguyen

1NT DPIR, Darwin, Australia, 2QDAF, Brisbane, Australia, 3DJPR, Melbourne, Australia, 4DPIRD, Perth, Australia

The first Australian detection of Cucumber green mottle mosaic virus (CGMMV) was in the NT in September 2014, on commercial watermelon farms. It was subsequently detected in cucurbit varieties including cucumber, pumpkin, squash and Asian cucurbit vegetables. After the NT detection, CGMMV was also found in isolated areas of Queensland, South Australia, cucurbit-growing areas of Western Australia and, more recently, New South Wales. Studies were conducted to help manage the disease, specifically investigating alternative hosts and non-hosts, studying CGMMV biology in contaminated soil, improving diagnostics for plant and seed detection and investigating the role of honey bees in CGMMV spread. Six alternative crops were identified as non-hosts of CGMMV from field and pot trials in the NT – sweet corn, snake bean, capsicum, okra, sorghum and peanut. Eight weed species were shown to be alternative hosts and some weed seeds also tested positive for CGMMV. Soil spiked with sap from CGMMV-contaminated plants remained infectious for up to 36 weeks; direct sowing of seeds into contaminated soil resulted in less infection than transplants, due to damaged root systems of transplant plants permitting virus entry. Molecular testing of cucurbit seeds showed that a broad range of cucurbit species can be tested, requiring sub-samples of up to 500 seeds for most species. A new lateral flow dipstick was developed and preliminary results showed it was able to detect the outbreak strain of CGMMV at a 1:103 dilution. A bee sampling protocol was developed, and bee products found to harbour CGMMV included bees, brood, pollen, honey, wax and propolis. Viable CGMMV was only found in adult bees, pollen and honey. A new project will investigate modes of transmission of CGMMV by honey bees. Future research should further investigate efficacy of disinfectants for new seedlings, the role of alternative hosts in CGMMV epidemiology and resistant/tolerant cucurbit varieties.

An integrated approach to manage Fusarium wilt on bananas

Dr Anthony Pattison, Dr Hazel Gaza, Mr David East, Mr Wayne O’Neill, Ms Jennifer Cobon, Mr Jeff Daniells, Mr Stewart Lindsay, Ms Sharon Hamill, Dr Lucy Tran-Nguyen, Dr Sharl Mintoff, Dr Paul Nelson, Mr Ryan Orr, Dr Jay Anderson, Dr Elizabeth Aitken, Mr Henry Birt, Dr Paul Dennis, Dr Rosie Godwin

1Department Of Agriculture And Fisheries, South Johnstone, Australia, 2Deaprtment of Primary Industry and Resources, Berrimah, Australia, 3James Cook University, Cairns, Australia, 4The University of Queensland, St Lucia, Australia, 5Australian Banana Growers’ Association, Rocklea, Australia

Fusarium oxysporum f.sp. cubense Tropical Race 4 (Foc TR4) causes Fusarium wilt, also known as Panama disease, and is currently spreading throughout banana producing nations. Foc TR4 was identified on a farm in the Tully region in March 2015 and threatens the viability of Australia’s $600 million banana industry. The Fusarium wilt Tropical Race 4 research program endeavours to build on short-term advances in biosecurity research, by investigating mid- and long-term strategies which would allow banana growers to profitably produce bananas in an integrated system in the presence of Fusarium wilt. Medium-term research outcomes have focused on development of more resilient banana production systems, by understanding the epidemiology of Fusarium within the banana plant, particularly chlamydospore production, how the pathogen survives on alternative hosts and the opportunities to incorporate pathogen suppressive crop rotations. Furthermore, a greater understanding of pathogen suppression has been achieved through characterisation of physicochemical properties of north Queensland banana producing soils and farm management practices. The longer-term outcomes include the development of TR4 resistant cultivars, by developing genetic material through a mutagenesis program, commencing with banana cultivars that are known to be resistant to TR4. Field screening and selection has been conducted in the Northern Territory and north Queensland for the identification of improved cultivars. Ultimately, an integrated system for banana growers will be developed based on biosecure farm systems using banana cultivars with improved resistance grown in a disease suppressive production system.
The development of robust molecular diagnostic assays for *Fusarium oxysporum* f. sp. *cubense* from environmental samples

**Dr Diane Mostert¹**, Me Megan Ceris Matthews¹, Mr Privat Ndayihanzamaso¹, Mr Paul-Henri Lombard¹, Dr Lindy Joy Rose³, Prof Altus Viljoen¹

¹Stellenbosch University, Stellenbosch, South Africa

Banana Fusarium wilt, caused by the soil-borne fungus *Fusarium oxysporum* f. sp. *cubense* (Foc), is a major constraint to sustainable banana production. The only means to manage Fusarium wilt effectively is by exclusion of the pathogen and by planting resistant varieties. Accurate diagnosis of Foc plays a vital role in the early detection and geographic mapping of Foc spread, which can be used to inform farmers and guide containment strategies. The development of accurate diagnostic assays that can detect pathogens from environmental samples, such as plant material, soil and water, relies on a good understanding of the ecology, evolution and epidemiology of the pathogen. In this study conventional and quantitative (q) PCR assays specific to Foc Lineage VI (containing Foc race 1 and 2 strains), Foc tropical race 4 (TR4) and subtropical race 4 (STR4) were developed for detection in environmental samples. Polymorphisms specific to each target were identified using a whole genome comparative approach and considered both regions within the core (relating to house-keeping function), and accessory (relating to pathogenic function) genome. For specificity testing, primer sets were tested using a culture collection that included all known Foc phylogenetic clades, lineages, pathogenic races and VCGs, as well as endophytes commonly isolated from banana tissue. The use of Propidium Monoazide (PMA) in combination with qPCR assays to distinguish between dead and living Foc cells were also investigated. Conventional PCR assays were specific and could be used to routinely monitor Foc spread and characterise Foc diversity. qPCR assays were sensitive and specific, and were able to detect Foc in environmental samples and could be used as an early screening tool for resistance. PMA-qPCR assays could be used to determine the efficacy of sanitiser treatments on Foc spores.

Loop-mediated isothermal amplification (LAMP) detection of *Calonectria ilicicola*, *Dactylonectria macrodidyma* and the *Dactylonectria* genus in avocado roots

**Dr Louisamarie Parkinson¹**, Dr Duy Le², Prof Roger Shivas³, Assoc Prof Elizabeth Dann¹

¹Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Brisbane, Australia, ²New South Wales Department of Primary Industries, Narrabri, Australia, ³Centre for Crop Health, University of Southern Queensland, Toowoomba, Australia

Black root rot of avocado, caused by soilborne nectriaceous fungal pathogens, is an aggressive disease of nursery avocado trees and young orchard transplants, causing rapid tree decline and death within a year after planting. *Calonectria ilicicola* and *Dactylonectria macrodidyma* are important pathogens in Australia, however multiple species in the *Dactylonectria* genus are also known to cause black root rot. Three loop-mediated isothermal amplification (LAMP) assays were developed for the rapid detection of *C. ilicicola*, *D. macrodidyma* and *Dactylonectria* spp. Species and genus-specific LAMP primers were developed from DNA sequence data of the β-tubulin gene for detecting *C. ilicicola* and Histone H3 for *D. macrodidyma* and *Dactylonectria* spp. The assays were optimized for detection in avocado root tissue, and were demonstrated to be sensitive at DNA concentrations of 1 pg/µl, 0.01 ng/µl and 0.1 ng/µl for *C. ilicicola*, *D. macrodidyma*, and *Dactylonectria* spp. respectively. The assays were validated with 82 fungal isolates across multiple genera in the Nectriaceae family, with 100% specificity demonstrated for *C. ilicicola* and *D. macrodidyma*, and 96.34% for the *Dactylonectria* genus-wide assay. Specificity of the genus-wide assay was dependent on isothermal amplification temperature and time. Detection in avocado roots averaged from 12–26 min for *C. ilicicola* and *D. macrodidyma*, and 14–30 min for *Dactylonectria* spp. The LAMP assays were adopted by the Australian avocado industry for laboratory and field diagnostic testing of symptomatic nursery trees. The assays are applicable to multiple agricultural industries as the target pathogens are important pathogens of other crops including soybean, peanuts, grapevine and apple.
Does timing of sporangia production and zoospore release influence the recovery of different *Phytophthora* species by baiting?

**Mrs Suchana Rani Sarker**1,2, Dr Jennifer McComb1, Prof Treena Burgess1, Prof Giles Hardy1

1Centre for Phytophthora Science and Management, Murdoch University, Perth, Australia, 2Plant Pathology Division, Bangladesh Agricultural Research Institute, Gazipur 1701, Bangladesh

The number of *Phytophthora* species is increasing rapidly due to extensive surveys of previously unexplored natural ecosystems and through the availability of High Throughput Sequencing (HTS). However, routinely many more *Phytophthora* species are detected from the same soil using HTS compared with the traditional soil baiting method, and many species have never been isolated into culture. This study investigated whether differences in the timing and abundance of sporangial production and zoospore release between species could be a reason for the lower number of species isolated using baiting. Stems of jarrah (*Eucalyptus marginata*) were inoculated with ten *Phytophthora* species (*P. nicotianae*, *P. multivora*, *P. pseudocryptogea*, *P. cinnamomi*, *P. thermophila*, *P. arenaria*, *P. heveae*, *P. constricta*, *P. gondwanensis* and *P. versiformis*), and lesioned sections for each species were baited separately in water. Leaves of *Scholtzia involucrata* and *Pimelea ferrunginea* previously shown to be suitable for many *Phytophthora* species were used as baits. There were significant species differences in timing of sporangia production and zoospore release. For most species there was a relationship between time of zoospore release and the number of days before a species could be isolated from a bait. *P. pseudocryptogea*, *P. nicotianae* and *P. multivora* which released zoospores within 8-12 hours could be isolated from lesioned baits 1-2 days after baiting. In contrast, *P. constricta* (which was not observed to produce zoospores within 48 hours) was only isolated 5-7 days after baiting. *P. heveae* and *P. versiformis* from which zoospores were not observed, were never recovered from the baits. Thus, when soil containing material infected with multiple species of *Phytophthora* is placed in water and baited, species differences in the timing of sporangia production and zoospore release may contribute to the ease of isolation of some species and not others.

Evaluating a protocol for the elution of *Plasmopara viticola* DNA from FTA® cards

**Dr Andrew Taylor**1,2

1Department of Primary Industries and Regional Development WA, Bunbury, Australia, 2Veterinary and Life Sciences, Murdoch University, Murdoch, Australia

*Plasmopara viticola*, the cause of grape downy mildew is an obligate biotroph, meaning conducting studies on population genetics are constrained due to biosecurity and long-term storage complexities. A solution to overcome these issues is the use of Whatman® FTA® cards. FTA cards have successfully been used to store and analyse the DNA of plant pathogens, including those of other oomycetes such as *Phytophthora infestans*. However, no protocol for *P. viticola* exists and the presence of polyphenol and polysaccharide contaminants in grapevine material can create difficulties in extraction or downstream processes. The aim of this experiment was to develop a protocol for processing *P. viticola* samples off FTA cards, allowing for optimal DNA analysis. The experiment involved comparing the Whatman Protocol BD08: Preparing an FTA Disc for DNA Analysis with a protocol describing the elution of DNA from FTA cards using virus infected leaf samples [1]. A comparison of DNA extracted from fresh leaf samples using commercial DNA kits and multiple primers were included to ensure consistency of results. The Ndunguru et al. (2005) method was the optimal protocol for PCR amplification and results were consistent with those from fresh samples. No PCR amplification occurred when using the FTA discs in the PCR reaction as described in protocol BD08. The addition of the 70% ethanol wash in the Ndunguru et al. (2005) protocol removes contaminants from the grape material and provides uninhibited PCR amplification. This protocol was successfully used for population genetic projects involving *P. viticola* using microsatellite and ITS primers.

Disease risk assessment of poppy downy mildew using qPCR analysis of two *Peronospora* spp. in naturally-infested soil

Dr Tamilarasan Thangavel\(^1\), Dr Jason Scott\(^2\), Mrs Krithika Krishnamoorthy\(^1\), Miss Chiranthika Singaloda\(^1\), Miss Suzie Jones\(^2\), Miss Harshitha Sri Ramakrishnan\(^1\), Dr Calum Wilson\(^1\)

\(^1\)Tasmanian Institute of Agriculture, 13, St. John’s Avenue, New Town, Australia, \(^2\)Tasmanian Institute of Agriculture, Cradle Coast Campus, 16-20 Mooreville Road, Burnie, Australia

Poppy downy mildew, caused by *Peronospora meconopsidis* and *P. somniferi*, is one of the most devastating diseases of opium poppy and continues to be a major constraint to commercial production in Australia. A real-time polymerase chain reaction assay was developed for the quantification of the two *Peronospora* spp. in leaves, soil and in spore traps. Based on the nucleotide differences within the cytochrome oxidase regions, species-specific Taqman and locked nucleotide acid probes were designed to perform a quantitative assay for the specific detection and quantification of *P. meconopsidis* and *P. somniferi*, respectively. To normalise between samples, an exogenous internal positive control, the marine bacterium *Pseudoalteromonas prydzensis* was included with samples prior to DNA extraction, and a primer and probe set targeting the control was also developed. Specificity of the assay to detect *P. meconopsidis* and *P. somniferi* was confirmed through testing against nine other closely related *Peronospora* spp. The assay was able to reliably detect a minimum of 30 pg/µl and 2 ng/µl of DNA for *P. meconopsidis* and *P. somniferi*, respectively. The capacity of the *P. somniferi* assay to quantify pathogen levels in soil was validated by testing 95 naturally-infested field soils collected between 2015 and 2017. Pathogen detection levels were 0.00 - 5,568 ng DNA/g of soil for *P. somniferi*, with only low levels recorded for *P. meconopsidis* (<1.0 ng DNA/g of soil). Successful disease transmission was shown in seven of the field soils, through measurement of infection in seedlings grown in tested soils under controlled conditions. A threshold of 20 ng DNA/g of soil was observed for reliable transmission of *P. somniferi*. No transmission of *P. meconopsidis* was detected from these samples. Utilization of this assay will enable risk prediction of field sites prior to planting. This assay can also be deployed for monitoring of pathogen dissemination via seed and airborne conidia, through spore trapping.
Leveraging metabarcoding to develop a molecular method to detect and quantify grapevine trunk disease-associated fungi present in New Zealand vineyards

**Dr Bhanupratap Vanga**, Dr Simon Bulman, Ms Rebecca Woolley, Ms Sarah Thompson, Mr Anish Shah, Ms Sandi Keenan, Ms Aliesha Kean, Mr Dion Mundy

1 *New Zealand Institute For Plant And Food Research, Lincoln, New Zealand*, 2 *New Zealand Institute For Plant And Food Research, Blenheim, New Zealand*

Grapevine trunk diseases (GTDs) are caused by a broad range of fungal species, leading to tissue rotting, shoot stunting, reduced berry yield, and ultimately vine death. Early diagnosis of GTD-associated pathogen communities is challenging, because of the presence of multiple co-infecting GTD pathogens within an individual wood lesion. Previously, the identification of GTD pathogens largely relied on traditional isolation methods that were time-consuming (up to four weeks), difficult to correctly identify to species level, and often underestimated incidence levels. To overcome these challenges, published quantitative polymerase chain reaction (qPCR) assays were initially chosen for two GTD pathogens, *Phaeomoniella chlamydospora* and *Eutypa lata*. Specificity was validated against related species of New Zealand (NZ) fungal isolates. Synthetic DNA constructs containing fungal and plant host target sequences were used to generate standard curves for optimising the amplification efficiencies, and a synthetic biomarker plasmid was used to verify the presence of PCR inhibitors. Recent work to confirm the status of fungal communities associated with GTD in NZ was conducted using DNA metabarcoding from grapevines (*Vitis vinifera*) located in the two main viticulture regions Marlborough and Hawke’s Bay. Based on the metabarcoding data, PCR primers were designed and a qPCR assay was developed for accurate detection and quantification of the native white rot fungus *Inonotus nothofagii*. The optimised qPCR assays have been applied to 328 grapevine wood samples collected from commercial vineyards to detect *P. chlamydospora*, *E. lata*, and *I. nothofagii*. This has resulted in a far more sensitive and accurate identification of pathogens than traditional microbiological re-isolation methods. Further qPCR assays are under development for pathogens belonging to the families of Phaeomoniellaceae, Diatrypaceae, Botryosphaeriaceae, and Hymenochaetaceae. Adoption of these qPCR assays will contribute to early and accurate detection of GTD pathogens, improving our understanding of disease aetiology and allowing deployment of early interventions for management.
Rapid evolutionary adaptation of powdery mildew fungi leads to the break-down of barley mlo resistance

Dr Stefan Kusch1, Dr Lamprinos Frantzeskakis2, Dr Mirna Barsoum3, Birthe Lassen3, Lina Pesch1,3, Prof Ralph Panstruga1  
1RWTH Aachen University, Aachen, Germany, 2DOE Joint Genome Institute, Walnut Creek, USA, 3Botanical Institute and Cluster of Excellence on Plant Sciences (CEPLAS), Köln, Germany

The obligate biotrophic ascomycete fungus Blumeria graminis causes the powdery mildew disease on grasses including Triticum aestivum (wheat) and Hordeum vulgare (barley). Different formae speciales of B. graminis exhibit strict host specificity, e.g. the barley powdery mildew (B. graminis f.sp. hordei, Bgh) can only complete its pathogenic life cycle on barley, but not on other grasses. In our newly generated near-chromosome level genome assembly of Bgh we noted copy number variation of candidate secreted effectors between B. graminis formae speciales as well as a recent lineage-specific expansion of transposable elements. We hypothesize that the evolution of the fungus is fast enough to detect changes in its virulence spectrum within one year. To identify the nature of genomic alterations underlying such putative rapid evolutionary adaptations, we performed experimental evolution experiments with Bgh by exposing the fungal pathogen to normally inaccessible host plant environments. We found that three experimentally evolved Bgh isolate K1 derivatives (designated as SK1-SK3) display comparable levels of virulence on otherwise fully resistant barley mlo (Mildew locus O) mutant plants. By whole transcriptome shotgun sequencing (RNA-Seq) we identified 123 genes that are differentially expressed between SK1 and K1 at 18 hours post inoculation (the time of host cell penetration), suggesting that mlo virulence is polygenic and quantitative. Furthermore, we discovered that a gene coding for a transcription factor known to affect virulence and hyphal development is part of a ~40 kb genomic deletion in the majority of the virulent population. By contrast, we observed no deleterious genomic alterations in genes encoding candidate secreted effectors, which are thought to be key determinants of the fungal virulence spectrum. Taken together, we observed that Bgh isolates quickly broke barley mlo resistance, indicating that the fungus is capable of rapid evolution and fast adaption towards new host environments.

Transcriptome analysis of resistant and susceptible sugarcane cultivars infected with root-knot nematode Meloidogyne javanica and identification of SNP markers linked to resistance

Dr Meredith McNeil1, Dr Shamsul Bhuiyan2, Dr Jiri Stiller1, Ms Jingchuan Li2, Ms Janneke Drenth1, Dr Karen Aitken1  
1CSIRO Agriculture and Food, St Lucia, Australia, 2Sugar Research Australia, Woodford, Australia

Root-knot nematodes (RKNs, Meloidogyne javanica) are widely distributed and are economically important endoparasites of agricultural crops with a wide host range. To date, no studies have been published on the global gene expression profiling in sugarcane infected with RKN. Very little information is available about the molecular mechanisms that contribute to pathogenesis and defense responses in sugarcane against these pests. In this study, we performed transcriptome analysis of resistant (QBYN04-26030) and susceptible (QBYN04-26137) sugarcane clones from a BC1 spontaneum population infected with RKN Meloidogyne javanica. A combined total of 4.2 billion paired-end reads were generated on an Illumina NovaSeq 6000 platform from RNA extracted from the roots of both clones at 1 week and 10 weeks post inoculation (pi). Trimmed reads were mapped against a de novo transcriptome assembled from the raw reads and, to identify linked SNP markers, against ~81,000 contigs generated from the development of the Affymetrix® Axiom® Sugarcane 48K SNP array. Differential gene expression analysis showed numerous defence-related genes induced in plants infected with RKN and included genes such as receptor-like kinases (RLK), nucleotide-binding site-leucine-rich repat (NBS-LRR) proteins, PR-proteins, transcriptional regulators as well as known anti-nematode proteins such as a jacalin-related lectin gene. SNP markers were identified from these differentially expressed genes and converted to Fluidigm SNPType markers. These SNP markers were validated against a panel of sugarcane cultivars that had different levels of resistance to RKN. Candidate genes that contribute to protection against M. javanica in sugarcane were proposed and the possibility of using SNP markers linked to these genes in marker-assisted breeding in sugarcane are discussed.
Identification of species-specific effector candidates in host-specific scab fungi

Assoc Prof Kim Plummer\textsuperscript{1,2}, Shakira Johnson\textsuperscript{1,2}, Oliviah Lines\textsuperscript{1}, Dr Thomas Shaffee\textsuperscript{1}, Dr Dan Jones\textsuperscript{3}, Amali Thrimawithana\textsuperscript{3}, Dr Jason Shiller\textsuperscript{4}, Dr Cecilia Deng\textsuperscript{3}, Dr Carl Mesarich\textsuperscript{5}, Prof Hideo Ishii\textsuperscript{6}, Dr Bruno Le Cam\textsuperscript{4}, Dr Vincent Bus\textsuperscript{3}, Dr Joanna Bowen\textsuperscript{3}

\textsuperscript{1}La Trobe University, Melbourne, Australia, \textsuperscript{2}Plant Biosecurity CRC, Australia, \textsuperscript{3}New Zealand Institute for Plant & Food Research Limited, New Zealand, \textsuperscript{4}INRA, IRHS, The University of Angers, France, \textsuperscript{5}Massey University, New Zealand, \textsuperscript{6}Kibi International University, Japan

Venturia inaequalis, V. pyrina and V. nashicola are host-specific fungi, causing scab disease on apples, European pears and Asian pears, respectively. As many as 40 fungicide applications per season are required for scab control, and fungicide resistance and residues are an ongoing issue. Disease-resistant germplasm for apple and pear exists, however identification of durable disease resistance is critical, as breeding is slow with these woody, outcrossing hosts. Genetics of host-cultivar resistance to the apple scab fungus follows the gene-gene model, whereby pathogen effectors are secreted into the host environment during infection. A subset of effector proteins may be recognised as avirulence (Avr) determinants by their cognate plant resistance (R) proteins to induce a resistance response. Few R genes, and no Avr genes have been cloned for apple scab resistance and none for the pear scab resistance. The molecular basis of the predicted more durable, non-host resistance is unknown. Comparison of predicted secretomes of Venturia spp. revealed few genus and species-specific effector candidates that may determine host range. Many expanded putative effector families were identified, including orthologues of known fungal effectors. Effector candidates, including conserved and species-specific effectors are currently being functionally characterized.

Investigating the ‘double life’ of Phytophthora cinnamomi

Mr Barry William Schroeter\textsuperscript{1}, Prof David Miles Cahill\textsuperscript{1}, Dr James Edward Rookes\textsuperscript{1}

\textsuperscript{1}Life and Environmental Sciences, Deakin University, Waurn Ponds, Geelong, Australia

Phytophthora cinnamomi (P. cinnamomi) is a ruinous soil-borne oomycete and is considered to be one of the most destructive plant pathogens. Almost globally distributed, P. cinnamomi is known to cause disease and death in close to 5000 plant species. The ability to overcome such a broad host range can be attributed to the hemibiotrophic mechanism of infection, in which P. cinnamomi orchestrates a complex and phase-dependent release of secreted effectors and elicitor molecules that produce structural, metabolic and transcriptional changes in the plant host. Initially, the biotrophic phase allows P. cinnamomi to penetrate and invade root tissues by actively avoiding plant host defences either by inhibiting plant receptors or suppressing programmed cell death. A subsequent shift to a necrotrophic phase shows P. cinnamomi switch to flooding the surrounding cells with a cocktail of effectors that modulate gene expression or elicit defence responses that promote cell death. This bio-necro switch of P. cinnamomi is poorly characterised, as few transcriptional studies follow the pathogen expression throughout the various phases of infection. In this study, a model resistant (Zea mays) and a model susceptible (Lupinus angustifolius) host plants were inoculated with P. cinnamomi. Root samples are taken at eight-time points over a 72-hour post-inoculation period representing all relevant infection phases. Putative homologs of infection-related genes expressed in similar oomycete species have been identified in P. cinnamomi and optimised for RT-qPCR analysis. Understanding the expression patterns of these genes (e.g. P. infestans suppressor of necrosis 1, Nep 1-like proteins and Crinkler effectors) will delineate the timing and events of the biotrophic and necrotrophic phases of infection. This valuable information will direct subsequent dual RNA studies using Illumina Novaseq to identify stage-specific promoters or gene pathways for functionalisation studies using gene editing approaches.
The stem rust fungus *Puccinia graminis* f. sp. *tritici* induces waves of small RNAs with opposing profiles during wheat infection

**Jana Sperschneider**, Silke Jacques, Bo Xu, Narayana Upadhyaya, Rohit Mago, Karam Singh, Eric Stone, Ming-Bo Wang, Peter Dodds, Jennifer Taylor

1The Australian National University, Canberra, Australia, 2Centre for Crop and Disease Management, Department of Environment and Agriculture, Curtin University, Bentley, Australia, 3Black Mountain Science and Innovation Park, CSIRO Agriculture and Food, Canberra, Australia, 4Centre for Environment and Life Sciences, CSIRO Agriculture and Food, Perth, Australia, 5Thermo Fisher Scientific, Scoresby, Australia

The fungus *Puccinia graminis* f. sp. *tritici* (*Pgt*) causes devastating stem rust disease on wheat. Infection occurs when rust spores germinate on the leaf surface and subsequently, specialized infection structures called haustoria form inside host cells. During the late stages of infection, urediniospore production commences and urediniospore pustules erupt through the leaf or stem surface. Small RNAs (sRNAs) are critical regulators of gene expression and can play a significant role in plant-pathogen crosstalk and in regulation of developmental processes. How *Pgt* utilizes sRNAs during infection has thus far been unknown. We use a fully phased chromosome-scale *Pgt* assembly as well as small RNA and transcriptome sequencing during *Pgt*-wheat infection to show that the *Pgt* RNA interference (RNAi) machinery has functionally diversified. A number of *Pgt* RNAi genes are strongly up-regulated during late infection and this coincides with the production of distinct *Pgt* sRNA profiles during infection. Strikingly, over 90% of *Pgt* sRNAs are differentially expressed during infection, compared to only 2% of wheat sRNAs. An early wave of *Pgt* sRNAs expressed during infection constitutes of 21 nt sRNAs with a 5’ uracil derived from genes, whereas the late wave of *Pgt* sRNAs encompasses 22 nt sRNAs with a 5’ adenine derived from repetitive centromeric regions. The late wave of *Pgt* sRNAs appears to target largely transposable elements (TEs) and genes located in close proximity exhibit reduced expression, resembling the epigenetic silencing mechanism in plants. We conclude that the *Pgt* RNAi machinery has functionally diversified and is under tight temporal control, resulting in differential accumulation of *Pgt* sRNAs during the infection cycle. Future research can use this knowledge to optimize methods of host-induced gene silencing where small RNAs from the plant operate via the fungus’s own RNAi machinery to silence genes important for causing disease.

Using comparative transcriptomics to dissect host specific virulence effectors of wheat and barley pathogen *Bipolaris sorokiniana*

**Ms Haochen Wei**, Dr Megan McDonald, Prof Peter Solomon

1The Australian National University, Canberra, Australia

*Bipolaris sorokiniana* is the causal agent of spot blotch (SB), common root rot (CRR) and helminthosporium leaf blight (HLB) of both wheat and barley (Kumar *et al.*, 2002). These diseases impact on grain yields globally and can cause up to 100% losses in wheat in humid growing areas in southern Asia. During disease *B. sorokiniana* undergoes a rapid switch in lifecycle from biotrophic to necrotrophic in the early stages of infection, ultimately resulting in the death of host tissue. The contribution of fungal effectors to this pathosystem is poorly understood. My research is focussed on identifying host specific fungal effectors that facilitate pathogenicity in the different cereal hosts and mechanisms behind it. To do this, I undertook deep transcriptomic sequencing during infection using a previously uncharacterized, highly virulent *B. sorokiniana* strain. A comparison of gene expression levels between biotrophic and necrotrophic stages of *B. sorokiniana* was conducted on both susceptible wheat and barley. In this dataset, key components of fungal infection machinery were expressed on both wheat and barley. However, multiple other genes, including those encoding putative effectors, showed strongly differentiated transcriptional profiles between the two hosts. Twelve novel small, secreted protein (SSP) effector candidates which were significantly differential expressed between wheat and barley through various infection stages were identified. CRISPR/Cas9 mediated homologous gene replacement was used to explore the virulence contribution of those candidates in *B. sorokiniana*. All mutants have now been generated and are currently undergoing infection assays to determine the requirement of these putative effectors on disease in wheat and barley.
Are “minor” pathogens playing a major role? Identification of oomycete species contributing to yield loss in Australian processing tomatoes

Miss Sophia Callaghan1, Prof Lester Burgess3, Dr Peter Ades4, Ann Morrison2, Elizabeth Mann2, Dr Len Tesoriero5, Prof Paul Taylor1

1Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Melbourne, Australia, 2Australian Processing Tomato Research Council, Shepparton, Australia, 3Sydney Institute of Agriculture, The University of Sydney, Sydney, Australia, 4Faculty of Science, University of Melbourne, Melbourne, Australia, 5NSW Department of Primary Industries, CCPI, Ourimbah, Australia

Phytophthora nicotianae was once considered the primary cause of yield loss in field-grown processing tomatoes in north-central Victoria. Since then, there have been major agronomic advances, such as the shift from furrow to sub-surface drip irrigation. However, growers rarely meet their optimal yields. Hence, the aim of this project was to investigate the oomycetes associated with the poor growth of processing tomato crops. During surveys between 2016 and 2018, a total of 145 oomycete isolates, including 117 Pythium and 28 Phytophthora were recovered from 20 sites. Thirteen species of Pythium and two species of Phytophthora were identified based on morphological examinations and sequencing of the ITS, Cox-1 and Cox-2 regions. Pythium dissotocum was the most abundant and widespread species during the three years of surveys being identified at 70% of surveyed sites overall. The Phytophthora species, Ph. melonis and Ph. nicotianae, were only found at 15% of sites overall. None of the 13 Pythium spp., nor Ph. melonis, have previously been reported on field tomatoes in Australia. This is also the first report of Py. carolinianum, Py. heterothallicum, Py. hordeum, Py. recalcitrans and a new Pythium sp. being isolated from field tomato crops anywhere in the world. All species caused varying degrees of pre-germination disease in-vitro except for Py. carolinianum and Ph. melonis which were not pathogenic in any trial. In glasshouse trials, Ph. nicotianae and five Pythium spp. caused moderate to severe post-germination damping-off. Two months after inoculation, plants inoculated with Ph. nicotianae, Py. aphanidermatum, Py. dissotocum, Py. irregulare, Py. recalcitrans and Py. ultimum were significantly stunted. These results confirmed the importance of Ph. nicotianae as a pathogen of tomatoes but also showed that several Pythium spp. could be contributing to yield loss in Australian processing tomatoes and should not be overlooked in the development of IDM strategies.
Comparison of the reproduction and pathogenicity of isolates of *Radopholus similis* (burrowing nematode) from Australia and Fiji on ginger (*Zingiber officinale*) and banana (*Musa spp.*)

**Ms Jennifer Cobon¹**, Dr Tony Pattison², Dr Lindsay Penrose³, Dr Kerri Chandra³, Mr Wayne O'Neill¹, Dr Mike Smith⁴

¹Ecoscience Precinct, Queensland Department of Agriculture and Fisheries, Brisbane, Australia, ²Centre of Wet Tropics Agriculture, Queensland Department of Agriculture and Fisheries, South Johnstone, Australia, ³ABARES, Department of Agriculture and Water Resources, Braddon, Australia, ⁴Maroochy Research Station, Queensland Department of Agriculture and Fisheries, Nambour, Australia

Ginger is an important commercial crop with global trade of 1.3 million tonnes, worth US$1,038 million in 2016, but is impacted by several soil borne diseases including plant-parasitic nematodes. *Radopholus similis*, the burrowing nematode, has been recorded as a persistent problem in Fijian ginger production, but has not been recorded on ginger in Australia. The objective of this study was to establish if differences in the pathogenicity of *R. similis* on ginger exist between isolates from Fiji and Australia. Four Australian and two Fijian isolates of *R. similis* were compared in the glasshouse for their impacts on plant growth and multiplication on ginger and banana. Harvest and plant assessments were conducted over a 10-week interval, beginning 12 weeks after inoculation. All isolates of *R. similis* were able to multiply on ginger, but the two Fijian isolates reduced above and below-ground ginger growth and caused significantly greater damage to rhizomes than the four Australian isolates. In contrast, the Fijian isolates did not multiply on banana or have any damaging effects, whereas, the Australian isolates multiplied and caused damage on this host. Thus, *R. similis* isolates from Fiji and Australia differed in pathogenicity on ginger and banana, indicating pathotype differences between isolates. Given the pathogenic variability observed in this study, care should be taken when soil and plant material (e.g. fresh rhizomes) are transferred between Fiji and Australia to avoid the potential introduction of infected material that could be used for plant propagation.
Resistant potato cultivars, an undervalued management tool for the potato cyst nematode *Globodera rostochiensis* Ro1 on infested land in Australia

Dr Rudolf de Boer

1Agriculture Victoria Research, Bundoora, Australia

The potato cyst nematode, a very serious pest of potatoes world-wide, is a quarantine pest in Australia. Its distribution is restricted to a relatively small number of infested parcels of land in Victoria, subject to strict quarantine regulations designed to minimise the risk of further spread of the nematode. Generally, except for one control area, growers sow infested parcels of land to long-term pasture. In overseas studies, the natural decline rates of *G. rostochiensis* (*Gr*) are about 30% pa, at which rate, it would take over a decade for populations to decline to non-detectable levels from an initial density (*Pi*) of 100 eggs/g soil. Many commercial potato cultivars have the H1 resistance gene that confers near absolute resistance to Ro1, the only pathotype of *Gr* known to occur in Australia. In a field trial in Victoria, *Gr* populations declined by between 20-40% after one crop of resistant cultivars, with no measurable difference between initial and final densities after a fallow from a high average *Pi* of 115 eggs/g. Susceptible cultivars increased densities by up to three times *Pi*. However, overseas trials showed that *Gr* population decline rates depended on *Pi* (0.5-27 eggs/g soil), and at these relatively low levels, averaged 80% each year a resistant cultivar was grown in a rotation. In one instance, populations were reduced to non-detectable levels after three years of resistant cultivars, showing that a resistant cultivar is potentially a more effective management tool than long rotations with non-hosts. The population decline with a resistant cultivar depends on the proportion of eggs remaining unhatched each season, which, at a *Pi* of 115 eggs/g soil, is likely to be relatively high. Therefore, in the UK for instance, it is recommended that highly infested soils be treated with a fumigant, and or, a nematicide before cropping resistant cultivars.

Organic amendments: Stimulation of nematode trapping fungi, *Arthrobotrys musiformis* and *A. oligospora*

Mr Khoa Le1, Dr Graham Stirling2, Prof David Guest1, Dr. Francine Perrine-Walker3

1The University of Sydney, Sydney, Australia, 2Biological Crop Protection, Brisbane, Australia

Organic soil amendments are well-known as beneficial factors affecting soil nutrients, soil physical and biological conditions, and crop capability. In some crop systems, they offer a supplementing control method to chemical control of plant-parasitic nematodes. We investigated the use of organic soil amendments to control nematode damage on coffee. Sugarcane trash, lucerne hay, cow manure and chicken manure were added at a rate equivalent to 20 t/ha (i.e. 10 g organic amendment/kg soil) into 13 L pots containing 18 kg sand and 2 kg soil obtained from grass pasture and natural vegetation. A non-amended control was also included. Specifically, this tropical-glasshouse experiment was conducted to determine whether the organic amendments affected two nematode trapping fungi: *Arthrobotrys musiformis*, a constricting ring-forming fungus, and *A. oligospora*, a network-forming fungus, and their trapping activity on *Pratylenchus coffeae*, an important nematode pest of coffee. Before and 2, 4, and 8 months after the organic amendments were incorporated, soil samples were collected to quantify population density of *A. musiformis* and *A. oligospora*, and their predacious activity in the laboratory. While the population density of *A. musiformis* was mostly stimulated by sugarcane trash, amending cow manure, chicken manure or lucerne hay to soil greatly enhanced the population of *A. oligospora. Pratylenchus coffeae* was trapped by *A. musiformis* much more efficiently than by *A. oligospora* and there was a correlation between the level of suppression to *P. coffeae* and the population density of *A. musiformis*. From an environmental and public health perspective, the results demonstrate an effective alternative to pesticides and soil fumigation using to control coffee-parasitic nematodes.
Verticillium wilt management using organic soil amendments - in search for parameters of disease suppressiveness

Miss Mee-Yung Shin, Dr Ee Ling Ng, Dr Pablo Galaviz, Dr Tonya Wiechel, Prof Paul Taylor

Verticillium wilt is an important soilborne disease of potato which is primarily caused by *Verticillium dahliae* and *V. albo-atrum*. To date, Verticillium wilt has predominantly been managed using chemical fumigation. However, increased concern for the environmental and human health costs associated with this method has led to growing interest in the utilisation of organic amendments (OA). OAs, such as animal and plant-based composts, as well as agricultural and municipal wastes, are thought to decrease the severity of Verticillium wilt in crops. As such, they offer great promise as a sustainable and effective component of long-term disease management strategies. The efficacy of OAs in suppressing Verticillium wilt has been variable when compared with chemical fumigation. Hence, a review of published literature was undertaken to assess the magnitude of successful Verticillium wilt suppression by OAs, and to identify factors that contribute to reduced disease severity. Articles were obtained for meta-analysis using the Web of Science (Clarivate Analytics) and Scopus (Elsevier) databases using key words “organic amendment/waste/matter”, “compost”, “manure”, “Verticillium”, and “suppress*”. The final dataset (n=131), sourced from 13 articles published between 2000-2019, included data on OA application rate (v/v) and disease severity (%). There was a 21.5% reduction in disease severity with every 10% increase in OA application rate based on metaregression analysis. There were large variations in effect size across studies, of which 19% of these variations were explained by OA application rate. Benefits in disease control were consistently seen at OA application rates of 20% and 30% (v/v) based on multi-level analysis, suggesting that high application rates of OAs are required. Further analysis investigating the effect of different OA sub-types on disease severity, as well as the inoculum threshold for successful disease suppression is needed to better understand the parameters for successful Verticillium wilt control by OAs.

Understanding *Verticillium* inoculum levels in cotton soil

Dr Karen Kirkby, Ms Sharlene Roser, Dr Toni Chapman, Dr John Webster, Dr Steven Harden, Ms Shelby Young

Understanding the risk of Verticillium wilt in cotton is made easier with knowledge of inoculum levels in the soil. The incidence and severity of disease is influenced by many factors including: inoculum levels, strain of pathogen, timing of infection, nutritional status in the soil, pH, soil moisture, soil and air temperature, variety of cotton, plants stand, row configuration, rainfall and humidity. Inoculum thresholds have been established elsewhere such as Texas, California and China but the thresholds vary and apply to the region in which they were developed. No thresholds have been available for Australian cotton growers until now. This presentation will provide a summary of the natural fluctuations of inoculum levels throughout the cotton growing season and results of the five field trials conducted by NSW DPI pathology over two seasons to develop a disease risk matrix with pre-season thresholds for *Verticillium dahliae* inoculum levels. One hundred and forty plots from two commercial cotton farms in two cotton growing valleys were combined to determine if there was a relationship between pre-season inoculum levels and disease incidence in the following crop. A positive relationship was found between the minimum disease incidence and increasing propagules per gram of soil. No direct relationship was found between inoculum levels and severity of disease. This may be explained by the fact that one propagule per gram of soil is sufficient to cause disease. Additionally, not every infected plant presents with external disease symptoms of wilting, leaf mottling/necrosis or defoliation. In the 2017/2018 season, 41% of infected plants had no external symptoms but when the stems were cut they all had vascular discolouration. The timing of infection plays a large part in the severity of the disease with early infection often having a greater impact than late infections.
General surveillance function of plant diagnostic clinics: new detections by Crop Health Services, Agriculture Victoria, 2017-2019

Dr Ramez Aldaoud1, Mrs Srikanthi de Alwis1, Dr Quang Dinh1, Mrs Soheir Salib1, Dr John Wainer1, Mr Con Skyllas1, Dr Brendan Rodoni2, Dr Mali Malipatil3, Dr Fiona Constable1, Dr Cliff Kinoti1, Mr Ruvinda Kankanamalage1, Dr Rachel Mann1, Ms Elisse Nogarotto1, Dr Linda Semeraro1, Dr Mark Blacket1, Mrs Robyn Brett1, Mr Chris Bottcher1, Dr Lixin Eow1, Dr Isabel Valenzuela1, Dr David Lovelock1, Mr Perrin Carter1, Mrs Ayfer Kocak1, Mr Stuart Wells1, Dr Jacqueline Edwards1

1Crop Health Services (CHS), a business of Agriculture Victoria, conducts plant diagnostic services of pests and diseases that mainly affect plants in the state of Victoria, and occasionally samples are submitted from other states. Diagnoses assist the management of productivity, biosecurity and market access for the State’s plant-based industries and the protection of the environment. CHS have well equipped labs, an up-to-date sample tracking and reporting system, and is underpinned by a comprehensive reference collection. CHS diagnostic staff apply a wide range of techniques, including cultural, morphological, biochemical, molecular and immunological techniques, to accurately identify suspect pathogens and pests, with many of the tests NATA-compliant. Staff are members of the National Plant Biosecurity Diagnosticians Network and participate in the annual national proficiency testing program. Fee-for-service clients are more likely to submit specimens with unusual symptoms that they cannot diagnose themselves. In this way, plant diagnostic services provide an important general surveillance function for Australia. CHS has an agreement with Biosecurity and Agricultural Services, Agriculture Victoria, to report suspect and confirmed exotic plant pathogens and pests and new host records to the Victorian Chief Plant Health Officer within 24 hours of detection under the State’s General Surveillance project. During 2017-2019, CHS conducted more than 6,000 diagnoses on samples submitted by the public, consultants, and State and Federal biosecurity agencies. In this time, we have detected many new records for Victoria and Australia (including new host records), which have been or are currently undergoing reporting to the Chief Plant Health Officers.
Established non-native forest pests and pathogens in Australia — accumulation, response to detection, and impact

Dr Angus Carnegie1, Dr Helen Nahrung2
1NSW Department Of Primary Industries - Forestry, Parramatta, Australia, 2Forest Industries Research Centre, University of the Sunshine Coast, Maroochydore, Australia

Geographic isolation and a robust biosecurity system have resulted in Australia remaining free from many devastating exotic pests and pathogens found in other countries. Nevertheless, around 260 non-native pests and pathogens of arborescent hosts have established in Australia since 1885. Although the risk of invasive species arriving and establishing in Australia is increasing through increased trade and travel, the rate of establishment of non-native forest pests and pathogens has remained relatively constant over the last 130 years, with non-native species accumulating at a rate of about two per year. Most of these affect host genera exotic to Australia, including the main plantation species, Pinus radiata; few are pests of Australian native genera. Less than 10% of these pests and pathogens have caused significant impact or resulted in ongoing management costs in commercial plantations, native forests or amenity trees. Thirty-four new detections of forest pests and pathogens were made since 1996, the majority (71%) via passive surveillance: 24% by public, 12% by industry, and 34% by researchers. More than half of all detections since 1996 were made by APPS or Australian Entomological Society members. This highlights the need for ongoing awareness campaigns and adequate systems for passive surveillance detection, reporting and response. There has been an increase in detections in recent years from active surveillance, but most exotic forest pests and pathogens were not detected early enough to attempt eradication. Early detection is key to successful eradication, yet only one pest of arborescent hosts has been successfully eradicated from Australia, the nematode Bursaphelenchus hunanensis. Cost:benefit analyses of key invasive species illustrated the benefit of biosecurity activities to the forest industry. However, all forest/tree stakeholders (industry, all levels of government, and environment) need to be involved for forest biosecurity to be effective.

Patho Blitz - an Atherton Tableland first

Ms Kathy Grice1, Mr Peter Trevorrow1, Dr Roger Shivas2, Mr Craig Marston3
1Department of Agriculture and Fisheries, Mareeba, Australia, 2Department of Agriculture and Fisheries, Dutton Park, Australia, 3Department of Agriculture and Water Resources, Brisbane, Australia

The aim of Patho Blitz was to develop the skills of early to mid-career pathologists and diagnosticians in various aspects of collecting and processing diseased plant specimens. Funding for the workshop was provided by the Department of Agriculture and Water Resources (DAWR), and convened by staff at the Mareeba Department of Agriculture and Fisheries, Queensland (DAF). Based on the Bush Blitz (www.bushblitz.org.au) concept, twenty six scientists from around Australia converged on the Atherton Tablelands (north Queensland) for the 5-day blitz in May, 2019. The location provided a diverse range of ecosystems within a 50km radius of home base. Sites surveyed included natural grassland, rainforest, horticultural, forestry and broad acre cropping systems. Mornings were spent out in the field collecting, followed by processing and curation of samples collected in the afternoons, conducted in a make-shift laboratory. Specialists in mycology, bacteriology, virology (including phytoplasmas) and botany were on hand, together with local pathologists and agronomists with in-depth knowledge of the region and cropping systems. The workshop provided a unique opportunity for those participants that were purely laboratory based or with limited to no field experience. The format allowed participants to hone their field skills in plant disease recognition, sample collection and handling in addition to the curation of samples and laboratory assessment (microscopy and isolation). A session in the use of Loop mediated isothermal amplification (LAMP) as a field diagnostic tool was conducted using bacterial wilt (Ralstonia pseudosolanacearum) and Queensland Fruit fly as case studies. In total, 202 specimens were collected of which 116 were fungal samples, including 19 entomopathogenic fungi. A further 60 suspected virus and 23 phytoplasma samples were collected for further assessment, along with 3 samples for bacterial determination. All of the fungal samples were lodged in the Queensland Plant Pathology Herbarium (BRIP).
Genomic analysis of a *Pseudomonas syringae pv actinidiae* outbreak in Australian kiwifruit production

Rachel Mann¹, Noel Djitro¹, Elisse Nogarotto¹, Soheir Salib¹, Tongda Li¹, Fiona Constable¹, Brendan Rodoni¹

¹Agriculture Victoria Research, Bundoora, Australia

*Pseudomonas syringae pv actinidiae* (Psa), the causal agent of bacterial canker of kiwifruit, is responsible for crop losses in kiwifruit production worldwide. The pathovar includes six distinct lineages of varying virulence and global distribution described as biovars. The strain responsible for the economically significant Psa pandemic across Europe, New Zealand, Asia and Chile is Psa biovar 3 or Psa3. In 2011, Victoria was surveyed for the presence of Psa but only *P. syringae pv. actinidifolium* (previously Psa4 or Psa-LV), a low virulence biovar, was detected. In October 2018, kiwifruit samples from Victoria with symptoms resembling Psa infection were submitted to Crop Health Services at AgriBio for diagnosis. Psa3 was detected on these samples and emergency response measures were enacted. Genomic analysis of more than 20 Psa isolates from this outbreak provides insight into the origin of this outbreak in a global context.

Innovative plant pathogen diagnostics using metabarcoding on biosecurity surveillance traps

Mr Conrad Trollip¹,², Dr Brendan Rodoni¹,², Dr Jacqueline Edwards¹,²

¹School Of Applied Systems Biology, La Trobe University, Bundoora, Australia, ²Agriculture Victoria Research, Department of Jobs, Precincts and Regions, Bundoora, Australia

Current diagnostic protocols used for the identification of plant pathogens in post-border biosecurity surveillance programmes still rely heavily on traditional microbial isolation and DNA barcoding techniques (1). Recent advances in environmental DNA (eDNA) sequencing and metabarcoding has brought about a more promising platform for early detection and broad spectrum monitoring of plant pathogens (1,2). To date, the majority of mycological metabarcoding studies have relied on using universal primers, such as those designed to amplify the internal transcribed spacer (ITS) region, to ensure broad coverage while assessing diversity (3). In a diagnostics framework, however, the use of ITS alone does not discriminate accurately for many groups of important pathogens (1,2). Additionally, the reliability of sequence clustering methods is brought into question when using short sequences to discriminate between closely-related taxa which can share more than 99% sequence similarity (4). In this study, the taxonomic resolution afforded by amplicon sequencing using high-throughput platforms is being investigated for the detection of high priority pathogens important for Australian biosecurity. The results of this study may provide a rapid and reliable diagnostics pipeline for improved post-border biosecurity surveillance.

Presence, absence, eradication and disappearance: potato diseases in Western Australia

Dr Margaret Uloth1, Mr Marc Poole1, Dr Nichole Hammond1

1Department of Primary Industries and Regional Development, South Perth, Australia

A critical re-evaluation of the pest status of potato pathogens in Western Australia was undertaken as part of a comprehensive policy review for the importation of ware potatoes. Historical records from 1133 potato samples submitted to the Department of Primary Industry and Regional Development for diagnosis between 1955 and 1992 were tabulated, and digital diagnostic records from 1993-2018, Western Australian Culture Collection lists, potato seed certification reports and survey data were examined for indications of disease presence. Annual reports of the Government Plant Pathologist from 1929 to 1974, historical correspondence and industry magazines were also checked.

Five potato pathogens previously recorded in published lists as present in Western Australia are now considered absent. They are bacterial wilt (Ralstonia solanacearum), potato cyst nematode (Globodera rostochiensis), late blight of potato (Phytophthora infestans), violet root rot (Helicobasidium purpureum) and stem nematode (Ditylenchus dipsaci).

Successful eradication campaigns eliminated R. solanacearum in 1987 and G. rostochiensis in 1989. Intermittent outbreaks of P. infestans occurred in Western Australia from 1909 -1954, although the disease was of minor importance and P. infestans has not been reported since 1966. Two doubtful records of H. purpureum exist from 1919 and 1931, but no cultures were retained for verification and the fungus has not been reported again. It is likely that 1950s records of D. dipsaci associated with cereals and clovers resulted from the erroneous identification of native Ditylenchus species, and extensive surveillance over the past 30 years has not detected D. dipsaci. Furthermore, there have been no reports of D. dipsaci from horticultural crops in Perth since 1964. Based on criteria listed in ISPM 8 – Determination of pest status in an area, these five pathogens are classed as absent from WA. Changes in pathogen distribution, improvements in identification methods and ongoing taxonomic revisions all contribute to the need for continuing revision of pathogen lists.
Extracellular vesicles as key mediators of plant-microbe interactions

Brian D. Rutter¹, Patricia Baldrich², Hana Zand Karimi¹, Ram Podicheti¹, Blake C. Meyers² and Prof Roger W. Innes¹

¹Department of Biology, Indiana University, Bloomington, Indiana, 47405 USA; ²Donald Danforth Plant Science Center, St. Louis, Missouri, 63132 USA

Exosomes are extracellular vesicles (EVs) that play a central role in intercellular signaling in mammals by transporting proteins and small RNAs. Plants are also known to produce EVs, particularly in response to pathogen infection. Our laboratory has developed methods for purifying EVs, which has enabled us to characterize their contents. These analyses have revealed that plant EVs are highly enriched in proteins involved in biotic and abiotic stress responses, and carry miRNAs and siRNAs. They are also highly enriched in single stranded RNAs of 10-15 nucleotides in length, which we have named ‘Tiny RNAs’ (tyRNAs). These tyRNAs are derived from diverse sources, and appear to be degradation products of longer RNA molecules. Recent work has established that EVs are rapidly taken up by filamentous pathogens from host plants and in vitro, and we are currently investigating the mechanism of uptake and the impacts of EVs on fungal physiology. These findings suggest that EVs represent an important component of the plant immune system.
Cross-Kingdom RNAi between plants and fungal pathogens

Qiang Cai, Baoye He, Shumei Wang, Prof Hailing Jin
Department of Microbiology & Plant Pathology, Center for Plant Cell Biology, Institute for Integrative Genome Biology, University of California, 900 University Ave., Riverside, CA 92521, USA.

Small RNAs (sRNAs) are a class of short non-coding RNAs that mediate gene silencing in a sequence-specific manner. We have demonstrated that some sRNAs from eukaryotic pathogens, such as Botrytis cinerea, the fungal pathogen that causes grey mold disease on more than 1000 plant species, can be transported into host plant cells and suppress host immunity genes for successful infection (1). We recently discovered that such cross-kingdom RNAi is bi-directional. Plants can also send small RNAs into pathogens using extracellular vesicles to silence its virulence genes as part of its immune responses. During the co-evolutionary arms race with the pathogen, plants have adapted exosome-like extracellular vesicles as one of the major pathways to deliver sRNAs into fungal cells and induce cross-kingdom RNAi (2). The potential mechanisms of sRNA loading into the plant extracellular vesicles will be discussed. Furthermore, we also discovered that B. cinerea can take up double-stranded RNAs (dsRNA) and sRNAs from the environment. Applying sRNAs or dsRNAs that target Botrytis Dicer genes on the surface of fruits, vegetables and flowers significantly inhibits grey mold disease (3). Such pathogen gene-targeting RNAs represent a new generation of fungicides that are durable and eco-friendly.

Assessment of fungicide resistance in *Botrytis cinerea* from cherry fruit

**Miss Elaine Tai¹**, Dr Tamieka Pearce¹, Dr Jason Scott¹, Dr Karen Barry¹

¹Tasmanian Institute Of Agriculture, Hobart, Australia

Botrytis cinerea is the main cause of rot of sweet cherry fruit in Tasmanian orchards. Despite good crop hygiene practices, crop management and extensive fungicide programs, disease prevalence can be high in conducive conditions. A study was conducted to determine if, and to what extent, resistance of *B. cinerea* has developed to currently registered fungicides used in sweet cherry orchards. Over 100 isolates of *B. cinerea* were obtained from mature, symptomatic fruit following surveys at three commercial sweet cherry orchards in southern Tasmania in December 2018 and January 2019. Using a hyphal tipping method these isolates were prepared as single genotypes for fungicide sensitivity screening. In addition, 11 single genotype isolates of *B. cinerea* were used a reference, which were collected prior to exposure to the selected fungicides. Several fungicides with different categories are used to control grey mould disease in cherry production, including succinate dehydrogenase inhibitors (SDHI; FRAC group 7), quinone outside inhibitors (QoI; FRAC group 11) and dicarboximides (DC; FRAC group 2). We selected two SDHI fungicides (boscalid and fluopyram), one QoI fungicide (pyraclostrobin, a strobilurin) and one dicarboximide (iprodione). Measurement of fungicide sensitivity was conducted on potato dextrose agar amended with each fungicide at five concentrations (0, 0.05, 0.5, 5 and 50 μg a.i./ml) in triplicate. Radial fungal growth was measured after 4 days growth. Data analysis included determining the EC50 discriminatory dose, modelled EC50 and calculation of resistance factors (RF). Preliminary results have detected evidence of reduced fungicide sensitivity in the *B. cinerea* isolates from cherry orchards to boscalid and fluopyram, and full results are forthcoming.

Developing a fungicide efficacy baseline for *Venturia inaequalis* in Western Australia.

**Dr Andrew Taylor¹**, Mr Lincoln Harper², Dr Fran Lopez Ruiz²

¹Department of Primary Industries and Regional Development WA, Bunbury, Australia, ²Centre for Crop and Disease Management (CCDM), School of Molecular and Life Sciences, Curtin University, Bentley, Australia

Apple scab, caused by the fungus *Venturia inaequalis*, has been present in Western Australia (WA) for several years after area freedom was lost in 2009. The origin of the apple scab in WA is unknown and its distribution within the state restricted, partially due to regular application of fungicides. However, *V. inaequalis* is considered a high-risk pathogen for the development of fungicide resistance and reliance on fungicides of the same mode of action for control could lead to management issues in the future. A survey was conducted in the 2018/19 season where 20 isolates of *V. inaequalis* were collected from commercial orchards and retail outlets in apple growing regions in the Perth Hills, Donnybrook and Bunbury. All isolates were assessed in vitro for growth rate against actives from four modes of action: DMI's (Group 3), QoI (Group 11), AP (Group 9) and SDHI's (Group 7). A range of sensitivities was found across the isolates when tested against a DMI (myclobutanil), SDHI (boscalid) and an AP (cyprodinil) fungicide. Calculated as a percentage radial growth (%RG) when compared to the untreated controls, these sensitives range from 123 – 38%, 155 – 56% and 112 – 0% for myclobutanil (DMI), boscalid (SDHI) and cyprodinil (AP), respectively. No growth for any of the isolates was observed on the trifloxystrobin (QoI) dose used in this study. The analysis of the target genes for the DMI, SDHI, AP and QoI fungicides (Cyp51, SdhB, cgs and Cytb, respectively) in each isolate revealed no correlation between the mutations found and the sensitivity shifts recorded for each of the fungicides. No changes were found in the known mutation “hot spot” region of the *cytB* gene. All isolates have been lodged in the WA plant pathology reference culture collection (WAC) as representative baseline samples for potential testing in later years.
Fluxapyroxad (Sercadis® Fungicide) activity on apple scab (*Venturia inaequalis*), powdery mildew (*Podosphaera leucotricha*), alternaria leaf blotch (*Alternaria mali*) in apple (*Malus domestica*) in Australia

**Mr Marco Montagna**¹, Mr Gavin Heard¹, Mr Ian Francis¹

¹BASF Australia Ltd, Southbank, Melbourne, Australia

Fluxapyroxad belongs to the group of the succinate de-hydrogenase (SDHI) class of fungicides. Within the SDHI, fluxapyroxad in part of the chemical family pyrazole carboxamide. Fluxapyroxad is foliar systemic and rapidly taken up from the leaf surface after foliar application. Fluxapyroxad controls pathogens at a number of stages in their lifecycle, including spore germination, preventing germ tube elongation, hyphal penetration and mycelium growth, giving it protective and curative activity. Furthermore, fluxapyroxad showed to be effective on a wide range of pathogens in several broadacre and horticulture crops. A total of 21 field trials in Australia tested the efficacy and crop safety of 1.0 to 6.0 g a.i./100 L fluxapyroxad in apple (*Malus domestica*) for apple scab (*Venturia inaequalis*), powdery mildew (*Podosphaera leucotricha*) and alternaria leaf blotch (*Alternaria mali*). The efficacy trials demonstrated that fluxapyroxad applied at 6 g a.i./100 L rate provided effective control of apple scab, powdery mildew and alternaria leaf blotch in apples. In addition, in the trials fluxapyroxad was compared to other fungicides commercially available and commonly used in apple, and its performance was equivalent or superior to those standards. No phytotoxicity symptoms were observed in any trial site. In light of the robust efficacy and crop safety data generated, and the resistance management option that will be offered, fluxapyroxad will be an excellent new tool for the control of apple disease for farmers.

The activity of mefentrifluconazole (Belanty® Fungicide) on powdery mildew (*Uncinula necator*) in grape (*Vitis vinifera* L.) in Australia

**Mr Marco Montagna**¹, Mr Gavin Heard¹, Mr Ian Francis¹

¹BASF Australia Ltd, Southbank, Melbourne, Australia

Mefentrifluconazole (Belanty® Fungicide) is the first Isopropanol-azole which belongs to the triazoles chemical family. Over many years, triazole-based fungicides have played a significant role in the fungicide programmes on many economically important crops. Mefentrifluconazole, with its unique chemistry, exhibits a very broad level of efficacy against many fungal pathogens in broadacre and horticulture crops. The efficacy and crop safety of mefentrifluconazole was evaluated in grape (*Vitis vinifera* L.) for the control of powdery mildew (*Uncinula necator*), across the major growing regions in Australia from 2013 to 2017. A number of different formulations of mefentrifluconazole were tested at the rates of 2.0 to 6.0 g a.i./100 L rates. Efficacy data showed that mefentrifluconazole had very high activity on *Uncinula necator* providing complete control of the disease in many situations. In addition, mefentrifluconazole out-performed or was at least equivalent to other commercial fungicide included in the trials. The trials also showed that multiple applications of mefentrifluconazole were safe to grape. The excellent level of efficacy and crop safety of mefentrifluconazole demonstrates it is an effective new tool for Australia grape farmers for the control of powdery mildew in grape.
Poster Session 1 - Agrichemicals & Managing Chemical Resistance 1  
Tuesday 26 November 2019, 5:15 PM - 6:15 PM

**Poster Board 35**

**Mefentrifluconazole (Belanty® Fungicide) activity on apple scab (*Venturia inaequalis*), powdery mildew (*Podosphaera leucotricha*), alternaria leaf blotch (*Alternaria mali*) in apple (*Malus domestica*) in Australia**

**Mr Marco Montagna¹**, **Mr Gavin Heard¹**, **Mr Ian Francis¹**  
¹BASF Australia Ltd, Southbank, Melbourne, Australia

Mefentrifluconazole (Belanty® Fungicide) is the first Isopropanol-azole which belongs to the triazoles chemical family. Over many years, triazole-based fungicides have played a significant role in the fungicide programmes on many economically important crops. Mefentrifluconazole, with its unique chemistry, exhibits a very broad level of efficacy against many fungal pathogens in broadacre and horticulture crops. The efficacy and crop safety of mefentrifluconazole was tested between the 2013 and 2017 growing seasons on apple scab (*Venturia inaequalis*), powdery mildew (*Podosphaera leucotricha*) and alternaria leaf blotch (*Alternaria mali*) across the major apple (*Malus domestica*) growing regions in Australia at the 2.0 to 6.0 g a.i./100 L rates. Mefentrifluconazole was safe to apple as no phytotoxicity was observed in any trial. Efficacy data showed that mefentrifluconazole provided excellent control on apple scab and very high activity on powdery mildew and alternaria leaf blotch. This demonstrate the wide spectrum of activity of mefentrifluconazole. Furthermore, in the trials mefentrifluconazole was compared to other fungicides commercially available and commonly used in apple. Mefentrifluconazole demonstrate to be equivalent or superior to the other active ingredients. In conclusion, mefentrifluconazole is a new effective diseases management tool for apple farmers in Australia.

**Poster Board 37**

**Pyraclostrobin+fluxapyroxad (Merivon® Fungicide): a new dual mode of action fungicide for the control of husk spot (*Pseudocercospora macadamiae*) in macadamia (*Macadamia integrifolia*) in Australia**

**Mr Marco Montagna¹**, **Mr Gavin Heard¹**, **Mr Ian Francis¹**  
¹BASF Australia Ltd, Southbank, Australia

Fluxapyroxad belongs to the succinate dehydrogenase inhibitors (SDHI) mode of action and to the chemical family pyrazole carboxamide. The compounds of this family bind to the ubiquinone-binding site of the mitochondrial Complex II inhibiting fungal respiration. These fungicides have a broad activity spectrum on several pathogens in a wide range of crops. Pyraclostrobin belongs to the quinone outside inhibitors (QoI) mode of action and to the chemical family methoxy carbamate. These fungicides inhibit the fungi’s ability to produce energy, blocking the transfer of electrons at the quinone site of the bc1 complex (complex III in the electron transport chain). Pyraclostrobin is a wide-spectrum fungicide, globally registered on a large number of broadacre and horticulture crops. Pyraclostrobin (Cabrio™ Fungicide) has been used at the rate of 10 g a.i./100 L for the control of husk spot (*Pseudocercospora macadamiae*) of macadamia (*Macadamia integrifolia*) for a number of years. The application of 10 g a.i./100 L fluxapyroxad in combination to 10 g a.i./100 L pyraclostrobin as pre-mixed commercial fungicide (Merivon™ Fungicide) decreased disease incidence on fruit by 58% and disease severity by 27% when compared to pyraclostrobin alone. This higher level of efficacy from the two different modes of actions also delays the development of *Pseudocercospora macadamiae* resistance to SDHI and QoI fungicides. The trials also showed that pyraclostrobin + fluxapyroxad was safe to macadamia. The high efficacy, together with the two modes of action allows Merivon® to be a very effective fungicide for husk spot control and fungicide resistance management in macadamia orchards.
Evaluation of fungicide soil drench treatments to manage black root rot disease in avocado seedlings

Dr AkilaDevi Prabhakaran1, Assoc Prof Elizabeth Dann1
1Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Australia.

Black root rot (BRR) caused by soil borne nectriaceae fungi Calonectria ilicicola (Ci) and Dactylonectria macrodidyma (Dm), is one of the major diseases of avocado (Persea americana) seedlings and young trees, causing losses within nurseries and new plantings around Australia. At present BRR is primarily managed by adopting good nursery and cultural practices. An integrated disease management program for BRR is yet to be established. Hence, glasshouse experiments were conducted to evaluate the efficacy of four fungicides: Scholar® (fludioxonil); Banrot®, (thiophanate-methyl and etridiazole); Octave® (prochloraz as the manganese chloride); and Sportak® (prochloraz). Chemicals were applied as post-infection drench treatments to suppress the pathogens and control BRR in avocado seedlings (cv. Reed). Of the four fungicides tested, Scholar® significantly reduced the frequency of re-isolation (4.25%) and root necrosis (10.8%), caused by C. ilicicola in seedlings 5 weeks after inoculation, compared to water drenched control seedlings (91.8% and 73.3% for re-isolation and root necrosis, respectively) and other fungicides. Root fresh weight and plant height was increased after Scholar® treatment compared to control (water) and other fungicide treatments. Similarly, in another experiment with D. macrodidyma, soil drenching with all three fungicides except Sportak® significantly reduced root necrosis (12.9, 13.3 and 15.4% for Octave®, Scholar® and Banrot®, respectively) in avocado seedlings 10 weeks after inoculation, compared to the control seedlings drenched with water (39.2%). Re-isolation frequencies of D. macrodidyma were reduced by Octave® (16.7%) and Scholar® (20.8 %) compared to water control (50%). Overall, the current study demonstrated that soil drenching with fungicides Scholar® (against Ci and Dm) and Octave® (against Dm) has the potential to suppress the nectriaceous black root rot pathogens sufficiently to allow successful establishment of new trees when planted in the orchard.
Poster Board 38

Festival of Plant Health 2020: a road map to promote the International Year

Mr Andrea Masino¹, Prof Lodovica Gullino M.¹,², Mr Ralph Lopian³
¹Centre for the innovation in the agro-environmental field, AGROINNOVA, University of Torino, Grugliasco, Italy, ²Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Grugliasco, Italy, ³Ministry of Agriculture and Forestry of Finland, Helsinki, Finland

The United Nations (UN) General Assembly declared 2020 as the International Year of Plant Health (IYPH). IYPH will be joined globally by all Plant protection’s actors to raise awareness about the role of Plant Health for our lives and the importance to protect the world’s plant resources from pests and diseases. The plant pathology’s worldwide community will promote a multitude of activities with the aim of positioning itself as main actor of the IYPH by 2020. In Italy, Agroinnova, the Centre of Competence for the innovation in the agro-environmental field of the University of Torino, works with the local Institutions to explain how environmental, biodiversity, biosecurity and crop protection’s research activities have impacted during the last 15 years. Several initiatives linked to each other by the theme of plant health, will lead to a cultural Festival in Torino from June 4 to 6, 2020. Artistic performances, concerts, exhibitions, shows, talks, round tables, workshops and open days are able to communicate the results of researches more effectively. As plant resources provide oxygen, foodstuffs and medicines to our society, it is crucial that citizens better understand how their health impacts sustainable agriculture and food security, as well as ecosystem protection. The IYPH should increase trust in science, innovation and in academic research and should function as an example that most of the challenges of our time can only be successfully addressed through science and research.

Poster Board 39

iMapPESTS: aiming for the sky in cross-industry plant pest surveillance initiative

Shakira Johnson¹, Rohan Kimber², Andrew Baker³, Brendan Rodoni⁴, Dusty Severtson⁵, Dean Brookes⁶, Nicole Thompson⁷, Darren Kriticos⁸, David Teulon⁹, Jessica Holliday¹⁰
¹AUSVEG, ²South Australian Research & Development Institute, ³ScIOT, ⁴Agriculture Victoria, Department of Jobs, Precincts and Regions, Victoria ⁵Department of Primary Industries and Regional Development, Western Australia , ⁶University of Queensland, ⁷Sugar Research Australia, ⁸The Commonwealth Scientific and Industrial Research Organisation, ⁹The New Zealand Institute for Plant & Food Research Limited, ¹⁰Hort Innovation, Australia

Australia’s agriculture and horticulture industries have joined forces to change the way airborne pests and diseases are detected. The iMapPESTS: Sentinel Surveillance Systems for Agriculture program (iMapPESTS for short) will provide the foundation for a nationwide plant pest surveillance system to monitor and report the presence of pests that threaten major agricultural sectors across Australia, including grains, cotton, sugar, horticulture, wine and forestry industries. A custom-designed prototype ‘sentinel’ mobile surveillance unit has been designed to offer optimal sampling of either airborne fungal spores or airborne insects. Samples captured by the sentinels are sent to entomologists and molecular diagnosticians for identification of target pests and diseases, such as powdery mildew and light brown apple moth. The sentinels also collect environmental data at the time of sampling, which are married with pest and disease information and stored in a secure cloud-based system for downstream reporting. Agriculture Victoria are using samples to test the application of Next Generation Sequencing diagnostic techniques for the broadscale detection of exotic pests and diseases. The iMapPESTS website aims to act as a centralised repository for all project-related data, reports and other materials generated across the eight distinct sub-projects nested within the overarching project.
Poster Board 67

The impact of the outbreak of tomatoes disease *Tuta absoluta* in Nigeria

**Mr Michael Oke**
*Michael Adedotun Oke Foundation, Federal Capital Territory, Nigeria*

In 2016 an outbreak of the tomato leaf miner pest *Tuta absoluta*, locally called 'tomato ebola' in Nigeria, resulted in adverse scarcity of tomatoes in the various markets of the affected states. The pest is known all over the world, as it originated from South America as far back 1912 and has ravaged tomato farms in many countries including Europe, Middle East, Asia and Africa. The leaf miner entered Nigeria through Niger Republic, as the adult moth stage with the larva boring into the fruits and stem of the tomato plant. The pest has invaded farms in Nigeria in Kastina, Kano, Kaduna, Jigawa, Nasarawa, Lagos, Oyo and Ogun States and other tomato producing states. Infestation by *T. absoluta* can be widespread throughout tomato farms within 48 hours. Pesticides cannot control the disease as it easily develops resistance. This paper describes the Nigerian experience of the infestation by *T. absoluta*, the impact on tomato production and the Federal Government's response to control the problem. Surveys of farms and markets were undertaken to ascertain the effect of this pest on supply, price and consumption of tomatoes. Further research is needed to study the effect and analyze the losses to farmers, and government support is needed to continue sustainable production of fruits for local consumption.

Poster Board 66

A review of red rot of sugarcane in Pakistan

**Mr Waqas Arshad**,* Miss Saman Shahzadi*,* Dr Shahid Afghan*
*1Sugarcane Research and Development Board, Faisalabad, Pakistan, 2University of Agriculture, Faisalabad, Pakistan*

Sugarcane is the main source of the world’s sugar that is valued at $US 97.2 billion (2017) and is projected to increase at 4.6% annually. Sugarcane is cultivated in 103 countries with Pakistan fifth in area under cultivation at 1.22 million hectares making it an important agro industrial crop. Diseases, particularly, red rot caused by Colletotrichum falcatum, are major factors for the Pakistan’s low yields of only 60.31 tons/ha. Losses estimated at 10-77% in cane yield and sugar recovery at 4-74% have been reported. Among sugarcane diseases, red rot, is the most destructive economically. Red rot was first reported in Pakistan in 1986, it affects quality and cane yield and in the most severe cases completely kills the plants. Red rot appears to infect and spread in the wet rainy (Monsoon) season in Pakistan. The pathogen, *C. falcatum*, is highly variable pathogenically making it extremely difficult to obtain stable resistant varieties though out the country. Keeping in view of the losses due to red rot in Pakistan’s sugar industry, this study focuses on red rot’s distribution, mode and source of infection, description of casual pathogen and disease management.
Poster Board 63

Comparison of aggressive and non-aggressive *Ascochyta lentis* isolates on lentil cultivar PBA Hurricane XT

Miss Jade Rose$^{1,2}$, Prof Eileen Scott$^1$, Dr Jenny Davidson$^{1,2}$, Mrs Sara Blake$^{1,2}$

$^1$South Australia Research and Development Institute, Adelaide, Urrbrae, 5064, Australia, $^2$The University of Adelaide, School of Agriculture, Food and Wine, Adelaide, Urrbrae, 5064, Australia

*Ascochyta lentis* is the causal agent of the foliar fungal disease ascochyta blight of lentil. Until late 2018, the cultivar PBA Hurricane XT was rated moderately resistant to ascochyta blight, when its rating was downgraded to moderately resistant–moderately susceptible in South Australia. Nine isolates varying in aggressiveness or virulence on PBA Hurricane XT were assessed on selected lentil cultivars. The objective was to determine whether the infection processes of those isolates differed on other lentil cultivars with different resistance ratings. Conidial length and width, conidia germination percentage, and cultural growth were assessed *in vitro* to investigate if aggressiveness of isolates could be associated with morphological characteristics. Conidial germination, germ tube length and development of appressoria were assessed *in planta*. Culture colony area *in vitro* increased over time however, all isolates were similar. Conidial length differed among isolates however, this difference was not associated with aggressiveness. The percentage of germinated conidia increased over time although all isolates were similar. Histopathology studies revealed the percentage of germinated conidia differed among cultivars however, not among isolates. The percentage of conidial germination and appressorium formation increased over time however, no differences were found for isolate or cultivar. Isolates differed in mean germ tube length *in planta* but this was not associated with aggressiveness. Controlled environment inoculation studies were undertaken to assess the range of aggressiveness among selected isolates on cvs PBA Hurricane XT and Cumra (susceptible check). Disease assessment showed a significant difference in the interaction between isolate and host for percentage of leaf area diseased. Both *in vitro* and histopathological studies indicated that aggressiveness among isolates cannot be determined solely from these methods. To elucidate the defence responses of PBA Hurricane XT, a larger study with more isolates and cultivars would be beneficial.

Poster Board 65

New pathogens on leafy vegetable for the ready-to-eat sector

Prof Lodovica Gullino M.$^{1,2}$, Dr Giovanna Gilardi$^1$, Mr Andrea Masino$^3$, Prof Angelo Garibaldi$^1$

$^1$Centre for the innovation in the agro-environmental field, AGROINNOVA, University of Torino, Grugliasco, Italy, $^2$Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Grugliasco, Italy

Italy is the second producer in Europe of fresh-cut leafy vegetables. During the past years many new diseases caused by soil-borne and foliar pathogens were observed for the first time worldwide on salads grown for this sector. Among foliar diseases, *Fusarium equiseti* on wild and cultivated rocket and lettuce, *Allophoma tropica* on lettuce, *Colletotrichum kahawae* on cultivated rocket, *Paramyrothecium roridum* on lamb’s lettuce and *Albifimbria verrucaria* on spinach and wild rocket were observed. Among the soil-borne pathogens, *Pythium aphanidermatum*, *P. irregularare*, *P. sylvaticum*, and *Pythium* Cluster B2a have frequently been isolated on spinach, Swiss chard, lamb’s lettuce and lettuce. *Fusarium oxysporum* f. sp. *lactucae*, present in Europe since 2002, is spreading in new countries. The new race 4 of the pathogen, first isolated in the Netherlands, has been recently found in Belgium, United Kingdom, Ireland and Italy. Some of these new pathogens are seed transmitted. The dynamism and specialization of such sector, together with the lack of adequate crop rotation and the globalization of the seed market, are the main causes of the development of many new pathogens that cause severe field losses. In the meantime, some of the newly introduced pathogens, typical of warmer areas, are easily spreading due to the increase in temperature. Newly observed diseases of the most important crops grown for this sector (lettuce, wild and cultivated rocket, lamb’s lettuce, chicory, endive, spinach and Swiss chard) are described.
Identification of the powdery mildew species infecting mungbean in Australian paddocks

Ms Lisa Kelly\textsuperscript{1,2}, Dr Niloofar Vaghefi\textsuperscript{2}, Prof Levente Kiss\textsuperscript{2}
\textsuperscript{1Department Of Agriculture And Fisheries, Toowoomba, Australia, \textsuperscript{2}University of Southern Queensland, Toowoomba, Australia}

Powdery mildew is a significant disease for mungbean (\textit{Vigna radiata}) growers in all areas of production across Australia. Recent field trials in Queensland have demonstrated that the disease can reduce yields by up to 40\% in conducive seasons when no management strategy is implemented. Despite spending more than ten years trying to breed cultivars with improved resistance to the powdery mildew pathogen(s), the Australian National Mungbean Improvement Program has only released cultivars that are regarded as moderately susceptible. Current disease management therefore, relies solely on multiple fungicide applications. In Australia, the mungbean powdery mildew is thought to be caused by \textit{Podosphaera xanthii}, although the description of the causal agent has changed over time. Research outside of Australia refers to the causal agent as \textit{Erysiphe polygoni}. This project was developed to validate the taxonomy of the species causing powdery mildew in Australia, and further understanding of the pathogens host range, virulence and potential resistance to DMI fungicides. Recent findings from this project have indicated that \textit{P. xanthii} and a second species, preliminary identified as \textit{Erysiphe sp.}, cause powdery mildew of mungbean in Australia. Future research aims to accurately identify the \textit{Erysiphe} sp., and determine the host range, virulence, fungicide resistance and yield loss caused by both pathogens. The results of this project will greatly improve our understanding of the pathogens and their life cycles, and provide the necessary foundations for the development of integrated disease management strategies.

Effects of grapevine trunk disease on wine composition

Miss Rebecca Woolley\textsuperscript{1}, Mr Dion Mundy\textsuperscript{1}, Mr Andrew McLachlan\textsuperscript{2}, Mrs Claire Grose\textsuperscript{1}
\textsuperscript{1Plant and Food Research, Blenheim, New Zealand, \textsuperscript{2}Plant and Food Research, Palmerston North, New Zealand}

Grapevine trunk diseases (GTDs) are associated with multiple fungal species that infect the vascular tissue in perennial organs of grapevines (\textit{Vitis vinifera}). Infections lead to rotting of woody tissue and produce a range of associated symptoms, including shoot stunting, foliar chlorosis and reduced berry yield. This project investigates whether trunk disease also affects the quality of wine produced from infected plants. Prior to vintage, two vineyards with Sauvignon blanc grapes in Marlborough, New Zealand, were visually assessed for symptoms of GTD (cankers, non-productive sections of head, and stunted foliar growth). For winemaking, 40 kg of grapes were hand-harvested for each treatment (with or without GTD symptoms) and replicated four times for each vineyard. The chemical composition of grape juice and wine from vines with and without GTD symptoms were evaluated. Combined results from both vineyards revealed small yet significant changes in the pH (-0.03) and optical density at 520 nm (+0.76) of grape juice from wines with trunk disease (p<0.05). Four characteristics of wine showed marginal differences between vines with trunk disease versus without: titratable acidity (+0.39 g/L with GTD symptoms; p=0.056), glucose (-0.24 g/L; p=0.058), and optical density at 420 nm and 420:320 (-0.061 and 0.0019; p<0.05 and p=0.052, respectively). These findings represent a snapshot from 1 year of a 3-year study. The small chemical differences detected thus far indicate that trunk disease may alter fruit composition enough to have some effect pre- and post-fermentation. Further sensory work to evaluate the perception of chemical changes in the wine is warranted. The findings from this project have economic impacts with respect to the quality of wine produced from vineyards with substantial incidence of trunk disease.
Poster Board 61

**Reaction of different species of Fabaceae and Solanaceae to three Cucumber mosaic virus isolates**

*Dr Mohammad Aftab¹, Dr Solomon Maina¹, Ms Narelle Nancarrow¹, Dr Piotr Trebicki¹*

¹Agriculture Victoria, Horsham, Australia

Amongst the seed-borne viruses, *Cucumber mosaic virus* (CMV) is the most important which significantly decreases yield in chickpea, lentil and lupin. CMV isolates collected from lentil and lupin crops from Horsham, Victoria in 2018 were compared to an isolate of CMV that had been maintained in tobacco plants. The test plants were grown in insect-proof cages in the glasshouse. Two weeks after germination 10-30 seedlings of *Nicotiana tabacum*, *N. glutinosa*, *Capsicum annuum*, *C. frutescens*, *Pisum sativum* and *Vicia faba* were mechanically inoculated with the three CMV isolates. Four weeks after inoculation, the seedlings were tested for the presence or absence of CMV using tissue blot immunoassay. Selected positive plants of tobacco and capsicum were kept longer for symptom observation. *Nicotiana tabacum*, *N. glutinosa* and the field pea cultivar Parafield were infected by all three isolates. The isolate of CMV from tobacco infected most of the faba bean cultivars but not many field pea cultivars. The isolate of CMV from lupin did not infect any faba bean cultivar. *Nicotiana tabacum* and *N. glutinosa* infected with all three isolates showed mosaic symptoms. Most of the capsicums infected with the isolates of CMV from lentil and lupin showed mottling. The isolate-host response variability will require high throughput sequencing studies such as RNASeq analysis to unravel any genomic differences.

Poster Board 60

**Diaporthe spp.: pathogen or saprophyte of persimmon?**

*Dr Cathryn Todd¹, Mrs Barbara Hall³, Dr Suzanne McKay³*

³SARDI, Adelaiade, Australia

*Diaporthe* spp. are common on several hosts and can be either parasitic or saprophytic. At least five species recovered from trunk cankers of persimmon in South Africa were shown to be pathogenic and recently *D. neotheicola* was identified as the cause of shoot blight symptoms on persimmon. In 2018, trunk canker symptoms including raised areas of damaged bark and sunken, brown necrotic lesions and vascular tissue were observed on young persimmon trees. Isolations confirmed the presence of a *Diaporthe* spp. and sequence comparison of the ITS region showed similarity to *D. fraxini-angustifoliae*, found in Australia on ash trees. The pathogenicity of the isolates was tested on 1 and 2-year-old wood of 2-yo persimmon trees maintained in a greenhouse. A circle of bark, 6 mm in diameter, was removed with a corer and agar containing mycelia or clean agar as control was inserted at the inoculation site and sealed with parafilm. Three months after inoculation the external, visual symptoms on both ages of wood consisted of minor darkening, sinking of tissue and dark staining below the bark that sometimes spread to 1 cm above and below the inoculation site. Reisolation of *Diaporthe* spp. from inoculated wood of both ages was possible from all the 8 inoculation sites and occasionally from the extension of staining. *Diaporthe* spp. was also reisolated from some controls, which could indicate the presence of *Diaporthe* in the wood prior to inoculation, or as a saprophyte on the bark. The symptoms after 3 months were not the same as those originally observed. We suggest that *D. fraxini-angustifoliae* is possibly a saprophyte that, given the right environmental conditions, becomes pathogenic and causes a slow progressing disease in persimmon. Pathogenicity tests will be undertaken on more plants using a longer incubation period.
Geographical distribution of two turf grass pathogens, *Wongia griffinii* and *W. garrettii*, in Australia

**Dr Percy Wong**¹, Mr Albert Leggett², Dr Peter Martin¹

¹Plant Breeding Institute, The University Of Sydney, Cobbitty, Australia, ²Turfcare Australia Pty Ltd, Rydalmere, Australia

In Australia, two serious turf diseases cause the grass hosts to decline over several years, resulting in unsightly patches of dead or dying grass. They are summer decline, caused by *Wongia griffinii*, and Adelaide patch, caused by *W. garrettii* (¹, ²). The pathogens are ectotrophic root-infecting fungi, which cause root and rhizome necrosis and the eventual death of plants. The diseases are mainly severe on intensively managed golf and bowling greens, but have occurred on home lawns and sports fields. A preliminary survey has found that *W. griffinii* has a wide geographical distribution in Australia, occurring on many golf and bowling greens in all the mainland states. The *W. griffinii* has been identified from diseased couch (*Cynodon dactylon*), hybrid couch (*C. dactylon* x *C. transvaalensis*), South African couch (*C. transvaalensis*) and kikuyu (*Pennisetum clandestinum*). By contrast, *W. garrettii* appears to have a more restricted distribution and has only been identified from three couch bowling clubs in Adelaide, South Australia, a couch bowling club in Carnarvon, Western Australia, and a buffalo (*Stenotaphrum secundatum*) lawn in Bourke, New South Wales. The diseases have not been successfully managed by fungicides.

Detection platforms of various crop plant fungal diseases using next generation molecular tools

Dr Prasannakumar MK1, Mr Gopal Venkatesh Babu2, Ms Parivallal P Buela1, Ms K Nandini1, Dr ManMohan Singh1, Ms Sanju Balan2, Ms Kavashree K1, Ms Jayashree A1, Mr Balanagouda Patil1, Mr Shridhar Shivakumar Hiremath1

1CAAST Project-Training, Department of Plant Pathology, University of Agricultural Sciences, Bangalore, India, 2Center for Excellence in Botany, Madras University, Chennai, India

Fungal diseases in commercially important crop plants result in a considerable reduction in both value and yield, often leading to the loss of an entire plant. In order to curtail the losses, it is crucial to detect and identify the pathogens at an early stage. There is a need for rapid and easy detection methods of fungal pathogens. In this study, cDNA was synthesised from fungal RNA followed by use of specific primers for the detection of fungal pathogens (Alternaria solani, Magnaporthe oryzae, Sarocladium oryzae and Sclerotium). Loop-mediated isothermal amplification (LAMP) is a useful DNA detection method with high specificity and sensitivity. We conducted a LAMP assay, as well as conventional PCR, and quantitative real-time PCR (RT-qPCR) assays to determine which of these techniques was less time consuming, more sensitive, and more accurate. We based on our assays on specific genes for all the four fungal pathogens. The LAMP assay provided rapid and accurate results, amplifying the target pathogen in less than 60 min at 63°C, with 10-fold greater sensitivity than conventional PCR. qPCR was the most sensitive among the assays evaluated, being 10-fold more sensitive than LAMP and conventional PCR for the least detectable DNA concentration (100 fg). The LAMP assay was simpler and faster than the other assays evaluated. The LAMP assay provided also higher specificity than qPCR. Hence, this technique has greater potential for developing quick and sensitive visual detection methods than do other conventional PCR strategies for detecting permitting early prediction of disease and reducing the risk of epidemics. The need for establishing next generation diagnostic tools is to prevent the introduction of new plant diseases. These tools can also be used for seeds and propagative plant materials to reduce disease incidence and spread in future.
Detection and quantification of plant pathogens using Droplet Digital PCR

Mr Mark Andersen1, Dr Simona Nardozza1, Ms Marcela Martinez-Sanchez1, Associate Prof Matt Templeton1,2
1The New Zealand Institute for Plant and Food Research Ltd, Auckland, New Zealand, 2University of Auckland, Auckland, New Zealand

The ability to rapidly detect and identify a pathogen is a valuable tool in combatting outbreaks and incursions of plant pathogens. New techniques and adaptations of existing techniques have assisted in the area of diagnostics providing new opportunities for improvement in speed and specificity of detection. One such method is the technology of Droplet Digital PCR (ddPCR). ddPCR is an extension of digital PCR, where partitioning and amplification are used to give an accurate measure (quantification) of target sequences without the need for external standards. Precise quantification of target sequence can help us understand host-microbe interactions by giving accurate assessments of pathogen load, and the role that plays in pathogenicity. It can also resolve uncertainties arising from faint bands produced in conventional PCR, or high C\textsubscript{T} values in real-time quantitative PCR (qPCR). We tested the utility of ddPCR in quantifying two distinct plant pathogens: *Pseudomonas syringae* pv. *actinidiae* (Psa), the bacterium responsible for bacterial canker of kiwifruit; and *Ceratocystis fimbriata*, a fungal disease complex responsible for numerous diseases in a diverse range of plants. Primers developed for qPCR were able to be used to detect and quantify Psa and *C. fimbriata* using ddPCR. As the two systems use different technologies this was not guaranteed, and may not apply in all cases. For *C. fimbriata* we were able to clearly identify samples which comprised a mixture of target sequences. This may be the result of a mixed infection, or heterogeneity within an organism of the target internal transcribed spacer (ITS) sequence. This can provide valuable information in understanding the evolution of the pathogen - helping elucidate close phylogenetic relationships or incidences of horizontal gene transfer. It is also important in the development of detection assays, as it can provide a greater understanding of the efficacy of the different assays.
Visual assessment is a customary means for disease detection. This limits its utility to symptomatic phases of disease, and by then significant damage may be underway. Recently, non-invasive and potentially high throughput proximal and remote sensing options have emerged, some with a potential for early disease detection. One such system involves hyperspectral sensors. Here, we report on preliminary results from a controlled infection study where by hyperspectral reflectance from wheat leaf surfaces were captured over several days from the time of infection. The results showed that reflectance spectra of inoculated (with *Parastagonospora nodorum*) and uninoculated (water or gelatine control) wheat leaves (cv. Emu Rock) became divergent within 72 hours post-inoculation. The spectral reflectance divergence became more pronounced with time. That the signals were related to disease caused by the fungal pathogen were verified from qPCR analysis of samples, which showed tight relationship between spectral response and qPCR estimates of fungal biomass. These results, while thus far are limited to one pathogen (hence needing assessment with a wider array of pathogens), provide a clear indication of the promising potential of hyperspectral sensing for early disease detection, and possible early management intervention.
Poster Board 70

Effects of light spectra on growth and defence in potted *Actinidia chinensis var. deliciosa* ‘Hayward’ kiwifruit plants

**Dr Tony Reglinski**¹, Dr Nick Gould¹, Dr Kirstin Wurms¹, Ms Nicola Haisman¹, Mr Patrick Snelgar¹, Dr Annette Ah Chee¹, Ms Rachelle Anderson¹, Mr Joseph Taylor¹

¹The New Zealand Institute For Plant & Food Research, Hamilton, New Zealand

Light is critical for plant growth and development. Moreover, spectral distribution has been found to affect plant defence signalling. This study investigated effects of artificial lighting on growth and on defence elicitation in potted *Actinidia chinensis* var. *deliciosa* ‘Hayward’ kiwifruit plants. Greenhouse plants under natural light were compared with counterparts grown in a temperature-controlled room under high-pressure sodium lamps (HPS; peaks at 570 and 589 nm) and light-emitting diodes (LED Red 440 nm and LED Red/Blue 440 nm and 670 nm). Shoot extension was not significantly affected by light source over the four-week experimental period; however, towards the end of the trial a trend emerged which suggested faster shoot elongation under HPS and LED Red than in the greenhouse or under LED Red/Blue. The chlorophyll content and photosynthetic rate were higher in greenhouse plants than under HPS or LED whereas the reverse was true for total phenolic content, which was greatest under LED Red and LED Red/Blue. Constitutive foliar resistance to *Pseudomonas syringae* pv. *actinidiae* (Psa biovar3) was greater on LED Red plants than LED Red/Blue or HPS. Treatment with acibenzolar-S-methyl (ASM) induced a reduction in Psa leaf necrosis in greenhouse plants, relative to controls, but not in plants grown under artificial lighting, suggesting that inducible resistance was affected by light spectra. The expression of putative markers of defence (PR1 and β-1,3, glucosidase) differed between treatments; PR1 was more strongly induced by ASM in the greenhouse than under artificial light whereas β-1,3, glucosidase was more strongly induced in ASM-treated plants after Psa inoculation under artificial light than in the greenhouse. These findings demonstrate the potential to manipulate plant growth and defence by modification of the light spectrum.

Poster Board 73

Effect of in-furrow phosphorus and zinc on Fusarium crown rot of hard red and soft white winter wheats in Oregon, USA

**Mr Duncan Kroese**¹, Mr Larry Lutcher², Mrs Christina Hagerty¹

¹Oregon State University, Columbia Basin Agricultural Research Center, Adams, United States, ²Oregon State University, Morrow County Extension, Heppner, United States

Fusarium crown rot is a major limitation to the two-billion-dollar winter wheat production region of the inland Pacific Northwest (PNW), USA. Genetic resistance to Fusarium crown rot is poorly understood, and major-gene resistance to Fusarium crown rot is not available in PNW-adapted cultivars. Furthermore, chemical control is not effective to control Fusarium crown rot and crop rotation to disrupt cycles of disease is not feasible in many water-limited environments of the inland PNW. As such, farmers seek relevant cultural control methods to help control yield loss from Fusarium crown rot. It is well established that an over-supply of plant available nitrogen and/or drought conditions can contribute to increased Fusarium crown rot. However, the relationship between other plant available macro- and micro-nutrients and Fusarium crown rot is less understood. We conducted a Fusarium crown rot inoculated study over two years and two locations in a 26-28 cm rainfall zone of Oregon, USA. We utilized a full factorial design with three rates of phosphorus (0, 11.2, 33.6 kg/ha) and two rates of zinc (0, 5.6 kg/ha) applied in-furrow on hard red and soft white wheats to test the following alternative hypotheses: Alternative hypothesis 1; Additional nutrients boost root growth and/or plant health to provide root disease robustness through disease avoidance and/or disease tolerance, Alternative Hypothesis 2; Additional nutrients contribute to plant biomass and thus late-season water stress to increase root disease. Preliminary data suggest that alternative hypothesis 2 is supported, as phosphorus and zinc applications increased yield and plant biomass but may also increase Fusarium crown rot.
A screening technique for alternative management options of *Thielaviopsis musarum*

**Mr Peter Trevorrow**, **Ms Kathy Grice**, **Ms Tegan Kukulies**

1. *Department of Agriculture and Fisheries, Mareeba, Australia*, 2. *Department of Agriculture and Fisheries, South Johnstone, Australia*

Crown end rot is a post-harvest disease of banana caused by a range of fungal organisms. Symptom expression can vary from a superficial mould to a severe breakdown of the crown end and pulp tissue. The latter is caused by the fungus *Thielaviopsis musarum* and is more prevalent during the winter months. The occurrence of the disease is sporadic but has a high consequence for growers as infected consignments are rejected at ripening facilities or the market place. An inoculation technique was required to achieve consistent and repeatable levels of disease, necessary to test the efficacy of the current registered fungicides. Experiments were undertaken to determine the spore concentration and the length of exposure time required to provide consistent disease incidence and severity. All experiments were conducted using commercially harvested Cavendish bananas and ripened under near commercial conditions. A ten-fold serial dilution ranging from $10^6$ to $10^1$ spores per ml was used and the most consistent results were achieved using concentrations of $10^5$ and $10^6$. For the exposure times, inoculation treatments comprised: 5, 15, 30 seconds and one minute duration. All durations resulted in infection, however, the 30-second treatment was chosen as the optimum exposure time due to the uniformity of disease development. Using a spore concentration of $10^6$ and a 30-second duration, an experiment was conducted to determine if the current registered fungicides Tecto® (thiabendazole) and Protak® (prochloraz) applied at recommended rates either as a dip or as a spray to the point of run-off had efficacy against *T. musarum*. Results suggest that prochloraz was more effective than thiabendazole when applied as a spray treatment, but they were of similar efficacy when applied as a dip. The efficacy of other fungicides and biological products will be tested as potential alternative management options for *T. musarum*.

The use of totally impermeable film with fumigants improves control of charcoal rot of strawberry

**Dr Dylan McFarlane**, **Mr Apollo Gomez**, **Dr Scott Mattner**, **Mr David Oag**

1. *Victorian Strawberry Industry Certification Authority, Toolangi, Australia*, 2. *Department of Agriculture and Fisheries, Brisbane, Australia*

Charcoal rot, caused by the soil-borne fungus *Macrophomina phaseolina*, is currently threatening the viability of the Australian strawberry industry. The disease has increased in importance in strawberry crops worldwide following the withdrawal of the soil fumigant, methyl bromide. Current industry practice of soil disinfestation with fumigants does not adequately control the disease. The greater the concentration and time (C x T) fumigants remain in soil, the more effective they are at controlling pathogens, including *M. phaseolina*. Traditionally, strawberry growers have sealed soils with semi-permeable film made from low density polyethylene (LDPE) to minimise emission losses of fumigants. Totally impermeable film (TIF) contains a layer of ethylene vinyl alcohol that makes it impermeable to the movement of fumigants. We conducted a series of soil-column and field experiments to evaluate the use of TIF with current soil fumigants for improved control of *M. phaseolina* and charcoal rot of strawberry, compared with LDPE film. Results showed that TIF significantly increased C x T values of the fumigants 1,3-dichloropropene and chloropicrin in soil by an average of 50-100%, compared with LDPE film. The use of fumigants with TIF significantly reduced concentrations of DNA of *M. phaseolina* in soil relative to LDPE film, over the course of a year. This resulted in significantly less charcoal rot in strawberry plants in soil treated with fumigants and TIF. Further, the use of TIF with fumigants significantly increased strawberry yield by 30% and revenue by $6/m, compared with LDPE film. This increase in revenue was considerably greater than the higher cost ($0.11/m) of TIF relative to LDPE film. We conclude that the use of TIF with fumigants is a cost-effective treatment for strawberry growers aiming to improve control of charcoal rot.
Effect of fungicides and variety resistance on the suppression of Fusarium head blight and Deoxynivalenol

Miss LeAnn Lux
North Dakota State University, Fargo, United States

North Dakota produces more than half of the total hard red spring wheat (HRSW) in the United States averaging, an annual total of 9740 metric tons. Fusarium head blight (FHB) is the most significant disease of HRSW in North Dakota (ND), the disease has been responsible for severe reductions in both yield and quality, resulting in billions of dollars in losses since the early 1990s. Fusarium graminearum, primary cause of FHB in ND, produces the mycotoxin deoxynivalenol (DON) which leads to dockage and, in some cases, rejection at the point of sale. The importance of FHB prompts the continual evaluation of varietal resistance and fungicides in suppressing FHB and DON in HRSW. Three integrated management experiments were conducted at three locations in eastern ND in 2019. The two varieties used in the experiments were WB-Mayville (susceptible) and ND-VitPro (intermediate resistance). Fungicides evaluated were the demethylation inhibitors metconazole, propiconazole, prothioconazole and tebuconazole, and the succinate dehydrogenase inhibitor pydiflumetofen. Fungicides were applied once either at Feekes 10.51 (early anthesis) or 3 to 7 days after Feekes 10.51. Research plots were inoculated using Fusarium-infected corn spawn to help elevate disease risk in the plots. Moderate to high levels of disease occurred at all three locations, with significant differences in FHB severity and incidence. Yield and DON levels will be obtained at season’s end and be reported. Results of the experiments will be used to help update management recommendations on FHB and DON for HRSW growers in ND.

Seed Potato Certification: an important role

Dr Nigel S. Crump, Ms Crystal Wilkinson, Ms Michelle Wilson, Mr Barry Strahan, Mr Mitchell Gorman, Ms Nellie A. Malseed, Ms Kerrie Hollis
AuSPICA, Toolangi, Australia

Certified seed potatoes underpin the multi-million-dollar national potato industry, including the increasing export markets. Total value of annual potato production in Australia is around $745 million (2017). All sectors (fresh/table and processing) of the Australian industry are underpinned by certified seed potato production. The successful development and administration of the seed certification scheme in Australia has meant that there has been: reliable high health seed production; increased yields and product quality of commercial crops in the fresh and processing industries; enhanced efficiency in the use of natural resources including land and water; management of potato diseases including many viral diseases that severely limit yield and quality; reduced necessity to use pesticides to manage pest problems; and a high adoption of Integrated Pest management practices. Seed potato certification contributes to the increased production of potatoes in Australia despite declining areas of production. Seed potato certification programs are designed and administered as a means to provide reasonable assurances of seed quality. Many potato diseases are systemic in potato plants and can be carried in or on the surface of seed tubers. Monitoring of seed crops for disease is largely by visual inspection supported by laboratory testing using ELISA or PCR technology. The tolerances of these diseases for seed certification vary from zero tolerance to an acceptable rating of incidence x severity. With trained field certification officers frequently monitoring over 2000 ha of seed crops, there is the ability for the early detection of new incursions of pests and diseases. Seed potato certification schemes have a considerable role in the biosecurity of the National Potato Industry for exotic pests such as Potato Cyst Nematode (PCN). There is a long history of soil testing for PCN, thereby minimising the spread of the PCN throughout Australia and true indication of pest free areas.
A brief historical review of fifty-year’s progress in South Australian management of grapevine downy mildew - once the major foliage disease in Australian viticulture

Mr Peter A Magarey

Magarey Plant Pathology, Loxton, Australia

In 1970, the inaugural year of APPS, when the SA Department of Agriculture’s plant pathologist Peter Dry began investigating the conditions favouring the disease, a 50-year investigation into improved management of downy mildew in the Riverland and Australian vineyards was initiated. First discovered in Australia in the wet-season 1917, downy subsequently spread across the eastern states. In the very wet 1950s, the disease spread further but spray machinery remained primitive. Severe national outbreaks in the mid-1970s catalysed the Loxton investigation into finer aspects of disease epidemiology. Prior to 1970, downy spread during ‘warm-wet’ days and ‘in wetter-than-average’ seasons. Hydraulic-boom and air-mist sprayers, if present, applied Bordeaux mixture or the new dithiocarbamates on a calendar-based schedule of 4-6 sprays/season but crop loss continued when protective applications were applied after infection. In this pre-electronic era, clockwork-driven weather instruments with ink-nibs drew wiggly lines across paper charts to monitor temperature, humidity, leaf wetness or rainfall. Significant research in Europe was still published in French or German, limiting Australian progress. International exchanges were few. In the 1980s-90s, long-term international collaboration with pathologists from Cornell University and elsewhere boosted progress. Networks of electronic weather stations were established in regional vineyards and DModel, an innovative computer-based simulator of downy epidemiology, was built to process weather data. Phone, fax and, later, email, provided growers advice of disease risk. In the late-1990s, national collaboration led to AusVit®, an advanced decision-support system that included downy and the other grapevine diseases and pests but it became a little-used market failure. Since 1995, CropWatch® and, latterly, the web-based GrowCare® services, combined with advanced spray technology, provide a disease risk advisory service for growers to make ‘decisions with precision’. SMS-based disease risk alerts are now sent within minutes of vineyard infection events. Downy mildew is no longer Australian viticulture’s major foliage disease.
Protecting the Australian capsicum industry from incursions of exotic Colletotrichum pathogens

Ms Awalikara De Silva\textsuperscript{1}, Prof Pedro Crous\textsuperscript{2}, Dr Peter Ades\textsuperscript{3}, Prof Paul Taylor\textsuperscript{1}
\textsuperscript{1}Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Australia, \textsuperscript{2}Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584 CT, The Netherlands, \textsuperscript{3}Faculty of Science, The University of Melbourne, Parkville, Australia

Anthracnose of chili (Capsicum annuum) causes major production loss throughout Asia where chili fruit are grown. Species identification from multigene phylogenetic analysis across five countries in Asia and Australia identified several pathogenic species including four novel species. Colletotrichum scovillei was recognised as a biosecurity threat to the Australian chili industry as it was the major pathogen of chili in Asia identified from all the surveyed countries in Asia but has yet to be identified in Australia. A species-specific PCR assay was thus developed and validated for reliable identification of C. scovillei along with two other exotic species, C. acutatum and C. nymphaeae, that cause anthracnose in chili. Three species-specific primer pairs were designed based on the intergenic spacer (IGS) region which identified each species in uniplex conventional PCR assays. These species-specific primer pairs showed high specificity to each of the respective species and were efficient at a range of annealing temperatures. In addition, a TaqMan real time PCR assay developed using C. scovillei primer pair qIGSF3-qIGSR2 and a MGB probe qIGSP was highly specific for the genomic DNA of C. scovillei and did not amplify the genomes of 14 related Colletotrichum species. The sensitivity limit of this assay, measured using the cycle threshold (Ct) value, ranged from 13.5 for 10 ng to 26.34 for 10 pg of genomic DNA of C. scovillei. The designed real time qPCR assay was suitable for detection and quantification of genomic DNA of C. scovillei in culture however, the assay will need further optimization to develop an in planta diagnostic test to detect C. scovillei in infected plant tissue. Developed species-specific diagnostic probes for pathogen detection is of great importance for biosecurity and will assist in the early detection of exotic pathogens and in the implementation of appropriate management techniques to prevent incursion of exotic species.

Development of loop-mediated isothermal amplification assay for the detection of seedborne fungal pathogen, Sarocladium oryzae causing sheath rot of rice

Dr MK Prasannakumar\textsuperscript{1}, Ms Parivallal Buela\textsuperscript{1}, Dr Manjunatha C\textsuperscript{2}, Mr Gopal Venkatesh Babu\textsuperscript{1}, Ms K Nandini\textsuperscript{1}, Mrs V V Kavyashri\textsuperscript{1}, Ms B N Ashwini\textsuperscript{1}, Mr Chittaragi Amoghavarsha\textsuperscript{1}, Mr B M Kiran\textsuperscript{1}, Mr Tripathy Abhisek\textsuperscript{1}, Ms A Sagna\textsuperscript{1}, Ms S E Navyashree\textsuperscript{1}, Dr K T Rangaswamy\textsuperscript{1}
\textsuperscript{1}CAAST Project-Training, Department of Plant Pathology, University of Agricultural Sciences, Bangalore, India, \textsuperscript{2}ICAR-Indian Agricultural Research Institute Regional Station, Wellington, Tamil Nadu, INDIA, OOTY, India

Sheath rot disease of rice caused by Sarocladium oryzae has become an important production constraint in all rice-growing countries. The detection of pathogens in rice seed is necessary to maintain high quality standards in order to avoid production losses. Thus, a simple, reliable, specific and sensitive method for surveillance is vital to screen infected seeds and seedlings at early developmental stages. In this study, we have developed an isothermal-mediated amplification technique (LAMP) for early and accurate detection of S. oryzae in rice seeds. The genomic DNA was extracted from rice seeds using a high-throughput DNA extraction method and was further used as template for PCR and LAMP assays. The LAMP assay could detect the presence of S. oryzae genomic DNA at a concentration as low as 100 fg within 15 min at 60 °C. Two DNA intercalating dyes (ethidium bromide and SYBR Green) and two pH indicator dyes (Neutral Red and Phenol Red) were used to visualize positive LAMP assays. Finally, the specificity of LAMP assay was validated against five isolates of S. oryzae and ten other fungal pathogens of rice. Our results demonstrate that LAMP is a useful and convenient tool for detecting S. oryzae in rice seeds, and it can be applied widely to detect sheath rot disease of rice.
Development of a multiplex-PCR approach for the accurate and rapid detection of *Gnomoniopsis smithogilvyi* in *Castanea sativa* (Mill.)

**Mr Matias Silva-Campos**, Dr Md Tohidul Islam¹, Prof David Cahill¹

¹School of Life and Environmental Sciences, Deakin University, Waurn Ponds, Australia

The fungus *Gnomoniopsis smithogilvyi* (syn: *castanea*) causes chestnut rot in the European chestnut (*Castanea sativa* Mill.) a disease that has been recently linked with production losses of up to 40% in Australia. To date, the diagnosis of this pathogen has been poorly explored. Chestnut growers rely on visual observations of healthy/diseased chestnuts to assess infection rates. This method underestimates the disease level, as asymptomatic chestnuts are not quantified. Therefore, an accurate diagnostic technique is essential to precisely estimate the pathogen impact in the industry. Herein we report the development of an accurate and rapid multiplex-PCR (mPCR) approach to detect *G. smithogilvyi*. Gene-specific primers were designed based on sequences from GenBank to amplify three DNA regions of *G. smithogilvyi* simultaneously: the translation elongation factor 1-α, internal transcribed spacer and β-tubulin. Amplification of the chestnut locus, *Cmcs1*, was used as internal control. The optimal mPCR conditions were determined experimentally. The annealing temperature for all primers was found at 55°C. The final concentration of primer pairs varied between 0.1 - 0.2 µM. The detection limit of DNA template was determined through serial dilutions and established at 1 x 10⁻² ng/µL. Analysis of primer specificity was performed firstly *in silico* with BLASTn (NCBI) and secondly under controlled experiments. Pure DNA from different *G. smithogilvyi* strains and other fungal species including *Penicillium* sp., *Alternaria* sp., *Mucor* sp., *Botrytis* sp., *Fusarium* sp., *Epicoccum* sp., and *Phoma* sp., were tested with the mPCR to confirm specificity of the primer sets. Only *G. smithogilvyi* DNA yielded bands that were clear and consistent with the expected sizes for the three target amplicons. To the best of our knowledge, this is the first report of the use of mPCR to detect *G. smithogilvyi* in chestnut.
Poster Board 29

NARH: confirmed as a robust isolation medium for *Phytophthora* species

*Mrs Suchana Rani Sarker*¹, Dr Jennifer McComb¹, Prof Treena Burgess¹, Prof Giles Hardy¹

¹Centre for Phytophthora Science and Management, Murdoch University, Perth, Australia, ²Plant Pathology Division, Bangladesh Agricultural Research Institute, Gazipur 1701, Bangladesh

Selective media for isolating *Phytophthora* species contains nutrient agar and antimicrobials to suppress other microorganisms. Hüberli et al. (2000) developed an isolation medium, NARPH, which has been widely used and appropriate for the species commonly reported over the last two decades. However Pentachloronitrobenzene, a carcinogen, is now rarely included. Many recently described species detected using high throughput sequencing (HTS) have never been isolated in culture. We investigated whether NARH (NARPH without Pentachloronitrobenzene) is an appropriate medium for the isolation of the wide range of *Phytophthora* species now known from Australia, and whether the antimicrobials used in NARH suppress growth of some *Phytophthora* species. Growth of 10 *Phytophthora* species across all clades was measured in media with the NARH antimicrobials in a range of concentrations, singly and in combination: nystatin 12.5 – 100 ppm (replacing the expensive pimaricin in the original formulation), ampicillin 62.5 – 500 ppm, rifampicin 5 – 40 ppm, hymexazol 12.5 – 100 ppm and, in addition, chloramphenicol 5 – 40 ppm. Two combinations of antimicrobials were selected: i) nystatin 12.5 ppm, ampicillin 250 ppm, rifampicin 10 ppm and hymexazol 12.5 ppm, and ii) these compounds with the addition of chloramphenicol 5 ppm. Growth of 48 *Phytophthora* species selected from all clades was tested in medium with these two combinations and standard NARH, in aseptic culture, and in plates for bait leaves from soils known to be infested with *Phytophthora*. Although growth of some *Phytophthora* species was better in the new combinations in aseptic culture, suppression of competing microorganisms was best in standard NARH. Thus, NARH is a robust and appropriate medium for isolation of *Phytophthora* species across all clades. Sensitivity to the NARH antimicrobials is not the reason for the difficulty of isolating many of the species detected using HTS. Hüberli D., et al. 2000 Australasian Plant Pathology 29, 164-169
Evaluation of different diagnostic methods for grapevine fungal trunk disease

**Miss Rebecca Woolley**, Mr Bhanupratap Vanga, Mr Simon Bulman, Mrs Sarah Thompson, Mr Anish Shah, Mr Dion Mundy

*Plant and Food Research, Blenheim, New Zealand, Plant and Food Research, Christchurch, New Zealand*

Detection of grapevine trunk disease (GTD) is complex and challenging because of the large number of associated fungal pathogens, long disease latency, and late appearance of disease symptoms. This project compares three GTD diagnostic methods: visual assessment of external disease symptoms, destructive vine sampling to evaluate internal staining, and molecular detection of GTD-causing pathogens using DNA extracted from mature grapevine trunk-wood tissue. Vineyards across Hawke’s Bay and Marlborough (two main viticulture regions in New Zealand) are being monitored over 3 years (2018–20), with over 100 individual vines assessed at each site. External GTD symptoms, such as cankers, stunted shoots and non-productive sections of trunk heads, are evaluated for each individual vine. Sites will be surveyed up to three times (once per year) before being destructively sampled, in order to evaluate both the incidence and progression of symptoms. Grapevine trunks are horizontally dissected at high and low regions, and internal infection determined by the extent and type of wood staining. Each cut is photographed with a unique QR code that identifies the specific location and other diagnostic data of the vine. The percentage staining within each trunk will be measured using image-processing software. To date, the prevalence of external GTD symptoms ranges from 0 to 67% per vineyard. Internal symptoms have been observed at higher rates than external symptoms at four vineyards, indicating an abundance of latent fungal infections. A total of 450 grapevine trunk samples have been collected to date, and analysis with qPCR assays for specific fungal pathogens is underway. Once data collection is complete, correlations between the three diagnostic methods for individual vines will be analysed. This project seeks to develop a reliable screening method for early diagnosis of GTD in vines before symptoms are too far progressed for remedial action to effectively prolong vineyard longevity.

Molecular diagnosis of *Ascochyta* spp. causing Ascochyta blight in Faba bean, Lentil and Vetch targeting the mitochondrial genome

**Dr Winnie Liu Heang**, Dr Joshua Fanning, Dr Grant Holloway

*Agriculture Victoria, Horsham, Australia*

*Ascochyta fabae*, *A. lentis* and *A. viciae-villosa* are the causal agents of Ascochyta blight in faba bean, lentil and vetch, respectively. Although considered to be host-specific, earlier studies have demonstrated that interspecific crosses between the species produced pseudothecia with viable ascospores. In our study, comparative analysis of the draft mitochondrial genomes of *A. fabae* strain 247/15, *A. lentis* isolate Al4 Alen and *A. viciae-villosae* strain ONG-16-641 was conducted. The results demonstrated that both protein-coding regions and non-coding regions are highly conserved between the three Ascochyta blight species, with 100% sequence identity between the *atp* gene in the three pathogens. Both introns and exons of the *nad1*, *nad4L*, *nad6*, *cob* and *cox1* encoding genes are shown to be identical between the *A. lentis* isolate Al4 Alen and *A. viciae-villosae* strain ONG-16-641, but different to the *A. fabae* strain 247/15. Genomic regions unique to the Ascochyta blight species complex were identified and used to develop molecular diagnostic tools targeting the mitochondrial genome. Different diagnostic strategies, including PCR, qPCR and loop-mediated isothermal amplification (LAMP) markers, were evaluated. The specificity of the molecular markers was further tested against isolates of common fungal pathogens. The highly specific nature of these markers allows reliable molecular diagnosis of Ascochyta blight in faba bean, lentil and vetch.
Poster Board 23

Rapid detection of Claviceps purpurea and quarantined Claviceps humidiphila by real-time PCR

Dr Kritarth Seth\textsuperscript{2}, Dr Jana Monk\textsuperscript{1}, Nik Grbavac\textsuperscript{1}
\textsuperscript{1}Asurequality Ltd, Lincoln, New Zealand, \textsuperscript{2}AgResearch Ltd, Lincoln Research Centre, Christchurch 8140, New Zealand

Claviceps purpurea is a fungus that infects the flowers of cereal crops and grasses (Poaceae) causing ergot disease. After floral infection, the seeds are replaced with fungal sclerotia or ergots. Recently, the genus Claviceps has been divided into four distinct species/lineages, of which, C. humidiphila has not been reported in Australia and New Zealand. Based on morphological characteristics or sequencing of common genes such as ITS, C. humidiphila is inseparable from C. purpurea. Within the genomes, there are very few nucleotide differences between the two species. A quick and robust method to identify the two species can therefore be beneficial in implementing biosecurity controls. Species-specific primers and probes were designed for the translation elongation factor 1-α (TEF1) gene. The assay was validated using 41 grass seed stocks. Ten samples contained C. humidiphila. Within the ten samples, three contained only C. humidiphila whereas seven samples were found to contain mixtures of C. humidiphila and C. purpurea. This is therefore the first report of the presence of C. humidiphila in New Zealand. The TaqMan assay developed in this study can accurately identify both species within 3 to 4 hours, compared with up to 2 weeks required for sequencing-based approaches. The assay can be a useful tool for biosecurity agencies and seed producers to monitor the distribution of ergot fungi and manage the disease.

Poster Board 25

Citrus black spot: Sex, lies and milenex tape

Dr Nga T Tran\textsuperscript{1}, Dr Andrew K Miles\textsuperscript{1}, Assoc Prof Ralf G Dietzgen\textsuperscript{2}, Prof André Drenth\textsuperscript{1}
\textsuperscript{1}Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Dutton Park, Australia, \textsuperscript{2}Queensland Alliance for Agriculture and Food Innovation, University of Queensland, St Lucia, Australia

Citrus black spot (Phyllosticta citricarpa) is characterised by fruit blemishes and premature fruit drop, resulting in economic losses in summer rainfall areas. Sexual reproduction plays a large role in the pathogen biology, resulting in pseudothecia and ascospores on leaf litter. The pathogen also produces asexual conidia on leaf litter and above-ground tree parts. Ascospores are considered more important than conidia in the disease epidemiology, such that ascospores are a recommended target for disease management. However, this strategy was ineffective in some cases, suggesting inoculum sources other than ascospores cause infection. We undertook volumetric spore trapping and infection timing studies in order to investigate the role of ascospores in disease development. Unexpected results made us wonder if our milenex spore tapes lied to us? Combined with determining the identity of the pathogen, artificial production of ascospores in vitro, and direct observation of their development in leaf litter, these experiments demonstrated that: ascospores and conidia are equivalently pathogenic in the glasshouse; pseudothecia in leaf litter and ascospore capture in the spore trap were closely related. However, ascospore production was not correlated with the timing of infection in the field. Furthermore, numbers of ascospores were far too low to cause the observed levels of disease. It may be that our milenex tapes lied to us about the link between ascospores and infection, but more likely our results suggest that inoculum sources other than ascospores play a role in the epidemiology of citrus black spot under Queensland conditions. Fortunately, our findings can now be applied to seeking direct evidence for the role of the different inoculum sources in order to better target disease management strategies.
Endogenous viral elements in Macadamia genome and its putative role in abnormal vertical growth

Mr Mohamed Cassim Mohamed Zakeel1, Assoc Prof Andrew D W Geering1, Assoc Prof Olufemi A Akinsanmi1
1Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Australia

Macadamia is a popular tree nut worldwide, and the demand is increasing globally. In Australia, a syndrome known as abnormal vertical growth (AVG) poses a serious threat to macadamia production. AVG is characterized by an upright growth habit, increased vegetative vigour, reduced branching, flowering and nut set, and over 70% reduction in yield. The cause of AVG remains unknown. In a preliminary study, the presence of a virus was investigated by Illumina sequencing of the sRNA population of AVG-affected trees, and sequences of a novel geminivirus obtained (M. Webb and ADW Geering, unpublished). We therefore tested the hypothesis that this virus is the cause of AVG. Using specific PCR primers, 95 DNA samples including AVG symptomatic (46) and asymptomatic (49) tissues were tested and geminivirus detected in both healthy and diseased trees. In order to test whether the AVG phenotype is strongly associated with geminivirus detection across different macadamia cultivars, a binary logistic regression analysis was done and no significant (p = 0.153) association was obtained. To search for circular, single-stranded DNA molecules, rolling circle amplification was done using a TempliPhi kit but no viral DNA was detected. The Rep protein sequence was then matched against the macadamia genome using tBLASTN, and significant hits were obtained, suggesting the existence of endogenous geminiviral elements.

Our data suggest that these endogenous geminiviral elements are replication-defective and the plants are not infected. However, it is possible that individual viral genes are expressed and could contribute to the AVG phenotype. This is the first record of an endogenous geminiviral element from the Proteaceae, an ancient Gondwanan plant family.

Transcriptomic analysis at different developmental stages of Root-knot nematode (Meloidogyne incognita)

Dr. Bum-Soo Hahn1, Dr. Chinreddy Subramanyam Reddy1, Dr. Vimalraj Mani1, Dr. Chang-Muk Lee1, Ms Soyoung Park1, Dr. Joon-Soo Sim1
1National Institute of Agricultural Sciences, RDA, Jeon-ju, South Korea

Meloidogyne incognita is a notorious plant pathogen but its sequence information still scanty. As a part of work we were anticipated to elucidate the M. incognita mRNA sequence across of all its developmental stages. After processing the data we found (Egg)-27,285,236 – (J2)-25,208,092 (J3)-19,962,672- (J4)-24, 502219 and (female)-26,329,321 clean reads from the respective stages. Based on FPKM value ≥ 0.3, we found 15,798 transcripts from egg, followed by 15,564-14,908-15,226 and 14,519 respectively from J2, J3, J4 and female stages. Further processed results were mapped to the currently available M. incognita reference genome with best quality reads and were able to mapped 51 to 62%. Across the five developmental stages namely egg, J2, J3, J4 and female, of the transcriptome, found to be expressed 17,423 genes and 12,803 were commonly expressed in all the five stages which is almost 73.48%. Expression analysis by heat-map revealed J3 and J4 stages to have similar mRNA profiles that were related to egg, J2 and female in a descending order. Minc01079, Minc06773, Minc0897, Minc0898, Minc0801, Minc01401, Minc2143, Minc02293 genes were highly expressed. Conclusively our data depicting basic clues regarding M. incognita life cycle as well as developmental stages that would ultimately may help for raising better strategies of its regulation.

Analysis of microRNA targets at different developmental stages of root-knot nematode (*Meloidogyne incognita*)

**Ms Soyoung Park¹, Dr Chinreddy Subramanyam Reddy², Dr Vimalraj Mani², Dr Joon-Soo Sim³, Dr Chang-Muk Lee¹, Dr Bum-Soo Hahn¹**

¹National Institute of Agricultural Sciences, RDA, Jeon-ju, South Korea

Root-knot nematode is highly destructive obligate plant parasite and has diverse host range of plants. In this study, we aimed to elucidate the targets of *M. incognita* miRNAs from the transcriptome data for all the five stages of its life cycle. First, we used three target prediction programs to find the potential miRNA targets. We obtained 3,036 miRNAs and 15,093 mRNAs using RNAhybrid, further 2,561 miRNAs and 10,056 mRNAs were found through miRANDA program, whereas using PITA 2,560 miRNAs and 9,018 mRNAs found. As a result, we found 2,431 common potential target miRNA genes of *M. incognita* that regulated the expression of 8,331 mRNAs by above three programs. We found the tendency that, the predicted potential targets of the miRNA are involved in biological processes, molecular function, cellular components. For example, stage-specific miRNA targets in the egg stage holds heat shock, transcriptional factors, DNA repair related proteins, whereas infective J2 stage each cell cycle stage, heat shock, ubiquitin conjugating pathway proteins and DNA replication related protein, while in J3 stage major sperm protein domain including proteins and in J4 stage we detected targets of translation related proteins. Finally in the female stages we found that regulate to ubiquitin mediated protein degradation and maintaining molybdopterin binding domain containing proteins. Our results may be useful for discriminate the potential regulatory networks which can be targeted to control the nematode induced agricultural losses.

Relative pathogenicity and molecular analysis of *Sporisorium scitamineum* isolates from Australia

*Mrs Nurul Hidayah*¹,², Dr Meredith McNeil³, Dr Shamsul Bhuiyan¹,⁴, Prof Victor Galea¹, Dr Karen Aitken³

¹School of Agriculture and Food Sciences, The University Of Queensland, Gatton, Australia, ²Indonesian Agency for Agricultural Research and Development, Jakarta, Indonesia, ³CSIRO Agriculture and Food, St Lucia, Australia, ⁴Sugar Research Australia, Woodford Station, Woodford, Australia

Previous research suggests that isolates of sugarcane smut (*Sporisorium scitamineum*) collected from various regions of Queensland exhibited different virulence levels on the same sugarcane genotype. Additionally, anecdotal evidence suggested that some sugarcane varieties were resistant to smut at one location but susceptible at another. Environmental factors, such as temperature, humidity and rainfall can influence the response of sugarcane plants to smut. There is limited information on the pathogenic variation and genetic characterisation of Australian isolates of *S. scitamineum*. Therefore, this study was conducted to determine relative pathogenicity and molecular analysis of *S. scitamineum* isolates collected from different locations in Australia including northern New South Wales (NSW), southern Queensland (Bundaberg, BND), central Queensland (Mackay, MCY), SRA Woodford Pathology farm (WDF) and northern Queensland (Burdekin, BRD).

Pathogenicity of these isolates was investigated through both microscopy on infected bud samples and molecular analysis of the whole genomic DNA sequence of isolates. Microscopic investigation of the pathogenicity of six *S. scitamineum* isolates was conducted by determining the extent of mycelial colonisation within sugarcane bud tissue. Sequence analysis was performed using CLC Genomic Workbench (v11.0) and utilizing the published Brazilian isolate sequence as a reference genome. The pathogenicity study demonstrated that the six *S. scitamineum* isolates varied in their virulence to four sugarcane genotypes although there was no significant isolate x genotype interaction indicating pathogenic variation was present among these isolates. Our results determined that the isolate from Mackay was most virulent, while the isolate from Burdekin was least virulent. Sequence analysis identified 4,400 SNP variants across the 7 isolates. This data was used to determine the genetic similarity between isolates. A number of SNP variants in genes related to pathogenicity were identified between the most and least virulent isolates indicating they may have a role in the aggressiveness of these isolates.
Field pea is the third most important legume food crop in the world after common bean and chickpea. It is an important source of food and feed for humans and animals, respectively. Its ability to fix nitrogen into the soil and provide disease break makes it a beneficial crop for sustainable cropping systems. Ascochyta blight is one of the most economically important diseases of field peas around the world. Yield losses can be up to 70% if conditions are favourable. Ascochyta blight is a fungal disease that affects foliage, stem and roots of the plant. The disease is caused by a complex of fungal pathogens from the order Ascomycota, mainly *A. pisi*, *P. pinodes*; *P. pinodella* and *P. koolunga* present in varying proportions. In Australia, only *P. pinodes*, *P. pinodella* and *P. koolunga* are found predominantly. Currently, there is no field pea variety that is known to be fully resistant to all ascochyta species. Understanding the host-pathogen interactions is vital as resistance to gene response has not been noted indicating that resistance is highly quantitative. Morphological characterization of ascochyta species is highly variable and depends largely on culture conditions. Distinguishing these species has rather been challenging as molecular markers have proved insufficient. To date, no known whole genome sequence of the ascochyta species has been published. Here, we employ the use of Oxford Nanopore long read sequence technology to generate whole genome sequences for *P. pinodes*, *P. pinodella* and *P. koolunga*. This will help in various ways such as identify genomic variations to differentiate the species, understand the epidemiology of the pathogen, and drive the development of in-field molecular tools for plant breeders to better manage disease.
Functional characterisation of the necrotrophic effector ToxA from wheat pathogen *Parastagonospora nodorum*

Dr Bayantes Dagvadorj¹, Prof Peter Solomon¹
¹Australian National University, Canberra, Australia

The wheat necrotrophic fungal pathogen, *Parastagonospora nodorum*, secretes effector proteins to manipulate host immunity and promote successful infection. One of the major determinants of the disease is the ToxA effector protein, which causes cell death in the presence of the wheat susceptibility gene, *Tsn1*. However, ToxA does not appear to directly interact with the *Tsn1* protein. Previous studies have identified host proteins that interact with ToxA, including ToxA-Binding Protein 1 (ToxABP1), plastocyanin and the Pathogenesis-Related 1 protein (PR1-5). Studies to date in the Solomon laboratory, though, have been unable to reproduce these interactions. As such, the molecular function of ToxA during infection remains poorly understood. To elucidate the molecular mechanisms of the ToxA effector, we are seeking to identify potential host target proteins of ToxA. For this purpose, we will use two high-throughput and large-scale approaches. First, host binding partners will be detected by Yeast Two-Hybrid using a prey library made from infected leaves and also ToxA-infiltrated wheat cultivars carrying the ToxA-specific susceptibility gene, *Tsn1*. An alternative to this approach, we will use co-immunoprecipitation (Co-IP) and liquid chromatography-tandem mass spectrometry to find interacting protein complexes from infected ToxA-susceptible cultivars by using tagged ToxA. After validating shortlisted interactions by Co-IPs and western blots, we will undertake assays that combine cell biology, genetics and biochemistry to determine their roles during necrosis. The knowledge gained from this study will be valuable not only for researchers working on plant necrotrophic pathogens, but also for scientists engaged with understanding and improving plant disease resistance.
The necrotrophic effector SnTox1 of Parastagonospora nodorum harbours a promoter variant associated with gene repression

Mr Evan John1, Dr Lifang Liu1, Dr Huyen Phan1, Mr Darcy Jones1, Prof Karam Singh1,2, Prof Richard Oliver1, Dr Kar-Chun Tan1
1Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Bentley, Australia, 2CSIRO Agriculture and Food, Wembley, Australia

The fungus Parastagonospora nodorum uses proteinaceous necrotrophic effectors (NEs) to cause tissue necrosis on Triticum aestivum (wheat). The virulence functions of three NEs, SnToxA, SnTox1 and SnTox3, have been well established. It has been observed that SnTox1 can epistatically suppress SnToxA and SnTox3, reducing their contribution to the disease. However, little is known about the mechanisms regulating these NEs. A recent breakthrough was the discovery that the Zn2Cys6 transcription factor PnPf2 is required for SnToxA and SnTox3 expression, but had no obvious role in regulating SnTox1. Maximal expression of SnTox1 occurs during the early stages of infection and it can be induced under in vitro conditions, but precise regulatory factors remain unidentified. An interesting discovery was that the Australian reference strain SN15 expresses SnTox1 at a higher level than the American reference strain SN4. Closer inspection has revealed a 401bp indel in SN4 positioned 267bp upstream of the SnTox1 start codon. The indel is absent in SN15 in an otherwise well conserved promoter. To investigate this, mutants with the same 401bp indel were produced in both the SN15 wildtype and a PnPf2 knockout mutant. SnTox1 expression was unaffected in the wildtype but abolished in the PnPf2 knockout. There was also no SnTox1 expression in an SN4 PnPf2 knockout mutant. This indicates that repressor elements associate with the indel and inhibit SnTox1 transcription but are suppressed when PnPf2 is present. Interestingly, the indel is present in the majority of isolates examined in a worldwide collection, but rare in an Australian collection. It remains to be seen whether SnTox1 is contributing more towards virulence in the Australian context. Promoter replacements in isolates carrying the indel will help establish its significance. In addition, the core SnTox1 promoter elements are currently being established through successive deletions upstream from the start codon in SN15.
Secretome profiling analysis of Pyrenophora tritici-repentis genes regulated by the Zn2Cys6 binuclear cluster transcription factor Pf2

Dr Pao Theen See1, Dr Caroline Moffat1
1Centre for Crop and Disease Management, Curtin University, Bentley, Australia

Pyrenophora tritici-repentis, the causal agent of tan spot (yellow spot) wheat disease, secretes necrotrophic effectors (NEs) (also known as host-selective toxins) to facilitate the colonisation of wheat tissue. This colonisation is promoted through the interaction of NEs with host susceptibility targets, and is governed by an inverse gene-for-gene relationship. Recently, a Zn2Cys6 binuclear cluster transcription factor, Pf2, was identified as a positive regulator of expression for the well-characterised NE gene, ToxA, in P. tritici-repentis race 1, with deletion of Pf2 rendering the race non-pathogenic. To further evaluate the role of Pf2 in P. tritici-repentis, a study to identify the genes regulated by Pf2 was performed using SWATH mass spectrometry (MS) on two different P. tritici-repentis races, race 1 and race 5. A comparative secretome analysis of in vitro culture filtrate between wild-type and Δpf2 mutants identified more than thirty unique secreted proteins from each race with lower abundances in the Δpf2 mutants. In the race 5 isolate, ToxB was amongst those found to have significantly lower abundance in the Δpf2 mutants. In addition to the known NE proteins, ToxA and ToxB, a number of additional proteins known to be associated with fungal virulence, including those that encode cell wall-degrading and protease enzymes, were found to show decreased abundance in the Δpf2 mutants. Notably, approximately 20% of uncharacterised proteins detected by MS had significantly altered abundance in the Δpf2 mutants. Proteins identified in this study will facilitate a better understanding of how P. tritici-repentis causes disease, and in doing so, may provide useful information in the discovery of novel targets for the control of this pathogen in wheat.

Cell death-inducing activity of a conserved family of small secreted proteins from Ciborinia camelliae, Botrytis cinerea and Sclerotinia sclerotiorum

Miss Hannah McCarthy1, Dr Matthew Denton-Giles1, Dr Carl Mesarich2, Assoc Prof Paul Dijkwel1
1School of Fundamental Sciences, Massey University, Palmerston North, New Zealand, 2School of Agriculture and Environment, Massey University, Palmerston North, New Zealand

Ciborinia camelliae, the causal agent of Camellia petal blight, is a necrotrophic fungus that specifically infects the blooms of susceptible Camellia plants. Candidate effector proteins that were identified from the secretome of C. camelliae included a highly conserved family of 72 proteins, termed C. camelliae-like small secreted proteins (CCL-SSPs). Notably, the CCL-SSPs are not unique to C. camelliae. Indeed, a single homolog of the CCL-SSP family is encoded by the genomes of the closely related necrotrophs Botrytis cinerea and Sclerotinia sclerotiorum (BcSSP and SsSSP, respectively). Previous work showed that BcSSP and SsSSP induce rapid cell death in Camellia ‘Nicky Crisp’ petals, whereas of the ten C. camelliae CCL-SSPs (CcSSPs) tested, only one induced very weak cell death. The aim of this study was to determine the specific regions of the SsSSP protein that confer cell death-inducing ability, and to further characterise the cell death-inducing capability of the CCL-SSPs. Infiltration of chimeric SsSSP (necrosis-inducing) and CCL-SSP37 (non-necrosis-inducing) proteins into Camellia ‘Nicky Crisp’ petals and Nicotiana benthamiana leaves demonstrated that the region encoded by exon 2 of SsSSP is essential for cell death-inducing activity. Differences in the intensity of necrosis elicited by SsSSP and BcSSP were observed. SsSSP was able to induce stronger cell death in Camellia ‘Nicky Crisp’ petals than BcSSP, while BcSSP and SsSSP induced strong and weak cell death in Arabidopsis thaliana leaves, respectively. The distinct responses in A. thaliana leaves suggest that these two proteins may target different molecules in plants, and therefore, may have different host specificity. The results of this study have shed further light on the CCL-SSP family as candidate effector proteins, and have provided several avenues to further elucidate the function of CCL-SSPs and their role in the virulence of these three necrotrophic fungi.
Charaterization of Brassicaceae smut fungal effectors responsible for plant infection

Miss Summia Gul

1 Heinrich-Heine University, Düsseldorf, Germany

The smuts are a prevalent group of plant-pathogenic fungi that affect agriculturally important cereal crops. In order to establish a biotrophic interaction with plants, these pathogens must secrete virulence factors termed effector proteins. Effectors promote virulence by suppressing plant defense responses or by altering plant physiology to assist fungal invasion. The infection biology of the grass smut fungi Ustilago maydis, Sporisorium reilianum and Ustilago hordei has been intensively analyzed at the molecular level, ultimately revealing both common and individual effector repertoires. The Brassicaceae smut fungus Thecaphora thlaspeos infects several Arabis species and the model plant Arabidopsis thaliana (a novel smut infection system). In contrast to the rapid infection cycle of U. maydis, T. thlaspeos establishes a long-lasting biotrophic interaction with perennial host plants without causing macroscopic symptoms. Therefore, it is of high interest to explore the unique and conserved effector repertoire of T. thlaspeos. Previous studies led to the identification of approximately 50 effector candidates that were grouped into conserved effectors with a homolog in grass smut fungi, and unique effectors. Stp1 is a conserved effector of smut fungi, essential for the penetration of maize by U. maydis. To investigate the function of the Stp1 homolog from T. thlaspeos, we complemented the U. maydis ΔStp1 deletion mutant with this gene. Interestingly, the homolog from T. thlaspeos cannot complement the infection phenotype of U. maydis, suggesting a specialized function. Among the unique and conserved effectors, a predicted nuclear localization was verified for Tue10, Tue17 and Tae2 using transient expression. As T. thlaspeos is not yet completely transformable, we used the Effector Detector Vector System to confirm the infection phenotype of effectors and prove them as virulence factors. This data might provide a platform for studying how T. thlaspeos effectors enable fungal colonization and disease establishment in the absence of macroscopic symptoms.
Structural prediction of ToxA-like and MAX effector proteins using threading and comparative modelling methods

Ms Lina Rozano\textsuperscript{1}, Mr Darcy Jones\textsuperscript{2}, Dr James Hane\textsuperscript{3}, Prof Ricardo Mancera\textsuperscript{1}

\textsuperscript{1}School of Pharmacy and Biomedical Sciences, Curtin Health Innovation Research Institute and Curtin Institute for Computation, Curtin University, Bentley, Australia, \textsuperscript{2}Centre for Crop Disease Management, School of Molecular and Life Sciences and Curtin Institute for Computation, Curtin University, Bentley, Australia

Effector proteins are of interest in the field of fungal plant pathology due to their ability to mediate disease infection in plants, particularly devastating fungal infections in economically important agricultural crops. The discovery of new fungal effector proteins is necessary to enable the screening of cultivars for disease resistance. Several sequence-based bioinformatics tools have been used for the discovery of effector proteins from proteome or secretome data, but only a limited number of functional effector proteins have been successfully predicted and subsequently validated experimentally. A significant obstacle is that fungal effector proteins appear to lack sequence similarity and conserved sequence motifs. Experimental determination of the three-dimensional (3D) structure of effector proteins is allowing the search for structural motifs to predict new effector proteins in fungi on the basis of similarities within effector protein families \cite{Franceschetti2017}. We have applied RaptorX threading and Rosetta comparative modelling to predict the 3D structures of candidate effector proteins from ToxA-like and MAX families. Effector candidate sequences were obtained from \textit{in-house} bioinformatics predictions for ToxA-like and published PSI-BLAST analysis for MAX \cite{deGuillen2015}. The best predicted models for these effector candidates have close resemblance to their respective template structures. Accurate selection of templates during threading was achieved by identifying the optimal target-template alignment and applying a scoring function to weigh the use of both sequence and structural features during threading, as implemented in RaptorX. This improved the conventional sequence-based alignment of target and template structures, overcoming the limitation of alignment accuracy in homology modelling, which works well only with highly conserved sequences. The predicted structural models of effector proteins can be further applied to the prediction of their interactions with plant receptors through molecular docking, which will greatly improve our understanding on their interaction with the host.

Opportunities through the Agricultural Microbiomes Research Coordination Network

**Dr JP Dundore-Arias,1,4, Dr Posy Busby,5, Prof Jan Leach,1, Dr Jude Maul,4, Dr Dan Tomso,3, Prof Linda Kinkel1**

1University of Minnesota, Saint Paul, USA, 2Oregon State University, Corvallis, USA, 3Colorado State University, Fort Collins, USA, 4USDA-ARS, Beltsville, USA, 5AgBiome, Raleigh-Durham, USA, 6California State University - Monterey Bay, Seaside, United States

Recent advances in sequencing technologies have resulted in a wealth of microbiome studies to catalog and describe plant-associated microbial communities. However, a lack of coordinated efforts, standard protocols, and communication among microbiome researchers has limited our capacity to understand the factors that influence the diversity, composition, and benefits of plant and soil microbiomes across diverse cropping systems. The Agricultural Microbiomes Research Coordination Network (RCN) seeks to advance understanding of agricultural microbiomes and their relationships with sustainable crop production and disease management. To accomplish this, we are building a coordinated global network of scientists from public and private entities working on developing and applying concepts, technologies, and analytical approaches for agricultural microbiome research. Network participants have the opportunity to engage in training and collaborative activities, and contribute to identifying research priorities and community needs to move agricultural microbiome science forward. The RCN facilitates the development of collaborative synthetic and cross-disciplinary research opportunities, taking advantage of existing research platforms and available resources. Diverse opportunities for plant pathologists to participate in RCN-sponsored collaborative research and publication projects, as well as in workshop attendance and organization, are currently available.
**Poster Board 11**

**The effect of *Verticillium dahliae* to cause Potato Early Dying syndrome in Victoria, Australia**

*Dr Prakash Nair*¹, *Dr Tonya Wiechel*², *Dr Nigel Crump*³, *Prof Paul Taylor*¹

¹*Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Australia*, ²*The Department of Jobs, Precincts and Regions, Bundoora, Australia*, ³*VICSPA, Toolangi, Australia*

Potato Early Dying (PED), caused by the interaction of *Verticillium dahliae* and *Pratylenchus* spp. (root lesion nematodes), is an important global disease of potato crops. PED is characterised by chlorosis of leaves with stunting and premature senescence, and early death of plants. Field soil was collected from a potato growing region (Cora Lynn) in Victoria that had a history of PED. The mean level of *V. dahliae* inoculum in the soil was 90 pg *V. dahliae* DNA/g soil and for *P. crenatus* was 3 nematodes/g soil. Other *Verticillium* and root lesion nematode species were not present in the soil. Potato cv. Shepody and eggplant cv. Black Beauty were used in the glasshouse trials to determine the threshold level of inoculum of *V. dahliae* and *P. crenatus* required to cause disease. Treatments included (i) naturally infested field soil supplemented with various concentrations of *V. dahliae*, (ii) nematicide treated soil, and (iii) pasteurised soil. After 8 weeks, potato plants growing in the field soil containing 3 *P. crenatus*/g soil and 4000 pg *V. dahliae* DNA/g soil inoculum had increased incidence and severity of PED and significantly reduced tuber yield. There was a threshold level of *V. dahliae* inoculum of between 300 and 1000 pg *V. dahliae* DNA/g soil required before infection and colonisation occurred in potato plants. In eggplant, *V. dahliae* inoculum as low as 85 pg DNA/g of field soil and 0.3 *P. crenatus*/g soil, resulted in higher disease severity, and significant reduction in plant growth and biomass. Eggplants needed low inoculum for infection and disease development hence can be used as bait plant for PED in naturally infested field soil.

---

**Poster Board 12**

**Surprises inside: cereal cyst nematodes induce striking changes in root vascular anatomy**

*Ms Kara Levin*¹, *Dr Pradeepa Bandaranayake*², *Assoc Prof Matthew Tucker*, *Prof Diane Mather*¹

¹*School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, Adelaide, Australia*, ²*Agricultural Biotechnology Centre, Faculty of Agriculture, University of Peradeniya, Peradeniya, Sri Lanka*

Like any parasite, cereal cyst nematode (CCN, *Heterodera avenae*) must secure nutrients from its host – without killing the host. To better understand this delicate balance, we used confocal microscopy to analyse infected tissue from roots of wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.). Stained root tissues were observed in sufficient cellular detail to assemble three-dimensional models of CCN feeding sites. Surprisingly, imaging also revealed striking changes in root vascular anatomy. In infected regions, metaxylem vessels consisted of a linear series of elements that are short and plump rather than long, narrow and cylindrical. Analysis of a developmental time course of root growth indicated that affected metaxylem cells grew radially at a stage when they would normally elongate. Later, their outer cell walls underwent secondary thickening. Some of the cell walls between these elements remained intact, rather than eroding to form a hollow tube for transport of water and solutes. Does this response help the host defend against the parasite? Or does it benefit the parasite at the expense of the host? It seems unlikely to be a defence response, given that (1) it is not specific to genetically resistant plants and (2) it blocks major water transport channels in the roots. We propose that modification of xylem development contributes to the nematode’s parasitic ‘strategy’. Xylem cells that avoid programmed cell death may serve as nutrient reservoirs that are accessed later by the expanding feeding site, providing a nutritional ‘boost’ that enables female cyst nematodes to mature and reproduce.
Modelling *Pratylenchus thornei* field populations over multiple soil depth intervals and trials to rank wheat genotypes for resistance in the northern Australian grains region

**Bethany Rognoni**, Jason Sheedy, Valeria Paccapelo, Clayton Forknell, Neil Robinson, John Thompson, Alison Kelly

1Queensland Department Of Agriculture And Fisheries, Rockville, Australia, 2University of Southern Queensland, Centre for Crop Health, Toowoomba, Australia

The root-lesion nematode *Pratylenchus thornei* is a soil-borne pathogen of significance in the northern Australian grains region. Three field experiments were conducted between 2013 and 2015 near Formartin (27.4676S, 151.42554E), Queensland. In each trial, three replicates of 36 wheat genotypes were sown into each of high and low *P. thornei* populations (disease levels) established in the preceding year by growing a susceptible and a resistant wheat genotype respectively. The initial (Pi) and final (Pf) *P. thornei* populations were quantified for 18 of these genotypes across three soil depth intervals (0-30, 30-60 and 60-90 cm) in each trial. Final *P. thornei* counts were analysed in a linear mixed model framework, where combinations of disease levels, depths and trials were labelled as unique environments in the model.

A factor analytic model was used for the genotype by environment interaction effects, which allows for heterogeneous genetic variance for each environment, and heterogeneous genetic correlations between environments. An exploration of the genetic correlations between environments revealed that they were consistently high between all combinations of disease levels, depths and trials. The highest genetic variance, as well as the lowest error variance, were generally found at the 0-30cm soil depth, providing the greatest ability to differentiate between genotypes, when compared with the other soil depths. In terms of resistance screening for *P. thornei*, the high genetic correlations between environments mean that consistent genotype rankings could be determined from any combination of disease level, depth and trial. Future work will consider whether the combined soil depth intervals 0-60 cm and 0-90 cm offer additional precision in ranking wheat genotypes according to resistance. These findings will help inform an effective and efficient soil sampling strategy to identify *P. thornei* resistant wheat genotypes suitable for use in wheat improvement programs.

Impact of deep soil amelioration treatments on *Rhizoctonia solani* and root lesion nematodes

**Dr Daniel Huberli**, Mr Tim Boyes, Dr Stephen Davies, Mr Geoff Thomas

1Department Of Primary Industries And Regional Development, South Perth, Australia, 2Ag Vivo, Central Wheatbelt, Australia, 3Department Of Primary Industries And Regional Development, Geraldton, Australia

An increasing number of grain growers in Western Australia (WA) are using a variety of deep tillage methods and soil amendments to overcome soil constraints such as compaction and water repellency. Little is known about how these deep soil amelioration practices effect soilborne diseases and nematodes pests which are often present at levels that are a major constraint to WA grain growers. Disease severity in cereal roots and DNA levels of *Rhizoctonia solani*, *Pratylenchus neglectus*, and *P. quasitereoides* in the top 10 cm of soil were measured after treatment (site 1) and 1-year post treatment (site 2) at two sites in four amelioration treatments in August 2018. The root lesion nematodes, *P. neglectus* and *P. quasitereoides*, levels were significantly reduced by all three treatments at site 1, while *R. solani* inoculum was not affected by any of the treatments. At this site disease in roots was reduced for one amelioration treatment compared to the control. At site 2 where only *R. solani* was present, one amelioration treatment significantly reduced the *R. solani* levels compared to the untreated control. Disease in roots at this site were low with no significant differences among all treatments. This is the first assessment of the impact on soilborne diseases and nematode pests post soil amelioration. Future studies need to consider changes in disease and inoculum at and post soil amelioration to determine how long the benefit of the treatments last. Additionally, assessment of changes in DNA levels of soilborne pathogens and nematode pests at different depths in the soil would indicate the effectiveness of the soil amelioration treatments and any spatial changes following amelioration.
An overview of site-specific nematode management in Louisiana cotton

Dr Manjula Kularathna1, Dr Charles Overstreet2, Mr Dennis Burns3
1Lincoln University, Lincoln, New Zealand, 2Louisiana State University, College of Agriculture, Baton Rouge, United States, 3Louisiana State University, College of Agriculture, St. Joseph, United States

Cotton (Gossypium spp.) is grown in tropical and subtropical regions in the world and considered a significant cash crop in several countries. Out of a variety of pests and diseases, nematodes are responsible for causing substantial damage to cotton. A variety of nematode species are capable of instigating significant yield losses in cotton and has been problematic for decades. Out of the available management strategies, nematicides have proven to be the most effective for control of cotton nematodes. Despite their effectiveness, their market availability is reducing due to adverse effects with excessive use on the environment and human health. Due to edaphic factors such as texture, organic matter and nutrient availability in soil, nematode distribution in a field can be highly sporadic. Site-specific management is a concept that corrects various problems within given areas of a field rather than the entire field. With accurate observations of nematode distribution in a field, site-specific management can be implemented with minimum use of a nematicide to correct nematode problems. Soil texture has a strong correlation with soil electrical conductivity (EC), and according to previous reports, soil texture also has a significant impact on the nematode distribution. Therefore, EC can be used as an indirect method to determine the distribution of the nematode populations in a field. In this research, we have utilised georeferenced data from Veris® 3100 Soil EC Mapping System, together with GIS software to generate nematode management zones. Depending on the nematode abundance in each management zone, nematicides can be precisely applied. Data has revealed around 50% reduction in nematicide application in some trials. Therefore, this method would enable growers to get the same amount of yield increase with minimal chemical inputs. This paper will summarise some of the work that had been done using site-specific technology in nematode management.

Wheat root histopathology and defensive biochemistry against root-lesion nematode Pratylenchus thornei

Md Motiur Rahaman1, John Thompson1, Rebecca Zwart1, Saman Seneweera1
1Crop Nematology, Centre for Crop Health, University of Southern Queensland, Toowoomba, Australia

Pratylenchus thornei is an economically damaging root-lesion nematode that has a world wide distribution. It is one of the major threats for wheat production in Australia and is particularly damaging in the northern grain region of the country. This nematode causes nutrient deficiency and water stress in wheat, which results in yield loss. Only moderately resistant wheat cultivars are available to date which reduce the reproduction of this nematode in soil and root in comparison to susceptible cultivars. The present study was intended to understand the role of different defensive bio-chemicals in reduced reproduction rate of P. thornei inside root of resistant wheat genotypes over the time of wheat growing period. Clear differences in P. thornei nematode egg deposition inside the root of moderately resistant and susceptible wheat genotypes were found at 8 weeks post nematode inoculation time. Biochemical defence in synthetic hexaploids (CPI133872 and CPI133859) against P. thornei were found to be constitutive in nature. However, the induction of the phenolic compounds were also recorded both in resistant and susceptible wheat genotypes at different time points (1-12 weeks of inoculation) tested. The induction of biochemicals in susceptible genotypes could be more related to symptomatic reaction than the defence.
Occurrence of Banana Wilt Associated Phytoplasma

Ms Cecilia O’Dwyer¹, Dr Lilia Carvalhais¹, Dr Vivian Rincon-Florez², Ms Jane Ray¹, Prof Andre Drenth³

¹Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, Australia

Banana Wilt Associated Phytoplasma (BWAP) was reported to cause a new wilt disease affecting banana plants in Madang province, Papua New Guinea (PNG) in 2012. By 2015, BWAP was confirmed to have spread to the Solomon Islands. BWAP is a bacterium that has a single cell membrane instead of a cell wall and can only live inside the plant phloem or an insect vector. Symptoms associated with BWAP include leaf yellowing and leaf death, poorly developed bunches, discontinuous brown or black vascular streaks associated with necrotic pockets of rot in the pseudostem, and decay of flowers in the male bell. Spread of the disease most likely takes place through infected planting material and insects. BWAP is currently exotic to Australia. The close proximity of Australia to countries in South East Asia that are affected by banana diseases not present in Australia is a major threat to Australian banana production. The prevention of movement of pathogens into Australia with planting material is covered under import conditions requiring holding of plants in post-entry quarantine glasshouses for assessing the expression of disease symptoms and testing for viruses and BWAP. To prevent further spread of BWAP, there is an urgent need for effective management of this phytoplasma disease through early detection, removal of symptomatic plants, restriction of movement of infected planting material, and the production of clean planting material.

A field survey conducted in August 2018 in PNG for BWAP assessed the distribution of BWAP across different plant organs and tissues. The symptomatic plant tissue was also used to test different diagnostics assays to detect BWAP. Our results reveal that the infection is systemic throughout the plant and that the currently available diagnostic assays have constraints, which we aim to alleviate through the development of a novel assay for this pathogen.

An overview of banana bunchy top virus (BBTV) in South Africa

Dr Anna Jooste¹, Miss Sinethemba Ximba¹,²

¹ARC-Tropical And Subtropical Crops, Mbombela, South Africa, ²University of KwaZulu-Natal (UKZN), Pietermaritzburg, South Africa

Banana bunchy top disease (BBTD), caused by Banana bunchy top virus (BBTV), is the most devastating viral disease of bananas worldwide. BBTV is a quarantine virus and is included in the South African Phytosanitary Services list of pathogens which must be absent in imported Musaceae propagation material. The disease is spread by the banana aphid (Pentalonia nigronervosa) Coquerel (Hemiptera: Aphididae), and through infected propagation material. In 2015, the detection of the virus was reported from an isolated area in the KwaZulu-Natal (KZN), South Coast region. The aim of the study was to conduct delimiting surveys across banana-producing regions in South Africa, focusing where the BBTD outbreaks were reported. Secondly, the distribution of the virus in the KZN region was determined and the molecular diversity in the plant- and aphid samples were determined. Over 400 plant- and aphid samples were collected from 15 commercial farms and 60 rural households in the region. A BBTV-specific PCR was done using primer pairs BBT-1 and BBT-2, amplifying a fragment of the putative replicase gene. The BBTV-positive PCR products were sequenced using Sanger sequencing. Phylogenetic analyses of the replicate genomic region clustered with the South Pacific group that included accessions from India, Pakistan, and other regions in Africa with a sequence identity of 99%. To date, the virus has been identified in another commercial farm 47km from the initial outbreak site. Management strategies, including removal of infected plants and controlling aphid populations have been implemented in areas where positive samples were identified Early detection of the virus in the aphid vector is used to determine early infections. Awareness campaigns were launched in the rural areas in KZN, but the disease is still spreading in these regions. Ongoing efforts by the ARC, commercial farmers and the Department of Agriculture is ongoing to limit the spread of the disease.
Surveillance of bacterial pathogens associated with blackleg symptoms in certified seed potatoes crops in South Eastern Australia

Dr Steven B Johnson, Ms Nellie A. Malseed, Dr Nigel S. Crump

1AuSPICA, Toolangi, Australia

The blackleg disease of potatoes is caused by various pectolytic bacteria including Pectobacterium carotovorum brasiliense, P. parmentieri, Dickeya dianthicola, P. polaris, P. carotovorum subsp. carotovorum, P. atroseptica. During the 2019 growing season, seed potato crops grown in South Eastern Australia and submitted for certification under the AuSPICA seed potato Scheme, were surveyed for the occurrence of blackleg symptoms. Samples from symptomatic plants were collected and sent to laboratory for identification using molecular and traditional methods. A total of 167 samples were collected from seed crops submitted for certification in Victoria and South Australia. Of these, 40 samples were negative to all blackleg causing pathogens. It was common for P. carotovorum brasiliense to be identified in the same plant sample as P. parmentieri, with 38 plant samples that were positive to both bacteria; and 21 plant samples were positive to P. carotovorum brasiliense and 44 plant samples were positive to P. parmentieri. D. dianthicola was detected in four plant samples. Based on disease symptoms, D. dianthicola presents the same as P. carotovorum subsp. brasiliense and pectobacterium parmentieri. This is the first report of P. carotovorum subsp brasiliense and P. parmentieri in Australia in potatoes.

Phylogenetic analysis of Cryphonectria parasitica (Chestnut blight) incursion in North-East Victoria

Dr Jacky Edwards, Dr Jackinder Kaur, Dr Dilani De Silva, Dr Quang Dinh, Dr Ramez Aldaoud, Dr SriKanthi de Alwis, Dr Martin Mebalds, Dr Ross Mann, Dr John Gilliland, Dr Cecile Robin

1Agriculture Victoria, AgriBio, Centre for AgriBioscience, Bundoora, Australia, 2School of Applied Systems Biology, La Trobe University, Bundoora, Australia, 3Biosecurity and Agriculture Services, Chief Plant Health Officer Unit, Attwood, Australia, 4INRA, UMR BIOGECO, Equipe Génétique et Ecologie des Maladies de la Forêt, Cestas Cedex, France

Chestnut blight, caused by the fungus Cryphonectria parasitica, is the most damaging disease of chestnut trees, including sweet chestnut (Castanea sativa) which is highly susceptible. In spring 2010, chestnut blight was detected for the first time in Australia. The detection was made in the Ovens Valley, North-East Victoria, the major chestnut growing region in Australia. Intensive surveys were carried out across Victoria and confirmed that chestnut blight was found on only 11 properties (IPs) in the Ovens Valley. An eradication program was initiated in 2010 and by the end of 2011, all visibly-infected trees had been removed and destroyed. Since then, ongoing surveillance detected a small number of infected trees on the same or neighbouring properties in 2014, 2016, 2017 and 2018, bringing the number of IPs to seventeen. To determine if the new detections were latent infections from the original outbreak, or were from different introductions, our study utilised 43 Cryphonectria parasitica isolates from all 17 properties that had been retained in the Victorian Plant Pathogen Herbarium, VPRI, or had been sent to France during the original incursion. DNA was extracted from single spore cultures and screened using 16 microsatellite markers in two multiplex PCR assays [1]. DNA from 17 European tester isolates were included in the assay. The Victorian isolates clustered into 3 distinct groups that correlated with location, except for one property. Isolates from Eurobin were identified as RE019 (widely distributed France, Italy, Switzerland); isolates from two properties in Bright were identified as H013 (newly identified lineage in northern France), and the remaining isolates from Wandiligong, Smoko and another property in Bright were identical to each other but did not match any of the European testers. The isolates from 2014-2018 matched isolates from 2010-2011 found in the same locations, providing evidence that the new detections are undetected latent infections from 2010-11, or were missed during earlier surveillance activities. Chestnut blight is under official control in Australia.

Biosecurity Pest Surveillance in Queensland

Ms Christine Horlock\textsuperscript{1}, Dr Ceri Pearce\textsuperscript{2}, Mrs Rosamund Allen\textsuperscript{3}
\textsuperscript{1}Biosecurity Queensland, DAF, Dutton Park, Australia, \textsuperscript{2}Biosecurity Queensland, DAF, South Johnstone, Australia, \textsuperscript{3}Biosecurity Queensland, DAF, Cairns, Australia

Queensland has an increased risk of exotic pest and disease incursions due to its proximity to South-East Asia and Papua New Guinea, where many exotic threats to our horticultural industries are present. Interstate and international movement of people, freight and machinery create an ever-increasing risk for pest entry and spread. Biosecurity Queensland conducts surveys for high priority plant pests (including pathogens, nematodes, insects and invertebrates) throughout Queensland. Data gathered from surveillance for pests of biosecurity concern is used to: 1) facilitate early detection, to support containment and potential eradication of exotic plant pests; 2) demonstrate area freedom from pests restricted to parts of Queensland or Australia, to continue market access; and 3) encourage stakeholder and general public awareness and reporting of suspect pests for further investigation. Standardised methodologies are used by trained plant health inspectors for the collection, storage and despatch of specimens to diagnostic laboratories. Identification is undertaken by specialist diagnosticians. Surveillance and diagnostic data are recorded and reported using Biosecurity Online Resources and Information Systems (BORIS) and Motion X, using handheld devices and desktop versions. Surveys are conducted in agricultural, urban and peri-urban areas. Individual sites for surveys are selected based on proximity to high-risk pathways of pest entry and establishment, volume of host plants/commodities produced, the biology of the pest being targeted, and interstate and international market access requirements. In recent years, Queensland has also prioritised surveillance in areas (urban and rural) accommodating high numbers of overseas tourists, student or transient workers, international airports or sea ports, and road and rail transport depots, etc. Surveillance results since January 1\textsuperscript{st} 2017 for high priority plant pests are presented.
Grapevine powdery mildew: from fundamental plant pathology to new and future vineyard technologies

Prof Eileen S. Scott
School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, South Australia, Australia

Grapevine powdery mildew, caused by the fungus *Erysiphe necator*, is a widespread disease which can reduce yield and quality of grapes and compromise wine quality. As an obligately biotrophic pathogen of a woody perennial crop, *E. necator* presents challenges for researchers studying aspects of biology, epidemiology and management. The disease can be difficult to detect, especially in the early stages, as signs and symptoms are often inconspicuous. Failure to control powdery mildew early, inadequate spray coverage and or fungicide resistance may lead to significant damage. Because of the negative effects on wine quality, many wineries set thresholds for acceptability of grapes for winemaking, typically 3-5% of the surface area of bunches affected. This is usually determined by visual inspection in the vineyard close to harvest or at the winery. Visual assessment is subjective and prone to inaccuracy, and the wine industry seeks a rapid and reliable objective measure for disease severity. I will describe some of the challenges of research on the biology and management of grapevine powdery mildew and how these have been addressed using fundamental approaches in plant pathology. Recent research towards development of objective measures will be presented and I will consider some of the technologies that have potential for application in the vineyard or winery in the future to facilitate disease diagnosis, quantification and management.
A biosecurity perspective of high-throughput sequencing for virus detection and diagnosis

Dr Thierry Candresse
UMR 1332 BFP, INRA, Univ. Bordeaux, Concurrent Session 20032, 33882 Villenave d’Ornon Cedex, France, (thierry.candresse@inra.fr)

The rapid development of high-throughput sequencing (HTS) technologies has impacted many research areas. In plant virology, HTS coupled with bioinformatics have dramatically changed the way virus discovery, etiology efforts or viral population analyses are performed. Key in this success is the ability, for the first time, to perform a complete viral indexing of a plant sample without the need for any prior knowledge (1). Protocols for the analysis of a variety of nucleic acids populations are now available, together with efficient pipelines for the bioinformatic analysis of the huge volumes of sequence data involved. These developments have wide ranging consequences in the diagnostics field and, in particular, in biosecurity. Still, HTS-based viral indexing has yet to be applied on a large scale in routine settings. The price of these technologies, which is still diminishing, is not a limitation for high value plant samples such as mother plants, and already compares favorably with the cost of an extensive indexing performed with classical techniques. Other pitfalls that will be discussed, and have yet to be overcome, include the definition and validation of detection thresholds, comparison of sensitivity with existing techniques or implementation of appropriate quality controls (1,2). In a biosecurity context, the discovery of agents for which no or very limited biological information is available, raises questions for risk assessment and for the ensuing decision making. The development of strategies for the analysis of the risks potentially posed by newly discovered agents is therefore of high priority as is the gathering of relevant biological information (3).

Control of foliar bacterial diseases: alternatives to copper

Dr Cherie Gambley1, Mr Peter Nimmo3, Dr Paul Campbell2, Dr Rebecca Roach3

1Department of Agriculture and Fisheries, Applethorpe, Australia, 2Department of Agriculture and Fisheries, Brisbane, Australia

Current industry standards for phytobacteria control include copper protectants and plant host resistance. The effectiveness of copper to manage bacterial diseases is often poor, despite registered application rates being about ten times greater than required to inhibit bacterial growth in vitro. This discrepancy between in vitro compared to in-field bacterial suppression is related to the low availability of the bactericidal form of copper (i.e Cu2+) in field environments. This is further exacerbated by copper tolerant bacterial populations. Host resistance, although an effective strategy to control bacterial diseases, is limited by low availability of suitable resistance genes which are often also overcome by pathogen evolution. Previous research has indicated plant oils could be useful as an alternative for disease control (1-3).

To identify new products for disease control, oil from clove, coriander, fennel, lavender, oregano and thyme were evaluated in vitro for efficacy to suppress Australian isolates of Pseudomonas syringae pv. porri, P. syringae pv. syringae, Xanthomonas euvesicatoria and X. vesicatoria, either as a volatile gas or through direct contact. Selected oils were then tested in pot trials to evaluate disease control in capsicum plants to X. euvesicatoria. An overview of the limitations of copper for disease control and results of potential oils for control of foliar phytobacteria will be presented.


Interspecies hybridisation and recombination events lead to the emergence of fungicide resistant clonal populations in Pyrenophora teres f. maculata

Mr Wesley Mair1, Dr Chala Turo1, Dr Anke Martin2, Dr Simon Ellwood1, Prof Richard Oliver1, Dr Francisco Lopez-Ruiz2

1Curtin University, Bentley, Australia, 2University of Southern Queensland, Toowoomba, Australia

Demethylase-inhibitor (DMI) fungicides have been frequently used to control net- (NFNB, causal agent Pyrenophora teres f. teres, Ptt) and spot- (SFNB, P. teres f. maculata, Ptm) form net blotch diseases of barley. While NFNB resistance to DMI fungicides has been described in Western Australia (WA), limited knowledge is available for resistance and its molecular basis in SFNB. A total of 43 Ptm strains collected 1996-2018 from WA barley growing regions were characterized for their sensitivity to several DMIs. The isolates differed in resistance factors ranging from a mean of 2.9 for propiconazole in moderately-resistant (MR) strains to 103 for prochloraz in highly-resistant (HR) strains. Sequencing of the DMI fungicide target region (Cyp51A) confirmed the presence in HR strains of a single amino acid substitution (F489L), identical to that reported in resistant Ptt. The Cyp51A promoter regions of both MR and HR strains also contained several different 134-bp insertion elements homologous to the ends of a Long Terminal Repeat retrotransposon. This was associated with constitutive overexpression of Cyp51A. Molecular markers specific to Ptt and Ptm showed HR strains carried both markers, suggesting the possibility that they were hybrids between the two forms. Diversity Array Technology (DArT) marker analysis was used to evaluate Ptm population diversity and structure. Cluster analysis of a total 13,943 DArT markers clearly distinguished barley grass, Ptm and Ptt isolates. While there was no genetic diversity among 40 HR isolates analysed, they were closely related to Ptm. Genome sequencing of selected isolates revealed evidence of recombination between Ptm and Ptt on aligned intergenic regions. Among 1,393 intergenic regions tested, 75 suggested presence of significant (P < 0.05) recombination. The results suggest that the HR hybrid isolates in WA may have arisen from an interspecific sexual recombination event with Ptt, followed by subsequent backcrossing to Ptm and clonal dispersion.
Functional characterization of a putative histone acetyltransferase (PnESA1) gene to investigate its potential as a new fungicide target

Ms Anjana Sharma1, Dr Weiwei Deng1, Dr Kar-Chun Tan1, Mr Steven Chang1, Dr Francisco J. Lopez-Ruiz1
1Curtin University, Bentley, Australia

Fungicides are a key component in the majority of crop disease management strategies. However, the widespread emergence of fungicide resistance together with the lack of new fungicides is threatening crop production worldwide. The current approach to discovering new fungicide molecules is based on random screening, involving a considerable investment in time and resources and often ending with molecules of unknown mode of action. Targeting histone modifiers involved in the regulation of gene expression to control fungal diseases in human has been previously evaluated, however, such studies are lacking in crop. Histone acetyltransferases (HATs) are responsible for histone acetylation, which is an important epigenetic modification involved in gene expression increase. Because HATs are conserved among diverse organisms and are involved in regulating important cellular functions, they have been suggested as potential drug targets for controlling fungal pathogens in both humans and plants. In this study, knock out and knock down strategies were applied for the functional characterisation of the Parastagnospora nodorum putative HAT gene PnESA1. Attempts to delete PnESA1 from P. nodorum were unsuccessful. In contrast, knock down of the gene using a long-hairpin RNAi approach showed successful silencing of PnESA1 in five P. nodorum transformants. All transformants exhibited reduced sporulation compared to the wild type and their phenotype was similar to that of P. nodorum strains under strong abiotic stress. Results suggest an essential function for PnESA1 in P. nodorum. Further studies aim to determine the processes disrupted by PnESA1 gene deletion in P. nodorum. This will facilitate the identification of fungal inhibition pathways that could be targeted for the control of plant pathogens.

Blackleg in Australia: resistance groups, fungicide resistance and upper canopy infection

Dr Alexander Idnurm1, Dr Steve Macroft2, Dr Susan Sprague3, Dr Angela Van De Wouw4
1University Of Melbourne, Parkville, Australia, 2Macroft Grains Pathology, Horsham, Australia, 3CSIRO, Australia

Blackleg disease, caused by Leptosphaeria maculans, remains the most significant disease of canola (Brassica napus) in Australia with yield losses ranging between 10-30% annually and epidemics resulting in yield losses of up to 90% in specific regions. Management of blackleg involves a three-pronged approach combining genetic, cultural and chemical practices. In Australia, the development of a differential set of field isolates allows the characterisation of resistance genes in all commercially released cultivars. Blackleg disease is minimised by rotation of cultivars with different resistance genes. At a population level, changes in the frequency of virulence alleles, as determined by molecular analysis for avirulence genes, shift dramatically under different rotation strategies but these shifts cannot always be predicted by the host resistance genes. Furthermore, stacking of multiple resistance genes in a single host selects for isolates virulent towards all resistance genes, preventing the use of rotation of single resistance genes as a management tool. Changes in cultural crop practices is having a large impact on the epidemiology of blackleg disease. Retention of stubble to conserve soil moisture has led to shifts in the quantity and timing of spore release. Furthermore, changes in crop management in the face of climate change have led to earlier flowering times leading to an increase in the incidence and severity of blackleg lesions on flowers, pods, upper stems and branches (collectively called upper canopy infection). Lastly, the use of fungicides has increased dramatically with 90% of growers currently using seed treatments and fungicide-amended fertilisers in combination at sowing. In addition, 50% of growers currently apply in-season foliar fungicides for blackleg control. Fungicide resistance to the demethylation inhibitor (DMI) class of fungicides was identified in 25% of Australian blackleg populations recently surveyed. To date, no fungicide resistance has been identified to succinate dehydrogenase inhibitor (SDHI) or Strobilurin fungicides.
Spatial and temporal distribution of copper-resistant strains of *Pseudomonas syringae pv. actinidiae* in a kiwifruit orchard and their control using copper

**Dr Joel L. Vanneste**, Dr Toan P. Hong, Ms Deirdre A. Cornish, Ms Magan M. Schipper, Ms Janet Yu, Dr Jenny M. Oldham

*Copper is one of the most cost-effective products for control of bacterial pathogens such as *Pseudomonas syringae pv. actinidiae* (Psa), which causes bacterial canker on kiwifruit. To determine whether copper could still control Psa in an orchard where copper-resistant (CuR) strains of Psa had been isolated, young potted plants of kiwifruit (*Actinidia chinensis* var. *chinensis* ‘Hort16A’) susceptible to Psa were hung in the canopy of a commercial orchard where CuR strains were present. The experiment was repeated 12 times between November 2017 and May 2018. At each time, plants treated with copper hydroxide (Kocide®, 70 g/100L), cuprous oxide (Nordox™, 37.5g/100L), or water were placed in ten locations in the orchard. After 1 to 3 weeks, depending on the weather conditions, the plants were brought into a glasshouse to express symptoms. The pathogen was isolated from each leaf spot and copper resistance was determined for c. 10 strains per leaf spot. In total about 30,000 strains were isolated and phenotyped. The comparison of disease incidence on treated and non-treated plants indicated that the two copper-based products reduced Psa incidence. To date there is no indication that CuR strains of Psa are not controlled by copper. However, copper treatments increase the ratio of CuR:CuS strains. The rate of infection at any time point within the block was highly variable; as was the percentage of leaf spots from which a CuR strain was isolated and the concentration of copper (0.64 mM to 2 mM) to which a strain was resistant. Whole genome sequence analysis led to the identification of different mobile genetic elements (MGE) in the strains isolated from this orchard. While we have determined the spatial and temporal distribution of CuR Psa strains in this orchard, we are now investigating the spatial and temporal distribution of the MGE responsible for copper resistance.*

Widespread resistance to SDHI fungicides in New Zealand populations of the barley pathogen *Ramularia collo-cygni*

**Ms Rachael M Warren**, Ms Shirley E Thompson, Dr David B Baird, Ms Joanne B Drummond, Dr Soonie F Chng

*Ramularia leaf spot (RLS), caused by the fungus *Ramularia collo-cygni* (Rcc), has recently become a serious threat to barley production in New Zealand and worldwide. Currently, management of the disease relies on the application of foliar fungicides. However, the development of fungicide resistance in Rcc populations is an increasing issue, with erosion of sensitivity to the quinone outside inhibitors (QoIs) confirmed overseas. To determine whether similar shifts in sensitivity were occurring in New Zealand Rcc populations, a microplate assay was used to screen field isolates against increasing concentrations of active ingredients within the SDHI, DMI and QoI fungicide groups. Estimates of the chemical concentration inhibiting growth by half (EC50 values) of 150 isolates, collected throughout the main barley growing regions of New Zealand between 2014 and 2018, have indicated a shift in sensitivity to the SDHIs, similar to those observed overseas. Analysis of the succinate dehydrogenase genes confirmed the presence of substitutions SdhC-H146R and SdhC-153R in highly-insensitive isolates. Isolates carrying these substitutions had EC50 values up to 100 times higher than the values of isolates carrying the wild-type version of the gene. Another substitution, SdhC-N87S, was identified in isolates showing a moderate-insensitivity to the SDHIs in *vitro*. The proportion of isolates identified carrying substitutions SdhC-H146R and SdhC-153R has rapidly increased, with over 96% of isolates screened in 2018 displaying a highly-insensitive SDHI EC50 profile, indicating SDHI insensitive isolates are now widespread within the New Zealand Rcc population. Field isolates showing resistance to the QoIs, and found to carry mutation G143A in the cytochrome b gene, were also identified.*
Development and application of a genome-informed loop-mediated isothermal amplification (LAMP) assay for the detection of *Pseudomonas syringae* pathovar *pisi* and *syringae*

**Dr Pragya Kant**

1. Agriculture Victoria, Grains Innovation Park, Horsham, Australia, 2. Biometry Hub, SAGI- STH, University of Adelaide, Adelaide, Australia, 3. Agriculture Victoria, AgriBio, Melbourne, Australia

The wide spread application of high throughput sequencing is being driven by low cost, ease of application, and advances in computational and bioinformatic capabilities. The vast amounts of data generated from sequencing technologies is facilitating the identification of novel targets for the design of specific and robust molecular diagnostics. This study reports the use of 10 draft genome sequences from the bacterial plant pathogen *Pseudomonas syringae* pathovar *pisi* (Ppi), the causal agent of bacterial blight in field pea, to identify unique diagnostic targets and design primers for a loop-mediated isothermal amplification (LAMP) assay. The assay reported here reliably differentiates strains of Ppi isolated from field pea from a range of other bacteria that are commonly associated with peas and other plants. The Ppi LAMP and a *Pseudomonas syringae* pathovar *syringae* (Psy) LAMP developed by collaborators, were validated with a range of *Pseudomonas* species and *P. syringae* pathovars including historical isolates from the VPR collection and recent isolates from the field. LAMP assay for both Ppi and Psy proved to be highly sensitive, accurate and versatile for application on bacterial colonies, and extracts or exudates from infected host plant material. The LAMP assay is a suitable diagnostic tool for the glasshouse and laboratory and as well as for in-field surveys.

Molecular diagnosis of viruses causing yellowing and stunting symptoms affecting pulse crops in Central West Asia and North Africa Countries

**Dr Safaa Kumari**, Dr Murray Sharman, Dr Fiona Filardo, Mr Abdul Rahman Moukahel, Mr Nader Asaad, Ms Samia Mghandef, Mr Joop van Leur

1. International Center for Agricultural Research in the Dry Areas (ICARDA), Terbol Station, Zahle, Lebanon, 2. Department of Agriculture and Fisheries, Brisbane, Australia, 3. General Commission for Scientific Agricultural Research (GCSAR), Al-Ghab, Hama, Syria, 4. Virology Laboratory, ICARDA, Tunis, Tunisia, 5. NSW Department of Primary Industries, Tamworth Agricultural Institute, Australia

Viruses causing yellowing and stunting are the most important virus diseases affecting pulses in many regions of the world, and were considered for many years to be caused mainly by infection with beet western yellows virus (BWYV, genus *Polerovirus*, family *Luteoviridae*). Knowing the exact identity of a virus affecting pulse crops is essential for breeding for resistance and crop management purposes. More than 5000 pulse samples (faba bean, lentil, and chickpea) with symptoms typical of virus infection including stunting, yellowing, necrosis and reddening were collected during the last two decades from different countries in Central West Asia and North Africa (CWANA). All samples were tested serologically by tissue-blot immunoassay (TBIA) technique using specific luteoviridae monoclonal antibodies. Selected samples were further tested by reverse transcription polymerase chain reaction (RT-PCR) using different luteoviridae primer pairs (generic and specific) followed by amplicon sequencing. RT-PCR results revealed clearly that there was a greater variation in polerovirus species detected than was indicated by TBIA alone. Molecular diagnosis has clearly shown that there are a number of *Polerovirus* species, in addition to BWYV (detected in Algeria, Ethiopia, Lebanon, Morocco, Sudan, Tunisia and Uzbekistan), each of which can produce yellowing and stunting symptoms in pulses in CWANA. These viruses are cucurbit aphid-borne yellows virus (detected in Algeria, Lebanon, Syria, Sudan and Uzbekistan), chickpea chlorotic stunt virus (detected in Algeria, Ethiopia, Lebanon, Morocco, Syria, and Tunisia), pepper vein yellows virus (detected in Morocco and Sudan), pepo aphid-borne yellows virus (detected in Sudan), and cotton leafroll dwarf virus (detected in Sudan and Uzbekistan). This study clearly showed that molecular characterization is an essential tool for accurate identification of plant viruses, which is the first step towards better crop management.
Rapid and sensitive detection of rice tungro virus by Loop-mediated isothermal amplification (LAMP)

Dr Fausiah Ladja1, MSi Yunimar Yunimar2, MSi Mansur Mansur1, Dr I Nyoman Widiarta3

1 Tungro Disease Research Station, Ministry of Agriculture, Sidenreng Rappang, Indonesia, 2 Indonesian Citrus And Subtropical Fruits Research Institute, Malang, Indonesia, 3 Indonesian Center for Food Crops Research and Development, Bogor, Indonesia

Several molecular methods have been developed for the detection of rice tungro spherical virus (RTSV) and rice tungro bacilliform virus (RTBV), the causal agent of rice tungro disease, but none are rapid methods and still need an expensive instrument. Developing a quick and accurate method to diagnose rice viruses in host plants and in insect vectors is very important for developing early warning systems to control rice tungro disease. Loop-mediated isothermal amplification (LAMP) assay is a molecular detection technique with high specificity and rapidity under isothermal conditions. The partial sequence of RTBV and RTSV, ORF1 and ORF3 genes, are used as the target template to design LAMP primers. Two extraction methods were evaluated, i.e: NaOH and CTAB. The DNA viruses from extracted sample were detected by LAMP with conventional PCR as a comparison. The results showed that RTBV and RTSV nucleic acid extracted from infected leaves with NaOH and CTAB were successfully amplified using conventional PCR with comparable DNA intensities. Based on the quality of amplified DNA, the NaOH method can be developed as an alternative DNA extraction method. Sensitivity and rapidity of detection using the LAMP technique is greater than conventional PCR.

Detached leaf assay to determine the host range and pathogenicity of citrus canker bacteria (Xanthomonas citri subsp. citri A*) causing the current Northern Territory outbreak

Dr Blessy Pathrose1, Dr Merran Neilsen1, Ms Karla Cardenas Gomez1, Mrs Shreya Patel1, Dr Lucy Tran-Nguyen1

1 Biosecurity & Animal Welfare, Department of Primary Industry and Resources, Makagon Road, Berrimah Farm, Darwin, Australia

Citrus canker is a bacterial disease affecting different varieties of citrus caused by Xanthomonas citri subsp. citri. This disease causes wide spread damage to citrus worldwide and severity of citrus canker disease differs with different varieties and the climatic conditions. In the Northern Territory (NT), citrus canker was first detected in April 2018 and the strain that causes disease in NT has been identified as Xanthomonas citri subsp. citri (Xcc) A* and the host range of Xcc A* is not fully known. To improve our understanding of the host range, 14 citrus varieties and a non-citrus host (Evodia hortensis) were tested by a detached leaf assay with wound inoculation. Symptoms on detached leaves were assessed and indicated that citrus varieties West Indian lime, Lemon Meyer and Star Ruby grapefruit were found to be highly susceptible to citrus canker disease on detached leaves. The moderate susceptible hosts were found to be Tahiti lime, Kaffir lime, Rio Red grapefruit, Pomelo and Evodia hortensis (non-citrus host). Desert lime, Lemon Lisbon, Mandarin Imperial, Orange Navel and Orange Valencia were found to be less susceptible to citrus canker disease on detached leaves. Mandarin Emperor was found to be resistant to citrus canker disease on detached leaves. The detached leaf assay was able to show varied levels of susceptibility within the citrus varieties and Evodia hortensis. All host varieties tested were found to be susceptible to citrus canker disease except Mandarin Emperor. However, host reaction to Xcc A* to any level of susceptibility indicates a potential source of inoculum to infect other hosts. Further study on whole plants is required to confirm this host range.
Assay validation in diagnostics: the missing link?

Dr Vivian Rincon Florez1, Dr Lília Carvalhais2, Ms Jane Ray1, Mrs Cecilia O’Dwyer1, Prof Andre Drenth1
1QAAFI, University of Queensland, Brisbane, Australia

Agricultural productivity and food security can be jeopardised by the emergence of new plant diseases. Increasing travel and trade have made the world more connected but also increased the rate of spread and invasion of plant pathogens. Diagnostic tools deployed to screen planting materials and investigate new disease outbreaks play a major role in early detection, eradication and containment of new pathogen incursions. However, the use of poorly validated diagnostic assays can lead to the occurrence of false positive or false negative results, lack of specificity and reproducibility making straightforward interpretation of the results less robust. Incorrect diagnostics has been shown to give rise to economic losses, confusion and lack of confidence. A key component in the development of diagnostic assays is the validation process to establish the fitness of an assay that has been optimised and standardised for a well-defined intended purpose. New or modified diagnostic tests require a rigorous ‘in-house’ verification to demonstrate the performance of the assay under a range of conditions. To ensure assay fitness, a range of assessments of the method are needed to be conducted, ensuring the inclusion of appropriate controls in each run and the use of the various organisms related to the target pathogen. Many published papers in the area of pathogen diagnostics lack a rigorous validation process. The validation process requires testing specific parameters that depend on the nature of the method and the sample size. For diagnostics, seven parameters are required to demonstrate that an assay is fit for purpose and adheres to the Australian National Association of Testing Authorities (NATA) for accreditation. Each parameter will be explained with relevant examples to portray how failures in validation can cause major interpretation problems and false positives. The end goal of assay validation in diagnostics is to ensure the method is accurate, reproducible and fit for purpose.

Development of new diagnostic antibodies for Banana bunchy top virus

Dr Megan Vance1, Assoc Prof John Thomas1
1Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, Australia

Enzyme-linked immunosorbent assay (ELISA) is a preferred method for detection of Banana bunchy top virus (BBTV) in many parts of the world due to its reliability and ability to be performed with simple laboratory equipment. The current commercially available diagnostic antibody reagents for ELISA testing for BBTV are in severe shortage worldwide. We have developed new antibodies for use in ELISA and potentially other immunoassays for detection of BBTV. BBTV purified from banana mid-rib tissue was injected into mice for monoclonal antibody production, and into a rabbit for polyclonal antibody production. To date, several monoclonal antibodies have been identified with a further 150 hybridoma lines still to be assessed. These new monoclonal and polyclonal antibodies are currently being characterised for use in ELISA. Initial results show that the polyclonal antibodies serve well as capture antibodies in a triple antibody sandwich ELISA, with two of the monoclonal antibodies being suitable for use as detection antibodies. These two monoclonal antibodies are also able to be used as capture antibodies in the assay. Specificity testing shows that these new antibodies are able to detect BBTV from both the Asian and South Pacific phylogenetic groups. Future work will include testing for cross-reactivity with the other babuviruses. Work is continuing to optimise the best antibody combinations and other assay parameters for ELISA. The new antibodies are also being tested in other immunoassay formats. These new antibodies will ensure that the availability of diagnostic reagents for detection of BBTV will continue into the future.
Palmageddon in Australia? A lethal disease of palms associated with a new phytoplasma in Cairns

**Dr Richard Davis**, Dr Brad Pease, Dr Lynne Jones, Dr Sandy Perkins, Dr Fiona Constable, Dr Cliff Kinoti, Dr David Warmington, Dr Pieter Taylor, Dr Ceri Pearce

1Department Of Agriculture, Cairns, Australia, 2Department of Jobs, Precincts and Regions, Bundoora, Australia, 3Cairns Regional Council, Cairns, Australia, 4Queensland Department of Agriculture and Fisheries, South Johnstone, Australia

A phytoplasma associated with a rapid lethal wilt of ornamental palms in Cairns was detected by nested and real time PCR. Leaf death progressed from older to younger leaves, culminating in meristem rot. With a maximum 16SrRNA gene sequence similarity of 96%, this phytoplasma is most closely related to, but not a member of, the novel taxon *Candidatus Phytoplasma noviguineense*. The next most closely related sequences all belonged to phytoplasmas in the 16SrIV and 16SrXXII groups. *Ca. P. noviguineense* and members of these groups are implicated in devastating diseases of coconut overseas and have never been recorded before in Australia. A key symptom in Cairns is shared with these exotic coconut diseases: dead leaves hang down, skirt like, before eventually falling. Phylogenetic trees comparing 16SrRNA and three ribosomal protein gene sequences against those of known candidatus phytoplasma species, plus other variants, confirmed the uniqueness of this phytoplasma. It was first detected in late 2017 in a *Dypsis poivreana* within the Cairns Botanic Gardens, (CBG). In 2018, it was also found in a *Euterpe precatoria* just outside the CBG and in a coconut palm (*Cocos nucifera*) and an Alexandria palm (*Archontophoenix alexandriae*), about 2 km south east of the CBG. Later investigations up to March 2019 detected the phytoplasma in more dying palms. These were a *Verschaffeltia splendida* and a *Brassiophoenix drymophloeodes* in the CBG, a *Euterpe* sp. about 600m west of the CBG, a *Phoenix* sp. 1.5 km west of the CBG, and a Carpentaria palm (*Carpentaria acuminata*) about 3 km south of the CBG. Detections at six separate locations suggests a capable insect vector is also present. During these investigations, a total of 33 other palms tested negative for phytoplasma, strongly suggesting this phytoplasma could be a causal agent of serious disease, rather than just an occasional phloem inhabitant.

Genetic identity, epidemiology and management of faba bean (*Vicia faba*) gall disease in Ethiopia

**Mr Beyene Eshete**

1Debre Birhan Agricultural Research Center, Debre Birhan, Ethiopia

Ethiopia is the world’s second largest producer of faba bean (*Vicia faba*) and there, it has largest share in terms of area and production of all pulses grown. It is valued as a cheap source of protein for human food, cash crop, its straw is a key animal feedstock, and it is an important rotational crop that enhances cereal yield. However, current productivity is very low due to susceptibility to a new emerging faba bean gall (FBG) disease. FBG causal agent remains unconfirmed, but it is likely an *Olpidium* sp. FBG is expanding across all major faba bean growing areas and has devastated faba bean production. Despite this, there has been relatively little comprehensive data on or understanding of the status of FBG across Ethiopia. Hence, a PhD study was initiated to address the following objectives: to assess the distribution, disease intensity and hosts of FBG disease; to determine the association of FBG disease intensity with major biophysical factors; to characterize the genetic identity of FBG disease causal pathogen; to develop integrated disease management options; and to identify the phenotypic reactions of genotypes and determine the stability of host resistance reactions to FBG disease under different agro-ecological conditions. Already 384 farmers’ fields have been surveyed, showing FBG to be particularly severe at altitudes >2300 m above sea level, in light soils, and at higher rainfall areas. Application of the fungicide triadimefon at 10 day intervals on moderately tolerant varieties significantly improved grain yield over that of the local faba bean variety. Variables such as later planting and later growth stage, increased crop density, previous susceptible crops, and poor drainage, all showed positive correlation with increased FBG disease severity. Studies to identify the causative agent, both morphologically and molecularly, are ongoing.
A new-to-science virus that infects karaka (*Corynocarpus laevigatus*), an endemic tree of New Zealand, is strongly associated with chlorotic ring spot symptoms

**Mr Lee Rabbidge**1,2, Dr Arnaud Blouin3, Dr Karmun Chooi2, Dr Robin MacDiarmid2, Dr Colleen Higgins1

1Institute for Applied Ecology New Zealand, School of Applied Sciences, Auckland University of Technology, Auckland, New Zealand, 2The New Zealand Institute for Plant and Food Research Limited, Auckland, New Zealand, 3Integrated and Urban Plant Pathology Laboratory Gembloux Agro-Bio Tech, University of Liege, Liège, Belgium

Chlorotic spot symptoms were observed on a specimen of a tree endemic to New Zealand, karaka (*Corynocarpus laevigatus*), leading to an investigation of the potential viruses associated with the symptoms. RNA-seq analysis identified a new-to-science emaravirus along with two other novel DNA sequences. We undertook full genome sequencing, a survey to identify the distribution of symptomatic karaka trees, and symptom correlation studies. Emaravirus is an established genus of viruses with plant hosts. Each species within the genus has a segmented, negative-sense monocistronic RNA genome comprising five to seven strands, and is vectored by eriophyid mites. We identified five negative-sense strands by high throughput sequencing, which were all confirmed by Sanger sequencing. The sequence of each strand was completed following rapid amplification of cDNA ends (RACE). Sequence comparison with other established emaravirus sequences revealed that this represents a unique virus, with only 33% amino acid identity within the replicase of its closest relative *Redbud yellow ringspot-associated virus*. A diagnostic test was developed and implemented to assess the virus’ distribution across New Zealand. The novel virus was primarily found throughout Auckland in both naturally occurring and planted karaka trees, with only a few examples identified beyond this region. Using the diagnostic test the presence of virus was confirmed to be highly correlated with the chlorotic spot symptoms. In addition, the virus was found to be only detectable within symptomatic regions of the leaf and not systematic. Systemic movement may be dependent on the suspected eriophyid mite vector, the endemic karaka gall mite. We present evidence for the sequence of a unique emaravirus, that represents the first endemic plant virus reported in New Zealand. The virus is strongly associated with the observed symptoms, therefore we suggest the name Karaka tīwata porohita virus, which describes the chlorotic spots in te reo Māori.
Spread, distribution and infection biology of banana blood disease (*Ralstonia syzygii* subsp. *celebesensis*)

Ms Jane Ray¹, Dr Vivian Rincon-Florez¹, Prof Siti Subandiyah², Mr Ady Prakoso², Dr. Lília Carvalhais¹, Dr. Alistair McTaggart¹, Ms Cecilia O'Dwyer¹, Prof Andre Drenth¹

¹University Of Queensland, Dutton Park, Australia, ²Gadjah Mada University, Jogjakarta, Indonesia

Banana blood disease (*Ralstonia syzygii* subsp. *celebesensis*) is a vascular wilt of banana that causes significant crop losses. This disease is characterised by a set of striking symptoms that include internal rot of green banana fruits and red/brown vascular discoloration in the centre of the pseudostem and peduncle. The disease was first documented in 1905 when an epidemic devastated banana plantations on a small island to the south of Sulawesi in the Selayar Islands, Indonesia. Shortly after, blood disease was reported from the island of Sulawesi. Quarantine preventing movement of banana planting material from Selayar and Sulawesi contained the disease until an outbreak occurred in West Java in 1987. From West Java the disease spread rapidly to many locations in the Indonesian archipelago and was detected more recently in peninsular Malaysia (2013). Our study aims to investigate (i) the spread and distribution of the disease, and (ii) how infection occurs in banana plants and the role insects play. We determined and confirmed the historical and current distribution of the disease through surveys, strains collected were identified and confirmed as *Ralstonia syzygii* subsp. *celebesensis* using biochemical and molecular diagnostics. Our field observations revealed that vascular staining generally progresses from the male bell through the peduncle towards the fruit. The inside of the fruit discolours, while the vascular staining continues to progress through the peduncle into the pseudostem. These observations imply that infection commonly occurs through the male bell. A field trial site with Cavendish and kepok banana plants has been established in Yogyakarta, Indonesia to investigate the infection biology of *Ralstonia syzygii* subsp. *celebesensis*. Insight into the distribution of banana blood disease and an understanding of the infection biology is important to be able to reduce the impact of this emerging disease threat to South East Asian and Australian banana production.
Soft rots of the Pectobacteriaceae – an old foe or an emerging threat to Australian horticulture?

Ms Elisse Nogarotto1, Mrs Soheir Salib1, Mr Perrin Carter1, Dr Fiona Constable1, Dr Brendan Rodoni1, Dr Rachel Mann1

1Agriculture Victoria, Bundoora, Australia

Autumn 2019 saw a significant outbreak of blackleg in potato crops across Australia’s south eastern states. Historical records indicated that there were two blackleg causing bacteria present in Victoria, South Australia and Tasmania, Pectobacterium atrosepticum and P. carotovorum subsp. carotovorum. Since these records the Pectobacteriaceae family has undergone substantial taxonomic reclassification with multiple new genera and species described. During the 2019 blackleg outbreak an additional five species of Pectobacteriaceae belonging to the Pectobacterium and Dickeya genera were isolated and identified from symptomatic plant tissues across multiple samples. Three of these Pectobacteriaceae species were first reports for Australia. Mixed infections of up to four bacterial species were detected in some plant samples. It is unclear how long the newly described Pectobacteriaceae species have been present in Australia. Have they always been present but, in the absence of significant blackleg disease, remained uncharacterised and therefore undetected? Or did the disease emerge with a recent introduction of new species into Australia? Detection, identification and origins of the Pectobacterium and Dickeya species contributing to the 2019 blackleg outbreak will be discussed.

A review of fungal pathogens associated with pyrethrum yield decline in Australia

Dr Azin Moslemi1, Professor Paul Taylor1

1University of Melbourne, Parkville, Australia

Pyrethrum (Tanacetum cinerariifolium) is commercially cultivated for the extraction of organic pyrethrin insecticides. Over the last 15 years pyrethrum crops have been in decline with reduced yields and non-sustainable crop production. Several major fungal plant pathogens have been identified associated with these yield decline plants. Ray blight caused by Stagonosporopsis tanaceti is one the most important diseases infecting leaves and crowns and reducing plant growth. Other important pathogens found to be associated with pyrethrum yield decline are Fusarium oxysporum and F. avenaceum, and Paraphoma vinacea, which caused crown rot and reduced growth of infected pyrethrum plants. Pathogenicity tests showed that F. oxysporum, F. avenaceum and P. vinacea significantly reduced below-ground and total biomass of pyrethrum plants. Dull-tan to reddish-brown discoloration of the cortical and sub-cortical crown tissue was observed in all plants infected with P. vinacea, and crown rot and stunting in plants infected with F. oxysporum. Specificity of pathogenic strains of F. oxysporum to pyrethrum needs to be further investigated as the pathogen was observed in xylem tissue of the infected plants. Alternaria infectoria and Stemphylium herbarum isolated from pseudothecia at the base of dead flower stems, and Paraphoma pye and P. chlamydocopiosa isolated from leaf lesions, were also identified as foliar pathogens of pyrethrum however, these pathogens has small affect on plant growth and will most likely only have a small impact on the commercial cultivation of pyrethrum in Tasmania Glasshouse trials with three-day waterlogging stressed plants infected with P. vinacea, F. oxysporum and F. avenaceum showed less photosynthesis ability, biomass and number of flowers and petioles compared to the controls. This study highlighted the need to assess the impact of the newly identified pathogens of pyrethrum in combination with abiotic stresses such as water logging to enable a better understanding of the cause of yield decline.
Transcriptome analysis of the *Rhynchosporium commune* infecting barley leaf to discover novel virulence factors of *R. commune*

**Mr Reynaldi Darma**, Dr Megan Camilla McDonald, Prof Peter Scott Solomon

1Division of Plant Sciences, Research School of Biology, The Australian National University, Australia

*Rhynchosporium commune* is the causal agent of scald disease in barley and is responsible for 10 to 15% yield losses annually. Subsequent to penetration, this necrotrophic fungus grows in the subcuticular region of the leaf for an extended period of time (7-12 days) prior causing visible necrosis in barley leaves. During that asymptomatic stage, this fungus is hypothesised to secrete small secreted cysteine-rich proteins, known as effectors, to evade plant defence and induce necrosis on the leaf. To date, only three effectors (NIP1, NIP2, and NIP3) have been discovered from *R. commune* that play a role in disease. To discover novel effectors or other virulence factors, a highly-contiguous assembly of *R. commune* genome was generated with the PacBio long-read sequencing technology resulting in 20 contigs with 57.7 Mb of the genome size. To identify genes potentially important for disease, RNA-seq will be performed from barley leaves infected with *R. commune*. To select the best time points for RNA extractions during the asymptomatic period (i.e. ensure enough fungal growth), biomass measurements and GFP visualization during infection have been used to characterize growth during this latent stage. RNA has subsequently been extracted from infected leaves at these time points and is currently being analysed. Subsequent bioinformatics analysis will identify likely virulence candidates that will be further characterised using reverse genetics.

Whole genome sequencing of putative somatic hybrids between formae speciales of *Puccinia graminis*

**Ms Michelle N. K. Demers**, Dr Priyanka Surana, Dr Davinder Singh, Dr Peter Dracatos, Dr Peter N Dodds, Prof Robert F Park

1The University Of Sydney, Parramatta, Australia, 2Commonwealth Scientific and Industrial Research Organization, Canberra, Australia

Isolates of *Puccinia graminis* have been found in Australia that have highly unusual pathogenicity profiles and cannot be categorized into any known forma specialis. These isolates have been referred to as ‘scabrum’ rusts, and are suspected of being the result of a somatic hybridisation event between *Puccinia graminis* f. sp. *tritici* (Pgt) and *Puccinia graminis* f. sp. *secalis* (Pgs). It is postulated that *Puccinia graminis* can exchange haploid nuclei between isolates and even between formae specialis, which would allow these clonally-propagating fungi to undergo a large genetic re-assortment within a single generation. This would have large implications for the use of resistance genes introgressed from different species and for hybrid crops such as triticale. Recent evidence suggests that somatic hybridisation may be a more significant driver of genetic change in *Puccinia graminis* than previously thought, and so this study aims to compare the similarity between the genomes of Pgs and Pgt and determine the origins of the ‘scabrum’ rust and whether it originated from a somatic hybridisation event. To test this hypothesis, the first genomes of Pgs and the ‘scabrum’ rust have been assembled using PacBio long-read sequencing and assembled de novo, and the degree of similarity of the genome and transcriptome of the ‘scabrum’ rust to both Pgt and Pgs will be determined. Understanding the mechanisms affecting genetic variability of highly-mutable pathogens such as *Puccinia graminis* is vital to the success of cereal breeding programs worldwide, and will influence the choice of resistance genes to incorporate into new resistant cereal varieties. This project is currently underway, and the results of these experiments will be presented at the conference.
Pan-genome and phylogeographic analysis of wheat-infecting *Parastagonospora nodorum*

**Mr Darcy Jones**¹, Dr Huyen Phan¹, Ms Kasia Clarke¹, Dr Kar Chun Tan¹, Dr James Hane¹⁻²

¹Centre for Crop and Disease Management, Curtin University, Bentley, Australia, ²Curtin institute for computation, Curtin University, Bentley, Australia

Management of fungal diseases relies on fungicides and crop resistance. Fungal pathogen genomes can mutate rapidly and can quickly adapt to overcome strong selective pressures from disease management. Continued management of fungal disease therefore requires deeper understanding of how fungal pathogen genomes change over space and time. Genomics studies have recently extended to sequencing multiple individuals of a species (pan-genomics), with potential to provide insights into local populations necessary to inform management decisions. *Parastagonospora nodorum* is an important pathogen of wheat which causes significant yield losses. To understand local evolution of the Western Australian (WA) *P. nodorum* population, we sequenced the whole genomes of 155 isolates collected between 1972 and 2016. Genome-based phylogeographic analyses revealed a core diverse WA population with several satellite sub-populations in northern areas of the WA wheatbelt. This may reflect adaptations to recent disease-resistant wheat cultivars, or to different environments and agricultural practices. Whole-genome alignments to the *P. nodorum* SN15, SN4, SN2000, and SN79 reference isolates indicate numerous generic and regional presence-absence variations (PAVs), including the previously described accessory chromosome 23. Analysis of SNPs and short variants revealed rapid accumulation of mutations in the WA *P. nodorum* pan-genome within a relatively short time span. GWAS analyses of SNPs and PAVs with virulence scores revealed several peaks corresponding to known and new candidate effector genes. Clustering of homologous genes between all isolates revealed conserved presence-absence profiles which correlated with phylogenetic and spatio-temporal groups. Several large contiguous gene clusters were common to a few co-located isolates, suggesting the presence of novel accessory regions in the WA *P. nodorum* population. Remote homology analyses using profile-HMMs revealed a number of distant ToxA, Tox1, and Tox3 necrotrophic effector paralogs, forming a set of strong effector candidates. Collectively these bioinformatic studies have given us a deeper understanding of the genome dynamics of *P. nodorum* in the field and a better understanding of the risks of crop disease emergence in fungal pathogen populations.

Genome-wide association mapping analysis to identify genomic regions associated with virulence in *Pyrenophora teres* f. *teres*

**Dr Anke Martin**¹, Dr Yongfu Tao², Mrs Judy McIlroy², Dr Ryan, A Fowler², Dr Lisle Snyman², Mr Greg, J Platz²

¹Centre for Crop Health, University of Southern Queensland, Toowoomba, Australia, ²Queensland Department of Agriculture & Fisheries, Hermitage Research Facility, Warwick, Australia

Net form of net blotch, caused by the fungal pathogen, *Pyrenophora teres* f. *teres* (*Ptt*), is an important foliar disease present in all barley (*Hordeum vulgare*) producing regions of the world. This fungus is a heterothallic haploid ascomycete and reproduces both sexually and asexually. Sexual recombination in *Ptt* can produce new combinations of pathogen virulences and lead to changes in disease expression in the host. Changes in virulence can be devastating to the barley industry especially if a limited number of barley varieties with common resistances are grown. Knowledge of the genetic structure and genes involved in virulence is vital to researchers and breeders to increase the durability of *Ptt* resistance in barley varieties. We have used a genome-wide association mapping approach to characterise genomic regions associated with virulence in Australian barley varieties. One hundred and eighty-seven *Ptt* isolates collected from five Australian states were genotyped using DArTseq (Diversity Arrays Technology Pty Ltd) markers and phenotyped across ten different barley genotypes. Association mapping analysis identified eleven unique genomic regions associated with virulence. The majority of these genomic regions were located on *Ptt* chromosomes 3 and 5. Four of the regions identified were confirmed via bi-parental quantitative trait loci mapping analysis in two different *Ptt/Ptt* populations. Knowledge of the virulence genes present in the Australian *Ptt* pathogen population will provide barley breeding programs with valuable information for future breeding of *Ptt* resistant barley varieties.
Identification of candidate virulence genes from the apple pathogen *Neonectria ditissima*

**Ms Brogan McGreal**¹, Ms Cecilia Deng¹, Dr Reiny Scheper², Ms Amali Thrimawithana¹, Ms Liz Flórez¹², Dr Joanna Bowen¹

¹The New Zealand Institute for Plant and Food Research Limited, Mt Albert, New Zealand, ²The New Zealand Institute for Plant and Food Research Limited, Havelock North, New Zealand, ³The University of Auckland, Auckland, New Zealand

*Neonectria ditissima* causes canker disease in many hosts, including apple and European pear, where the disease in apple, European canker, can be severe. It is currently controlled by pruning and fungicides, thus alternative, more sustainable, and less labour intensive solutions, are desirable. Different apple cultivars show different susceptibilities to canker. Thus, an understanding of the disease process at the molecular level may reveal the presence of susceptibility genes and matching virulence genes underlying this specificity. Therefore, candidate virulence genes were identified by comparative genomic and transcriptomic approaches. These approaches were facilitated by an improved *N. ditissima* RS324p genome, combining PacBio single-molecule real-time (SMRT) sequencing technology with Illumina data. The 45.7 Mb genome comprises 30 scaffolds (previously 172), including six complete chromosomes. OrthoMCL analysis comparison of high (RS324p) and low (RS305p) virulent isolates predicted 194 proteins either unique to RS324p or highly dissimilar between the isolates. Candidate virulence genes were also identified by transcriptomic analysis of infection by virulent isolate RS324p. Gene expression at 6 weeks (where symptoms start to appear) and 12 weeks post inoculation (obvious symptoms) in planta was compared to that in vitro. Mapping of RNASeq reads to the draft genome of RS324p, followed by differential expression tests, identified 379 upregulated genes in planta compared to in vitro, with thresholds of the absolute value of logFC (log2 fold changes) greater than 4 and a false discovery rate smaller than 0.00001. These candidate virulence genes include those that encode putative plant cell wall-degrading enzymes (pectate lyases), proteases and a chitinase similar to proteins in PHI-base (http://www.phi-base.org/), which when knocked out results in reduced virulence. In addition, three small, secreted proteins were identified that are predicted to be effectors by EffectorP (1). Functional characterisation of candidate virulence genes is currently underway.


Small RNA profiling of *Sclerotinia sclerotiorum* while infecting *Brassica napus*

**Mr Roshan Regmi**¹², Dr Toby Newman¹, Dr Lars Kamphuis¹³, Dr Mark Derbyshire⁴

¹Centre for Crop and Disease Management, Curtin University, Perth, Australia, ²CSIRO Agriculture and Food, Floreat, Perth, Australia

Pathogen secretes different classes of molecules to infect its host. Recently, small RNA from the pathogen evolved as a new kind of pathogenicity factor during host infection. *Sclerotinia sclerotiorum* is a necrotroph fungus having broad host range. It incites Sclerotinia stem rot in *Brassica napus* (canola) and causes huge economic loses to canola industry annually in Australia and other canola growing part of the world. Despite new insights and efforts, limited fact is known about its molecular interaction with the host. To unravel the role of *Sclerotinia* small RNA in pathogenicity, we sequenced the small RNA from fungal mycelium while infecting *Brassica napus* leaves at 0, 12 and 24-time points. On an average, more than 60 M clean reads were obtained. The size class distribution enriched 22 nt length reads and 5 prime biased reads are uracils in those reads. We aligned those reads with the *Sclerotinia* genome and predicted the locus that has abundant 22 nt reads. The abundant putative small RNAs targets were identified in *Brassica napus* and *Arabidopsis*. We developed GFP transformed Sclerotinia strains to facilitate our sRNA knock out strains to accommodate in silico analysis with in vitro validation. The findings from this result would add more understanding on molecular mechanism of *Sclerotinia sclerotiorum* and *Brassica napus* patho system.
Colonisation of weeds by *Fusarium oxysporum* f.sp. *cubense*

**Dr Jay Anderson**, Ms Amelie Soper, Ms Fiona Hill, Ms Eliza Seymour, Prof Elizabeth Aitken

1School of Agriculture and Food Sciences, The University of Queensland, St Lucia, Australia

*Fusarium oxysporum* f.sp. *cubense* (*Foc*) is a soil-borne fungus which causes Fusarium wilt (Panama disease) of banana. *Foc* has been isolated from common weeds of banana plantations in field samples and from pot trials. However, it was not known how extensively *Foc* colonised these weed species. In order to examine the colonisation of *Foc* on various potential non-banana hosts we conducted glasshouse studies with a green fluorescent protein (GFP) transformed isolate of Subtropical Race 4 *Foc*. We inoculated *Bidens pilosa* (Asteraceae), *Solanum nigrum* (Solanaceae) and *Leucaena leucocephala* (Fabaceae) in separate glasshouse trials using high inoculum loads. The susceptible controls of ‘Williams’ Cavendish or ‘Lady Finger’ bananas developed characteristic discoloration of the corm. There were traces of vascular discoloration in crowns of some of the inoculated *L. leucocephala*, but there were no macroscopically visible symptoms on *B. pilosa* or *S. nigrum*. When examined with scanning confocal microscopy, colonisation of the roots by the fungus was very limited. On each weed species there were occasional hyphal nets, chlamydospores and colonisation of some epidermal cells. Stem sections were examined with scanning confocal microscopy but there was no evidence of colonisation in any of the weeds. However, isolations were performed on the *S. nigrum* plants and the GFP-*Foc* was reisolated from the stem, crown and roots. To examine the effect of herbicides on the GFP-*Foc* in planta we sprayed *L. leucocephala* and *B. pilosa* with glyphosate and used scanning confocal microscopy to examine sections from roots and stems. The GFP-*Foc* was able to colonise the dead weeds extensively and the fungus sporulated on the *L. leucocephala*. These results have implications for inoculum management in *Foc* infested banana plantations.

Root infections will make the long-term management of invasive *Phytophthora agathidicida* challenging in New Zealand kauri forests

**Dr Stanley Bellgard**, Elsa Paderes, Dr Chantal Probst

1Manaaki Whenua Landcare Research, Auckland, New Zealand

*Phytophthora* species have a unique life-history, that lies between biotrophy and saprophytic - hemi-biotrophy. This unique choice, enables the pathogen to complete its life cycle in and on the host, as well as being able to live semi-independently, as a subsistence saprotroph. The pathological consequences of completing the life cycle on the host and in situ in the forest soil, means that primary hosts of *Phytophthora agathidicida* will serve as primary inoculum source for further infections on other kauri tree roots. Beyond the primary or terminal host, if *P. agathidicida* can infect and colonise the roots of other plant species in the kauri forest, then these non-target hosts may represent a “cryptic” or hidden source of inoculum, as there may not be the visual symptomology associated with kauri and *P. agathidicida* - i.e. trunk bleeding, and crown and canopy collapse (“dieback”). This paper reports on some no-choice glasshouse studies that demonstrate spill-over from *P. agathidicida* and its ability to complete part of its life cycle on other native plant species in New Zealand kauri forest. The implications of these glasshouse studies for field-based research are discussed in terms of managing kauri dieback and strategic use of control tools, e.g. phosphite trunk injections.
Fusarium wilt of watermelons in southern Lao PDR – socio-economic impact and race determination

Prof Lester Burgess1, Dr Virgilio Balmas5, Miss Sengphet Phanthavong3, Ms Phitsamay Phitsanoukane3, Ms Kaisone Sengsoulchan2, Dr Victor Puno, Miss Nina Potts, Mr David Coleman, Dr Bevan Weir4, Miss Sophia Callaghan3, Mr Adam Williams4, Mrs Jillian Burgess3

1Sydney Institute of Agriculture, University of Sydney, Sydney, Australia, 2Agriculture Section, Provincial Agriculture and Forestry Office, Themeang Village, Lao PDR, 3Agriculture Section, Provincial Agriculture and Forestry Office, Thaluang Village, Pakse, Lao PDR, 4Landcare Research, Auckland, New Zealand, 5Dipartimento di Agraria, Università degli Studi di Sassari, Sassari, Italy

Watermelons, an important dry season cash crop for many small-holder rice farmers, contribute to poverty alleviation in Savannakhet and Champasak provinces in southern Lao PDR. Fusarium wilt caused by *Fusarium oxysporum* f.sp *niveum* (Fon) was identified in 2015 in both provinces. The disease has been a focus of on-going studies, with extension of information on IDM strategies appropriate to each province. In Savannakhet watermelons are mainly grown in small round pits in rice paddies and hand-watered. Wilt was recorded on a limited number of farms but with up to 90% wilted plants. Small holders adopted advice to relocate their watermelon crops to ‘clean’ rice paddies, a practice which led to effective wilt management. In contrast, in Champasak watermelons are grown with furrow irrigation. Inoculum of Fon was disseminated throughout these areas via the furrows. Consequently, a high incidence of wilt has led to most small holders ceasing production, a significant socio-economic impact on the affected communities. None of the cultivars available in southern Lao PDR have shown resistance so a study was initiated to determine the race(s) present. Wilt samples were collected across the watermelon areas of both provinces and a population of isolates of (FON) was preserved (University of Sassari). Four isolates of Fon were randomly selected from each province for race determination using four differential cultivars and a non-wounding technique. All isolates caused 100% wilt in the Race 0 differential, Sugar Baby, and caused severe wilt in Race 1 and Race 2 differentials, Crimson Sweet and Allsweet, respectively. None of the isolates affected the Race 3 differential, SP6. This study indicates that Race 2 is common in both provinces. None of the cultivars available in Lao PDR appear to have resistance to wilt. Grafting of transplants onto resistant rootstocks is being discussed as an IDM strategy for Champasak.
Metabolomic approaches for the discrimination of disease suppressive soils for *Rhizoctonia solani* in cereal crops using 1H NMR and LC-MS and identification of potential biomarkers

**Dr Helen Hayden**, Dr Simone Rochfort\(^1\)\(^2\), Mr Vilnis Ezernieks\(^1\), Dr Keith Savin\(^1\), Assoc Prof Pauline Mele\(^1\)\(^2\)

\(^1\)Agriculture Victoria, Bundoora, Australia, \(^2\)School of Applied Systems Biology, La Trobe University, Bundoora, Australia

Rhizoctonia root rot and bare patch disease, caused by the fungus *Rhizoctonia solani* anastomosis group (AG) 8, results in significant losses in cereal crops with patches of infected plants having stunted growth, fewer tillers, reduced vigour and producing less grain. The suppression of soilborne pathogens such as *R. solani* AG8 may offer a sustainable and enduring method of disease control. It is difficult, however, to identify soils that have disease suppressive properties. In this study, we analysed the soil metabolic profiles of suppressive and non-suppressive soils over two years of cereal production in adjacent paddocks. We collected bulk and rhizosphere soil at different cropping stages and subjected soil extracts to liquid chromatography-mass spectrometry (LC-MS) and proton nuclear magnetic resonance spectroscopy (\(^1\)H NMR) analyses. Community analyses of suppressive and non-suppressive soils using principal component analyses and predictive modelling of LC-MS and NMR datasets respectively, revealed distinct biochemical profiles for the two soil types with clustering of these samples based on suppressiveness and cropping stage. NMR spectra revealed the suppressive soils to be more abundant in sugar molecules than non-suppressive soils, which were more abundant in lipids and terpenes. LC-MS features that were significantly more abundant in the suppressive soil were identified and assessed as potential biomarkers for disease suppression. The structures of a potential class of LC-MS biomarkers were elucidated using accurate mass data and MS fragmentation information. The most abundant compound found in association with suppressive soils was confirmed to be a macrocarpal, which is an antimicrobial secondary metabolite. Our study has demonstrated the utility of environmental metabolomics for the study of disease suppressive soils. This has resulted in the discovery of a macrocarpal biomarker for *R. solani* AG8 suppressive soil which can be further studied functionally in association with suppression pot trials and microbial isolation studies.
Influence of pre-conditioning and germination temperatures on the carpogenic germinability of diverse *Sclerotinia sclerotiorum* populations within the south-western Australian grain belt

*Dr Pippa Michael*, Dr Sarita Bennett, Ms Linda Thomson, Ms King-Yin Liu

Curtin University, Kent St, Bentley, Australia, Department of Primary Industries and Regional Development, Esperance, Australia

In Australia, infection of canola by the plant pathogen *Sclerotinia sclerotiorum* can lead to severe outbreaks of sclerotinia stem rot (SSR) disease. Currently, management of SSR relies heavily on cultural and chemical control, which are under pressure due to increased plantings and long-term inoculum persistence. Furthermore, application of foliar fungicides is challenging, as efficacy is dependent on accurately predicting when ascospores are released and present on floral tissue. Therefore, an understanding of temperature requirements under Australian conditions necessary for carpogenic germination of sclerotia in addition to the influence of pre-conditioning temperatures over summer is vital. To determine optimal germination temperatures, sclerotia were collected from four canola and one lupin populations. Four replicates of ten sclerotia per population were placed on trays containing moist vermiculite:sand (1:1), incubated at 30/15°C, 20/15°C, 20/4°C and 15/4°C (12/12 hr light/dark) and days to apothecia emergence assessed for 180 days. To examine the impact of pre-conditioning temperatures, five replicates of 15 sclerotia from five populations were incubated for 0, 30, 60 and 120 days at 4°C, 20°C, 35°C, 50°C and field temperature. Sclerotia were incubated on moist trays at 20/15°C as described above and apothecia emergence recorded for 160 days. The highest and most rapid germination occurred at 20/15°C (84%, 42 days), followed by 15/4°C (70%, 48 days) and 20/4°C (59%, 60 days). No germination was recorded at 30/15°C. Temperature and population had an effect (P<0.01) on total germination, however only temperature had an effect (P<0.01) on onset of germination. Pre-conditioning of sclerotia at higher temperatures led to more rapid germination and greater overall germination, compared to no preconditioning or low temperatures. Optimal temperature required for preconditioning was found to vary significantly between populations of sclerotia in relation to their original location, suggesting an adaptation of *S. sclerotiorum* populations to their local Australian environment.

*Phytophthora* and allies along a river salinity gradient

*Dr Bevan Weir*, Rose Williams, Natalie Morse, Dr David Waite, Dr Kim Handley

Manaaki Whenua - Landcare Research, Auckland, New Zealand, Auckland University, Auckland, New Zealand

*Phytophthora* are ‘water moulds’ found in wet soils and water bodies such as streams and rivers. Some rivers as they eventually flow into the ocean become progressively more saline as they pass through an estuarine environment, this raises the question about what happens to *Phytophthora*. Are *Phytophthora* species salt tolerant and can they survive in saline water? Are there marine specific *Phytophthora*? Nine sites were sampled along a salinity gradient in the Waikouaiti river north of Auckland, New Zealand. At each site filtered bulk water and sediment was collected and stream baits set for one week. The most inland sample was in fresh water, and the most saline sample on the beach at the mouth of the river. *Phytophthora* cultures were isolated using selective media from filter fragments and from leaf baits. Total metagenomic DNA and metabarcoding loci were sequenced from the filters and sediment, and metabarcoding loci from the leaf baits. The results of the stream baiting show a striking pattern of a decline in the abundance of *Phytophthora*, *Phytophthoria* and *Pythium* species as salinity increases, and the reciprocal relationship with *Halophytophthora* species increasing in abundance as salinity increases. *Halophytophthora* has not previously been confirmed as present in New Zealand. The biological implications, and utility of the different methods of detecting *Phytophthora* for diagnostics will be discussed.
Poster Board 15

Using fungicide mixtures with multi-site fungicides for managing resistance of *Cercospora beticola* in sugar beet

Prof Mohamed Khan

1North Dakota State University & University Of Minnesota, Fargo, United States

*Cercospora beticola* causes Cercospora leaf spot (CLS), the most destructive foliar disease of sugar beet (*Beta vulgaris*) worldwide. Growers integrate tolerant varieties, husbandry practices, and timely fungicide applications to manage CLS. *C. beticola* has developed resistance to several classes of fungicides. In 2016, widespread resistance to quinone outside inhibitor (QoI) fungicides resulted in a CLS epidemic and over $200 million reduction in revenue for sugar beet growers in the United States. Field studies were conducted in Minnesota, USA to evaluate the efficacy of fungicides for controlling *C. beticola* resistant to QoI fungicides and with reduced sensitivity to demethylation inhibitors (DMI). Results demonstrated that QoI fungicide treatments resulted in disease severity that was not significantly different from the non-treated check, and DMI fungicides were becoming less efficacious. Mixtures of multi-site with site-specific fungicides typically provided better disease control compared to using a single mode of action fungicide. Results also showed that the use of only multi-site fungicides in a rotation program provided season-long control of CLS. Deploying only multi-site fungicides for CLS control for several growing seasons may be a strategy to provide effective disease control and managing the *C. beticola* populations that are resistant to site specific fungicides.

Poster Board 14

Determination of fungicide efficacy for management of rust of field pea in North Dakota, U.S.A.

Miss Jessica Halvorson

1, Mr Bryan Hansen1, Mr Casey Schuh1, Mr Scott Meyer1, Mr Scott Fitterer2, Mr Dave Carruth2, Dr Sam Markell1

1North Dakota State University, Fargo, United States, 2BASF Corporation, Davenport, United States

Dry edible pea (*Pisum sativum*) acreage in the two United States north central states of Montana and North Dakota has recently approached 0.5 M Ha. Reports of rust, caused by *Uromyces viciae-fabae* (Pers.) Schr., have recently increased in the region and could be cause for concern. The objective of this study was to evaluate the efficacy of numerous fungicides for the management of rust on field pea. Fungicide experiments were conducted in Davenport, ND in 2018 and Fargo, ND in 2019. Both experiments were conducted in a randomized complete block with four replications, and included 12 to 14 treatments with different modes of action, including; QoIFRAC 11), DMIFRAC 3) and SDHIFRAC 7). Experiments were artificially inoculated with fresh *U. viciae-fabae* urediniospores and fungicides were applied once after the occurrence of disease. Disease severity was determined visually by evaluating the percent leaf area covered with pustules on ten arbitrarily-selected plants within each plot. In 2018, disease severity in plots treated with pyraclostrobin, fluxapyroxad + pyraclostrobin, and difenoconazole + benzoavindiflupyr was statistically lower than the non-treated control in at least one location. Data in 2018 suggests that multiple fungicides may be useful for the management of field pea rust, should it become an economic concern in the region. In 2019, the study was expanded.
Blast in northern Queensland: not so nice for rice!

Dr Nirodha Weeraratne¹, Assoc Prof Adam Sparks¹
¹University Of Southern Queensland, Centre for Crop Health, Toowoomba, Australia

Rice blast disease, caused by the fungus *Magnaporthe oryzae*, is considered to be the most destructive disease affecting rice cultivation globally. Traditionally, Australian rice crops are thought to be safe from this disease, given that it has not been reported from southern New South Wales where the majority of rice has historically been grown. However, with the recent renewed interest in rice cultivation in tropical north Queensland, rice blast has been identified to be the most important disease in this area. Out of the diagnostic samples received during the dry season of 2017, when disease pressure is expected to be low, 50% were found to have characteristic signs of rice blast. Additionally, the disease was found throughout northern Queensland in all rice-growing areas that were surveyed and the currently grown cultivar, Doongara, is susceptible. Previous studies suggest that wild rice (*Oryza spp.*), which are naturally occurring in northern Queensland could be a source of pathogen inoculum. Our study on the genetic diversity of *M. oryzae* strains isolated from diagnostic samples showed single nucleotide polymorphisms in nucleotide sequences of internally transcribed spacer region 1 indicating local adaptations of the pathogen. Control of rice blast disease is usually achieved by fungicides and cultivar resistance. Commercially available fungicides containing Azoxystrobin and Difenoconazole were found to inhibit the growth of the fungus on culture media at a concentration 1 ppm. Applications of a commercial fungicide formulation containing Azoxystrobin were recommended for disease control based on the timing practiced in USA and south east Asia. With no currently identified resistance in Australian rice cultivars, fungicides will remain necessary to control this disease in northern Queensland. Further work is being conducted to determine the best timing for fungicide applications in Australia and screening for resistance in Australian rice breeding germplasm.

Barley Disease Cohort Project: a co-innovation approach to managing fungicide resistance

Mrs Megan Jones¹, Mrs Linda Thomson¹, Dr Fran Lopez-Ruiz¹, Prof Mark Gibberd¹, Assoc Prof Lorenzo Covarelli¹,²
¹Centre for Crop and Disease Management, Curtin University, Perth, Australia, ²Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy

Research into fungicide resistance in the Australian grains industry has, to date, focused around the molecular detection of fungicide resistance and the quantification of fungicide sensitivity. However, there is a recognised shortage of research addressing the growers’ need for evidence-based solutions to manage fungicide resistant pathogens once detected at the paddock level. In 2019, the Centre for Crop and disease management (CCDM) established the Barley Disease Cohort Project, a pilot project designed to use a co-innovation approach to find local, regionally relevant solutions for growers to manage fungicide resistant pathogens on barley. The project is enlisting a large and diverse population of barley growers from across the South of the Western Australian wheatbelt, with a particular focus on spot-form and net-form net blotches of barley, caused by *Pyrenophora teres f. maculata* and *P. teres f. teres*, respectively, two pathogens recently identified as resistant to group 3 demethylation inhibitor (DMI) fungicides in this region. This “cohort” approach will directly connect CCDM researchers with growers with three yearly cycles of co-innovation, by sharing data, experiences and knowledge together, finding out exactly where resistance is occurring and carrying out glasshouse and field trials to find solutions to manage the problem locally and nationally. The success of this project will see the establishment of other cohorts in other parts of Australia’s grain growing regions, ensuring growers from any region in Australia will have access to regionally relevant information when it comes to managing fungicide resistance.
In vitro inhibitory activity of different selenium compounds towards a *Fusarium proliferatum* strain isolated from rice

Dr Giovanni Beccari¹, Dr Roberto D’Amato¹, Dr Elisabetta Troni², Assoc Prof Daniela Businelli¹, Dr Francesco Tini², Dr David Baldo², Dr Antonio Prodi², Prof. Gian Maria Beone³, Dr Maria Chiara Fontanella³, Assoc Prof Lorenzo Covarelli¹,⁴¹ Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy, ²Department of Agricultural and Food Sciences, Alma Mater Studiorum University of Bologna, Bologna, Italy, ³Department for Sustainable Food Process, Catholic University of the Sacred Heart of Piacenza, Piacenza, Italy, ⁴Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Perth, Australia

The aim of the present study was to investigate the *in vitro* activity of different concentrations of selenium (Se) compounds on the growth and development of a *Fusarium proliferatum* strain, previously isolated from rice (*Oryza sativa* L.) seedlings. It is well known that Se, at very low doses, is an important element in the physiologic and metabolic processes of living organisms. However, there is relatively little known about the inhibitory activity of Se on fungal microorganisms. In this study it was shown that the addition of different Se compounds (sodium selenite, sodium selenate, Se–L–cysteine, Se–DL–methionine) at various concentrations (5, 10, 15, 20 and 100 mg kg⁻¹ of Se), to fungal growth medium (potato dextrose agar), considerably inhibited *F. proliferatum* growth after 10 days of incubation at 22°C in the dark. Regardless of the Se compounds, it was found that the dose of 10 mg kg⁻¹ significantly reduced *F. proliferatum* growth whilst at the dose of 100 mg kg⁻¹ growth was completely inhibited. Concerning Se chemical forms, sodium selenite and Se–L–cysteine were the most effective compounds at the lowest doses. Scanning Electron Microscopy analysis showed appreciable modifications in the morphology of *F. proliferatum* hyphae following the application of sodium selenite in the growth medium. This study identified combinations of Se compounds and concentrations required for the *in vitro* inhibition of *F. proliferatum* strain development. These results could be also interesting to obtain a Se–biofortification of cereal grains coupled to fungal control. Further studies will evaluate Se speciation, Se activity towards other *Fusarium* species and Se ability to control *Fusarium* infections of cereals in controlled environmental conditions as well as in the field.
**Variability in fungicide sensitivity in the *Pyrenophora teres f. maculata* population in South-eastern Australia**

**Miss Hayley Wilson**, Dr Mark McLean², Dr Fran Lopez-Ruiz³, Assoc Prof Kim Plummer¹, Dr Wesley Mair³, Dr James Hunt¹, Dr Grant Hollaway²

¹La Trobe University, Bundoora, Australia, ²Agriculture Victoria, Horsham, Australia, ³Curtin University, Perth, Australia

Spot form of net blotch (SFNB) is the most common foliar disease of barley (*Hordeum vulgare*) in South-eastern Australia and can cause production losses of up to $20 million annually (1). SFNB is caused by fungus *Pyrenophora teres f. maculata* (Ptm) and susceptible varieties are commonly treated with triazole fungicides to reduce both grain yield and quality loss (2). *Pyrenophora teres f. maculata* is genetically diverse and regular fungicide application has led to selection for mutations in the Cyp51A gene region which produces an enzyme vital to the key ergosterol pathway (3). Such mutations have become established in Western Australia (3) and possibly in south-eastern Australia. This is one of the first studies into SFNB resistance to the triazole fungicides tebuconazole and propiconazole in southeastern Australia. In vitro radial growth sensitivity assays were conducted for thirty-eight single spore Ptm isolates collected in south-eastern Australia during 2007-18. There was considerable variation in the sensitivity to tebuconazole among isolates with percentage growth inhibition (PGI) ranging from 0% to 84.75%. For propiconazole, PGI varied between 60.29% and 95.82%. Isolate sf61/18a (obtained from Dr Hugh Wallwork, South Australian Research and Development Institute) and isolate ptm17-066 were not inhibited by tebuconazole and are likely candidates for identifying mutations in the Cyp51 gene region in further molecular analysis. This study indicates that barley growers should continue to get effective control from propiconazole, but should avoid using tebuconazole for SFNB management.

Evaluation of fungicide timing and efficacy for management of Phoma black stem in Sunflower in the USA

Bryan Hansen1, Michelle Gilley1, Brandt Berghuis1, Jessica Halvorson1, Blaine Schatz2, Febina Mathew3, Scott Fitterer4, Dave Carruth5, Sam Markell1

1Department of Plant Pathology, North Dakota State University, Fargo, United States, 2NDSU Carrington Research Extension Center, Carrington, United States, 3Agronomy, Horticulture and Plant Science Department, South Dakota State University, Brookings, United States, 4BASF North Dakota Research Farm, Davenport, United States

Sunflower (Helianthus annuus) production in the United States is concentrated in the Northern Great Plains States of North and South Dakota, where 777,775 metric tons of sunflower seed were produced in 2018. Phoma black stem, caused by Phoma macdonaldii, has been one of the most prevalent diseases of sunflowers in the US in the last two decades. While Phoma black stem is not generally considered yield-limiting in the Dakotas, a statistical increase in yield was observed when Phoma black stem was managed with fungicides in a single experiment in 2017. The objective of this study is to evaluate fungicide efficacy and timing for management of Phoma black stem. To evaluate fungicide timing, two different trials were established using two hybrids in Davenport, ND. The fungicide pyraclostrobin (Headline) was applied singly or in combination at three sunflower growth stages: late vegetative stage (V8-V12), budding stage (R1), and flowering stage (R5). To evaluate fungicide efficacy, a trial was established at Davenport, ND. Nine fungicides with differing modes of action, including demethylation inhibitors (DMI), succinate dehydrogenase inhibitor (SDHI), and quinone outside inhibitors (QoI), were applied at growth stage R1. All trials were designed as a randomized complete block design with four reps, planted under natural disease pressure, and disease was evaluated visually using a disease severity index (DSI). A statistically lower DSI was recorded for V8-V12 and R1 treatments than the non-treated control in both timing trials. All fungicide treatments had statistically lower DSI than the non-treated control in the efficacy trial. While the use of fungicides reduced DSI in all trials, yield impacts were not observed in 2018. Trials are being repeated in 2019.
Symbionts of the tomato potato psyllid

Dr Rebekah Frampton¹, Gabrielle Drayton¹, Shea Addison¹
¹The New Zealand Institute for Plant and Food Research Limited, Lincoln, New Zealand

The tomato potato psyllid (Bactericera cockerelli Šulc; TPP) is a significant pest on solanaceous crops in New Zealand. It transmits Candidatus Liberibacter solanacearum (Lso), the putative causal agent of Zebra Chip disease in potatoes. TPP also has a range of other bacterial symbionts associated with it. Carsonella is an obligate endosymbiont and therefore associated with all psyllids. It produces essential amino acids and other metabolites for the psyllids that they cannot obtain from feeding on plant phloem. Other bacteria are also known to be associated with the suborder of Hemiptera which includes psyllids, and are thought to influence the insect’s behaviour and metabolism. However, little is known about the interactions between different associated bacteria species and their interactions with the host insect. To understand the role of symbionts in the biology of TPP, bacterial profiles from over 500 individual TPP were generated and compared in this study. TPP were collected from different regions in New Zealand, California (USA), and Honduras. The microbial profile of individual TPP from these collections were assessed using several methods: sequencing of total DNA, 16S sequencing of PCR amplicons, and multiplex qPCR. The obligate endosymbiont, Carsonella, was found in all samples as expected. The DNA sequences revealed a range of other bacteria also associated with TPP, including Wolbachia and Hamiltonella. Species from both these genera are known to influence the fitness and fecundity of their host insects. The major differences in the composition of bacteria associated with TPP were related to the geographic location and the insect biotype. Most noticeably, Wolbachia was not detected in individuals from Canterbury and Manawatu (New Zealand). This information will be used, in conjunction with colony experiments, to determine if the bacterial symbiont profile influences the acquisition and transmission of Lso.
Grapevines (*Vitis vinifera* L.) contain diverse communities of culturable fungi that differ between organic and standard management systems in New Zealand

**Mr Noureddine Besselma**¹, Dr Hayley Ridgway², Mr Dion Mundy³, Dr Eirian Jones¹

¹University Of Lincoln, Christchurch, New Zealand, ²The New Zealand Institute for Plant & Food Research Limited, Private Bag 4704, Christchurch, 8140, New Zealand, ³The New Zealand Institute for Plant & Food Research Limited, Marlborough Wine Research Centre, 85 Budge Street, 7201, Blenheim, New Zealand

Grapevines contain a diverse community of microorganisms that includes pathogens and beneficial fungi. Some pathogenic fungi are causal agents of grapevine trunk disease (GTD) and are considered latent pathogens. For GTD, understanding of the factors affecting latency is lacking. The aim of this study was to describe the fungal endophyte community in vines of Sauvignon blanc that were symptomatic and asymptomatic for GTD and grown under standard and organic management practices. Samples were taken from 90 grapevines in nine vineyards in the Marlborough region, the largest winegrowing area in New Zealand. The samples encompassed 30 young vines (<9 years), 60 mature vines (>10 years) of which equal numbers were symptomatic (visual canker) and asymptomatic (no visual canker). Samples were collected from the trunk using a sterilized 4-mm drill bit after removing the bark by a knife. Three samples were taken from each vine, with samples from within the canker, at the margin and beyond the canker in symptomatic vines. Samples were plated onto a range of agars and a collection of approximately 2000 endophytic fungi recovered. Taxonomic identification using morphology and DNA sequence information has identified at least 42 genera. Trunk microbiota was dominated (85.25%) by species of the genera *Alternaria*, *Aureobasidium*, *Diplodia*, *Epicoccum*, *Phaeomoniella*, *Eutypa*, *Botrytis*, *Cladosporium* and *Diaporthe*. Differences in the taxa recovered into culture were observed between vines of different ages, symptomology and those under different management systems. For example, seven and six taxa were found exclusively in vines under conventional and organic management, respectively. This live collection will be complemented by further work using metabarcoding to characterise the complete fungal community and their relative abundance. This study has produced new baseline information on fungal endophytes in Sauvignon blanc and further work will determine the impact of these microbial communities on the latency of GTDs.

**Poster Board 6**

**Acid soils in Pacific Northwest, USA wheat production and impacts on the soil microbiome**

Mrs Chuntao Yin¹, Mr Dan Schlatter¹, **Mr Duncan Kroese**², Mr Timothy Paulitz¹, Mrs Christina Hagerty²

¹USDA-ARS, Wheat Health, Genetics and Quality Research, Pullman, United States, ²Oregon State University, Adams, United States

Soil acidity is an emerging issue in the $2B wheat industry of the Pacific Northwest, USA. The process of nitrification is a bacterial mediated process that converts ammonium to nitrate but also acidifies the soil. Our recent survey of the PNW wheat production region indicates 73% of surveyed fields are below pH 5.5, the threshold for optimal wheat production. Acidic soil can have a negative impact on wheat yields, favor some yield limiting plant pathogens such as *Cephalosporium*, and can lead to aluminum toxicity. However, the influence of soil acidity on the soil microbial community is less understood. We established winter wheat plots in two rainfall zones with pH ranging above and below the critical threshold of pH 5.5 and conducted fungal and bacterial microbiome analysis. Preliminary results indicate bacterial soil communities may be more strongly influenced by soil pH than fungal soil communities. Liming significantly increased the relative abundances of some bacterial families, including *Pseudomonadaceae*, *Opitutaceae*, and *Flavobacteriaceae*, while decreasing others, such as the *Bradyrhizobiaceae*, though this effect was often seen only at the 0-3 inch depths. Among fungal families, liming significantly reduced the relative abundances of *Teratosphaeriaceae*, *Hypocreaceae*, and *Piskurozymaceae*, though these patterns often depended on location and soil depth. Results suggest that liming may reshape soil communities, primarily impacting bacteria, in ways that may influence plant health.
Impacts of cropping sequences on rhizosphere microbiome and root disease in sugarcane

Dr Belinda Stummer¹, Ms Bhanu Nidumolu¹, Dr Paul Harvey¹
¹CSIRO Agriculture & Food, Glen Osmond, Australia

The research aimed to deliver novel information on sugarcane rhizosphere-fungal interactions and factors impacting on root disease incidence and suppression. Culture-dependent and culture-independent analyses of rhizosphere fungal and oomycete communities were conducted across two cropping seasons at two sites in northern Queensland. Agronomic treatments included replant continuous cane, cane-legume rotations and longer-term (LT) ratoon. A native forest soil was included as a comparison with cane cropping. Relative abundances of fungal taxa (Order, Family, Genus OTUs) in sugarcane pre-plant and rhizosphere soils were used to define impacts of agronomic treatments on the structure of the fungal microbiome. Fungal community structure of LT ratoon cane was significantly different (P<0.003) from replant continuous cane and cane-legume rotations, the latter 2 treatments not significantly different. Forest soil fungal communities were highly differentiated (P<0.001) from the adjacent sugarcane cropping treatments and had the greatest (P<0.001) diversity and taxonomic eveness. The majority of differences among sugarcane fungal rhizosphere soil communities were attributed to to 33 taxa, their abundance differing (0.0001<P<0.05) among cropping treatments. These included numerous root-associated saprophytes, potentially pathogen antagonistic Trichoderma, Epicoccum, Humicola, Bullera and Clonostachys spp., plant pathogenic Fusarium spp. and functionally diverse Helotiales, Hypocreales, Myriangiales and Pleosporales comprising mycorrhizal, mycoparasitic and plant pathogenic species. Culture-dependent root endophytic fungal communities were dominated by saprophytic Chaetomium, Mortierella and Penicillum, pathogen antagonistic Trichoderma and plant pathogenic Fusarium spp. Oomycete communities were dominated by plant pathogenic Pythium spinosum. The oomycete Pachymetra chaunorhiza was not isolated from roots or rhizosphere soils. Saprophytic and plant pathogenic taxa were more abundant (P<0.001) in the roots and rhizosphere (OTUs) of replant continuous cane and cane-legume rotations. Trichoderma and Epicoccum spp. were more abundant under LT ratoon cane (P<0.001) and produced metabolites that inhibited root pathogens in vitro, implying a mechanism for rhizosphere selection and disease suppression by these taxa.
**Poster Board 5**

**Effects of host plant on the endosymbionts in *Bemisia tabaci***

**Miss Fang-Yu Hu**, **Prof Chi-Wei Tsai**

1Department of Entomology, National Taiwan University, Taipei City, Taiwan

*Bemisia tabaci* is considered as a serious pest worldwide. It not only infests a broad range of host plants but also transmits over 200 plant viruses. *Bemisia tabaci* harbors several endosymbiotic bacteria. *Portiera aleyrodidarum* is the primary endosymbiont that provides *B. tabaci* with essential nutrients, whereas the functions of secondary endosymbionts (e.g. *Hamiltonella denfensa*, *Rickettsia* sp., etc.) are still poorly understood. *Bemisia tabaci*, endosymbionts, and host plants have intimate interactions. It has been reported that the amounts of endosymbionts in *B. tabaci* vary when it feeds on different host plants; however, few studies further examine this phenomenon. In this study, *B. tabaci* MEAM 1 species harboring *P. aleyrodidarum*, *H. denfensa*, and *Rickettsia* sp. was reared on five host plants (Chinese kale, cotton, cucumber, poinsettia, and tomato) respectively for more than 10 generations. The whiteflies were collected from each host plant every generation, and the population dynamics of endosymbionts were determined. The fitness of *B. tabaci* and the expressions of nutrient-related genes of *P. aleyrodidarum* were examined in the first generation and the tenth. The results demonstrated that the populations of *P. aleyrodidarum* and *H. denfensa* decreased when the whiteflies were transferred to new host plants in the first or second generation and then restored to the original amounts after five to 10 generations. Also, the fitness of *B. tabaci* significantly decreased after it fed on new host plants. Since *P. aleyrodidarum* has mutualistic nutritional relationship with *B. tabaci*, we found that the expressions of some nutrient-related genes were regulated to help *B. tabaci* adapt to new host plants. Altogether, host plant shifting affects *B. tabaci*, endosymbionts, and also their interactions. More knowledge of the interactions between host plant and the endosymbionts of *B. tabaci* may lead to a novel strategy to control *B. tabaci*.

**Poster Board 7**

**Blueberry Replant Decline: an inheritance worth avoiding**

**Mr Michael Norman**, **Dr Rosalie Daniel**, **Prof David Guest**

1School of Life and Environmental Sciences, University Of Sydney, Sydney, Australia, 2Department of Primary Industries, Ourimbah, Australia

Replant decline is described as the poor growth of crops in soil previously used for the same or similar crop. This study was conducted to evaluate potential biological, chemical and physical soil characteristics contributing to replant decline in blueberry orchards on the mid-north coast of NSW, Australia. Soils were assessed from two sites on a commercial blueberry orchard planted with Southern highbush blueberry cv. ‘Snowchaser’ in 2014. The ‘poor’ site (Site 1) yielded 9 tonnes/ha of fruit, and the ‘good’ site (Site 2) 20 tonnes/ha fruit. Site 2 was fumigated prior to replanting. Soil pH and electrical conductivity were higher in soil sampled from Site 2 than soil sampled from Site 1. Low pH can reduce the availability of most plant nutrients, resulting in less vigorous and productive plant growth. A low electrical conductivity indicates a reduced quantity of salts within the soil and can result in further reductions in nutrient availability. Manganese and aluminium levels were greater at Site 1 than at Site 2. Aluminium toxicity can result in poor root growth and affect water and nutrient uptake; manganese can be toxic to plant cells in high concentrations. To determine the contribution of bacteria, fungi and nematodes to replant decline, microbial and nematode fractions of the soils were extracted and used to inoculate blueberry seedlings in the glasshouse. Fungal, bacterial and nematode community analyses were conducted to assess the role of microbial composition in soil in Blueberry replant decline. Soil respiration was also measured but no significant differences were detected between the two sites suggesting overall soil microbial activity was unlikely to play a role in plant differences observed at these sites.
How does peanut crop rotation influence plant health?

Asfakun Siddika\(^1\), Prof Gavin Ash\(^1\), Dr Dante Adorada\(^1\), Dr Niloofar Vaghefi\(^1\)

\(^1\)University of Southern Queensland, Toowoomba, Australia

Peanut (Arachis hypogaea L) is a highly nutritious economically important summer crop. Control of peanut seedling, foliar and soil borne diseases is crucial to maintain peanut yields in Australia. To ensure management of peanut diseases in Australia, varieties that are partially resistant, appropriate cultural management and extensive quantities of synthetic fungicides are used in combination. Synthetic fungicides have potential adverse consequences to the environment and to human health. Consequently, plant and rhizosphere microbial populations have received greater attention as a means of environmentally sound disease management and sustainable yield improvement. There is a global demand for the development of potential microbial inoculants for disease management and this could be achieved through identifying plant–microbe interactions. A glasshouse experiment was conducted to explore the relationship between peanut rotation and plant growth. Soil samples were collected from the major peanut cropping rotation in Australia. Two peanut varieties and one maize variety were used as planting material. Soil was collected from four crop rotations 1) Three years continuous mono-cropping of peanut, 2) Five years sugarcane-one season peanut 3) Five years sugarcane-peanut-barley–peanut 4) No sugarcane-two years peanut 5) Pasture soil and one potting mix were used as a planting material. Maize was used as a model plant common in the rotation. Plant growth measurement data were recorded from the pot trial and some of the parameters showed significant difference among the rotations. Rhizosphere soil were also collected for metagenome sequencing along with isolation of fungi and bacteria from the bulk soil. It is important to use sequencing technology to reveal how the pre-existing microbial community impacts peanut health and growth. Understanding and comparing underground microbiomes with above ground plant parts will help to identify microbial communities with the potential for disease control through interacting with the host plant and pathogen and, accordingly, ensure yield of peanut.
Epidemiology of cereal viruses in southern Hungary

Dr András Takács¹, György Pásztor¹, Miklós Aczél¹, Dr Mária Papp²

¹University of Pannonia, Georgikon Faculty, Plant Protection Institute, H-8360 Keszthely Deák F. 16., Hungary, ²Cereal Research Non-Profit Ltd., H-6726 Szeged, Alsó kikötő sor 9, Hungary

In recent years cereal diseases, including virus diseases have been increased in Hungary as well as worldwide. The aim of our work was to survey the virus infection of south Hungarian wheat fields. Wheat leaf samples were collected in Szeged at the experimental station of Cereal Research Non-profit Ltd. in April in 2017. Most of the investigated plants showed mosaic and chlorotic symptoms. Collected samples were stored in ELISA plastic bags at 4 °C. Natural virus infection of Barley stripe mosaic virus (BSMV), Brome mosaic virus (BMV), Wheat dwarf virus (WDV), Barley yellow dwarf virus (BYDV), Wheat streak mosaic virus (WSMV) and Brome streak mosaic virus (BStMV) were tested serologically. Kits for ELISA derived from Loewe Biochemica. Substrate absorbance was measured at 405 nm. Test samples were considered positive if their absorbance values exceeded three times those of the healthy control samples. Among the 60 investigated leaf samples 25 was BMV, 24 BStMV, 31 WSMV and 3 WDV infected. BYDV infection was not detected. Complex virus infection was revealed in 24 cases. Forecasting plays a key role in protection against vectors. The massive outbreaks of vector pests, therefore the transmission of viruses can be significantly reduced by prevention. The bad agricultural technology (e.g. monoculture) promotes the spread of pests, like weed species, virus vectors and viruses. But if we stubble the fields and carry out the cultivation works in time, the spread of pests can be reduced. If it is possible, it is advisable to choose resistant varieties. Because of various virus spectrum in the studied years, cereal breeders need to focus on achieving complex resistance to viruses.
Can bacterial plant pathogens be written off from grain discolourations observed on rice in northern Queensland?

Mr Peter Buyoyu1, Dr Nirodha Weeraratne1, Dr Dante Adorada1, Professor Gavin Ash1
1Centre for Crop Health, Institute of Life Sciences and the Environment, University Of Southern Queensland, Toowoomba, Australia

Grain discolouration affects the head rice yield and physical properties of rice, hence reducing the profitability of rice production. Although grain discolouration can be attributed to both fungi and bacteria, previous studies have largely ignored the involvement of bacterial pathogens in grain discolouration in Australia, except for a few reports in southern New South Wales. The purpose of this study was to investigate the involvement of bacteria in rice grain discolouration in northern Queensland (QLD). More than 40 bacterial isolates were obtained from discoloured grains collected from northern QLD during the wet and dry seasons in 2018 and the wet season in 2019. Identification based on 16S rRNA gene sequencing was performed for all the isolates, followed by a pathogenicity test on two rice cultivars, Opus and Doongara. Sequencing results revealed that more than 40% of the isolates belonged to the genus Pantoea. Isolates representing P. agglomerans, P. ananatis and P. stewartii were tested for pathogenicity by spray-inoculation method on both rice cultivars. Grains of inoculated panicles showed symptoms of grain discolouration with varying severity levels. These results indicate that bacterial pathogens could be responsible for the rice grain discolouration observed in northern QLD. Whilst bacterial diseases are not considered a significant threat to temperate rice in Australia, our results suggest that bacterial pathogens could pose a threat to the emerging tropical rice industry in northern QLD.

Diseases of Roselle and implications for small-holder farmers

Mr Nicholas Pain1, Dr Bevan Weir2, Ms Sengphet Phanthavong3, Mr Andrew Daly4, Dr Len Tesoriero4, Dr Lester Burgess5
1CSIRO Agriculture and Food, Floreat, Australia, 2Landcare Research, Auckland, New Zealand, 3Provincial Agriculture and Forestry Office, Pakse, Lao PDR, 4NSW Department of Primary Industries, Sydney, Australia, 5Sydney Institute of Agriculture, Sydney, Australia

Roselle (Hibiscus sabdariffa var. sabdariffa) has been promoted as a novel crop in Lao PDR for production in small plantations and by small-holder farmers for over ten years. The bright red fleshy calyx is dried and used as a base for jams, jelly, tea and cordial, and exported to Europe. Despite the interest in the crop by aid agencies and commercial entities, there is a paucity of information on disease constraints in the Lao environment. Therefore, we have monitored roselle crops for diseases on a plantation in Sekong province in southern Laos since 2015. A severe leaf and stem blight developed late in the 2016/17 crop and caused serious losses. A fungal pathogen was suspected but the diseased plants were extensively colonized by saprophytes precluding accurate diagnostics. In November 2017, a tropical storm led to serious mechanical damage to leaves, stems and calyxes. Two weeks later, abundant pycnidia were observed on lesions that were spreading rapidly from the wound sites. The fungus was identified as Coniella hibisci and was shown to be an opportunistic pathogen on roselle in pathogenicity tests. In November 2018, wilting and dead plants were observed in a young roselle crop. Symptoms also included collar rot typical of Phytophthora infection, vascular discolouration, and bacterial oozing. An Agdia disease test kit suggested the presence of Ralstonia solanacearum. Cultures of Fusarium oxysporum and Phytophthora nicotianae were also isolated from the diseased plant and from the soil around the plant respectively. Ralstonia pseudosolanacearum and several Phytophthora species have been observed commonly in this region on other crops. Studies on this root, crown and wilt complex on roselle are continuing. These findings demonstrate the importance of assessing the disease constraints of novel cash crops in developing countries before they are promoted to small-holder farmers.
Occurrence of seed-borne pathogens in wheat grains across the Western Australian wheatbelt

Lucia Giordano¹, Steven Chang¹, Ian Sprowl², Dr Ayalsew Zerihun¹, Prof Mark Gibberd¹, Assoc Prof Lorenzo Covarelli¹,³
¹Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Bentley, Australia,
²Co-operative Bulk Handling (CBH), Forrestfield, Australia, ³Department of Agricultural, Food and Environmental
Sciences, University of Perugia, Perugia, Italy

Seed health is an important requirement to reduce the spread, incidence and severity of crop diseases in the following season. Furthermore, pathogen-free seed minimises downgrading of grain stocks due to postharvest decay. The purpose of the present study was to investigate the occurrence of seed-borne pathogens in 73 wheat grain samples collected in 2018 at grain delivery to CBH depots from diverse agro-ecological zones across the Western Australian wheatbelt. For each sample, a subset of 100 wheat kernels was subjected to visual assessment and surface sterilisation and then fungal mycelia were allowed to develop on Potato Dextrose Agar. Individual morphotypes were sub-sampled and used to obtain monosporic cultures for DNA extraction. PCR assays were carried out to amplify ITS gene regions or Translation Elongation Factor 1-alpha and amplification products were sequenced. BLAST analyses were performed to identify the individual strains. qPCR assays were also carried out on the DNA extracted directly from the grain samples to check for the presence of Parastagonospora nodorum and Pyrenophora tritici-repentis in the seed. The most frequent seed-borne fungi found in the kernels belonged to the genus Alternaria. Cladosporium oxysporum and Nigrospora oryzae were also frequently present. The importance of the above results for grain quality and the carry forward of diseases are discussed.

Are groundcover and native plants potential reservoirs of pathogens within vineyards?

Dr Vaughn Bell¹, Dr Kar Mun Chooi¹, Vicky Davis¹, Dr Daniel Cohen¹, Rebecca Gough¹, Franziska Grab¹, Samantha Hansen¹, Tara Taylor¹, Manoharie Sandanayaka¹, Victoria Raw¹, Dr Arnaud Blouin², Dr Gardette Valmonte¹,³, Dr Robin Macdiarmid¹
¹The New Zealand Institute for Plant & Food Research Limited, Auckland, New Zealand, ²Integrated and Urban Plant
Pathology Laboratory Gembloux Agro-Bio Tech, University of Liege, Liege, Belgium, ³Institute for Applied Ecology New Zealand, School of Applied Sciences, Auckland University of Technology, Auckland, New Zealand

Several pathogens of grapevines are hosted by other plants; there is even an example of a ‘grape-specific’ pathogen, grapevine leafroll-associated virus 3 (GLRaV-3), that was recently identified in a non-Vitis host. To investigate the possibility of grapevine pathogens in the flora growing beneath and between the vines of New Zealand commercial vineyards, we identified plant species to undertake high throughput sequencing on RNA isolated from their samples. We identified multiple viruses spanning 13 viral families in groundcover and native plants in the four vineyards tested. Included were eight new-to-science virus species and other new viruses identified to the family level. In addition, one virus constituted a new host record and was also new to New Zealand. No GLRaV-3 was identified from any of the non-Vitis plants tested from the vineyard samples despite our recent demonstration that GLRaV-3 can be transmitted to a Nicotiana species by the cosmopolitan citrophilus mealybug, Pseudococcus calceolariae. Similarly, no known grapevine virus pathogens were identified in groundcover and native plants. However, some of the new viruses fall within taxonomic families from which pathogens are described for grapevines. Whether the new viruses infect grapevines and thus pose a risk to the wine sector may be confirmed in the future during high throughput sequencing of adjacent grapevines. This research is part of the “Future-proofing the wine sector with innovation: evaluation of groundcover and native plants as potential reservoirs of pathogens of grapevines” project funded by the Bragato Research Institute (BRI), New Zealand.
Incidence of *Puccinia punctiformis* within and between populations of *Cirsium arvense* in New Zealand

**Miss Caitlin Henderson**, Dr Michael Cripps, Dr Seona Casonato

1 Lincoln University, Lincoln, New Zealand, 2 AgResearch, Lincoln, New Zealand

*Cirsium arvense* is a highly problematic weed in agricultural systems throughout New Zealand. *Puccinia punctiformis* is a potential biological control agent of *C. arvense*. In the field, the biotrophic fungus systemically infects the thistle and subsequently reduces shoot abundance. This research determined the varying levels of *P. punctiformis* infected shoots in New Zealand. A survey was conducted in the North and South Island of New Zealand at 22 different *C. arvense* sites. For each *C. arvense* population, nine 1m² quadrats were surveyed. Within each quadrat, the total number of thistle shoots and the number of *P. punctiformis* diseased shoots were recorded. *Puccinia punctiformis* was visually observed in all 22 sites surveyed throughout New Zealand but was not detected by the survey method at eight of the sites (< 1% incidence of disease). The Ruakura site, in the Waikato in the North Island, had the highest percentage of *P. punctiformis* infected shoots (11.1%, ± 3.0) within the surveyed area. There was an average of 4.2% infected shoots across the sites where rust was detected. Six other sites had high levels of infected shoots that did not differ significantly to the Ruakura site. The percentage of *P. punctiformis* infected shoots varied within and between locations. The different *C. arvense* sites have varying climatic and habitat ranges. There were no obvious characteristics that differed between the populations exhibiting higher levels of *P. punctiformis* infection compared to those with low or nil infected shoots. This study indicates that all *Cirsium arvense* populations have *P. punctiformis* present with varying levels of infection. There appears to be no obvious indication as to why some populations have higher concentrations of *P. punctiformis* infection than others.

A spore trapping network for the early detection of potato pathogens in the USA

**Dr Phillip Wharton**, Dr James Woodhall, Dr Carlos Pizzolotto, Ms Miranda Harrington, Ms Katie Fairchild, Mr Alan Malek, Dr Kasia Duellman

1 University Of Idaho, Aberdeen, United States

Recent developments in spore sampling technology and molecular diagnostics mean that airborne spores of plant pathogens can be detected prior to symptoms developing and the results disseminated in a timely manner. Spore traps placed in a network could provide a powerful tool to warn growers of disease risk, thereby allowing early treatments or conversely alleviating the need for unnecessary treatments in the absence of disease pressure. In 2018, a spore trap network for key foliar potato pathogens was established in Idaho. The network consisted of 15 Burkard multi-vial cyclone samplers in southern Idaho operating from May to September. Daily samples were collected and real-time PCR was used to determine the relative levels of *Phytophthora infestans*, *Alternaria solani*, *Alternaria alternata*, *Botrytis cinerea* and *Sclerotinia sclerotium* spores. Results were disseminated to the potato industry each week with an indication of risk, two days after collection of samples. In 2019, the network was expanded to additional states (Washington, Oregon and Michigan) and Sporenado spore samplers were also used to augment the network. Initial results suggest a relationship between temperature, relative humidity and *P. infestans* and *A. solani* spore quantities detected. Spore trap networks can provide useful real-time information to growers as well as giving researchers useful insights into trends in plant pathogen populations.
**Poster Board 62**

**Area wide management of bacterial and viral pathogens in the vegetable industry**

*Mrs Shannon Mulholland*¹  
¹*NSW Department Of Primary Industries, Ourimbah, Australia*

Bacterial and viral pathogens are a significant limiting factor in vegetable production, affecting a wide range of commodities. NSW DPI, in collaboration with a National project team and as part of a Hort Innovation supported project, has embarked on the development of an Area Wide Management project investigating bacterial pathogens of brassicas and viral pathogens of cucurbits. A key focus of the project is disease surveillance to map the diversity of bacterial and viral pathogens across key vegetable production areas of NSW. Pathogen incidence and distribution is being assessed in conjunction with widespread screening of alternative plant hosts which may be enabling pathogens to overwinter in the landscape in the absence of primary host crops. This is a particular issue for cucurbit production, typically a summer production crop, that experiences recurrent viral infections each season. Linkages with growers across NSW and diagnosticians nationally are also being cultivated as a key outcome of the project to help build capacity and knowledge to support the vegetable industry. Genomic analysis of the historic *Xanthomonas campestris* collection will facilitate the development of better diagnostic tools. Seed disinfestation and soil longevity of *X. campestris* is being investigated to identify potential management strategies. Novel cultural and biological options for virus management are being explored in an effort to validate their suitability for Australian production systems. Surveillance operations have already identified a disconnect between research outcomes and grower knowledge particularly for viral pathogens which is contributing to poor uptake of current best practice virus management options. Supporting better education initiatives aligned with a combination of cultural and biological options, understanding of current disease populations and better management of inoculum load in the environment will assist growers in managing key viral and bacterial pathogens that beset Australian vegetable production.

**Poster Board 55**

**Surveillance of potato spindle tuber viroid (PSTVd) in certified seed potato crops in South Eastern Australia**

*Dr Nigel S. Crump*¹, Ms Nellie A. Malseed¹, Ms Crystal Wilkinson¹, Ms Michelle Wilson¹, Mr Barry Strahan¹, Mr Mitchell Gorman¹, Ms Kerrie Hollis¹  
¹*SUISPICA, South Melbourne, Australia*

Potato spindle tuber viroid (PSTVd) is a pathogen that poses a significant risk to potato crops in Australia. Ensuring there is clean disease-free seed through effective seed certification schemes is paramount in the prevention of this disease. To provide assurance that PSTVd is not known to occur in certified seed potatoes in Australia, the seed certification authority AusPICA conducted targeted surveillance for PSTVd in potato crops submitted for certification from 2016 to 2019. This included surveillance of potato crops in Victoria, South Australia and northern New South Wales. Samples of potato leaves were collected from 10% of all seed crops submitted for certification per farm. A leaf sample included fifty randomly collected leaves. The leaf samples were sent to an approved laboratory with NATA accreditation for analysis using RT-PCR. No PSTVd was detected in any samples collected during the 4-year surveillance period. This data provides some evidence that PSTVd does not occur in the areas of certified seed production in Victoria, South Australia, and New South Wales.
Identification and detection of soft rot of carrot caused by *Klebsiella variicola* – a new pathogen on carrot

Dr MK Prasannakumar1, **Ms K Nandini**1, Ms Parivallal Buela1, Mr Gopal Venkatesh babu1, Mr BS Chandrasekhar1, Mrs K Priyanka1, Mr KL Nandeesha1, Mr Alase Saddamhusen1, Mr Boda Praveen1, Ms SM Jayasudha1, Ms Dasgupta Amrita1

1CAAST-Project Training, Department of Plant Pathology, University of Agricultural Sciences, Bangalore, India

The carrot (*Daucus carota*) is a root vegetable often claimed to be the perfect health food. Recently soft rot disease has become a serious threat which affects the taproot leading to decay and with foul odour. The pathogen attacks in all the stages (early, mid and late) accurate diagnosis of this disease is therefore important. In the present study, we isolated the causal organism of soft rot of carrot from the diseased samples, using nutrient agar and/or the enrichment host (Bell pepper) technique. Successful isolates were purified by sub-culturing and all the isolates were positive for oxidase, catalase and nitrate reductase and negative for indole. The isolates were identified as *Klebsiella variicola* using 16S rDNA amplicon sequencing. For accurate and sensitive detection a loop-mediated isothermal amplification (LAMP) assay was used by comparing with the conventional polymerase chain reaction (PCR). In the LAMP assay, six primers (two inner primers, two outer primers and two loop primers), targeting 16S rDNA sequences of *K. variicola* were used for the LAMP reactions which could detect the *K. variicola* at 60 °C within 30 min. The sensitivity of PCR was at 10ng where the LAMP assay was found to amplify less than 50 fg. The specificity was confirmed with five other bacterial pathogen isolates which showed negative results. A set of two DNA intercalating dyes were used such as Ethidium Bromide and SYBR Green which helped in the visual detection of the amplified LAMP products. Hence, this technique has greater potential for developing quick and sensitive visual detection methods than the other conventional PCR strategies for detecting *Klebsiella variicola* in the infected plants.

Isothermal detection of the *Dickeya* genus and *Clavibacter michiganesis* subsp. *sepedonicus*, prominent potato tuber pathogens

**Mr Bryant Davenport**1, Dr Rugang Li1, Dr Shulu Zhang1, Mr Keith Schuetz1

1Agida, Inc., Elkhart, United States

Recent outbreaks of black-leg disease in potato in the United States have prompted international awareness to the aggressive bacteria of the *Dickeya* genus. Symptoms produced in potato by *Dickeya* are indistinguishable from those produced by *Pectobacterium* species, requiring laboratory analysis for bacterial identification. *Dickeya* outbreaks also raise concern for other tuber diseases such as bacterial ring rot in potato, caused by *Clavibacter michiganensis* subsp. *sepedonicus* (Cms). Cms is highly contagious and persistent in tissues leading to classification as an A2 quarantine pest by EPPO. Both *Dickeya* and Cms require molecular detection for identification and confirmation, which poses issues with sample inhibition due to starchy potato tissue and laboratory training to perform testing. We present genus and subspecies level isothermal assays using recombinase polymerase amplification for both *Dickeya* and Cms, respectively, to combat the inhibition posed from tuber tissue and simplify molecular diagnostics for these pathogens in potato tubers. The tests run at a constant 39°C for 20 minutes, producing results in real-time on a portable fluorometer or traditional qPCR machine, such as the Agdia AmpliFire and BioRad CFX 96. Each assay can detect the respective bacteria from a crude tuber soak with a sensitivity matching that of traditional PCR assays routinely used for black-leg and bacterial ring rot detection.
Population analysis and subgroup diagnosis of Lettuce necrotic yellows virus in New Zealand

Ms Toni Darling\textsuperscript{1}, Ms Priyadarshana Ajithkumar\textsuperscript{1}, Dr Colleen M. Higgins\textsuperscript{1}
\textsuperscript{1}Auckland University of Technology, School of Science, Auckland, New Zealand

Lettuce necrotic yellows virus (LNYV) causes lettuce crop losses in Australia and New Zealand (NZ). The virus can be differentiated into two subgroups, of which subgroup I appears to have died out in Australia but was still detected in NZ in 2011. It has been suggested that subgroup II is outcompeting subgroup I, and recent high crop losses in NZ may indicate stronger presence of subgroup II in New Zealand. Current diagnostic methods require each sample to be tested separately for each subgroup. To diagnose LNYV subgroups, and assess if subgroup I is disappearing from NZ, a one-step diagnostic method for both subgroups would reduce time and costs. I have been developing a diagnostic assay based on RT-qPCR with High Resolution Melting (HRM). Primers designed previously for use in a RT-PCR-RFLP assay were tested for their usefulness in RT-qPCR-HRM. It was found that these primers could diagnose LNYV, but couldn’t confidently distinguish one subgroup from another since their HRM profiles overlapped. New primers were designed- these have been shown to diagnose LNYV, and have been tested for their ability to diagnose each subgroup. Once this test is finalised, samples collected from around NZ in 2018 will be tested for LNYV subgroup. Phylogenetic analysis of the LNYV N gene from the same samples will update our knowledge of subgroup distribution. The N gene has been amplified by RT-PCR and was sequenced using Sanger sequencing. These sequences have been compared to other LNYV N gene sequences using phylogenetics to analyse the relationships between these and published sequences from 2011. The diagnostic testing of samples together with phylogenetic analysis will help us understand if the virus population is changing, which may help determine the cause of recent lettuce crop losses in NZ.

Rapid detection of Sweet Potato Virus G using novel LAMP detection technology

Ms Winnie Maso\textsuperscript{1}, Ms Myla Deros\textsuperscript{2}, Miss Emma Coleman\textsuperscript{4}, Mrs Sandra Dennien\textsuperscript{3}, Dr Anthony Young\textsuperscript{1}, Prof Victor Galea\textsuperscript{1}
\textsuperscript{1}The University Of Queensland, Gatton, School of Agriculture and Food Sciences, Gatton, Australia, \textsuperscript{2}The National Agricultural Research Institute, Lae, Papua New Guinea, \textsuperscript{3}Agri-science, Department of Agriculture and Fisheries, Gatton, Australia, \textsuperscript{4}Australian Centre for International Agriculture Research, Canberra, Australia

Sweet potato virus diagnoses of planting materials is a key task in a clean seed system to support commercial production in Papua New Guinea (PNG). Sweet potato virus G (SPVG) detection is masked when other potyvirus like sweet potato feathery mottle virus (SPFMV) is present in nitrocellulose membrane enzyme-linked immunosorbent assay (NCM-ELISA) tests, thus a complementary detection method is required. SPVG positive samples will be preserved onto FTA cards to facilitate preliminary screening of PNG samples to develop a LAMP (loop-mediated isothermal amplification) assay in Australia. Vine sections of sweet potato virus G (SPVG) infected sweet potato will be graft inoculated onto seedlings of sweet potato virus sensitive indicator plant Ipomoea setosa for virus transmission. I. setosa leaves will be collected three times at two weekly intervals from the top, middle and base of the respective nodal vines. One disc from each leaf for the respective nodes will be cut out from the main mid rib and pressed onto labelled FTA cards, air dried and stored at room temperature for two and four weeks respectively after sampling to mimic shipment conditions. A LAMP assay will be developed for the detection of SPVG to amplify products in real time to show results of positive reaction in samples with SPVG infection. This study will provide information on suitable protocols to sample I. setosa onto FTA cards and its efficacy to store nucleic acids for a reverse transcriptase LAMP assay for SPVG detection.
Poster Board 63

The development of loop mediated isothermal amplification (LAMP) diagnostic assays for the detection of Deformed wing virus and Sacbrood virus in bees

Dr Linda Zheng1, Dr David Lovelock1, Dr Brendan Rodoni1, Dr Fiona Constable1
1Agriculture Victoria Research, Bundoora, Australia

The European honey bee (Apis mellifera) is the mainstay of the managed pollination industry in Australia. Bees are used to pollinate a broad range of horticultural and agricultural crops and are used for honey and beeswax production. More than 25 viruses infect bees, and some can have a significant impact on hive health, such as the exotic species Deformed wing virus (DWV), vectored by the Varroa mites. DWV can also be transmitted horizontally between bees within a hive and vertically, from queen to progeny. Varroa mites also transmits several other bee viruses including Sacbrood virus (SBV), Kashmir bee virus (KBV) and Varroa destructor virus 1 (VDV1). An uncontained incursion of varroa mite, and associated bee viruses, is estimated to cost producers and consumers of pollination-dependent crops an estimated billion over 30 years. Therefore, surveillance activities for viruses prior to, during or after a varroa mite incursion will be required. High throughput lab based diagnostic assays and field deployable molecular testing capability will support these surveillance activities and can also support the screening of illegally or legally imported bee products at the point of entry. Providing the bee industry with simple field deployable diagnostics assays for virus detection will assist in the maintenance of healthy hives. For this purpose, loop mediated isothermal amplification diagnostic assays have been designed for the detection of two bee viruses, the exotic DWV and the endemic SBV. Findings from the development and validation of these two assays will be presented.

Poster Board 64

Microscopic examination of Ralstonia pseudosolanacearum and R. solanacearum colonies and the response of tomato breeding lines to bacterial wilt caused by the two species

Dr Mark Angelo Balendres1, Mr Villamor Ladia Jr.1, Dr Fe Dela Cueva1
1University of The Philippines Los Baños, Los Baños, Philippines

Potato bacterial wilt is caused by Ralstonia pseudosolanacearum and R. solanacearum. These two genomic species can be discriminated by using the Phylotyping scheme and by Biovar analysis. Differentiation of the two species by colony morphology is rarely reported and only by visualization of colony growth. The latter, relative to the first two methods, is simpler, less time-consuming and economical. The use of resistant cultivars is the most sustainable approach to bacterial wilt. However, most tomato breeding lines were assayed only against R. solanacearum. A study conducted between 2018 and 2019 shows that microscopic examination of colony morphology can be also used to discriminate potato isolates of R. pseudosolanacearum from R. solanacearum. Visual observation of the colony in growth media was not sufficient to separate the two species. By examining individual colonies under 40X microscope magnification, colony characteristics of the two species were found distinct. Color and the ratio of the white and reddish portion of the colony proved to be the two discriminating factors. The variations were observed in repeated tests conducted on reference isolates and in representative Ralstonia spp. collection. The study further identified, from repeated glasshouse trials in 2018 and 2019, several tomato breeding lines with resistance to R. solanacearum and moderate resistance to R. pseudosolanacearum. These results demonstrate how colony morphology examination, with microscopy, can still be used to identify species causing bacterial wilt in potato. This test may be used to partially screen large number of isolates, may be used alongside biovar analysis and may substitute the Phylotyping scheme for potato isolates. Further, results from the disease assays of tomato breeding lines indicate that sources of resistance to bacterial wilt caused by the two genomic species are available for further breeding trials.
First report of *Phytophthora capsici* as a causal pathogen of blight disease of chilli (*Capsicum annuum* L.) in Bhutan

**Mr Ganja Singh Rai**, Mr David Ian Guest, Mr Brian Jones, Mr Thinley Thinley

1*Agriculture Research and Development Centre, Samtenling 31101, Bhutan*, 2*Sydney Institute of Agriculture, The University of Sydney, Sydney, Australia*, 3*National Plant Protection Centre, Simtokha 11001, Bhutan*

Chilli (*Capsicum annuum* L.) is an important crop, nutritionally and economically in Bhutan. It is consumed both as a spice and a vegetable in Bhutan. However, a blight disease, suspected to be caused by the oomycete pathogen, *Phytophthora capsici* Leon., is a serious production problem of chilli in all growing areas in Bhutan. No studies have been carried out in Bhutan to find out the causal agent of this disease in chilli prior to this research although the disease was first reported in 1995. For management of any disease to be effective, it is important to identify the causal pathogen first. Thus, in this study, we isolated 54 isolates in Bhutan from diseased chilli plants from 18 different farms with elevations ranging from 337 to 2408 masl in 2018 for identification of causal agent using morphological and molecular methods. The purified isolates produced stellate (40.7%), cottony (25.9%), petalloid (18.5%) and rosaceous (14.8%) colony characters in carrot agar media. All isolates produced caducous sporangia on long pedicels that were mostly papilllate (77.8%). The mean length of sporangia among the isolates ranged from 33.8 to 61.2 μm, and mean breadth of sporangia varied from 21.6 to 44.3 μm. The length to breadth ratio of sporangia ranged from 1.3 to 2.2 among the isolates. All 54 isolates of *P. capsici* tested were A1 mating type. The mean oospore diameter varied from 25.6 to 52.4 μm. Further, all isolates produced a PCR product of 172 bp when tested with the *P. capsici* specific primer PCAP paired with ITS1 primer. These findings confirmed the pathogen as *P. capsici* that causes chilli blight in Bhutan.

Differences in the acquisition of *Candidatus Liberibacter solanacearum* by two New Zealand tomato potato psyllid genotypes

**Mrs Gabrielle Drayton**, Mrs Shea Addison, Dr Ruth Butler, Dr Rebekah Frampton

2*The New Zealand Institute For Plant & Food Research Limited, Lincoln, New Zealand*

The plant pathogen, *Candidatus Liberibacter solanacearum* (CLso) is vectored by the tomato potato psyllid (TPP; *Bactericera cockerelli*). This pest and pathogen combination can cause significant damage to plants and severely affect crop yield and quality. However, information regarding the acquisition and transmission of CLso by TPP is limited and often conflicting. TPP were collected from around New Zealand, and isofemale colonies of the dominant mitochondrial genotype were developed in both the North and South Islands. Screening of a small subset of TPP from the colonies suggested that both were CLso negative. Laboratory-based experiments were conducted to determine the ability of these two colonies to acquire CLso. Adult TPP were released onto CLso-positive tomato plants and removed after 3 days (G0). TPP eggs were allowed to develop through to adults. TPP adults (G1) were then collected and released onto a fresh CLso-positive tomato plant. The TPP were removed after 3 days and the second generation of eggs allowed to develop through to adults (G2). Controls using CLso-negative plants were also included in the experiment. DNA was extracted from individual TPP and screened for CLso using a multiplex qPCR. The number of TPP that tested positive for CLso increased at each collection point. Differences in the rate and percentage positive differed between the colonies. This suggests that further genetic differences are present and may influence the ability of TPP to acquire CLso. CLso was detected in a low number of G2 individuals from the CLso-negative plants. This suggests that a low rate of CLso exists in the colonies. It appears that feeding on a CLso-positive plant is required for the rate of CLso to increase. Understanding the role of TPP genetics and differences in CLso acquisition rates is important for the development of targeted, regional TPP management strategies.
Revisiting tomato pith necrosis: a new *Pseudomonas* species associated with the disease

**Dr Merje Toome-Heller**¹, Dr Luciano Rigano¹, Dr Katharina Hofer¹, Dr Brett Alexander¹

¹*Plant Health and Environment Laboratory, Ministry for Primary Industries, Auckland, New Zealand*

Tomato pith necrosis is caused by a group of closely related bacteria: *Pseudomonas corrugata*, *P. mediterranea* and a more recently reported undescribed *Pseudomonas* sp. Group 3. Bacterial isolation from tomato stem material from New Zealand showing pith necrosis symptoms, resulted in a culture which was shown to be genetically very similar to the isolates of *Pseudomonas* sp. Group 3 detected in Japan. Pathogenicity testing with the isolate from New Zealand demonstrated that it causes pith necrosis in tomato with similar disease symptoms as caused by *P. corrugata* and *P. mediterranea*. Full genome sequencing was carried out to characterise the virulence genes of the bacterium and to complete a more comprehensive phylogenetic analysis. This confirmed that the isolate represents a previously undescribed *Pseudomonas* species and has a few unique traits compared to the other pith necrosis pathogens. This case highlights the need to revisit known plant pathogen groups and use the most up-to-date diagnostic tools as numerous organisms can cause phenotypically similar signs and symptoms but potentially possess different traits.

Chocolate streak disease of tomatoes in Australia is caused by a unique strain of *Fusarium oxysporum*

**Miss Sophia Callaghan**¹, Prof Lester Burgess², Dr Peter Ades⁵, Elizabeth Mann³, Ann Morrison³, Dr Len Tesoriero⁴, Prof Paul Taylor¹

¹*Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Melbourne, Australia*, ²*Sydney Institute of Agriculture, The University of Sydney, Australia*, ³*Australian Processing Tomato Research Council, Shepparton, Australia*, ⁴*NSW Department of Primary Industries, CCPIC, Ourimbah, Australia*, ⁵*Faculty of Science, University of Melbourne, Australia*

In recent years, a new disease has been observed in field-grown processing tomatoes in north-central Victoria, characterised by stunted plants with chocolate coloured vascular streaking in the collar and tap root regions. The objective of this study was to identify and characterise the causal pathogen of this disease. During surveys of processing tomato crops during the 2016/17, 2017/18 and 2018/19 seasons, the “chocolate streak” symptom was observed at approximately 65%, 80% and 40% of crops surveyed, respectively. *Fusarium oxysporum* was consistently isolated from the chocolate coloured necrotic tissue of affected plants. Subsequent pathogenicity trials confirmed that representative isolates of *F. oxysporum* could cause pre and post-germination seedling death, as well as stunting, dry root weight reduction, and collar and root lesions in mature tomato plants. In host range trials, rye, barley, maize, clover, wheat and faba beans were asymptomatic hosts, harbouring *F. oxysporum* without exhibiting any visible symptoms of infection. In multi-gene phylogenetic studies using the ef1, pgx4 and ITS regions, there was no clustering of Australian chocolate streak isolates with international *F. oxysporum radicis-lycopersici* or *F. oxysporum f. sp. lycopersici* isolates. In growth rate trials on artificial media, the optimum temperature for the chocolate streak isolates was 30°C. The symptomology of this disease matches overseas descriptions of Fusarium Crown and Root rot of tomato (FCRR), caused by *Fusarium oxysporum radicis-lycopersici*. However, FCRR has never been reported in Australia, and is typically described as being a colder climate disease (18°C optimum) caused by a pathogen with a wide-host range. The growth rate, host range and phylogenetic results of this study suggest that the chocolate streak pathogen in Australia might be a genetically and biologically unique pathogen to those affecting foreign tomato industries. This has implications in terms of disease management, especially breeding for resistance and plant biosecurity.
Is Sugarcane an alternative host of Panama Disease?

**Mr Wayne O’Neill**, Ms Jenny Cobon, Dr Tony Pattison

1Queensland Department Of Agriculture And Fisheries, Dutton Park, Australia, 2Queensland Department Of Agriculture And Fisheries, South Johnstone, Australia

Sugarcane is extensively cropped in the wet tropics of north Queensland, including areas that are in close proximity to confirmed infestations of Panama disease Tropical Race 4 (TR4). Recent work on the Panama disease pathogen (*Fusarium oxysporum* f.sp. *cubense*, Foc) suggest that it is capable of colonising and surviving on a wide variety of alternative host species. Previous field studies on the use of sugarcane as a rotation crop give mixed reports on its ability to suppress or exacerbate Panama disease incidence. A glasshouse inoculation study was carried out with four current sugarcane varieties, popular in the wet coastal tropics of Queensland (Q200, Q208, Q228 and Q250). Sugarcane plants were grown in field soil and inoculated with Subtropical Race 4 (SR4) of the pathogen. Williams Cavendish was included in the experiment as a susceptible control. Once the banana plants showed signs of disease, sugarcane roots were surface sterilized and plated to determine if they had been colonised by the pathogen. Colonies identified as *Fusarium oxysporum* were purified and characterised using vegetative compatibility group testing to determine whether they were Foc. All four varieties in the experiment demonstrated the ability to host SR4 Foc as an endophyte in their roots, in at least 50% of the replicates. This finding concurs with recent work on Foc that suggests it is capable of colonising and surviving on a wide variety of alternative host species. Some means of pathogen spread (eg feral animals, flooding) can bypass on-farm biosecurity measures, and potentially move the pathogen into other crops such as sugarcane. Foc does not cause any obvious symptoms when persisting on these alternative hosts, so they can potentially mask the presence of the pathogen at a site. Further work is advisable to determine whether the fungus reaches the harvested portion of the sugarcane plant for TR4 biosecurity.

First report of mango stem-end rot, caused by *Lasiodiplodia theobromae*, in the Lao PDR

**Mr Andrew Daly**, Ms Sengphet Phanthavong, Dr Virgilio Balmas, **Prof Lester Burgess**, Dr Bevan Weir

1NSW Department of Primary Industries, Menangle, Australia, 2Provincial Agriculture and Forestry Office, Pakse, Laos, 3University of Sassari, Sassari, Italy, 4University of Sydney, Camperdown, Australia

The authors have observed stem-end rot of mango in both local and imported mangoes in Lao PDR. However the disease has not been formally reported. Ripe eating mangoes cv. ‘Keo Romeat’ probably of Cambodian origin were purchased at a local roadside market in Champasak town, Champasak Province, (14° 53’ 11” N, 105° 52’ 36” E) in November 2019. Two days later an aggressive stem-end rot symptom characteristic of infection with a systemic fungal pathogen developed in some of the mangoes. Surface sterilised pieces of pulp from just below the surface of the skin at the margin of the infection zone were plated onto quarter-strength potato dextrose agar medium amended with cephalxin monohydrate (500 mg/l). Fungal colonies typical of the morphology of Botryosphaeriaceae species were consistently isolated. A representative culture was purified by hyphal tipping for molecular identification. Amplification of the ITS region of nuclear rDNA extracted from this culture, gave a 536 bp product with 100 % identity with a number of GenBank accessions of *Lasiodiplodia theobromae*, a common cause of mango stem-end rot. Green mangoes were obtained from a local market for a pathogenicity test. The peduncle of each of five fruits was inoculated with an agar plug colonised by the fungus. The peduncle of five more fruits were inoculated with a sterile agar plug (controls). All fruit were incubated at room temperature. Six days after inoculation, symptoms typical of a systemic stem-end rot pathogen infection were recorded on three of the inoculated fruit. Control fruit did not develop symptoms. *L. theobromae* was consistently re-isolated from the diseased fruit. This is the first report of mango stem-end rot and *L. theobromae* in Lao PDR.
Calonectria quinqueseptata associated with a leaf spot disease of Macadamia integrifolia in the Laos PDR

Ms Sengphet Phanthavong1, Mr Andrew Daly2, Dr Virgilio Balmas3, Prof Lester Burgess4, Dr Bevan Weir
1Provincial Agriculture and Forestry Office, Pakse, Laos, 2NSW Department of Primary Industries, Menangle, Australia, 3University of Sassari, Sassari, Italy, 4University of Sydney, Camperdown, Australia

Macadamia integrifolia (Proteaceae) is a rainforest species native to Queensland, Australia and a high-value crop. Leaf spot diseases of M. integrifolia in Australia and other countries are not known. In November 2018, tan-coloured irregular to circular leaf spots randomly distributed across the leaf surface and measuring up to 20 mm in diameter and with a prominent yellow halo were observed on mature M. integrifolia trees in a garden on the Bolavan Plateau, Champasak Province, Lao PDR (15° 11’ 22” N 106° 8’ 20” E). Initial disease symptoms were characterised by small chlorotic flecks and tan-coloured spots 1 mm in diameter. Mature spots were often coalesced and had a grey papery centre. There was a high incidence and severity on affected leaves. Samples of affected leaves were collected for isolation of a putative fungal pathogen. Small (2 x 2 mm) segments were excised from the margin of the tan-coloured tissue of several lesions selected at random, surface sterilised in 70% ethanol for 10 sec and plated onto quarter-strength potato dextrose agar amended with cephalxin monohydrate (500 mg/l). Nine-day-old colonies on PDA were tan-coloured and flat with sparse white cottony aerial mycelium and irregularly-shaped diffuse margins. Conidia were hyaline, cylindrical, up to 5-septate and rounded at both ends. To confirm species identification, the internal transcribed spacer region (ITS) was PCR-amplified and sequenced. BLAST searches showed 99.82% identity with an existing sequence of Cylindrocladium quinqueseptatum, the anamorph of Calonectria quinqueseptata (current name), deposited in GenBank (Accession No. EU285555). The anamorph C. quinqueseptatum is a well-known cause of leaf and twig blight disease in nurseries and plantations of Eucalyptus spp. in Australia and SE Asian countries including Lao PDR, however this is the first report of its association with a leaf spot disease of M. integrifolia.
Poster Board 23

Adaptation in a near-clonal pathogen, *Dothistroma septosporum*, over 50 years in New Zealand pine forests

Prof Rosie E. Bradshaw¹, Ms Shannon Ormond¹, Dr Pierre-Yves Dupont², Dr Pranav Chettri¹, Dr Kutay Ozturk¹, Dr Rebecca L. McDougal³, Dr Lindsay S. Bulman¹, Prof Murray P. Cox¹

¹Massey University, Palmerston North, New Zealand, ²Institute of Environmental Science and Research, Christchurch, New Zealand, ³Scion, NZ Forest Research Institute Ltd, Rotorua, New Zealand

Dothistroma needle blight is one of the most serious pine tree diseases worldwide. Its increasing occurrence and severity over the last few decades have been associated with human-mediated movement of the pathogen and with changing weather patterns. The main pathogen responsible for this disease, *Dothistroma septosporum*, was introduced into New Zealand in the 1960s and has remained there as a virtually clonal population, unlike in many Northern hemisphere countries where there is high genetic diversity. The existence of stored historical isolates of New Zealand *D. septosporum* at Scion (NZ Forest Research Institute), and their almost clonal nature, provided a unique opportunity to study the evolution and adaptation of a forest pathogen after its introduction into a new country. Whole genome sequencing and phenotype analyses were performed on isolates collected in the 1960s, 1990s and 2000s from central North Island forests in New Zealand. Low genome diversity, but increasing diversification over time, supported the hypothesis of a single introduction of *D. septosporum*, but suggest that a number of isolates, rather than just one, were introduced. The more recent isolates did not show any change in tolerance to copper compared to 1960s isolates, despite decades of copper fungicide spraying of forests with Dothistroma needle blight. Surprisingly, in pathogenicity assays carried out under controlled conditions, isolates from the 1990s and 2000s produced lower levels of the virulence factor dothistromin and significantly reduced virulence to *Pinus radiata* compared to 1960s isolates. *D. septosporum* thus appears to have adapted over time to become less virulent, possibly in part to secure the continued viability of its long-lived host. These studies highlight the importance of long-term pathogen studies and have broad implications for the health of forests subject to incursions of exotic pathogens.

Poster Board 78

Multi-domain interactions between *Fusarium oxysporum* and the banana microbiome

Mr Henry W.G. Birt¹, Dr Anthony B. Pattison², Mr Adam Skarshewski¹, Dr Jeff Daniells², Dr Anil Raghavendra¹, Dr Paul G. Dennis¹

¹The University Of Queensland, Brisbane, Australia, ²Centre for Wet Tropics Agriculture, Department of Agriculture and Fisheries, South Johnstone, Australia

Global banana production is greatly undermined by the fungus, *Fusarium oxysporum* f. sp. *cubense* (Foc) Tropical Race 4 (TR4), which causes vascular wilt (Panama Disease) in susceptible varieties. At present, there are no effect chemical treatments for Foc, but evidence indicates that like other macro-organisms, bananas host diverse microbial communities (i.e. the microbiome) that influence their susceptibility to disease. Using high-throughput sequencing, we have characterised the banana microbiome across a range of soils, genotypes and plant compartments, and reduced its complexity to a core set of taxa that are associated with bananas worldwide. Using network and other analyses we have identified a range of taxa that significantly interact with *Fusarium oxysporum* and suggest how they may influence plant health.
Using genome-wide screening to identify genes important for bacterial colonisation of plant surfaces

Ms Belinda Fabian¹, Dr Christie Foster¹, Dr Amy Asher¹, Dr Liam Elbourne¹, Dr Amy Cain¹, Dr Karl Hassan², Dr Sasha Tetu¹, Dr Ian Paulsen¹

¹Department of Molecular Sciences, Macquarie University, North Ryde, Australia, ²School of Environmental and Life Sciences, University of Newcastle, Newcastle, Australia

One of the major factors limiting global food and fibre production is the loss of crop yields due to plant disease. Pesticides are used to control many plant diseases, but pathogens are becoming increasingly resistant, and new disease control methods are needed. One such approach is the use of biological control agents. Pseudomonas protegens Pf-5 is one of the best characterised biocontrol bacteria and in lab studies has the ability to control crop diseases. However, field trials of biocontrol bacteria often show unreliable colonisation and persistence on plant surfaces, hindering their efficacy. Our aim is to identify the genes that are important for colonisation of plant surfaces by Pf-5 by conducting genome wide studies using Transposon Directed Insertion Site Sequencing (TraDIS). This technique combines the creation of a dense library of randomly generated loss-of-function mutants with massive parallel sequencing to allow the simultaneous study of all non-essential genes. Applying TraDIS also allows us to see biological stories that aren’t visible using traditional methods of assaying gene function, such as targeted gene knockouts. We challenged our Pf-5 mutant library in conditions related to colonising plant surfaces (e.g. seed and root attachment, motility and interactions with other microbes) so we can identify the genes involved in successfully colonising and persisting in this niche. As an example, motility is a crucial part of colonisation and biocontrol activity. From these motility assays we have identified ~400 genes important for Pf-5 motility, with chemotaxis and flagella genes important for both motility types. In addition to these common functions, there are genes that are important for just one type of motility. Some of these functions haven’t been previously linked to these conditions. A greater understanding of the roles these genes play in colonisation may improve our ability to effectively use biocontrol bacteria in Australian agriculture.
A high-quality reference genome for the plant pathogen *Phytophthora cinnamomi*

**Miss Amy Longmuir**1,2, Assoc Prof Peter Beech3, Dr Mark Richardson1,2  
1Deakin University, Genomics Centre, School of Life and Environmental Sciences, Waurn Ponds, Australia, 2Deakin University, Centre for Integrative Ecology, School of Life and Environmental Sciences, Waurn Ponds, Australia, 3Deakin University, Centre for Cellular and Molecular Biology, School of Life and Environmental Sciences, Burwood, Australia

The plant pathogen, *Phytophthora cinnamomi* results in noteworthy crop losses globally, including the avocado and macadamia industries in Australia, while also posing a significant threat to the biodiversity of Australia’s native flora. To date, attempts to sequence and assemble the genome of *P. cinnamomi* using first and second generation sequencing techniques have resulted in hugely fragmented genomes, with large gaps of missing information. Specifically, significant sections of the genome containing abundant repeat regions and virulence genes are not adequately resolved, limiting the utility of such genomic resources. Utilising recent advances in long-read sequencing by Oxford Nanopore Technologies we sequenced ~5.5 gigabases of an Australian *P. cinnamomi* isolate (~50x coverage). By optimising the assembly process to include error-correction and repeat graphs we have produced the first genome assembly under 1,000 contigs for any *Phytophthora* sp.; a 107 Mb assembly in 965 contigs plus 11 scaffolds with an N50 of 325,473. The presented genome is a vast improvement on the current available reference genome which consists of 9,537 contigs in 1,314 scaffolds, but importantly enables us to understand the importance of large scale structural variations in the genome. Here, we present the results of our assembly and annotation work, and highlight how this improved contiguous assembly enables us to investigate and answer fundamental evolutionary questions regarding *Phytophthora* genomics and pathogenicity. I will then go on to detail our future work (enabled by this assembly) where we use CRISPR to study the mechanism of *P. cinnamomi* infection in important native flora.

**Poster Board 21**

Implementing molecular techniques develops our understanding of a devastating bacterial disease of mungbean, halo blight

**Mr Thomas Noble**1, Prof Sagadevan Mundree1, Dr Brett Williams1, Dr Anthony Young2, Mr Col Douglas3  
1Queensland University of Technology, Brisbane, Australia, 2The University of Queensland, Gatton, Australia, 3DAF Qld Gov, Warwick, Australia

Mungbean (*Vigna radiata* L. Wilczek var. radiata) is grown as a high-value export crop and established as the main dryland rotation in the northeastern Australian summer cropping region. Its short duration of 55–70 days, capacity to fix atmospheric nitrogen, and high returns make it a desirable option for growers. Crystal and Jade released in 2005 and 2014 respectively, dramatically increased the areas planted for mungbean production. Both cultivars have trusted vigorous plant types yielding beyond what was thought possible at the time. However, production volatility arising from seed-borne bacterial disease halo has proved a constant threat to the Australian mungbean industry. Breeding for resistance and the production of clean seed is critical to managing the spread and effects of bacterial disease, particularly as there are no in-crop chemical options. To integrate the most effective long-term resistance into commercial cultivars, knowledge of genetics underlying the multiple epidemiologically significant strains present in the environment is vital. Research of the pathogens genome is providing insights into the population structure and the mechanisms giving rise to highly pathogenic strains. In addition to resistance breeding, testing seed lots for the presence of halo blight DNA will aid in the early detection of infected seed lots minimising the risk of epidemics and limiting the spread of disease. Implementation of these technologies today and into the future will control the threat of this disease, providing farmers a dependable source of income.
Spot form of net blotch (SFNB) caused by *P. teres f. maculata* (*Ptm*) is a major foliar disease of barley worldwide. Potential annual losses caused by SFNB are estimated to be $192 million to the Australian barley industry. Quality parameters such as kernel size, bulk density and plumpness are negatively affected by SFNB and SFNB can cause yield losses of 10-40%. To manage spot form of net blotch resistance in barley varieties it is important to understand the genetics of *Ptm* virulence. This information will provide us with knowledge to better understand the pathogenic structure and host/pathogen interactions. Most of our current understanding of barley-*P. teres* interactions is of the genomic regions involved in resistance of the barley host. This project aims to identify the genomic regions conferring virulence in *Ptm* isolates via association mapping (AM). One hundred and fifty-one *Ptm* isolates collected from Victoria, New South Wales and Queensland were genotyped using DArT-seq (Diversity Arrays Technology (DArT) Pty Ltd) and over 10,000 markers were obtained. Isolates were phenotyped across twelve different barley genotypes. The genotyping and phenotyping data will be combined and the GAPIT (Genomic Association and Prediction Integrated Tool) package in RStudio and TASSEL (Trait analysis by association, evolution and linkage) software used to analyse the data. This project will contribute towards a better understanding of the complex host–pathogen interactions and it will be important for barley germplasm enhancement to develop resistant cultivars. Also, it will provide insight into the pathogenicity caused by *Ptm* and provide information about disease management strategies.
Fusaristatin production negatively contributes to the aggressiveness of the crown rot pathogen *Fusarium pseudograminearum*

Mr Mohammed Khudhair1,2, Dr Kemal Kazan3, Dr Louise Thatcher3, Dr Friday Obanor4, Dr Elizabeth Aitken1, Mrs Anca Rusu2, Dr Donald Gardiner2

1 School of Agriculture and Food Science, The University of Queensland, Brisbane, Australia, 2 CSIRO Agriculture and Food, 306 Carmody Road, St Lucia, Qld, 4067, Brisbane, Australia, 3 CSIRO Agriculture and Food, 147 Underwood Avenue, Floreat, WA, 6014, Perth, Australia, 4 The Grains Research and Development Corporation (GRDC), 4 National Circuit, Barton ACT, 2600, Canberra, Australia

*Fusarium pseudograminearum* (*Fp*) is an important pathogen of cereals in many countries and regions including Australia, causing Fusarium crown rot that causes significant economic losses. *Fp* produces number of secondary metabolites throughout its life cycle; one of these metabolites is fusaristatin. The presence and absence of a gene cluster responsible for fusaristatin production was investigated amongst a large number of isolates (429 isolates) collected from Western Australia (WA) in 2008 (n=134) and 2015 (n=164) and from New South Wales, Victoria, Queensland and South Australia (n=131). The study results revealed that the fusaristatin gene cluster is unique to WA finding no evidence of this gene in *Fp* isolates from the eastern states. Mutants of the gene cluster were generated in two different parental backgounds. By comparing the mutants and their respective parental strains, the parental strains were significantly less aggressive than the mutants. Similar trends were obtained for head blight tests. The increased aggressiveness may be linked to increased growth rates of the mutant strains. The possible reasons for the geographically restricted presence of the fusaristatin gene cluster is discussed.

Fungal Effectors and Their Potential Role in Infection

Dr Joanna Bowen3, Ms Cordelia Dravitzki1, Dr Carl Mesarich2, Assoc Prof Kim Plummer1, Dr Janet Wheeler1

1 La Trobe University, Melbourne, Australia, 2 Massey University, New Zealand, 3 Plant & Food Research, Auckland, New Zealand

*Venturia inaequalis* causes apple scab worldwide, resulting in a high cost to growers who spray fungicides up to every two weeks as a method of control. Whole genome sequencing of *V. inaequalis* enabled the identification of candidate effectors in the *V. inaequalis* infection arsenal. Amongst these candidate effectors, a family of secreted proteins were found that were similar to plant natriuretic peptides (PNPs) (1). In plants, PNPs are involved in water and ion homeostasis, stomatal regulation, and biotic and abiotic stress (2). Although PNPs are ubiquitous and well characterized in plants, PNPL-like (PNPL) proteins found in *V. inaequalis* are rare in pathogens. PNPLs released by *Xanthomonas axonopodis* pv. *citri* affect stomatal aperture in its host. VdAve1, a PNPL in *Verticillium dahliae*, has been shown to trigger resistance mediated by the tomato immune receptor, Ve1 (3). Ave1 (avirulence on Ve1) is a single copy gene important to pathogenicity, however its role in plant homeostasis is unknown. Our lab has shown that synthetic *V. inaequalis* PNPL (ViPNPL) peptides cause stomata to close in *Tradescantia fluminensis*. We hypothesise that *V. inaequalis* regulates host stomata to maintain biotrophic infection, and that it releases these ViPNPL proteins to modify guard cell homeostasis, resulting in the closure of stomata. We are measuring guard cell aperture of apple leaves +/- *V. inaequalis* to test this hypothesis. The behaviour of guard cells in a range of plant leaves exposed to synthetic ViPNPL peptides will also be analysed. Plants will be transiently transformed to express ViPNPL proteins, and the effect on guard cell behaviour will be examined.

Initial characterisation of extracellular vesicles from the fungal wheat pathogen *Zymoseptoria tritici*

**Miss Erin Hill**, Prof Peter Solomon

*The Australian National University, Canberra, Australia*

The fungal pathogen *Zymoseptoria tritici* is responsible for Septoria Tritici Blotch (STB) of wheat. Despite STB posing a significant threat to wheat production in Australia, we are still limited in our understanding of the molecular interactions that underpin disease. *Z. tritici* is an apoplastic pathogen, proliferating in the apoplast during the long, latent phase of infection. Given this, the apoplast is likely an important site for these host—pathogen molecular interactions. An outstanding question is how *Z. tritici* secrets pathogenicity-associated factors into the harsh apoplastic environment and/or delivers them to host cells. Many molecules are likely secreted by classical pathways, but recent evidence suggests some plant pathogens may also use non-classical secretory pathways to deliver pathogenicity factors. Extracellular vesicles (EV) have emerged as a potential mechanism of non-classical secretion and cross-kingdom communication. We hypothesise that EVs may play a role in mediating pathogen-host communication during *Z. tritici* infection of wheat, and have begun examining putative EVs produced by *Z. tritici*. Putative EVs have been isolated from axenic fungal cultures using ultracentrifugation and size exclusion chromatography. Transmission electron microscopy and nanoparticle tracking analysis showed the isolated structures varied in size, with most structures between 50 – 200 nm in diameter, and morphologically resembled previously described EVs. High-resolution bottom-up proteomics will provide preliminary insight into the protein composition of putative *Z. tritici* EVs. The characterisation of *in vitro*-derived EVs will provide a foundation from which we can begin to examine the role of EVs during *Z. tritici* infection of wheat. We anticipate this study will further our understanding of the molecular activities occurring in the apoplast during *Z. tritici* infection and more broadly, how fungal pathogens communicate with their hosts.
Identification and characterization of the interactions between the key plant protein RIN4 and the plant exocyst subunit Exo70B1 protein in kiwifruit using yeast two-hybrid system

Dr Wei Cui¹, Dr Jay Jayaraman¹, Dr Minsoo Yoon¹, Dr Erik Rikkerink³
¹Host-Microbe Interactions team, The New Zealand Institute For Plant And Food Research Limited, Auckland, New Zealand

The exocyst complex for vesicle secretion was first discovered in yeast. Homologues of the eight exocyst subunits, including Exo70, have subsequently been identified in all eukaryotes. In plants, multiple Exo70 genes have been reported. In contrast, only a single Exo70 gene occurs in the yeast and human genomes. This suggests that plant Exo70 proteins may have evolved novel functions. Plant immunity is mediated by disease resistance (R) proteins. Some R proteins can directly or indirectly recognize secreted pathogen effector presence and trigger immunity. Most characterised R proteins are intracellular nucleotide-binding and leucine-rich repeat-containing receptors (NLR). Recently, Arabidopsis Exo70B1 was shown to interact with TN2, an atypical NLR, and disruption of this interaction leads to constitutive activation of defence. One possibility is that Exo70B1 is associated with TN2 and that TN2 is activated by an undiscovered effector that manipulates Exo70B1. This manipulation of Exo70B1 could involve proteins from pathogen or plant. Pseudomonas syringae pv. actinidiae (Psa) is responsible for bacterial canker in kiwifruit. Psa genome sequencing has revealed a substantial type III secreted effector (T3E) repertoire. Identification of the key plant R proteins that recognise and/or interact with Psa effectors is a crucial step in management of bacterial canker of kiwifruit. Arabidopsis RIN4 protein is a critical component in plant immunity and is targeted by several T3Es from Pseudomonas syringae. At least two host NLR resistance proteins monitor this pathogen interference and trigger plant defence responses. Homologues of Arabidopsis RIN4 and Exo70B1 have been cloned from Actinidia chinensis (AcRIN4 and AcExo70B1, respectively). The cloned AcExo70B1 protein strongly interacts with Arabidopsis RIN4 and AcRIN4 in yeast, suggesting that there exists a similar RIN4-associated exocyst secretory complex in kiwifruit plants. This is the first study of the kiwifruit exocyst protein complex, and will make a significant contribution to plant immunity research.
A polyethylene glycol-mediated protoplast transformation system for the Basal Stem Rot causal fungus, *Ganoderma boninense*

**Mr Fook Hwa Lim**1,2, Omar Abd Rasid1, Mui-Yun Wong2,3, Abu Seman Idris1, Abdul Wahab Mohd As’wad2, Ganesan Vadamalai2, Ghulam Kadir Ahmad Parveez1
1Malaysian Palm Oil Board (MPOB), Selangor, Malaysia, 2Department of Plant Protection, Faculty of Agriculture, Selangor, Malaysia, 3Institute of Plantation Studies, University of Putra Malaysia, Selangor, Malaysia

Oil palm (*Elaeis guineensis* Jacq.) is a tropical perennial crop that has become one of the important contributors to the world edible oil supply and feedstock for oleochemical and biodiesel productions. Malaysia is one of the major palm oil producers and its palm oil products have been exported to more than 150 countries globally. However, the most efficient oil bearing crop has been threatened by various devastating diseases and Basal Stem Rot (BSR) disease has gained serious attention in Malaysia and Indonesia. The basidiomycete fungus, *Ganoderma boninense* has been identified as the main causal of oil palm BSR. Various efforts have been initiated to study and understand the oil palm BSR and this plant pathogen. This paper describes the development of a PEG-mediated protoplast transformation system for *G. boninense*.

The establishment of a PEG-mediated *G. boninense* protoplast transformation system will contribute to a deeper understanding of this plant pathogen and the oil palm BSR disease. About $5.145 \times 10^7$ cells/ml of protoplasts with the viability of more than 90% were successfully obtained from the *G. boninense* mycelium tissue. Based on the minimal inhibitory concentration study, the selection agent, hygromycin was effective against *G. boninense*. No *G. boninense* mycelium could survive on the medium containing 60 µg/mL of hygromycin and above. The PEG-mediated *G. boninense* protoplast transformation was performed and the parameters including amount of transformation vector, percentage of PEG, pre- and post-incubation periods during transformation were successfully identified and optimized. The putative *G. boninense* transformants could be visible on the selection medium at day five after the transformation. The integration of transgene, *hygromycin phosphotransferase* (*hpt*) in the putative *G. boninense* transformants was confirmed via PCR analysis. Southern blot analysis will be conducted for further verification.
Phenotypic evaluation of *Sclerotinia sclerotiorum* resistance in wild *Cicer* germplasm under greenhouse conditions

**Mrs Virginia Mwape**, Dr Mark Derbyshire, Dr Toby Newman, Dr Kefei Chen, Dr Lars Kamphuis

*1Center for Crop and Disease Management, Curtin University, BENTLEY, Australia, 2Commonwealth Scientific and Industrial Research (CSIRO), Wembley, Australia, 3Statistical for the Australian Grain Industry (SAGI-West), Curtin University, BENTLEY, Australia*

Evaluation of wild germplasm collections for traits of value for breeding programs is a common practice in Australia. A recent collection of wild *Cicer* germplasm [1] allowed us to screen this resource for sources of resistance to a range of diseases. Sclerotinia Stem Rot (SSR) of chickpea (*Cicer arietinum*) caused by *Sclerotinia sclerotiorum* is a serious problem in Australia and worldwide [2]. The aim of this study was to identify accessions with resistance to *S. sclerotiorum* for yield improvement in cultivated chickpea. Initially, this research evaluated aggressiveness of nine *S. sclerotiorum* isolates using a domestic and two wild *Cicer* accessions. The study identified two isolates CU8.24 and CU10.12 as “aggressive” and “less aggressive” respectively. The results were similar with a previous study by that demonstrated that these isolates also showed different levels of aggressiveness on canola (*Brassica napus*). Subsequently, the two isolates were used to screen 88 wild *Cicer* accessions (*C. reticulatum* and *C. echinospermum*) and two Australian chickpea varieties (PBA HatTrick and Kyabra) for resistance using a stem inoculation method [3]. A subset of 11 wild *Cicer* accessions were found to have superior levels of resistance to *Sclerotinia* than the two Australian varieties. The subset will be further evaluated following the same inoculation protocol and the accession with high levels of resistance will be crossed with a local variety to develop mapping populations to identify the loci that confer resistance to *Sclerotinia*. This research thus aims to identify novel sources of resistance, which will be a high value resource in chickpea breeding programmes to enhance *S. sclerotiorum* resistance.

Storage requirements of *Puccinia sorghi* urediniospores

**Mrs Aurelie Quade**

*University Of Southern Queensland, Wagga Wagga, Australia*

The causal agent of common rust of maize, *Puccinia sorghi*, is increasing in incidence and severity in Australia. Testing the virulence of isolates against disease resistance genes necessitates adequate parameters for storage and revival of spores. urediniospores of *P. sorghi* can be kept long term when induced into a cold dormancy after being exposed to temperatures of -80°C or below. A heat shock of 40°C is used to revert dormancy in other species of *Puccinia*, and an adequate moisture level prior to induced cold-dormancy is a critical factor for spore longevity. No research had been conducted to determine the drying requirements prior to long term cold storage, nor the effect of heat shock temperature and duration on urediniospore germinability of *P. sorghi* post-cold storage. Therefore, the germination of urediniospores at the time of collection (fresh) was compared with those exposed to different drying times prior to cold storage (-80°C; 7 days) and heat-shock parameters. There was no significant difference between germination of fresh spores and those placed directly in cold storage without drying. However, a germination loss of 88.38% was recorded between dried spores and undried spores. There was no significant difference in germinability between drying time of 24h, 48h and 144h. Heat shock temperatures of 35°C, 40°C and 45°C did not significantly impact on spore germination. However, compared to the germination of spores subjected to a 40°C heat shock, a significant decline in germination was observed at temperature of 50°C and 30°C. Thawing duration was not significant and there was no interaction between thawing duration and temperature on spore germination. This study established that drying urediniospores of *P. sorghi* adversely affects germinability following cold storage and that the optimum temperature for heat shock was between 35°C and 45°C.

The impact of waterlogging tolerance on Phytophthora root rot resistance in chickpea

**Ms Nicole Dron**

*NSW Department of Primary Industries, Tamworth, Australia, South Australian Research and Development Institute, Adelaide, Australia, School of Agriculture, Food and Wine, University of Adelaide, Adelaide, Australia*

A link between Phytophthora root rot (PRR) resistance and waterlogging tolerance has been discovered in soybean (*Glycine max*). Screening chickpea (*Cicer arrietinum*) germplasm for PRR (oomycete: *Phytophthora medicaginis*) resistance in the presence of waterlogging stress could further improve the robustness of resistance. A controlled environment seedling experiment investigated the effect of waterlogging on PRR resistance, ranking material from the Pulse Breeding Australia (PBA) chickpea program. Material included the PRR resistant wild *Cicer* backcross line 04067-81-2-1-1(B) and the moderately resistant variety Yorker, along with selected F₆ derived RIL progeny from a cross between these genotypes. Results showed that the level of waterlogging tolerance in PBA chickpea material is minimal. However, 04067-82-2-1-1(B) and selected RIL progeny had improved waterlogging tolerance; significantly outperforming the moderately resistant variety Yorker in dry root weight following two and six days of waterlogging in the presence of *P. medicaginis*. The experiment supports prior findings in lucerne (*Medicago sativa*) that waterlogging in combination with *P. medicaginis* increases the level of PRR disease. The ability of 04067-82-2-1-1(B) and selected RIL progeny to maintain higher levels of resistance and root mass consistently is an indication that waterlogging tolerance may contribute to novel PRR resistance in chickpea. The RIL population developed from the cross of 04067-82-2-1-1(B) and Yorker will be further investigated to specifically identify and measure traits which could confer waterlogging tolerance, including root length, presence of adventitious roots, cell wall and root exudate composition. The interaction of these traits and susceptibility or resistance to PRR in chickpea will also be investigated.

1. Nguyen et al. 2012 Crop Science 52: 2481-2493
2. Kuan and Erwin 1980 Phytopathology 70: 981-986
Poster Board 42

**Monitoring virulence of the *Pyrenophora teres f. maculata* pathogen population on barley to aid breeding for host plant resistance**

**Ms Jennifer Cutajar\(^1\), Dr Mark McLean\(^1\), Dr Grant Hollaway\(^1\)**

\(^1\)Agriculture Victoria, Horsham, Australia

*Pyrenophora teres f. maculata* (Ptm) is a fungus that causes spot form of net blotch (SFNB) in barley. Spot form of net blotch is a major foliar disease worldwide and has been shown to cause up to 44% grain yield loss and losses to grain quality in Australia. Sowing barley with host plant resistance is an effective way of controlling SFNB and reduces reliance on costly fungicides. *Pyrenophora teres f. maculata* is genetically and pathogenically diverse and has the potential to overcome resistance. This study monitored the current Ptm pathogen population in Australia to identify emerging virulence’s of importance for barley breeders. Thirty-two single spore Ptm isolates from grain growing regions around Australia were isolated and tested with a differential set of 27 barley lines of known reaction. Abundant diversity of virulence’s were observed, but no new virulent isolates were identified when compared with previous years testing. These results indicate that barley breeders and growers can continue to use current resistance sources and varieties for SFNB management.

Poster Board 32

**Mapping of quantitative trait loci for seedling and adult plant resistance to *Blumeria graminis f. sp. tritici* in wheat**

**Rebecca Fox\(^2\), Dr Hossein Golzar\(^1\), Prof Diane Mather\(^2\), Prof Stephen Neate\(^3\), Dr Manisha Shankar\(^1\)**

\(^1\)Department Of Primary Industries And Regional Development, Perth, Australia, \(^2\)University of Adelaide, Glen Osmond, Australia, \(^3\)University of Southern Queensland, Toowoomba, Australia

Powdery mildew (*Pm*) caused by *Blumeria graminis f.sp. tritici* is an important foliar disease of common wheat worldwide. The economic loss occurs sporadically on commercial wheat cultivars in Western Australia. Deployment of quantitative trait loci (QTL) conferring resistant genes in wheat breeding programs is an effective approach in preventing yield loss. The double haploid mapping populations CPI33842/Janz (C/J), Magenta/7HRWSN58 (M/7H), Scout/Mace (S/M), Cobra/ZIN09QNo27 (C/Z), Emu Rock/ZWW09Q149 (E/Z) and Mace/ZWB10Q127 (M/Z) were phenotyped over the years 2016 to 2018. Trials were conducted under a controlled environment using a randomised complete block design in duplicate. A composite of *Pm* isolates that were collected from various locations across WA was used for inoculation. Plants were assessed at seedling and head emergence using percentage leaf area diseased on seedling and adult plant flag leaf. Frequency distribution of individuals within each population for various levels of *Pm* resistance was continuous and a few lines within some populations showed higher levels of resistance than both parents indicating additive gene effects. Genetic and QTL analysis showed loci for *Pm* resistance at adult plant on chromosomes 4B, 6B and 7A in C/J; on 1A, 3A, 4B, 6B, and 7A in M/7H; on 4B, 4D and 5B in S/M; on 3B and 4D in C/Z; on 1B and 4D in E/Z; and on 1A, 1B, 2A, 2B, 2D, 3B, 4A, 6B, 7A and 7D in M/Z populations. Loci for *Pm* seedling resistance were detected on 2B, 3B, 4A and 7A in C/J; on 1A, 4B, 5B, 6B and 7A in M/7H; 1B and 5D in S/M; 3B and 4A in C/Z; on 1A, 1B and 4D in E/Z; and on 1B, 2B, 3B, 4A, 5A, 6A, 6D and 7A in M/Z populations.
Mapping of quantitative trait loci for seedling and adult plant resistance to nodorum blotch in wheat

Rebecca Fox, Dr Hossein Golzar, Prof Diane Mather, Dr Manisha Shankar

1Department Of Primary Industries And Regional Development, Perth, Australia, 2University of Adelaide, Glen Osmond, Australia

Nodorum blotch (syn. septoria nodorum blotch) caused by Parastagonospora nodorum is an important disease of common wheat (Triticum aestivum L.) worldwide. The disease is prevalent in wheat growing regions in Western Australia causing significant yield losses. Resistance to nodorum blotch is complex and quantitatively inherited. This research provides information on additional genes that can be deployed by wheat breeding programs for effective improvement of resistance. Three doubled haploid mapping populations: EGA Blanco/AUS20917 (B/A), Magenta/7HRWSN58 (M/7H) and Cobra/ZIN09QNo27 (C/Z) were phenotyped for resistance to P. nodorum at seedling and adult plant stages over the years 2016 to 2018. Trials were conducted in a controlled environment. Plants were sprayed using an inoculum mixture of P. nodorum isolates, then assessed for percentage leaf area diseased at seedling and adult plant stages. Populations showed continuous distribution and transgressive segregation for both traits. Correlations between assessments made at the same growth stage in different years were moderate (r = 0.6). Correlations between assessments made at seedling and adult stages within the same trial were low to moderate (r = 0.2 to 0.7) indicating independent inheritance of resistance at the two growth stages. The populations were genotyped and resistance loci for leaf resistance at the adult plant were identified on chromosomes 2B, 2D, 3A, 3D, 4A, 4B, 4D, 5D, and 7B in B/A; on 1B, 3B, 4A, 4B, 7A and 7D in M/7H and on 1B and 3A in C/Z. Loci for SNB seedling resistance were detected on 3B, 4D, 5D, 7A and 7B in B/A; on 1B, 2A, 3B, 4B, 5A, and 5B in B/A; and on 1B, 2A, 3B, 4B, 5A, and 5B in M/7H and on 4D and 5B in C/Z.

Field Screening of Resistance to Didymella arachidicola in peanuts (Arachis hypogaea)

Ms Shona Wood, Dr. Graeme Wright, Dr Mark Dieters, Prof Gavin Ash

1University Of Southern Queensland, Toowoomba, Australia, 2Peanut Company of Australia, Kingaroy, Australia, 3University of Queensland, Brisbane, Australia

Peanuts (Arachis hypogaea) are a globally important legume crop grown for human consumption, oil and animal fodder. Biotic stressors, such as the foliar pathogen Didymella arachidicola, are a major constraint to production. D. arachidicola causes premature defoliation and yield reductions of up to 50%. In south-east Queensland, Australia, D. arachidicola epidemics only occur periodically making screening for resistance difficult. A method to effectively screen for D. arachidicola resistance in the field was developed. A recombinant inbred line (RIL) population segregating for D. arachidicola resistance was partially replicated with six check lines spanning the spectrum of resistance/susceptibility over the summer of 2018/19 at the Department of Agriculture and Fisheries, Kingaroy, Queensland, Australia. One end of each plot was inoculated with mycelium suspension of the pathogen in January and February 2019. Plots were irrigated with overhead sprinklers for 20 minutes each evening for the week proceeding inoculation. Disease progress was assessed on a 0-9 scale (0 = no disease, 9 = plant defoliated at the non-inoculated end of each plot). Twenty-three RILs were classified as resistant (<3) and 45 lines were classified as highly susceptible (>7). These results demonstrate that the screening method is useful at distinguishing resistant and susceptible lines and can be implemented in breeding programs for identifying resistance to D. arachidicola.
Screening of a macadamia breeding population for resistance to husk spot

**Miss Jasmine Nunn**, Dr Mobashwer Alam, Assoc Prof Olufemi Akinsanmi, Dr Craig Hardner, Assoc Prof Bruce Topp

Queensland Alliance for Agriculture and Food Innovation, Nambour, Australia, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Australia

Infection of macadamia by the fungal pathogen, *Pseudocercospora macadamiae* results in lesions on the fruit pericarp and accelerated fruit abscission (husk spot disease). If nuts abscise prior to the development of commercial characteristics required by processors, they may be rejected. In Australian farms, losses of up to 33% of saleable yield have been recorded due to the disease. The pathogen overwinters on diseased pericarps that fail to abscise (stick-tights) from where the conidia are dispersed by rain splash to new fruit in the following season. Proficient control is costly and typically involves fungicide spray applications or mechanical removal of stick-tights. This study aimed to identify genotypes resistant to infection by *P. macadamiae* using an Australian macadamia breeding population. Trees included in the field trial consisted of open-pollinated progeny seedlings of diverse commercial cultivars and replicated clones of the parents. Published methods for husk spot were used to inoculate and assess disease incidence of 370 trees, being 281 progeny from 32 families and 24 maternal parent genotypes. Husk spot symptoms were observed on fruits of all inoculated genotypes. Mean disease incidence of families ranged from 69 to 100% and from 75 to 96% for parents. Preliminary findings suggest that all genotypes included in the trial were susceptible to infection, however future trials are planned to expand on these results. For families with the lowest incidence means, increased numbers of progeny will be inoculated and more complex phenotypic data will be collected and compared. Results will be used to determine more specific differences in disease expression in order to guide selection and crossing for future breeding populations.

Comparison of measurement methods for determining *Macrophomina phaseolina* isolate aggressiveness

**Dr Dante Adorada**, Mrs Encarnacion Adorada, Dr Precila Gonzales, Dr Adam Sparks

University Of Southern Queensland, Centre for Crop Health, Toowoomba, Australia

Charcoal rot, caused by the fungus *Macrophomina phaseolina*, is an economically important sorghum stalk disease in the northern grains region of Australia. It is often associated with lodging and yield losses that usually occur during hot and dry conditions during the growing season. There are few management strategies to minimise its effect, and so far, no resistance in sorghum has been reported. An effective charcoal rot resistance screening method requires both an aggressive isolate, representative of the pathogen population, and a repeatable inoculation method. The area under disease progress curve (AUDPC) has been used for identifying disease resistance and can be used in the selection of aggressive plant pathogen isolates for screening purposes. This study aimed to investigate if current methods of inoculation and measurements used to determine *M. phaseolina* isolate aggressiveness being used in Australia are effective. Two trials were conducted using 33 isolates from the northern grains region. The first trial used a single timepoint assessment at 28 days after inoculation (DAI). The second used four timepoints measured weekly ending at 28 DAI to calculate AUDPC using two timepoints and then all four time-points for traditional AUDPC. In both trials, sorghum plants were inoculated by inserting *M. phaseolina* infested toothpicks into the stalk ~5 cm above the soil surface. Stalks were split and lesion length was measured. The single timepoint method was unable to detect any difference in isolate aggressiveness. The two timepoint AUDPC method was not feasible due to some measurements not exceeding zero until the final reading, while the four timepoint AUDPC method showed significant differences at \( p > 0.05 \), but a Tukey’s post-hoc test was unable to determine any groupings. The current method of inoculating the lower stalk generated variable lesion lengths and should be re-evaluated to find methods that can generate more consistent results.
Development and assessment of genetic stocks with four genes for yellow spot resistance

Mrs Dorthe Jorgensen¹, Dr Manisha Shankar¹, Assoc Prof Ken Chalmers², Ms Rebecca Fox², Dr Julian Taylor², Dr Grant Hollaway³, Dr Mark McLean³, Ms Melissa Cook³, Prof Stephen Neate⁴, Prof Diane Mather⁵

¹Department of Primary Industries and Regional Development, South Perth, Australia, ²The University of Adelaide, Glen Osmond, Australia, ³Department of Jobs, Precincts and Regions, Horsham, Australia, ⁴University of Southern Queensland, Toowoomba, Australia

Yellow spot, caused by *Pyrenophora tritici-repentis*, is an important disease of wheat. The objectives of this research were to: 1) identify novel quantitative trait loci for yellow spot resistance and 2) develop fixed lines derived from elite Australian wheat cultivars that carried multiple resistance loci and were suitable for use in resistance breeding programs. Three double haploid mapping populations Calingiri/Wyalkatchem (C/W) (247 lines), IGW2574/Annuello (I/A) (97 lines) and Machete/Magenta (M/M) (220 lines) were screened for yellow spot resistance at various growth stages, environments and national sites. Of these, populations C/W and M/M were fixed for the ToxA-insensitivity allele *tsn1* while population I/A was fixed for the ToxA-sensitivity allele *Tsn1*. Resistance loci were mapped on 1A in I/A, 2A in C/W and 2A and 5A in M/M. These loci were significantly associated (LOD > 3) with reduced yellow spot severity in all experiments. Loci 1A and 2A were combined with *tsn1* by crossing selected lines from the I/A and C/W populations and using single seed descent (SSD) and marker assisted selection (MAS). Sixteen F₅ lines, homozygous at the three yellow spot resistance loci and fixed for the *vrn-1* locus, were developed. One of these lines was crossed with a selected line from the M/M population and the three resistance loci 1A, 2A and 5A were combined with *tsn1* using SSD and MAS. Ten F₅ lines, homozygous at all four yellow spot resistance loci and fixed for the *vrn-1* locus, were developed and screened for yellow spot resistance at various growth stages and environments in Western Australia, Victoria and Queensland. All ten lines expressed high levels of broad-spectrum resistance effective at various growth stages, environments and national sites. These lines are important resources for breeders to use for rapid development of varieties with high levels of resistance.
Management of Carlavirus in beans through varietal tolerance

Ms Visnja Steele¹, Dr Julia Cremer¹, Mrs Kerri Chandra¹, Mr Denis Persley¹
¹DAF, Brisbane, Australia

Queensland is the major producer of green beans (*Phaseolus vulgaris*) in Australia. In 2016, bean crops in one production area in south east Queensland were severely impacted by a virus disease that caused leaf mottling, stunting and discoloured, deformed pods. Crop losses were estimated at several hundred thousand dollars over several months of the autumn production period. The virus responsible was identified as a Carlavirus within the cowpea mild mottle virus clade by serology, RT-PCR and particle morphology. This Carlavirus can be transmitted by the silver leaf whitefly (*Bemisia tabaci*) and has now been detected in most summer and winter bean production areas of Queensland. Effective disease management requires vector monitoring, strategic insecticide applications and growing varieties with virus tolerance during high-risk periods. To provide data for the latter management option, 23 bean varieties were evaluated. Varieties were planted in three metre plots with two replicates per variety in a field trial in south Queensland, 2019. All plants within a one metre section in each replicate, were sap inoculated with an isolate of bean Carlavirus, at the first trifoliate leaf stage. Varieties were classed as tolerant according to the severity of leaf and pod symptoms. A tolerant variety had no or very mild leaf symptoms and few deformed pods at maturity. In contrast, a susceptible variety developed severe leaf and pod symptoms. Tolerance was not reflected in yields of varieties as several varieties with good tolerance as defined above, had yield losses approaching 30% compared with uninoculated plots of the same variety. Virus could be detected in leaf samples by ELISA from varieties ranked as either tolerant or susceptible. Of 23 varieties tested, 10 were ranked as tolerant and 13 as susceptible. Several varieties identified as tolerant in this work will be tested in semi-commercial plantings to further evaluate their role in Carlavirus management.

Incidence of and resistance to *Heterodera avenae* and *H. filipjevi* in cereal production regions of Idaho in the United States

Dr Juliet Marshall¹,², Dr Pooria Ensafi², Dr James Woodhall³, Dr Arash Rashed⁴, Dr Richard Smiley⁵
¹University of Idaho, IDAHO FALLS, United States, ²University of Idaho, Aberdeen, United States, ³University of Idaho, Parma, United States, ⁴University of Idaho, Moscow, United States, ⁵Oregon State University, Pendleton, United States

In the United States, Idaho produces more barley than any other state and in 2018 ranked 5th for wheat production. The high-elevation environment is very conducive to high quality cereal production but also results in limited options for crop rotation and consequently high pressure from soil-borne diseases. *Heterodera avenae*, or cereal cyst nematode (CCN), reaches damaging levels in many areas in eastern and southern Idaho, reducing yields by as much as 30-50% in spring cereals. Screening varieties and breeding for CCN resistance has therefore received a renewed focus, as presently only a few varieties of wheat (hard red spring wheat WB-Rockland with Cre5 resistance) and barley (two-rowed spring barley LCS Odyssey of unknown Rha resistance) are available to Idaho growers that appear to have effective levels of resistance. High incidence and populations of *H. avenae* were documented throughout the region, from northern Snake River Plain to the Magic Valley region. The study also detected *H. filipjevi* in Idaho (first report), but only in one field in the northernmost region of production in the Snake River Plain. Both morphological and DNA sequence analyses were used to accurately determine the identity of the isolate as *H. filipjevi*. Host resistance to *H. avenae* does not confer resistance to *H. filipjevi*; however due to the limited incidence of *H. filipjevi*, recommendations to growers focus on incorporation of Cre and Rha resistance in wheat and barley cultivars, respectively, while emphasizing appropriate pest management practices if resistant varieties are not available.
Visual scores and normalised difference vegetation index can be used to screen wheat cultivars for tolerance to *Pratylenchus thornei*

Mr Neil Robinson\(^1\), Mr Jason Sheedy\(^1\), Ms Bethany Macdonald\(^2\), Dr Kirsty Owen\(^1\), Dr John Thompson\(^1\)

\(^1\)University Of Southern Queensland, Toowoomba, Australia, \(^2\)Queensland Department of Agriculture and Fisheries, Toowoomba, Australia

Wheat breeders select cultivars tolerant to the root-lesion nematode (*Pratylenchus thornei*) by measuring grain yield when grown in fields with damaging populations (>2000kg/soil). Biomass, visual scores and normalised difference vegetation index (NDVI) can be predictive of yield and used to estimate tolerance. Three, two-stage field experiments were grown to test whether NDVI is more predictive of yield, and hence tolerance than visual score. In Stage 1, moderately-resistant and susceptible wheat cultivars were grown to establish plots with either low or high initial population densities (Pi) prior to sowing 36 wheat cultivars in Stage 2. The Pi ranged from 578–9,901 *P. thornei*/kg soil. NDVI values were obtained using a Greenseeker™ at various days after sowing (DAS), and visual scores were recorded twice at mid-stem elongation, by assessing leaf yellowing and inter-row canopy growth, using a 1 (intolerant) to 9 (tolerant) rating scale. Plots were harvested for yield at maturity. At 78 DAS, the genetic correlation matrix for each experiment between NDVI, visual scores and yield showed higher correlation coefficients at high Pi compared to those at low Pi. NDVI and visual scores were highly correlated in all experiments ranging from 0.83–0.95. The correlations of NDVI and yield ranged from 0.32–0.79 (low Pi), and 0.69–0.93 (high Pi), and visual scores and yield ranged from 0.35–0.85 (low Pi) and 0.74–0.99 (high Pi). From these results, it was established that Pi affects both assessment methods, and it is therefore important that experiments are grown on high Pi to best discriminate for tolerance. NDVI has the advantage of being a quantitative measurement that is independent of operator experience. This technology could be adapted for use on unmanned aerial vehicles to increase the efficiency of phenotyping for tolerance to *P. thornei* in wheat cultivars.
Iranian landrace wheats are a valuable source of dual resistance to the root-lesion nematodes *Pratylenchus neglectus* and *P. thornei*

**Mr Jason Sheedy¹**, Valeria Paccapelo², Prof John Thompson¹

¹USQ, Toowoomba, Australia, ²QDAF, Toowoomba, Australia

The root-lesion nematodes (RLN) *Pratylenchus neglectus* (Pn) and *P. thornei* (Pt) reduce the yield of many cereal and pulse crops globally. Wheat is a preferred host with intolerant cultivars losing up to 65% of their grain yield. Mixed RLN populations commonly occur in Australian farming systems, therefore the incorporation of genetic tolerance and resistance to both species into crop cultivars is the most effective management strategy. Currently, Australian wheat cultivars depend on the *Rlnn1* Pn resistance gene that is linked with yellow flour colour; a quality defect that reduces the marketability of resistant cultivars. Iranian landrace wheat (ILW) accessions are a genetically diverse group that offer resistance to several fungal and insect diseases, including 91 accessions that are resistant to Pt. In this study, these Pt-resistant accessions were characterised for Pn resistance in four replicated glasshouse experiments and compared with standard cultivars ranging from resistant to susceptible. Final Pn populations were log-transformed and individual experiments analysed in a linear mixed model framework. A factor analytic model that allows for heterogeneous genetic variance for each experiment, and heterogeneous genetic correlation between environments was used for the simultaneous analysis of all experiments. The genetic correlations between the experiments ranged from 0.54 to 0.77, producing a single factor model that explained 70% of the genetic variation. From this model, seven ILW accessions were identified as resistant to Pn, producing similar final populations to the *Rlnn1*-carrying wheat cultivar Yenda. These accessions originated from the northwestern Iranian provinces of West Azerbaijan, Kermanshah and Hamaden. Given that these seven accessions are resistant to both RLN species, they are a valuable genetic resource for wheat breeders to develop cultivars with dual resistance to better manage mixed RLN field populations and offer the possibility of novel Pn resistance that is not linked with the yellow flour colour defect.

Variations in macadamia varietal susceptibility to *Phytophthora multivora* and *P. cinnamomi*

**Ms Olumide Jeff-Ego¹**, Assoc Prof Bruce Topp¹, Dr Juliane Henderson², Prof André Drenth¹, Assoc Prof Olufemi Akinsanmi³

¹The University of Queensland, Queensland Alliance for Agriculture & Food Innovation, Dutton Park, 4102, Australia, ²Department of Agriculture and Fisheries, Dutton Park, 4102, Australia

Incidence of diseases caused by various *Phytophthora* spp. in macadamia is increasing worldwide. In Australia, a recent study showed more than six species of *Phytophthora* are associated with the macadamia rhizosphere. *P. cinnamomi* and *P. multivora* were isolated from active stem cankers on mature macadamia trees in commercial orchards. There is limited information on the aggressiveness of these *Phytophthora* spp. on macadamia. Therefore, using *in planta* stem wound-inoculation method and a newly developed *in vivo* bioassay, over 300 macadamia genotypes collected from a macadamia arboretum in Queensland, were screened for their disease severity response to *P. cinnamomi* and *P. multivora*. The overall objective of the study was to identify genotypes with acceptable levels of tolerance to *Phytophthora* spp. potentially useful in macadamia varietal improvement program. In terms of the disease severity, there was no significant (*P >0.05*) statistical differences between *P. cinnamomi* and *P. multivora*, however, the mean lesion length and stem diameter growth over the inoculation period in *P. cinnamomi* trees were higher than those inoculated with *P. multivora*. Our results showed macadamia genotypes are partitioned into a spectrum of susceptibility and tolerance to both *Phytophthora* spp.
Field evaluation of Cavendish somaclones and mutants for Fusarium wilt race 4 resistance and agronomic performance in northern Mozambique

Miss Sheryl Bothma

1University Of Stellenbosch, Stellenbosch, South Africa, 2Jacaranda, Namapa, Mozambique, 3Matanuska, Namapa, Mozambique

Banana (Musa spp.) is considered one of the most important agricultural commodities and provides a source of income to millions of people in the tropics and subtropics. Fusarium wilt (Panama disease), caused by the soil-borne fungus Fusarium oxysporum f. sp. cubense (Foc), is considered the most destructive disease of bananas. The only sustainable management option for the disease is to replace Foc-susceptible with Foc-resistant varieties. In this study four ‘Cavendish’ somaclones (GCTCV-106, GCTCV-119, GCTCV-218, GCTCV-247) generated through extended in vitro multiplication, and one gamma-irradiated mutant of the Cavendish cv Dwarf Parfit (AAA) (DPM-25), were screened for Foc TR4 resistance and agronomic performance at two banana farms in northern Mozambique. Nandi, a Cavendish cv Grand Naine selection (AAA) was used as the control for disease progression and agronomic traits. Banana variants were planted according to randomised complete block design with 40 plants in each block and five replicates. Data on disease progression was collected monthly, commencing three months after planting, and agronomic data was collected as required for the crop and first ratoon. Disease susceptibility was determined by calculating the area under the disease progression curve. Of the varieties evaluated, GCTCV-119 was most resistant to Foc TR4. GCTCV-106, -218 and -247 did not differ significantly from each other, but were significantly more resistant than DPM-25 and Nandi, and had higher annual yields with shorter growth cycles than GCTCV-119. DPM-25 had poor resistance combined with the shortest growth cycle and large annual yields. With further improvement of agronomic traits, GCTCV-218 could be used as a replacement for susceptible Cavendish cultivars in Foc TR4-infested fields.
Poster Board 49

**Fusarium pseudograminearum and F. culmorum** in cereal stubble after harvest

**Dr Margaret Evans**
Department Of Primary Industry And Development Institute, Urrbrae, Australia

Crown rot caused by *Fusarium pseudograminearum* and *F. culmorum* results in significant yield losses in winter cereals in Australia. Keeping pathogen levels low is the most effective method for reducing yield losses, but infected cereal residues can host the pathogen for many years. Managing infected residues requires an understanding of where and in what concentrations the pathogen occurs within those residues. This paper presents information on concentrations of *F. pseudograminearum* and *F. culmorum* DNA over time and also vertically in cereal stubble in South Australia. Post-harvest *Fusarium* spp. DNA concentrations (pg/g of sample) in cereal stubble were monitored every two months at two sites and vertically in stems of up to seven cereal types/varieties in three field trials. Whole plant bases were collected, tillers and main stems separated, and roots and soil removed. Stems were cut into lengths, dried at 40 °C, ground and submitted for DNA analysis to the PREDICTA® B service at the South Australian Research and Development Institute. Time-series samples were examined in two sections - up to the second node and above the second node. Vertical distribution of DNA was quantified in three 7 cm sections up to 21 cm. *F. pseudograminearum* DNA concentrations: were, with one exception, higher in main stems than in tillers and leaf sheaths; decreased over time after harvest; were higher in fallen than in standing stubble; were highest at the base of the stubble, decreasing vertically; and, usually, were highest for the most susceptible and lowest for the least susceptible cereal types/varieties. For the one *F. culmorum* data set, DNA concentrations were not as high as for *F. pseudograminearum* but followed similar trends except that triticale stubble had lower than expected concentrations. Implications for management of crown rot infected cereal residues are discussed.

Poster Board 50

**Identification of alternative hosts in the management of Fusarium oxysporum f.sp. cubense Tropical Race 4 in the Northern Territory**

**Dr Shari Mintoff, Ms Samantha Cullen, Ms Nadine Kurz, Dr Tuan Nguyen, Dr Lucy Tran-Nguyen**
Department Of Primary Industry And Resources (NT), Darwin, Australia, Queensland Department of Agriculture and Fisheries, Brisbane, Australia

Panama disease Tropical Race 4 (TR4) poses a significant threat to banana production nationally and worldwide. Panama disease caused by the causal agent *Fusarium oxysporum* fsp. *cubense* (*Foc*), is a soil borne fungus which invades the root system of the host and impedes water flow through the xylem leading to wilting, leaf yellowing and death of the plant. As with most *Fusarium oxysporum* plant pathogens this fungus produces long term survival structures, chlamydospores, which have been reported to survive in the soil for decades in the absence of the host. Although the survival of these spores is not well understood, it is thought that the presence of alternative hosts may aid in its survival, whereby *Foc* colonises the roots of other plant or weed species without causing disease symptoms. Work carried out in the Northern Territory aimed to identify potential alternative hosts of *Foc* TR4 through field surveys and a pot trial. Results from the pot trial and field surveys have identified weed species, common to the Darwin area, which can act as potential alternative hosts, with *Foc* TR4 successfully being isolated from surface sterilised root systems from several weed species. This study demonstrates the importance of understanding the role alternative hosts play in the survival and potential spread of plant pathogens such as *Foc* TR4.
Fungal pathogens threatening quinoa (*Chenopodium quinoa* Willd.) cultivations in central Italy

Dr Giovanni Beccari¹, Dr Mara Quaglia¹, Dr Francesco Tini², Dr Euro Pannacci¹, Assoc Prof Lorenzo Covarelli¹,²

¹Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy, ²Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Bentley, Perth, Australia

In 2017, in a quinoa variety field trial located in Perugia (Umbria, Central Italy), emergence failures of the varieties “Titicaca”, “Riobamba” and “Real” were observed. For these varieties, seeds had been self-produced in the same area the year before. Conversely, “Regalona” seeds, imported from Chile, showed an optimal emergence. However, inside “Regalona” plots, a very high incidence of chlorotic plants was detected. Therefore, investigations both on seed lots of the four varieties and on “Regalona” leaves were carried out. Visual observations on “Titicaca”, “Riobamba” and “Real” seeds showed a higher incidence of browning/necrosis symptoms in comparison to “Regalona” seeds. Symptomatic seeds of the first three varieties showed no *in vitro* germination, while almost all symptomatic “Regalona” seeds were able to germinate. Isolation and molecular identification of fungi associated with seeds showed a high incidence of a member of the *Fusarium incarnatum* species complex (FIESC) in the symptomatic seeds of “Titicaca”, “Riobamba” and “Real”. A FIESC member was also detected in the asymptomatic seeds of these varieties, while no FIESC species was recovered in “Regalona” seeds. On the upper side of “Regalona” leaves, visual observations showed the presence of yellow/chlorotic spots corresponding to an efflorescence erupting from stomata on the adaxial surface consisting of zoosporangioles and zoosporangia. Morphological features and molecular identification carried out on the leaves revealed the presence of *Peronospora variabilis*. This pathogen was also detected in “Regalona” seeds. FIESC and *P. variabilis*, here reported for the first time on *C. quinoa* in Italy, can be important threats to this crop given the lack of registered fungicides on quinoa in Italy. This study also underlines the importance of healthy seed production for successful quinoa cultivations.

Assessing the efficacy of pot bioassays to indicate soil microbial changes related to suppression of banana Fusarium wilt

Dr Hazel Gaza¹, Mr David East¹, Dr Anthony Pattison¹

¹DAF, South Johnstone, Australia

Banana is seriously threatened by a soil borne disease, Fusarium wilt (FW) caused by the pathogen *Fusarium oxysporum* f.sp. *cubense* (Foc). Utilisation of a farm management practice that creates a Foc-suppressive environment in the soil can be an alternative strategy to cope with the disease. A field experiment to determine the effects of nitrogen fertiliser and vegetated ground covers on disease suppression was conducted. The soil from this field experiment was collected at three time points (39, 45 and 51 months after establishment) and was then used to assess the soils ability to suppress FW using a pot bioassay. The soil microbial community dynamics for both field experiment and pot bioassay were assessed using the MicroResp™ system with fifteen different C substrates, and the activity of six different soil enzymes. Redundancy analysis on pot bioassay data revealed a negative correlation between the plant height and the external disease rating. On the other hand, a positive correlation was found between the percentage of rhizome necrosis and the percentage carbon dioxide released using carboxylic acids, citric acid, fumaric acid, malic acid and oxalic acid, as a C substrate was observed. Microbial respiration resulting from the degradation of carboxylic acids appears to be a promising indicator for the soils ability to suppress banana FW. However, only the data for oxalic acid from pot bioassay corresponded with the field experiment measurements determined by linear regression analysis (P=0.024). Likewise, only the enzyme activities of beta-glucosidase (P=0.035), chitinase (P<0.0010) and alpha-glucosidase (P=0.015), out of six enzyme activities monitored, corresponded between the pot bioassay and the field experiment data. These results indicate the complex inter-relationship that exist between plant, soil pathogen and the environment; hence, caution needs to be exercised when extrapolating pot bioassay results to reflect field performance.
Infected strawberry crop debris is a source of inoculum for charcoal rot disease

Mr Apollo Gomez¹, Mr David Oag¹, Dr Dylan MacFarlane², Dr Scott Mattner², Dr Frank Greenhalgh²  
¹Department of Agriculture and Fisheries, Australia, ²Victorian Strawberry Industry Certification Authority, Australia

*Macrophomina phaseolina* is a soil borne fungus and causes the crown rot disease charcoal rot in strawberry. The disease became an issue in strawberry crops across Australia and worldwide following the withdrawal of the soil fumigant, methyl bromide. Alternative fumigants do not effectively eradicate the pathogen from infected crowns buried in soil. The objective of this study was to examine the role of infected strawberry crowns as a source of inoculum. Strawberry plants (cv. ‘Albion’) were artificially inoculated with the pathogen and the resultant infected crowns buried individually in the soil at a depth of 10 cm. Whole crowns and half-crowns were collected at fortnightly intervals during the first four months, and monthly thereafter. Laboratory isolations confirmed a decline in surviving *M. phaseolina* over a 6-month period. However, viable *M. phaseolina* was detected in up to 30% of infected whole crowns and 20% of infected half crowns, six months after burial. The transmission of *M. phaseolina* from infected crowns to new plants was investigated, using strawberry runners (cv. ‘Albion’) grown in sterilised potting mix. One, two or four half-crowns, or one or two whole crowns, artificially infected with *M. phaseolina*, were placed within the root zone in each pot. At eight weeks after planting, 40% of plants exposed to one or more half-crowns had died, compared to around 10% of plants exposed to whole crowns. However by 24 weeks, irrespective of quantity of inoculum, most or all of the plants were dead due to *M. phaseolina*. Control plants remained healthy. Infected strawberry plant debris is a source of *M. phaseolina* inoculum, which can infect new runners and lead to outbreaks of charcoal rot disease in the subsequent crop. Understanding the role of infected crop debris as a source of inoculum will allow practices to be developed to reduce carryover inoculum load.
Pathogenicity and aggressiveness of *Macrophomina phaseolina* isolates to strawberry (*Fragaria x ananassa*)

**Mr Apollo Gomez**, Ms Joanne De Faveri, Dr Yu Pei Tan, Dr Jodi Neal, Dr Mark Herrington, Prof Elizabeth Aitken

1Department of Agriculture and Fisheries, Nambour, Australia, 2Department of Agriculture and Fisheries, Mareeba, Australia, 3Department of Agriculture and Fisheries, Dutton Park, Australia, 4University of Queensland, St Lucia, Australia

The fungal plant pathogen *Macrophomina phaseolina* causes charcoal rot on a range of important crops including strawberry where, in Australia it causes significant industry losses. Consequently, the development of resistant genotypes is a major focus of the Australian Strawberry Breeding Program. To assist the strawberry breeding efforts, it is important to ascertain if isolates of *M. phaseolina* used in pathogenicity tests are host specific to strawberry. For this reason, pathogenicity studies were conducted on strawberry using isolates of *M. phaseolina* obtained from both strawberry and non-strawberry sources. The relative aggressiveness of the isolates was compared, and any potential host specialisation identified. Under glasshouse conditions, thirty isolates of *M. phaseolina* were assessed, including 17 from *Fragaria x ananassa* (strawberry), five from *Sorghum bicolor* (sorghum), and two each from *Vigna radiate* (mung bean), *Arachis hypogaea* (peanut), *Citrullus lanatus* (watermelon) and *Cicer arietanum* (chickpea). Strawberry plants (cv. Albion) were drenched with an inoculum suspension from each isolate. Data (dead/alive) was recorded weekly for fourteen weeks and analyses on survival and isolate comparisons performed. All isolates of *M. phaseolina* assessed, regardless of origin, were able to cause charcoal rot symptoms on strawberry. However, there were significant differences in the level of pathogenicity of the thirty isolates which fell into two different groups based on the aggressiveness towards strawberry. With the exception of one isolate, strawberry isolates were more aggressive to strawberry, as were isolates from sorghum grown as cover-crop in a cultivated strawberry field, compared with isolates from sorghum, chickpea, mungbean, peanut and watermelon. The result suggests isolates that originated from strawberry fields showed host-specialisation. Investigation of host-pathogen interactions is integral to develop further understanding of the diversity between *M. phaseolina* isolates in Australia and assist in the efforts to breed strawberry cultivars resistant to charcoal rot.
Poster Board 27

**Morpho-molecular characterization and control of *Guignardia bidwellii* causing leaf spot of jackfruit**

Mrs Nabila Yesmin¹, Dr Abdul Mannan Akanda¹, Dr Tofazzal Islam¹, Dr Md. Abdullahil Baki Bhuiyan¹
¹Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh

Jackfruit is an important fruit tree in tropical and sub-tropical countries of the world. Jackfruit is the national fruit of Bangladesh. However, its production is hampered by diseases and pests. Among the diseases, leaf spot is one of them. This study was conducted to determine the cause of the disease; to characterize the pathogen based on morphology, cultural and molecular characteristics; to perform the pathogenicity test; and *in-vitro* control of the pathogen. The cause of the leaf spot was identified as *Guignardia bidwellii* (anamorph: *Phyllosticta artocarpi*) using ITS primer. This fungus was pathogenic to jackfruit seedlings and detached mature leaves and therefore satisfied Koch's postulates. There was a negative correlation found between the age of jackfruit and occurrence of leaf spot. Infection process began with the germination of conidia at 3 hours after inoculation (hai) followed by formation of appressoria at 12 hai then direct penetration of germ tube through the epidermis at 2-3 days after inoculation (dai). Colonization of the hyphae occurred through the epidermis and endodermis at 7 dai. Finally, pycnidia were produced at 10 dai. Among the artificial media, significantly highest and lowest mycelial growth were found in potato dextrose agar (PDA) and oatmeal agar (OA), respectively. The highest and lowest mycelial growth were recorded at 25 °C and 15 °C and at pH 6 and 4.5, respectively. Autostin 50 WDG, Tilt 250 SC, Sunfighter 25 SC were completely inhibited the growth of *P. artocarpi*. However, Sunvit 50 WP and Ridomil Gold MZ 68 were least effective against the pathogen. This was the first report of *G. bidwellii* causing leaf spot of jackfruit seedlings in Bangladesh.

Poster Board 30

**Four New *Pythium* Species of Clade B from Rice Paddy Fields**

Prof Reza Mostowfizadeh-Ghalamfarsa¹,², Ms Fatemeh Salmaninezhad¹, Prof Treena Burgess²
¹Shiraz University, Shiraz, Iran, ²Murdoch University, Perth, Australia

Investigation of oomycetes biodiversity in rice paddy fields of Fars Province, Iran, led to the identification of four new *Pythium* species. The identification based on morphological and physiological features was verified with molecular phylogenetic approach using Bayesian inference and maximum likelihood analyses of nuclear (ITS and *Btub*) and mitochondrial (*cox2*) loci. Their unique morphological traits including sexual and asexual structural characteristics (*i.e.* sporangial type; oogonial type and ornamentations; type and the number of antheridia per oogonium; and oospore type), cardinal temperatures, and colony morphology on various media separated them from other known species. Among the four new species, including *Pythium banihashemianum*, *P. izadpanahii*, *P. kamfiruzense* and *P. rosarium*, only *P. izadpanahii* didn't produce asexual structures such as vesicle and zoospores. All species belong to clade B of ITS phylogenetic tree of *Pythium* species. These species were extremely pathogenic on rice seedlings, except for *P. izadpanahii*, isolates. We described the morphological characteristics of the new four species as well as their phylogenetic relationships with other *Pythium* species.
Poster Board 28

**Phytophthora diagnoses and species associated with plant health in Victoria**

Dr Quang Dinh¹, Dr Ramez Aldaoud¹, Dr Srikanthi DeAlwis¹, Soheir Salib¹, Dr Jacky Edwards¹²

¹Agriculture Victoria Research, Department of Jobs, Precincts and Regions, Bundoora, Australia, ²School of Applied Systems Biology, La Trobe University, Bundoora, Australia

In the period 2016-2019, Crop Health Services, Agriculture Victoria, received 407 samples for *Phytophthora* testing. Samples were soil, water, and plants showing symptoms of wilting and decline. Some samples were submitted as part of targeted surveillance for the exotic species *P. ramorum*. Others were commercial samples submitted by growers for soil health and plant pathogen testing, and these support Victoria’s general surveillance program. When detected, clean cultures of *Phytophthora* were identified to species using either ITS and/or Cox I, Cox II, beta-tubulin gene sequence data, and accessioned into the Victoria Plant Pathogen Herbarium (VPRI) for future reference. Sixteen species were recovered from 54 *Phytophthora* positive samples, including water, soil and plant roots. The isolates recovered from soil and roots were associated with root rotting, wilting and decline of horticultural and ornamental plants. No exotic species were detected, but there was a *Phytophthora* sp. nov. isolated from soil associated with a declining olive tree.

Poster Board 29

**Identification of the Colletotrichum spp. causing anthracnose diseases of citrus in Australia**

Miss Weixia Wang¹, Miss Dilani De Silva¹, Miss Azin Moslemi¹, Dr Jacqueline Edwards²³, Prof Paul Taylor¹

¹Faculty Of Veterinary And Agricultural Sciences, The University of Melbourne, Melbourne, Australia, ²Agriculture Victoria, Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia, ³La Trobe University, Bundoora, Australia

*Colletotrichum* spp. are important pathogens of citrus which cause dieback of branches and post-harvest disease. Recent studies in Europe identified eight species of *Colletotrichum* involved in anthracnose of citrus. However, only *C. gloeosporioides* has been recorded in Australia. Thirty-two *Colletotrichum* isolates were collected from infected citrus fruits from Victoria, New South Wales and Queensland, Australia and from State herbaria. *Colletotrichum gloeosporioides, C. siamense, C. fructicola, C. grossum* and a new *Colletotrichum* species *Colletotrichum australianum* sp. nov. were identified using multi-gene phylogenetic analysis based on six genomic loci (ITS, GAPDH, ACT, TUB2, ApMat and GS) and morphological characters. *Colletotrichum australianum* sp. nov. was similar to *C. queenslandicum* isolates that infect *Capsicum annuum*. However, it is proposed that these capsicum and citrus isolates will be renamed as a new species. This was the first report of *C. grossum* isolated from citrus, the first detection of *C. grossum* in Australia, the first detection of *C. fructicola* on citrus outside of China and the first report of *C. siamense* associated with citrus anthracnose disease in Australia. Pathogenicity tests on *Citrus reticulata* imperial mandarin with 11 isolates revealed that *C. siamense* was the most virulent species and *C. gloeosporioides* was least virulent. On *Citrus × sinensis* orange fruit, *C. gloeosporioides* was the most virulent species.
Secondary metabolite clusters distinguish different species of *Teratosphaeria* pathogens

**Dr Janneke Aylward**1,2, Prof Brenda Wingfield1, Prof Francois Roets3, Prof Leanne Dreyer3, Prof Michael Wingfield1

1Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa, 2Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa, 3Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa

The genus *Teratosphaeria* (Dothideomycetes) accommodates numerous species associated with *Eucalyptus* hosts. At least 10 of these have emerged as important pathogens in areas where *Eucalyptus* spp. are grown as non-native trees in forestry plantations. Most *Teratosphaeria* pathogens, including for example *T. destructans* and *T. pseudoeucalypti*, infect leaves causing diseases known collectively as *Teratosphaeria* Leaf Blight (TLB). In contrast, only two species cause necrotic stem lesions known as Teratosphaeria stem canker. In some cases, subtle differences exist between diseases caused by different *Teratosphaeria* species, but pathogen morphology and disease symptoms are ambiguous. Consequently, sequencing barcoding genes provides the only reliable means for their identification. In this study we used 11 genomes from seven *Teratosphaeria* species to (a) investigate secondary metabolite biosynthesis clusters; (b) consider their evolutionary history and (c) explore their potential use for diagnostic assays. Four of these genomes are in public repositories, while the remainder are available from our research group. A maximum likelihood phylogenomic tree was constructed using RAxML and >1000 single-copy orthologous genes identified with BUSCO (Benchmarking Universal Single-Copy Orthologs). Secondary metabolite clusters were characterised with antiSMASH, compared among the genomes with reciprocal BLASTn searches and mapped onto the phylogeny. Clear differences in secondary metabolite content emerged between the clades comprising *Teratosphaeria* leaf and stem pathogens. Four species had species-specific clusters, while a combination of clusters had the potential to identify a further two species in the leaf pathogen clade. Preliminary diagnostic assays, based on PCR amplification of different combinations of these secondary metabolite clusters, have emerged from this study and now require validation and further exploration.

Re-inventory of *Fusarium* species in the Victorian Plant Pathology Herbarium (VPRI)

**Dr Quang Dinh**1, Dr Matthew Laurence2, Dr Edward Liew2, Dr Brett Summerell2, Dr Jacky Edwards1,3

1Agriculture Victoria Research, Department of Jobs, Precincts and Regions, Bundoora, Australia, 2Royal Botanic Gardens and Domain Trust, Sydney, Australia, 3School of Applied Systems Biology, La Trobe University, Bundoora, Australia

In Victoria, *Fusarium* species cause an array of diseases including crown rot of wheat, stalk and cob rot of maize and sorghum and Fusarium wilts of many fruit and vegetable crops. Victorian grain and forest industries are potentially endangered by several species of *Fusarium*, especially the exotics such as *F. circinatum* causing pitch canker of pine and *F. virguliforme* causing soybean sudden death syndrome. The Victorian Plant Pathology Herbarium (VPRI) has 1094 records of *Fusarium* recovered from various plant-related materials over more than 100 years. Recent taxonomic revision of the genus in light of molecular information has demonstrated that species identification based purely on morphological characters is no longer valid, with the implication that the identity of *Fusarium* species held in VPRI could be outdated and need to be re-examined. Using TEF1-alpha and RPB1 gene sequence data, 87 *Fusarium* isolates selected from VPRI were re-examined. 42 isolates have been named and/or renamed. There were 19 new records, including new host records and some unknown *Fusarium* sp. nov. from ornamental plants. This study emphasises the importance of taxonomic research to maintain the currency of our herbaria, which provide specimen-based records of the plant pathogens present in Australia.
Phylogeny of *Fusarium* associated with *Euwallacea*-vectored branch dieback of avocado and other woody tree hosts in Australia

**Dr Louisamarie Parkinson¹, Ms Kaylene Bransgrove¹, Assoc Prof Elizabeth Dann³, Assoc Prof Andrew Geering¹**

¹Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Brisbane, Australia

Fusarium dieback of avocado (*Persea americana*) trees in Australia is vectored by branch-boring ambrosia beetles in the *Euwallacea fornicatus* cryptic species complex, viz. the Tea Shot Hole Borer (TSHB). Ambrosia beetles carry symbiotic fungi in mycangial sacs in their mouthparts as an obligate food source, and the fungus is deposited on xylem gallery walls for the larvae and beetles to feed on. The fungal infection results in branch dieback, leaf wilt and symptoms of frass and persitol at the pin-hole entry sites in affected branches. Dieback associated with TSHB was identified in avocado orchards on the Atherton Tableland in Far North Queensland, and in suburban tuckeroo (*Cupaniopsis anacardioides*) in South East Queensland. This study aims to investigate the phylogenetic diversity and pathogenicity of *Fusarium* species associated with branch dieback of avocado and other woody tree hosts in Australia. A collection of over 100 fungal isolates of *Fusarium* spp. were obtained from symptomatic heartwood of borer-beetle affected branches of avocado, tuckeroo, macadamia (*Macadamia integrifolia*), wattle (*Acacia* sp.) and mango (*Mangifera indica*), and from TSHB specimens in Queensland. Fungal isolates were identified to genus-level with PCR and sequencing. Other fungal genera were also isolated, which mostly consisted of *Lasiodiplodia*, *Bionectria* and *Phomopsis*. A multigene phylogenetic analysis of the ITS, TEF1–α and RPB2 loci was performed on the *Fusarium* isolates. Two putative novel *Fusarium* sp. were identified in the Ambrosia Fusarium Clade (AFC) and will be described. These species were found to be unique to Australia, with one species exclusively found in avocado, while the other *Fusarium* sp. nov. shares hosts in avocado and tuckeroo. Further work to identify the full *Fusarium* spp. collection to species-level will be completed and pathogenicity testing of selected fungal isolates will be carried out on avocado and alternate hosts in future experiments.
Towards sub-species resolution profiling of plant and soil microbiomes

**Dr Paul Dennis**, Mr Henry Birt, Dr Edward Liew, Dr Brett Summerell, Dr Alistair McTaggart, Prof Roger Shivas, Dr Tony Pattison

1UQ, Brisbane, Australia, 2Department of Agriculture and Fisheries, South Johnstone, Australia, 3The Royal Botanic Garden Sydney, Sydney, Australia

Sequence-based studies to characterise microbial communities remain dominated by platforms that offer ultra-high output of short (100-250 bp), high-quality reads. This is largely because platforms capable of generating much longer, and potentially more informative reads (>10 kb), are prone to high error rates. Recent advances in library preparation and bioinformatics, both internationally and in our lab, make it possible to generate long-high-quality reads that can be used to profile microbial diversity at sub-species-resolution, and enhance the recovery of genomes from metagenomic datasets. Here, we present results from our work with the microbiomes of banana plants and soils and their interactions with *Fusarium* spp. This novel technology has the potential to revolutionise pathogen diagnostics and our understanding of pathogen-microbiome ecology.

Suppression of crown and root rots in wheat by endophytic *Trichoderma gamsii*

**Dr Belinda Stummer**, Ms Mahshid Roohani Dezfooli, Ms Bhanu Nidumolu, Dr Xinjian Zhang, **Dr Paul Harvey**

1CSIRO Agriculture & Food, Glen Osmond, Australia, 2CSIRO Agriculture & Food, North Ryde, Australia, 3Shandong Academy of Sciences, Jinan, China

Strategies to effectively manage cereal crown and root rot disease complexes are limited. The inoculant *Trichoderma gamsii* ASMH is an endophytic colonist of wheat root and crown tissues and can suppress Fusarium crown and Pythium and Rhizoctonia root rots. Wheat inoculant trials were run for 2 consecutive years on a site expressing Fusarium crown and Pythium root rots. In each year soil and rhizosphere samples were taken at pre-inoculation (T0), emergence (T1), tillering (T2), harvest (T3) and from post-harvest standing stubble (T4). This research delivered agri-ecological analyses of inoculant-pathogen rhizosphere dynamics, ASMH disease suppressive efficacies, rhizosphere microbiome impacts and crop performance. In both years ASMH actively colonised (P<0.001) wheat rhizosphere soil, crown and root tissues and persisted throughout the growing season (T1-T3). The inoculant did not persist post-harvest (T4) in year 1 but did persist after harvest in year 2 (T3-T4). Endophytic ASMH was recovered in high frequency from crown and root tissues and decreased (P<0.001) isolation of plant pathogenic *Pythium irregulare* (root rot), *F. pseudograminearum* (crown rot), *Diaportha* spp. (stem canker) and *Eutiarosporella* spp. (white grain disorder) over both growing seasons. Inoculation also resulted in a 5-fold decrease (P=0.015) in *F. pseudograminearum* biomass in crown and root tissues at harvest (T4). Rhizosphere microbiome analyses indicated no significant inoculant impacts in year 1. However, inoculation in year 2 caused differentiation (P<0.002) of fungal microbiomes at tillering. Overall, ASMH significantly increased crop establishment (P<0.001), biomass at tillering (P=0.004) and whilst not statistically significant, increased harvest biomass and grain yields by 12 % and 16 %, respectively. *In vitro* pathogen antagonism assays showed that ASMH significantly (P<0.002) reduced *Fusarium* and *Rhizoctonia* biomass and killed *Pythium*. Metabolites produced by the strain provide a potential mechanism to enhance rhizosphere competition, inoculant abundance and disease suppression in the field.
Effect of copper on the leaf epiphytic microbiome of kiwifruit

Dr Toan Phuoc Hong1, Ms Janet Yu1, Dr Alfonso Eposito2, Ms Magan Schipper1, Ms Deidre Cornish1, Dr Dan Jones3, Dr Joel Vanneste1

1The New Zealand Institute for Plant and Food Research Limited, Ruakura Research Centre, Hamilton, New Zealand, 2Department of Cellular, Computational and Integrative Biology - CIBIO University of Trento, via Sommarive 9, 38123, Trento, Italy, 3The New Zealand Institute for Plant and Food Research Limited, Mt Albert Research Centre, Mt Albert, Auckland, New Zealand

Copper-based products are the main bactericide for control of the bacterial pathogen Pseudomonas syringae pv. actinidiae (Psa) on kiwifruit. However, the effect of copper use on Psa populations and epiphytic bacteria sharing the same ecological niche is not known. To answer this question, we examined the kiwifruit epiphytic bacterial microbiome before and after copper application using 16S rDNA metabarcoding. The experiment was carried out in the Plant and Food Research orchard at Ruakura, Hamilton, New Zealand on Actinidia chinensis var. deliciosa ‘Hayward’ and Actinidia chinensis var. chinensis ‘Zesy002’, also known as Gold3. Leaves were sampled before copper application and at 1, 3, 7 and 14 days after application of Kocide at summer rate (70 g/100 L). For each time point, leaves were taken from eight different vines of each cultivar. The experiment was carried out in February 2017 (summer) and repeated in November 2017 (spring). Leaf samples were washed with solution containing cetyltrimethylammonium bromide (CTAB), the DNA was extracted using the CTAB-based phenol/chloroform protocol. The V5-V7 region of 16S rDNA was amplified using the primers 799F and 1193R. Amplicon libraries were sequenced with Illumina Mi-Seq. Sequence data were analysed with the Qime2 workflow. We revealed that the bacterial epiphytic microbiome on kiwifruit leaf is strongly associated with cultivars and seasons. Copper was found to reduce the operational taxonomic units (OTUs) richness of the bacterial epiphytic microbiome in summer for both cultivars 1 and 3 days after copper spraying. Conversely, copper had little effect on the kiwifruit bacterial epiphytic microbiome in spring, particularly in the ‘Hayward’ cultivar. This could be because of the heavy dominance of the Pseudomonadaceae family or the regular use of copper in the orchard selecting for bacterial strains that are not affected by copper.

Seed microbiomes of pasture species and their role in plant protection and plant growth

Dr Ross Mann1, Dr Jatinder Kaur1, Dr Dilani De Silva1, Dr Piyumi Ekanayake1, Mr Desmond Auer1, Miss Holly Hone1, Mr Tongda Li1,2, Mr Ian Tannenbaum1,2, Dr Tim Sawbridge1,2, Prof German Spangenberg1,2

1Agriculture Victoria, AgriBio, Centre for AgriBioscience, Coburg, Australia, 2School of Applied Systems Biology, La Trobe University, Bundoora, Australia

Plant seeds harbour microbes that assist in critical stages of a plant’s life, including germination and early seedling development. The seed microbiome is thought to play an integral role in the protection and growth of the host plant during these life stages. In the case of pasture grasses the seed transmitted, mutualistic fungal endophyte Epichloë spp. assists the host in protection against biotic and abiotic stress. However, the broader seed microbiome of pasture species is largely unknown. The seed microbiome of tall fescue was profiled across global accessions to establish a core seed microbiome, while the seed microbiome of perennial ryegrass was assessed to determine the effect of the resident fungal endophyte on the seed microbiome and the seed transmissibility of the seed microbiome. The microbiome of perennial ryegrass was isolated and strains were assessed via in vitro, in planta and in silico analyses to predict their function. Key isolates were shown to possess a range of putative functions including bioprotection against common Poaceae pathogens and biostimulation via nitrogen and phosphorous acquisition. This study sheds new light on pasture grass microbiomes and has identified some bacteria of potential commercial significance due to their seed transmissibility and likely importance in seed germination, early seedling vigour, and protection of the host against pests and disease.
Community structure and functional potential of endophytes of the New Zealand native medicinal plant *Pseudowintera colorata* (horopito)

**Dr Neeraj Purushotham**, 1,2 Dr Eirian Jones2, Dr Jana Monk3, Dr Hayley Ridgway2,4

1University Of Southern Queensland, Toowoomba, Australia, 2Lincoln University, Christchurch, New Zealand, 3AsureQuality, Christchurch, New Zealand, 4The New Zealand Institute of Plant & Food Research Ltd, Lincoln, New Zealand

Medicinal plants harbour unique endophytes with key roles in maintaining plant health, tolerating biotic and abiotic stresses and producing secondary metabolites. However, in New Zealand there is a significant knowledge gap of endophytes with functional roles in native medicinal plants, with no studies on the medicinal plant and primitive angiosperm *Pseudowintera colorata*. Denaturing gradient gel electrophoresis (DGGE) of plants from ten sites revealed tissue type as the main factor influencing the endophytic communities in *P. colorata* (PERMANOVA, *P*=0.001). For a subset of three sites, the interaction of plant location with maturity influenced the Actinobacteria, Betaproteobacteria and Gammaproteobacteria communities (PERMANOVA, *P*=0.010, *P*=0.005 and *P*=0.030, respectively). Further analysis by Illumina MiSeq confirmed that tissue type affected the bacterial communities with Gammaproteobacteria being the most abundant class (89.1%) followed by Alphaproteobacteria (10%). In addition, two OTUs belonging to *Pseudomonas* were identified as members of *P. colorata* “core endomicrobiome”. To complement the molecular studies, a total of 405 endophytic bacteria, 200 endophytic fungi and nine endophytic Actinobacteria were recovered from *P. colorata* plants. The majority of endophytic bacteria were isolated from the stem (58.1%, *n*=235), followed by roots (32.1%, *n*=130) and leaves (9.8%, *n*=40). Eleven endophytic bacteria showed strong antagonism towards phytopathogenic fungi *Neofusicoccum luteum*, *N. parvum*, *Neonectria ditissima*, *Ilyonectria liriodendri* and four endophytic bacteria were active against bacterial phytopathogens *Pectobacterium atrosepticum* and *P. brasiliensis*. This is the first study to identify endophytic Actinobacteria communities in *P. colorata* and to examine the functional traits of cultured representatives. The reintroduction of a *Bacillus* sp. TP1LA1B and *Nocardia* sp. TP1BA1B as a soil drench increased shoot height, shoot and root biomass and the number of internodes of seedlings (*P*=0.016, *P*<0.001, *P*=0.007 and *P*<0.001, respectively). This study indicated that *P. colorata* harbours unique endophytes which have a key role in the growth of the plant.
The temporally and spatially dynamic endomicrobiome of New Zealand myrtaceous species is diverse and contains members that inhibit germination of urediniospores

Dr Hayley Ridgway1, Dr Fernanda Jacobo-Nieto1, Dr Soonie Chng1, Dr Julia Soewarto2, Mrs Monika Joshi1, Ms Kirsty Boyd-Wilson1, Dr Beccy Ganley3

1The New Zealand Institute for Plant and Food Research Ltd, Lincoln, New Zealand, 2Scion, Rotorua, New Zealand, 3The New Zealand Institute for Plant and Food Research Ltd, Te Puke, New Zealand

Plant resistance to disease is modulated by the microbial endophytes, collectively termed the endomicrobiome, resident within their tissues. Research has demonstrated that members of the endomicrobiome can help plants defend themselves against pathogens. For New Zealand Myrtaceae it is unknown whether microbial community-related fitness phenotypes influence infection by Austropuccinia psidii (myrtle rust). In other countries it has been shown that new season’s growth is less resistant to infection by A. psidii. Thus, the hypothesis tested in this work was that endomicrobiome would differ between last and this season’s growth (stem and leaf) and that endophytes found in last season’s growth would be antagonistic towards rust spores. The research focused on the foliar endomicrobiome of Leptospermum scoparium (mānuka) and Metrosideros excelsa (pōhutukawa). A live collection of 815 endophytes was obtained, of which 71% were fungi and 29% were bacteria. Of these, 56% and 44% were from L. scoparium and M. excelsa, respectively. This work was complemented by amplicon sequencing to characterise the complete endomicrobiome. The results from both approaches showed that host, tissue type and age were major drivers of the endophyte community structure. The community in new foliage was dynamic, changing within a season. An in vitro assay was developed to assess the ability of bacterial endophytes to inhibit the germination of rust spores in comparison to a fungicide control. Using poplar rust (Melampsora larici-populina) the results showed that the endomicrobiome of L. scoparium and M. excelsa contained bacteria that were antagonistic towards germination of urediniospores, to an equivalent degree as the fungicide control. Future work will validate the findings on A. psidii urediniospores. Collectively, the findings show the dynamic nature of the microbiome and support the possibility that there is a role for the microbial community in tolerance to infection by rust pathogens.
Monitoring shifts in the pathogen population of *Ascochyta lentis* in southern Australia

**Ms Sara Blake**1,2, Ms Michelle Russ1, Ms Jade Rose1, Dr Liz Farquharson1,2, Dr Jenny Davidson1,2

1South Australian Research & Development Institute (SARDI), Urrbrae, Australia, 2The University of Adelaide, Urrbrae, Australia

*Ascochyta lentis*, the causal agent of ascochyta blight of lentil, is a necrotrophic heterothallic polycyclic fungal pathogen with a broad and variable range of aggressiveness in the pathogen population. Recently in SA, intensive cropping of cv PBA Hurricane XT has raised concerns of resistance breakdown. Annual monitoring has identified a shift in the pathogen population towards increasingly aggressive isolates on resistant cultivars and elite breeding lines. From 2015 to 2018, isolates were collected from commercial crops and field trials in SA and VIC. Forty single spore isolates plus a check isolate were inoculated on a differential lentil host set in controlled environment conditions. Percent leaf area of disease was assessed and split plot ANOVA produced a significant host by isolate interaction each year (p<0.001). Isolate reactions on each lentil host were also categorically grouped according to severity using Least Significant Difference. Aggressiveness of isolates on individual cultivars varied over time. In 2015, 11 of 40 isolates infected PBA Hurricane XT at low severity only compared to 27 isolates in 2018 ranging from low to moderate severity. PBA Hurricane XT was rated moderately resistant when commercially released in 2013 but downgraded to moderately resistant-moderately susceptible for SA in late 2018 after disease observations. Conversely, cv Nipper, no longer popularly sown, was infected at a low to moderate severity by 18 of 40 isolates collected in 2018 compared to 40 of 40 isolates in 2015 with a low to high severity. This shift in the pathogen population has occurred as isolates that are capable of infecting resistant lentil material like PBA Hurricane XT are selected for over time. Anecdotally, cultivar rotation appeared to have a strong influence on the pathogen population. Continued monitoring of changes in the *A. lentis* pathogen population remains important for the lentil industry.

Dashboards – a novel method for visual interrogation of large data sets

**Dr Margaret Evans**1, Dr Jennifer Davidson1, Dr Rohan Kimber1, Prof Mary Burrows2, Ms Danielle Allen3,1, Mr Jamus Stonor1

1South Australian Research And Development Institute, Urrbrae, Australia, 2Montana State University, 207 Plant BioScience Building (PBB), Bozeman, USA, 3APAL Australian Precision Ag, Unit 3/11 Ridley St, Hindmarsh, Australia

Interpretation and analysis of data begins with visual inspection. For large data sets which track multiple diseases in relation to weather over multiple years at multiple sites, visual inspection is not a simple task. This paper presents a novel option for visual inspection of large data sets, using spore trapping and weather data from South Australia. Spores were collected for up to 11 fungal pathogens at 8 sites over 5 years using static Burkard volumetric spore traps which collect spores from air actively pulled over an adhesive tape (impact sampling) on a rotating drum. Trapping was undertaken in the period March to December. Adhesive tapes were changed monthly, stored and processed at the end of the trapping period. Sections of tape from selected time zones were cut and submitted for DNA analysis to the PREDICTA® B service at the South Australian Research and Development Institute. Weather data were collected from automated weather stations or from BOM data where weather stations were not co-located with spore traps. Data were entered into Excel spreadsheets and graphed however, Excel graphics did not allow adequate inspection of data. An alternative, interactive graphic option (flexdashboard) managed by the statistical package R and commonly used to look at weather data was then considered. Data were entered into R and programming was undertaken which presented information in an interactive graphic format (the flexdashboard). The flexdashboard allowed easy visual inspection of viewer-specified combinations of information for selected pathogen(s) and weather parameters. Robust discussions ensued when examining these graphs with colleagues. Interpretation of the data were discussed, statistical analysis options considered and possibilities for further research and extension were identified. Statistical analysis will be facilitated as data are already entered into R. Automation of data entry into R is being explored, as is inclusion of mobile and smart trap data.
Distribution of viruses infecting shallot in Indonesia and the potential of true shallot seed as virus-free plant material

Prof Sri Hidayat¹, Ms Heri Harti¹, Ms Ana Septiani Saputri¹
¹IPB University, Bogor, Indonesia

Shallot is one of the most important vegetable crops in Indonesia. The use of true shallot seed (TSS) as starting material is recommended to improve productivity of shallot in Indonesia. Research was conducted to detect major viruses and fungi from initial planting materials (TSS and seed bulb), and harvested bulbs; and to compare the growth and yield of TSS and seed bulb crops. Virus and fungi detection was based on serological assay and morphology observation, respectively. Field experiment involved growing TSS and seed bulb crop of four shallot cultivars, i.e. ‘Bima’, ‘Bauji’, ‘Thailand’, and ‘Tuk-Tuk’. The results showed that infection of viruses on TSS was not detected, meanwhile high incidence of Onion yellow dwarf virus, Shallot latent virus, Garlic common latent virus, and Shallot yellow stripe virus, was detected from seed bulb. *Fusarium solani* was successfully isolated from both TSS and seed bulb; whereas *F.oxysporum* was only found from seed bulb. Disease incidence in the field caused by virus infection was lower in the TSS crops (up to 5.6%) than those in seed bulb crops (up to 93.6%); likewise with basal rot disease caused by *F.oxysporum* infection. The average of virus and fungi infection on bulbs harvested from seed bulb crops was also higher than those from TSS crops. Over all the growth of TSS crops is better than seed bulb crops; this corresponds also to the better yield of TSS crops (11.1 to 12.3% tons/ha) than seed bulb crops (5.2 to 6.2 tons/ha).

Avocado sunblotch viroid: present status and future prospects of the pathogen in South Africa

Dr Anna Jooste¹, Miss Zanele Zwane¹,²
¹ARC-Tropical And Subtropical Crops, Mbombela, South Africa, ²University of KwaZulu-Natal (UKZN), Pietermaritzburg, South Africa

Avocado sunblotch disease (ASBD), caused by *Avocado sunblotch viroid* (ASBVd), is an important disease of avocado worldwide that affects yield and quality. Typical symptoms are found on leaves, fruit and bark of the tree, however, some trees do not display any visible symptoms and these are referred to as symptomless carrier trees. The most important control measure for ASBD is careful selection of pathogen-free bud wood and seeds that are used for propagation, which is achieved through indexing. The distribution of ASBVd within a single plant was studied and an uneven distribution of ASBVd between branches and in the fruits was detected. This finding has huge implications for optimising detection methods and sampling strategies for avocado tree indexing. For example, a tree displaying no symptoms on the leaves or on the fruit tested positive in all branches and in all symptomless fruit. These symptomless carrier trees are currently the main concern for the avocado industry in South Africa and precise sampling strategies and detection systems need to be in place to reduce the spread of ASBVd. A summary of the indexing status of nurseries and commercial growers will be presented and the strategies towards an ASBVd-free avocado industry in South Africa will be discussed. The ultimate aim is to mobilise all role players in the South African avocado industry to ensure an ASBVd-free industry that will lead to optimal production.
The incidence and genetic diversity of viruses infecting Prunus species in Australia

Dr Wycliff Kinoti1, Dr Alison Dann2, Ms Narelle Nancarrow2, Dr Brendan Rodoni2, Dr Fiona Constable1
1Agriculture Victoria, Bundoora, Australia, 2Department of Primary Industries, Parks, Water and Environment, Hobart, Australia

The biosecurity of the Australian summerfruit and almond industries is maintained at the border by the Department of Agriculture in post entry quarantine (PEQ) facilities. Prunus germplasm imported into Australia requires a minimum of 18 months post entry quarantine testing using a range of diagnostic techniques for the detection of diseases and pathogens of quarantine significance. Post-border, the biosecurity of these industries is maintained through certification schemes that supply high-health planting material throughout Australia which was tested only for apple chlorotic leafspot virus, apple mosaic virus, prune dwarf virus and prunus necrotic ringspot virus, which are endemic. However, there are now 55 virus species and three viroids that have been reported to infect almonds, stone fruit and/or ornamental Prunus species overseas. The incidence and genetic diversity of these viruses and viroids in Australian Prunus species was unknown. Consequently, a national survey of summerfruit and almond growing regions of Australia was conducted. The survey was used to update the disease status for viruses and viroids of almond and summerfruit industries in Australia and to update the list of viruses and viroids requiring testing during PEQ. Metagenomic next generation sequencing was used to characterise the genomes of several viruses that had not been found previously in Australia as well as viruses that were known to occur. The genomes of Australian isolates of Prunus infecting viruses were compared to other isolates occurring overseas. In undertaking the survey, the molecular diagnostic assays used for detection of these viruses were also validated. The results of the survey will be discussed.

Cotton diseases: the ‘big four’ in New South Wales

Dr Duy Le1, Ms Aphrika Gregson1, Mr Rodney Jackson1, Dr Linda Smith2
1New South Wales Department Of Primary Industries, Narrabri, Australia, 2Queensland Department of Agriculture and Fisheries, Brisbane, Australia

Cotton (Gossypium hirsutum), a billion-dollar crop is mainly grown under irrigated conditions in regional areas of New South Wales (NSW) and Queensland. Diseases are of major constraints to production in both states. In NSW, the ‘big four’ diseases of concern are regional dependent. Black root rot (BRR) was a prevalent seedling disease across NSW. The average disease incidence varied from 15 to 90% in the last two survey seasons. However, BRR was more severe in the south, where lower temperatures were recorded during seedling establishment. The BRR pathogen, Berkeleyomyces rouxiae (syn. Thielaviopsis basicola) was proposed to be spread from northern NSW, where it was first detected, based on uniform sequences of ITS, TEF1 and RPB2 loci. Soil drench with myclobutanil (3ml/l) reduced BRR severity slightly in a pot trial. Alternaria leaf spot (ALS) has long been considered minor, but ALS outbreaks were recorded on cotton seedlings in the south in 2017/18 season. The ALS also remained prevalent on mature crops, especially before crop defoliation in the last two seasons. The main pathogen, Alternaria alternata was re-identified. Of 10 fungicides tested, all showed strong suppression of A. alternata in vitro, except for azoxystrobin which suppressed growth of A. alternata as little as 10%. Fusarium wilt associated with Fusarium oxysporum f. sp. vasinfectum (Fov) and Verticillium wilt (Verticillium dahliae) were mainly detected in northern NSW, where disease incidence was recorded up to 70% and 90%, respectively. F. oxyporum was also prevalent on seedlings exhibited Rhizoctonia-like rot; and the pathogen was well-clustered with both Australian Fov and non-Australian races based on TEF1 sequences. Of the V. dahliae population recovered in 2017/18 and 2018/19 seasons, 17.4% and 34% were molecularly characterised as defoliating pathotype, respectively. Continued efforts in surveillance of the ‘big four’ will provide insights into their etiology and epidemiology.
Towards an understanding of virulence mechanisms in the necrotrophic fungal phytopathogen *Neonectria ditissima*, the causal agent of European canker of apple

Ms Liz Flórez1,2, Dr Saadia Arshed1, Mr Brent Fisher3, Mr Paul Sutherland1, Dr Mark Wohlers1, Ms Brogan McGreal1, Dr Matthew Templeton1,2, Dr Reiny Scheper1, Dr Joanna Bowen4

1The New Zealand Institute for Plant and Food Research Limited, Auckland, New Zealand, 2The University of Auckland, Auckland, New Zealand, 3The New Zealand Institute for Plant and Food Research Limited, Havelock North, New Zealand

The necrotrophic fungal phytopathogen *Neonectria ditissima* causes canker disease in many hosts, although the disease in apple (European canker) can be severe and therefore economically important. European canker is currently controlled by pruning and fungicides, thus alternative, more sustainable, and less labour-intensive solutions are desirable. However, little is known about the molecular basis of *N. ditissima* virulence to aid formulation of novel control strategies. Therefore, expression profiles of four candidate virulence genes were measured during an infection time-course using reverse transcriptase real-time PCR (RT-qPCR): *g8150*, predicted to encode a protein kinase, and *g4542, g5809* and *g7123* predicted to encode small, secreted proteins, i.e. similar to fungal effectors (microbial-derived molecules that enhance virulence). Prior to RT-qPCR, eight housekeeping genes were assessed for suitability as reference genes; *actin* and *gapDH* were selected. The expression of all four candidate virulence/effectors genes was upregulated in planta compared with in vitro, suggesting a role in the *N. ditissima*-apple interaction. The expression of *g8150* was the most highly upregulated, peaking at 8 weeks post-inoculation (wpi), whereas the expression of the three candidate effector genes peaked 5 to 6 wpi, prior to symptom expression. Whilst the precise role of these effectors remains to be elucidated, their identification raises the possibility that an inverse gene-for-gene interaction may contribute to *N. ditissima* infection success. To enable functional characterisation of *N. ditissima* candidate virulence genes, a protoplast-mediated transformation protocol was developed and used to trial gene knockout mutation in *N. ditissima* for the first time, targeting *g8150* in a virulent isolate. Use of a homologous recombination knockout vector with ~600bp flanks generated a single *g8150* knockout transformant. This transformant caused significantly smaller lesions in apple fruit and fewer, less severe symptoms in detached apple twigs than the wild-type and an ectopic transformant, suggesting a role in virulence for *g8150*.

Isolation and characterization of extracellular vesicles from *Fusarium graminearum* and *Fusarium oxysporum* f. sp. *vasinfectum*

Mr Donovan Garcia Ceron1, Dr Mark Bleackley1, Prof Marilyn Anderson1

1La Trobe University, Melbourne, Australia

Members of the genus *Fusarium* are severe human, animal and plant pathogens. *F. graminearum* (Fgr) and *F. oxysporum* f. sp. *vasinfectum* (Fov) are pathogens of wheat and cotton, respectively, with worldwide occurrences that cause important economic losses. Extracellular vesicles are particles enclosed by a lipid membrane that transport macromolecules such as protein, nucleic acids and polysaccharides. These particles facilitate intercellular communication between fungi and in many cases, EVs elicit immune responses in the host. EVs are increasingly studied as a component of the host-pathogen interaction in humans and animals, and now also in fungal plant pathogens. We have isolated EVs from Fgr and Fov, with a purification procedure that uses size exclusion chromatography as opposed to the standard ultracentrifugation methods. EVs from Fov and Fgr were between 100-200 nm, as determined by nanoparticle tracking analysis, and had similar morphologies to vesicles from other fungal organisms as observed by transmission electron microscopy. To determine if stress and nutrient availability have an effect on EV production, Fov was grown in different culture media. Results show that there are significant changes in vesicle size and abundance across the tested media. Currently, protein composition of EVs is being analyzed by mass spectrometry to assess if cargo sorting differs between growth media. This is the first report of the production of EVs from fungal pathogens of agricultural importance, and results will lead to a better understanding of the roles for EVs in disease progression caused by fungi.
Host susceptibility factor, MLO, supports fungal symbiosis and pathogenesis

Ms Catherine Jacott\textsuperscript{1}, Dr Myriam Charpentier\textsuperscript{2}, Dr Jeremy Murray\textsuperscript{2}, Dr Christopher Ridout\textsuperscript{1}
\textsuperscript{1}John Innes Centre, Norwich, United Kingdom, \textsuperscript{2}Chinese Academy of Sciences, Shanghai, China

Understanding how plants balance the ability to both resist pathogens and accommodate symbionts has direct implications for fundamental plant biology and optimal use of crop plants in agriculture. Host susceptibility genes enable colonization of plants by harmful pathogens. \textit{Mildew resistance locus o} (\textit{MLO}) is a host susceptibility factor, first identified in barley, which confers infection by biotrophic powdery mildew fungi. In loss-of-function \textit{mlo} mutants, fungal development is restricted at host cell entry, thus \textit{mlo} mutants provide robust immunity. We considered, why do plants have susceptibility factors? We reasoned that \textit{MLO} may have a role in supporting an ancient plant-microbe interaction, such as arbuscular mycorrhizal symbiosis. Arbuscular mycorrhizal fungi form beneficial biotrophic symbioses with most land plants, including important crops. We demonstrate that, in addition to powdery mildew susceptibility, \textit{MLO} contributes towards arbuscular mycorrhization and this function is conserved across species: barley, wheat and \textit{Medicago truncatula}. Our research shows that during mycorrhization, barley and wheat powdery mildew-resistant \textit{mlo} mutants show delayed formation of arbuscules, the nutrient exchange structure of mycorrhiza. barley \textit{MLO} transcript levels are upregulated in response to both powdery mildew and mycorrhiza. Thus, induction during mycorrhization was used to predict which \textit{M. truncatula} \textit{MLO} (\textit{MtMLO}) orthologs may be functionally analogous to barley \textit{MLO}. Three \textit{MtMLO} candidates were identified using this approach, one of which is conserved exclusively in mycorrhizal host plants. Mutants in two \textit{MtMLO} candidates show delayed arbuscule formation, leading to reduced symbioses. Promoter-GUS assays suggest that these \textit{MtMLO} genes are induced in root cells containing arbuscules. To explore the mechanism of \textit{MLO} in fungal biotrophy, we performed RNA sequencing of barley wild-type and \textit{mlo} mutant during powdery mildew infection and mycorrhization. In addition to our genetic and phenotypic data, we will present the extent to which \textit{MLO} controls analogous processes during these pathogenic and symbiotic interactions.

Fol SIX6: a semi-specific necrosis-inducing protein

Mr Pravin Khambalkar\textsuperscript{1}, Mr Daniel Yu\textsuperscript{1}, Dr Simon Williams\textsuperscript{1}, Dr David Jones\textsuperscript{1}
\textsuperscript{1}Research School of Biology, The Australian National University, Canberra, Australia

The soil-borne fungus \textit{Fusarium oxysporum} f. sp. \textit{lycopersici} (\textit{Fol}) causes fusarium wilt of tomato. In the \textit{Fol} pathosystem, small secreted fungal proteins, called SIX (Secreted In Xylem) proteins, have been identified in the xylem sap of infected tomato plants. Fourteen SIX genes have been identified so far (designated \textit{SIX1–SIX14}). In agroinfiltration experiments, \textit{Fol SIX6} was found to cause cell death when expressed in leaves of \textit{Nicotiana benthamiana} and \textit{N. tabacum}. Purified \textit{Fol SIX6} protein produced using an \textit{E. coli} expression system was found to cause cell death in leaves of tomato as well as \textit{N. benthamiana} and \textit{N. tabacum}. Infiltration of \textit{Fol SIX6} protein into cotyledons/leaves of representative species from various plant families, including the Solanaceae, Cucurbitaceae, Brassicaceae and Leguminosae, revealed not only widespread sensitivity to \textit{Fol SIX6}, but also considerable variation in sensitivity, indicating an unexpected degree of specificity. For example, \textit{Fol SIX6} protein causes a strong cell death response in cotyledons/leaves of bean, calendula, capsicum, eggplant and watermelon; wilting and curling of cotyledons/leaves in cotton, cucumber and flax; but no response in cabbage, pea, radish, spinach, wheat or zucchini. Homologues of \textit{Fol SIX6} have been found in other \textit{formae speciales} of \textit{F. oxysporum} including \textit{F. oxysporum} f. sp. \textit{cubense} TR4 (\textit{Foc SIX6}) which causes panama disease in banana and plantains, \textit{F. oxysporum} f. sp. \textit{vasinfectum} (\textit{Fov SIX6}) which causes fusarium wilt in cotton, \textit{F. oxysporum} f. sp. \textit{melonis} (\textit{Fom SIX6}) which causes fusarium wilt in melons and many other \textit{formae speciales} of \textit{F. oxysporum}, but not all, as well as some species of \textit{Colletotrichum}. \textit{Foc SIX6}, \textit{Fom SIX6} and \textit{Fov SIX6} proteins have also been found to cause plant cell death, but the patterns of response differed between plant families. An investigation of \textit{Fol SIX6} function suggests that it may affect plant transpiration.
Dissecting the dual functionality of the Tox3 effector protein from the wheat pathogen *Parastagonospora nodorum*

Yi-Chang Sung¹, Megan Outram¹, Bayantes Dagvadorj¹, Chen Wang¹, Simon Williams¹, Peter Solomon¹

¹ Division of Plant Sciences, Research School of Biology, The Australian National University, Acton, Australia

It has recently emerged that some necrotrophic fungi facilitate disease through a strict gene-for-gene mechanism as observed in biotrophic pathogens. For the wheat pathogen *Parastagonospora nodorum*, the basis of this host specific interaction is small cysteine-rich effector proteins secreted during infection (ToxA, Tox1 and Tox3). These effectors interact with specific dominant susceptibility genes in the host leading to a programmed cell death response and disease. However, whilst we now understand the requirement of these effector proteins for disease, their modes of action remain poorly understood. To characterise these necrotrophic effectors, a search for potential host protein binding partners for the Tox3 effector was conducted. From this work, the wheat TaPR1-1 protein was validated through three independent approaches to interact with Tox3. We have now generated high-resolution crystal structures of several PR-1 proteins as well Tox3 and are using these to dissect the basis and function of this protein interaction. In this talk I will present our latest findings on dissecting the dual functionality of the Tox3 effector protein. Together with its function in causing cell death through its interaction with Snn3, we demonstrate that Tox3 has an important role in mediating PR-1 defence signalling and is required for disease development. These data have not only significantly advanced our understanding of necrotrophic diseases, but also provided a rare insight into the function and mechanism of the enigmatic plant PR-1 proteins.

The flax-rust effector AvrM14 is a nudix hydrolase with mRNA decapping activity

Mr Carl McCombe², Dr Ann-Maree Catanzariti¹, Dr Anna Desai³, Prof Steven Brenner², Dr Peter Dodds³, Prof Bostjan Kobe⁴, Assoc Prof David Jones¹, Dr Simon Williams¹

¹ Plant Sciences Division, Research School of Biology, Australian National University, Canberra, Australia, ² Plant and Microbial Biology Department, University of California, Berkeley, USA, ³ CSIRO Agriculture, Canberra, Australia, ⁴ School of Chemistry and Molecular Biosciences, University of Queensland, Brisbane, Australia

While the lifestyles and infection strategies of plant pathogens are diverse, a prevailing feature is the use of an arsenal of secreted proteins that aid in microbial infection. Collectively known as effectors, these proteins promote pathogen virulence and aid in host colonisation. Effectors can also be recognised by plant immune receptors, known as resistance (R) proteins, leading to host immunity. Utilising the flax/flax-rust pathosystem, we are working to understand the virulence function of recognised pathogen effectors. Here, I will report our recent work on the flax-rust effector protein AvrM14. Structural studies of AvrM14 revealed homology to the nudix family of phosphohydrolases. After an exhaustive substrate screen, we found that AvrM14 has hydrolase activity that is specific towards molecules that are chemically related to the 5' cap associated with mRNA in eukaryotes. Using *in vitro* assays, we subsequently demonstrated that AvrM14 can remove the 7-methylguanosine cap from synthetic mRNA. The capping of mRNA in eukaryotes is important for mRNA stability and other RNA processing events. I will present preliminary data on how we think this decapping activity is linked to the virulence function of the AvrM14 effector in plants.
Discovery of diverse sources of stripe rust resistance from pre-Green Revolution wheat genotypes and their deployment in future wheat cultivars

Prof Harbans Bariana¹, Dr Urmil Bansal¹
¹The University of Sydney Plant Breeding Institute, Cobbitty, Australia

Various thoughts about food security for the future include increased area under crop production, higher yield and high fertiliser use efficiency. We often forget the losses caused by biotic and abiotic stresses. Technological advances in the 21st century have enabled us to tackle at least biotic stresses in a more efficient manner. Stripe rust, caused by *Puccinia striiformis* f. *sp. tritici* (Pst), is currently the most important disease of wheat worldwide. It has the potential to cost the wheat industry around AUD 1 billion per annum. Almost 50% of stripe rust resistance genes were catalogued in the last century through highly time-consuming cytogenetic technology and were derived from short-statured cultivars and wild relatives of wheat. The discovery and characterisation of about 50% of these stripe rust-resistance genes has happened in the last two decades. This efficiency can be attributed to the rapid improvement in genotyping technologies where the application of bioinformatics to resolve large DNA sequence databases has led to the rapid cloning of rust resistance loci. Screening of a pre-Green Revolution collection of wheat genotypes (Watkins Collection) against a diverse group of Pst pathotypes led to the identification of putatively new sources of resistance that subsequently underwent detailed characterisation. The stripe rust-resistance genes *Yr47*, *Yr51*, *Yr57*, *Yr63*, *Yr72*, *Yr80*, *Yr81* and *Yr82* were characterised from the "Watkins Collection' and DNA markers closely linked with these genes were developed. *Yr47*, *Yr51* and *Yr57* have been transferred to modern wheat cultivars and the remaining four resistance genes are currently being backcrossed into modern wheat cultivars.

Understanding the impact of management in canola to reduce the incidence of sclerotinia stem rot

Dr Sarita Bennett¹, Dr Pippa Michael¹, Ms Linda Thomson¹, Ms King Yin Lui²
¹Curtin University, Bentley, Australia, ²Department of Primary Industries and Regional Development, Esperance, Australia

Sclerotinia stem rot (SSR), caused by the fungal pathogen *Sclerotinia sclerotiorum*, produces significant yield loss in canola where conditions are conducive to disease infection. Crop rotation is the recommended management to reduce risk, as sclerotia remain viable for up to seven years in the soil. In 2018, 10 canola-SSR field trials were conducted across the Western Australian grainbelt from Greenough to Cranbrook. Trials were comprised of four varieties (two hybrid and two open-pollinated) +/- fungicide treatment at 30% flowering, the industry recommended time to spray for *S. sclerotiorum* infection. To determine the impact of previous *S. sclerotiorum* infection on in-season SSR, trial sites were: 1) soil sampled prior to seeding for background sclerotia inoculum, 2) petals collected at 30% flowering to determine spore load at the time of spraying, 3) plants assessed for disease incidence, and 4) five diseased plants collected from each plot/site to record infection characteristics, including sclerotia development within the stem. A low incidence of SSR was recorded, with <15% infection in most plots at all sites except for Bolgart, which had up to 36%. Despite the low infection, significant differences in disease incidence were recorded between locations, fungicide treatments and varieties (*P*<0.05). In contrast *S. sclerotiorum* spores were present on >75% of collected petals at most sites. Despite this, significant differences between sites were recorded (*P*<0.05) for petal spore load. Soil testing was variable between sites, and between plots within a site. Most plots recorded zero sclerotia/m², but ranged from 0 to 66 sclerotia/m²/plot across the ten locations. There was no correlation between plots with high sclerotia numbers in the soil, and a high *S. sclerotiorum* petal spore load. Final yields showed a significant difference between locations (*P*<0.05) and between varieties (*P*<0.05), but not between fungicide treatments. Multivariate analysis highlighted differences between varieties in stem infection and sclerotia development.
Trials and tribulations — Ramularia leaf spot of barley in New Zealand

**Dr Soonie Chng¹, Miss Rachael Warren¹, Ms Joanne Drummond², Ms Shirley Thompson¹, Dr Ruth Butler¹**

¹The New Zealand Institute for Plant and Food Research Limited, Christchurch, New Zealand, ²Foundation for Arable Research, Christchurch, New Zealand

Ramularia leaf spot (RLS), caused by the fungus Ramularia collo-cygni, is a key disease affecting New Zealand’s barley production, reducing yield by up to 30%. Fungicide application has been the only measure used in New Zealand to control RLS. However, like Europe, growers in New Zealand are experiencing difficulty controlling the disease, even with fungicides. Insensitivity to quinone outside inhibitors and succinate dehydrogenase inhibitor fungicides by R. collo-cygni was confirmed in New Zealand in the 2017-18 season. Although demethylation inhibitor based fungicides are currently effective in controlling RLS, they remain at risk of becoming ineffectual given that resistance to this group of fungicides has already occurred in the United Kingdom and Germany. Attempts to develop reliable varietal resistance ratings for barley cultivars has proven difficult. Many factors including varying crop maturity, amounts of seedborne and airborne inoculum, presence of other diseases and seasonal variability have all contributed to the inconsistent ratings.

Analyses of seedborne R. collo-cygni DNA before sowing and from their harvested grains in the 2018–19 autumn (11 lines) and spring (15 lines) field trials have shown that despite not detecting R. collo-cygni DNA in some pre-sown lines, the pathogen’s DNA was detected in the harvested grains of all lines. This suggests that when the disease is present on the plants in the field, airborne inoculum may contribute substantially towards infection of the offspring. When similar seed lines were sown at two different sites, RLS developed on the plants at only one of the sites, indicating that regional weather conditions affect the development of the disease. These findings contribute to our understanding of RLS epidemiology, however, further research is required to understand the persistence of the inoculum within the host and in the field, and to develop best management options to restore the yield potential of barley.

A new class of gene confers resistance in barley to *Puccinia hordei*

**Mr Hoan Dinh¹, Prof Robert Park¹, Dr Davinder Singh¹, Dr Mohammad Pourkheirandish¹,²**

¹Cobbitty, Australia, ²Melbourne, Australia

Resistance genes have long been used as a cost effective and sustainable approach to protect barley crops. However, the molecular mechanisms behind such resistance are largely unknown. We have recently isolated the gene *Rph3*, which confers a high level of resistance to the barley leaf rust pathogen *Puccinia hordei* at all growth stages. High-resolution mapping using 10,411 F₂ individuals derived from six segregating populations delimited the region carrying *Rph3* to 0.023 cM, equivalent to a 9-kb interval in a parent carrying the resistance allele (Scarlett). Two genes were identified in this region based on the gene prediction software FGENESH, designated ORF1 and ORF2. Sequencing of the whole 9-kb region among four independent EMS-induced mutants revealed sequence alterations in ORF1 only, demonstrating that ORF1 is the *Rph3* gene. One of the mutants generates stop codon; one alters the splice site; and the other two lead to amino acid substitutions. The RPH3 protein is a novel disease resistance protein as it does not carry the classical nucleotide-binding domain fused with leucine-rich repeat, or the kinase domain. The discovered gene expresses only in leaf tissues that are infected by *P. hordei*. The gene is only found in barley, *Brachypodium* and *Aegilops tauschii*, suggesting it has a recent evolutionary origin. Our study has discovered a new class of gene that has evolved to protect barley against *P. hordei*, adding to our developing knowledge of the structure and function of resistance genes in plants. This study opens the door to study an undiscovered angle of the molecular interactions that define cereal-rust pathosystem.
Investigation of the basis behind selection of superior and inferior garlic lines from uniformly virus-infected cultivars

Mrs Sari Nurulita¹, Assoc Prof Andrew Geering¹, Dr Kathy Crew², Dr Stephen Harper², Assoc Prof John Thomas¹

¹QAAFI - The University Of Queensland, Brisbane, Australia, ²Queensland Department of Agriculture and Forestry, Brisbane, Australia

Viruses infecting garlic and shallot are economically important in many countries, including Australia and Indonesia. These viruses are transmitted through planting material and by insect vectors. Infected planting material is the primary source of inoculum, as garlic and shallot are vegetatively propagated by farmers. Worldwide, garlic is infected by a complex of viruses, including potyviruses, carlaviruses and allexiviruses, and the majority have been identified on garlic in Australia. Chronically infected garlic plants show symptoms of yellow stripes, mosaic, stem lesions, and leaf deformation. The objective of this study was to investigate why inferior and superior lines of garlic can be selected and maintained from a uniformly, chronically-infected garlic crop and whether improvements are associated with the loss of one or more viruses. As an indexing tool, ten virus-specific PCR primer pairs for the main viruses infecting garlic in Australia have been developed. Field trials were conducted in two successive seasons, in which the second trial was planted with cloves that derived from either mildly or severely diseased plants in the first trial. Second-generation plants from severely diseased plants had significantly lower yields than those from mildly diseased plants. The severe-disease phenotype was highly heritable, although there were some reversions, mild to severe and severe to mild. No consistent association was found between the severity of disease symptoms and the profile of viruses but there were some instances where a virus species was lost during the vegetative propagation process. We speculate that differences in disease severity may related to differences in virus titre, which may be associated with RNAi silencing mechanisms. During the course of virus indexing, we detected garlic virus E in some plants, which is the first detection of this allexivirus in Australia.

Strong indication of susceptibility of faba bean (Vicia faba) genotypes to the root-lesion nematode Pratylenchus thornei, under field conditions

Dr Kedar Adhikari², Mr Tim Clewett¹, Dr Kirsty Owen¹, Ms Emily Plant³, Dr John Thompson¹

¹University Of Southern Queensland, Toowoomba, Australia, ²The University of Sydney, Narrabri, Australia, ³Department of Agriculture and Fisheries, Toowoomba, Australia

Faba beans (Vicia faba) are susceptible to the root-lesion nematode Pratylenchus thornei, therefore a range of cultivars and advanced lines were tested to determine if there was genetic variation in resistance to potentially exploit in breeding programs. Two field experiments in Queensland measured the resistance to P. thornei of faba bean cultivars and compared them with wheat cultivars (Triticum aestivum) ranging from moderately-resistant to susceptible, and a very susceptible narbon bean cultivar (Vicia narbonensis). In the first experiment, in-crop rainfall was 271 mm and plant biomass ranged from 7.3 to 9.2 t/ha, whereas the second experiment, in-crop rainfall was 116 mm and plant biomass ranged from 3.9 to 4.6 t/ha. Despite the differences in seasonal conditions and plant growth, the effect of cultivars on nematode populations was consistent in an across site analysis (P<0.001). All faba bean cultivars were susceptible with final P. thornei populations increased 7 to 14-fold (48 P. thornei/g soil after cv. 11NF001-10 to 90/g soil after cv. Cairo at 0–30 cm soil depth at harvest) when compared with the moderately resistant wheat cultivar (6 P. thornei/g soil). There was a 10-fold increase after the susceptible wheat cultivar (73/g soil) and 22-fold increase after narbon bean (148/g soil). Screening cultivars for resistance to diseases in the field can be confounded by environmental constraints, but not so in these experiments, reflecting the strong genetic control of crop genotypes on P. thornei reproduction. The range of P. thornei populations measured after growing the faba bean cultivars means that targeted breeding can be used to improve resistance levels of all faba bean cultivars so that growers will be able to derive the maximum benefit from this valuable pulse crop in the farming systems of the Australian northern grain region.
Re-inventory of Australia’s plant pathogen reference collections – why is it important and what is being done?

Dr Jacqueline Edwards\(^1,2\)

\(^1\)Agriculture Victoria Research, Bundoora, Australia, \(^2\)La Trobe University, Bundoora, Australia

In Australia, the effectiveness of biosecurity measures relies heavily on the accuracy of specimen-based databases of plant pathogens. Pathogen incidence data is essential for ‘evidence of absence’ that underpins market access and biosecurity for Australian produce, and plant pathogen reference collections and associated databases provide this evidence. With recent advances in fungal taxonomic research, identification of specimens based on the phenotype has been demonstrated to be inadequate and unreliable. This has enormous implications for quarantine and biosecurity, which rely on accurate diagnostic methods and accurate names. There is an urgent need for re-examination of herbarium specimens and living cultures using DNA-based methodologies. Examples from the Victorian Plant Pathogen Herbarium (VPRI) demonstrate the concerted effort that has been made over the past decade to update the identities of living cultures using single and multi-locus sequencing and NGS. More recently, breakthroughs have been made in techniques to re-examine preserved specimens of biotrophic plant pathogens up to 100 years old using sequencing technology.

Australia: A continent without native powdery mildews?

Prof Levente Kiss\(^1\), Dr Niloofar Vaghefi\(^1\), Ms Kaylene Bransgrove\(^2\), Assoc Prof John D. W. Dearnaley\(^1\), Dr Yu Pei Tan\(^3\), Mr Craig Marston\(^4\), Prof Roger G. Shivas\(^1\), Prof Susumu Takamatsu\(^5\)

\(^1\)University of Southern Queensland, Centre for Crop Health, Toowoomba, Australia, \(^2\)Department of Agriculture and Fisheries, Plant Pathology Herbarium, Brisbane/Dutton Park, Australia, \(^3\)Department of Agriculture and Fisheries, Biosecurity Queensland, Ecosciences Precinct, Brisbane/Dutton Park, Australia, \(^4\)Department of Agriculture and Water Resources, Brisbane, Australia, \(^5\)Mie University, Faculty of Bioresources, Tsu, Japan

In contrast to Eurasia and North America, the powdery mildews (Ascomycota, Erysiphales) are largely understudied in Australia. There are over 900 species known globally, with less than 50 recorded from Australia. Some of these records are doubtful as the identifications were presumptive, being based on host plant-pathogen lists from overseas. Australian herbaria contain many undetermined powdery mildew specimens and an outdated nomenclature is still in use. The Department of Agriculture-sponsored Modern Diagnostics Project identified the Erysiphales as a diagnostic gap that was addressed by a 5-day workshop in 2018. This resulted in (i) an up-to-date list of all the taxa that have been identified in Australia based on published DNA barcode sequences prior to the workshop; (ii) precise identification of 117 specimens freshly collected from across the country; and (iii) precise identification of 30 herbarium specimens collected between 1975 and 2013. Identifications were done based on both morphology and DNA barcodes. Altogether, 39 species representing 10 genera were confirmed in Australia, including two genera and ten species newly recorded during the project. In Eurasia and North America the number of powdery mildew species is more than 10 time greater. Interestingly, powdery mildew infections have been recorded on only eight native Australian plant species in the genera Acacia, Acalypha, Eucalyptus, Ixodia, Jagera, Senecio and Trema. All but one of these infections were caused by polyphagous species that infect many other host plants both overseas and in Australia. The data indicates that (i) the native Australian vegetation may have evolved without being exposed to any native powdery mildews; and (ii) all the species of the Erysiphales that are known to occur in Australia may have been introduced since the European colonisation of the continent.
Identification of rust fungi in Australia a century after McAlpine

Dr Alistair McTaggart1, Dr Dean Beasley2, Dr Julia Kruse3, Prof Andre Drenth1, Prof Roger Shivas2,3
1University of Queensland, Brisbane, Australia, 2Queensland Department of Agriculture and Fisheries, Brisbane, Australia, 3University of Southern Queensland, Toowoomba, Australia

Daniel McAlpine’s The Rusts of Australia: Their structure, nature and classification, published in 1906, has been the first point of contact for plant pathologists to identify rust fungi in Australia. Changes in taxonomy, new introductions and new discoveries have outdated this key reference. In order to update these changes, we developed a publicly available interactive online identification guide (Lucid) for the Australian rust fungi - collections.daff.qld.gov.au/web/key/rustfungi/. The guide is dynamic in that taxa can be added and renamed in line with changing taxonomies. Molecular barcodes were provided for most taxa featured on this website, including reference DNA sequences of many exotic taxa. In the course of this study, we have sequenced and assembled genomes of five endemic rust fungi, including a close relative of the introduced and established Austropuccinia psidii (myrtle rust), as well as rust taxa unique to the Southern Hemisphere. These genomic data will complement studies on model rust fungi and comparative studies on rust fungi that have evolved in rainforest habitats.

A revision of Phytophthora parsiana complex

Dr Zahra Mirsoleymani1,2, Dr Xiao Yang3, Prof Chuanxue Hong3, Prof Reza Mostowfizadeh-Ghalamfarsa1,4
1Shiraz University, Shiraz, Iran, 2Shahid Chamran University of Ahvaz, Ahvaz, Iran, 3Virginia Tech, Virginia Beach, USA, 4Murdoch University, Perth, Australia

Phytophthora parsiana, described in 2008, is an important pathogen in Iranian pistachio orchards causing crown rot and gummosis as well as root rot. As more isolates have been recovered considerable variability has been observed in sequence data, morphological and physiological traits and host range. These isolates are now considered to comprise a species complex which warrents further investigation. For this purpose, Phytophthora isolates collected from pistachio and other hosts over the past 30 years, were re-evaluated by sequencing the internal transcribed spacers (ITS) region, β-tubulin (Btub), and mitochondrial cytochrome c oxidase subunit 1 (cox1) genes. Among the three genetic markers, cox1 was the most informative, followed by ITS, while Btub sequences had numerous ambiguous reads in some isolates. Phylogenetic analysis of sequences indicated that the isolates formed four subgroups (namely taxa A, B, C and D) all which were located in subclade 9a of Phytophthora phylogenetic tree. All isolates originated from either pistachio or, in a few cases, almond trees except the type culture of P. parsiana (taxon C) that originated from fig. Close examination of extensive polymorphisms in Btub sequences of taxon D indicated the pistachio isolates examined in this study could be a stable hybrid of P. virginiana × P. parsiana while the other two taxon are distinct species that should be described. These results indicate that there is tremendous genetic diversity among the isolates previously identified as P. parsiana.
Towards improving phytoplasma taxonomy using phylogenetics and phylogenomics: A focus on Australian 16Sr II phytoplasmas

Miss Bianca Rodrigues Jardim¹,², Dr. Wycliff M. Kinoti¹, Dr. Lucy T.T. Tran-Nguyen³, Dr. Cherie Gambley⁴, Dr. Brendan Rodoni¹,², Dr. Fiona E. Constable¹

¹Agriculture Victoria Research, Department of Jobs, Precincts and Regions, AgriBio, Melbourne, Australia, ²School of Applied Systems Biology; La Trobe University, Melbourne, Australia, ³Biosecurity and Animal Welfare, Department of Primary Industry and Resources, Darwin, Australia, ⁴Horticulture and Forestry Science, Department of Agriculture and Fisheries Applethorpe Research Station, Applethorpe, Australia

Phytoplasmas are unculturable, pleomorphic Mollicutes that infect plant and insect hosts. As such, the taxonomy of this group has relied on molecular phylogenetics rather than the polyphasic approaches often used for culturable bacterial species. Phytoplasmas are classified into groups and subgroups based on sequence similarity and RFLP analyses of the 16Sr gene. Routinely, a novel phytoplasma group is identified and classified into the provisional genus ‘Candidatus Phytoplasma’ when the 16Sr gene shares less than 97.5% sequence similarity with any previously described ‘Candidatus Phytoplasma’. RFLP analysis of the 16Sr gene is then used to further assign a subgroup to a phytoplasma strain. There is some doubt however, around the robustness of this classification scheme. The number of subgroups can be inflated when using an RFLP-based approach where subgroups are differentiated based on a single nucleotide polymorphism without the support of meaningful biological or ecological data. Additionally, the 16Sr gene presents two challenges to phytoplasma taxonomy. The 16Sr gene shows limited phylogenetic resolution between closely related strains and is duplicated in the phytoplasma genome, where these two copies can show sequence heterogeneity. Due to these limitations, phytoplasma taxonomy has moved to a multilocus-based approach where additional genes, more variable than the 16Sr, are being evaluated. In this study, we investigate the usefulness of combining different genomic resources to explore the taxonomic relationships of members within the ‘Candidatus Phytoplasma’ genus. The results of this study will contribute to the understanding of phytoplasma evolution and genetic diversity within Australia, and to identify robust markers for improved monitoring, disease management, and diagnostics of these plant pathogens.
Molecular phylogenetic resolution of *Podosphaera clandestina* in Australia from 130 year old herbarium specimens

Dr Jaqueline Edwards$^{1,2}$, Dr Ross Mann$^1$, Dr Tom May$^3$, Dr Tim Sawbridge$^{1,2}$, **Ms Reannon Smith**$^{1,2}$

$^1$Agriculture Victoria Research, Bundoora, Australia, $^2$La Trobe University, Bundoora, Australia, $^3$Royal Botanic Gardens Victoria, Melbourne, Australia

Monitoring potential biological threats to the Victorian horticultural industry is an on-going process which engages boarder security, disease monitoring and incursion management across the country. The cherry industry is an important Victorian export commodity which generated 1,235 tonnes of fruit for export at $18.4 million dollars in 2018 [1]. The most destructive cherry disease is cherry powdery mildew, which has not been recorded in Australia, although the pathogen, *Podosphaera clandestina*, is reported in Australia on the host *Crataegus* (hawthorn). Cherry powdery mildew affects tree foliage which reduces the photosynthetic capabilities of the tree leading to reduced fruit production. Severe powdery mildew infection can lead to infection of the fruit, resulting in further crop losses. Cherry powdery mildew can over winter in chasmothecia in tree bark or on the orchard floor providing inoculum for the next season [2]. *Podosphaera clandestina* is described as a species complex by Braun and Cook [3] who reinstated Blumer’s [4] distinction between *P. clandestina* s. str. on *Crataegus* and *P. clandestina* on *Prunus* as genetically different species. The Victorian Plant Pathology Herbarium (VPRI) includes powdery mildew on *Crataegus* collected in Australia and powdery mildew on cherry collected in the USA. Molecular phylogenies are being generated in order to resolve the taxonomic question of whether the species present in Australia is different from the cherry infecting *Prunus* strain.

Pursuing durable, broad-spectrum disease resistance in plants

Jan E. Leach
Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, Colorado 80523-1177

Disease resistance is the foundation for managing many plant diseases, because resistant varieties have the strongest impact with minimal environmental effects or cost. Sources of broad-spectrum resistance (BSR), or resistances that are effective against multiple and/or diverse pathogens, are of particular interest. Frequently, BSR are quantitative traits, which, due to their complexity, can be difficult to identify and to transfer into elite germplasm. To guide improvement of BSR in rice, we have used novel genetic resources, such as Multi-parent Advanced Generation Inter-Cross (MAGIC) populations, advances in genomics and associated computational tools, and knowledge of plant disease defense responses. These resources and tools have improved detection of BSR QTL, enabled identification of the genes contributing to QTL function, and, importantly, allowed discovery of how those genes contribute to disease resistance. Overall, this progress provides steps forward to improving BSR, and possibly durable disease resistance, in rice.
Genetic dissection of the *Erwinia amylovora* disease cycle

**Prof George W. Sundin**  
*Michigan State University*

Fire blight, caused by the pathogen *Erwinia amylovora*, is the most devastating bacterial disease of pome fruits in North America and around the world. The pathogen infects flowers, fruits, shoots, and rootstock crowns, and also moves systemically through hosts via cortical parenchyma and sometimes xylem tissue. The type III secretion system (TTSS), the type III effector DspE, and the exopolysaccharide (EPS) amylovoran are all critical pathogenicity factors. Amylovoran and two other EPSs levan and cellulose also contribute to biofilm formation, which is an important phase of development whereby cell populations increase in leaves at shoot tips. We have been determining the genetic bases of *E. amylovora* infection of different apple tissues, and also studying the regulation of virulence determinants by the second messenger compound cyclic di-GMP and by noncoding small RNA translational regulators. I will provide an update on our progress in this regard, discuss specific proteins whose regulatory function is affected by binding to cyclic di-GMP, and specific sRNAs that play critical regulatory roles in functional transitioning that is needed at distinct phases of the disease cycle.
Translational taxonomy: balancing utilitarian and theoretical taxonomies of plant pathogenic bacteria

Prof Carolee T. Bull
Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, State College, PA, United States

Despite 60 years of evidence against it, the ‘new host-new species cliché’ remains alive and well in phytobacterial taxonomy and continues to excite controversy. Though Starr in 1959 clearly outlined that the cliché was false, the advent of the pathovar system of classification and nomenclature exacerbated and reinforced the myth. Current controversies surrounding the pathovar system are largely based on the erroneous notion that the pathovar system requires a one host-one pathovar relationship and lack of use of species elevated from groups of former pathovars. Despite misinterpretations, the ability to identify and detect pathogens of particular hosts remains critical to growers, regulators, and researchers. Thus, it is essential that any taxonomic system must applicable to real world situations. The coupling of comparative genomics to published taxonomic frameworks made from reference strains with valid names and known host ranges, is allowing researchers to understand what genetic differences make a difference with regard to pathogenic capabilities on a given host. Diagnostic metagenomics coupled to spatio/temporal functional genomics will explain why and when certain pathogens cause disease on a given host and why other organisms with the capability to cause disease are not identified as the culprits at the scene of plant disease epidemics.
Sustainable crop protection: BioClay technology to deliver RNAi

Prof Neena Mitter
Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation, the University of Queensland, St Lucia, Australia

Can we really feed ten billion people as we head towards the next century? The current world population of 7.3 billion is expected to rise to 9.7 billion in 2050 and 11.2 billion in 2100. A staggering $1.1 trillion worth of agricultural products are traded internationally each year with 80 per cent of the total made up by the food component. In this globalized world and interconnected economies, we need to address to ensure that our food crops are protected from pests and diseases as they account for 20-40% losses in productivity. The ongoing usefulness of chemical pesticides suffers from issues such as residual toxicity, run off, specificity and resistance. Genetic modification (GM) is not available for all crops/pathogens, and it is not the preferred choice for all producers and consumers. The aim to deliver transformative clean green technologies is the key driver for agricultural nanotechnology innovations for crop protection. Nanoparticles as carriers of innovative biological ‘active ingredients’ could be a game changer for future crop protection strategies. BioClay is one such non-toxic, non-GM, biodegradable crop protection platform that delivers pest targeting RNA interference (RNAi) as a topical application using clay nanoparticles. The discovery of RNAi as a natural regulatory mechanism that plays critical roles in growth, development and host defence against viruses and transposons, has proved to be a powerful strategy to engineer disease resistance against viruses, viroids, nematodes, insect pests and fungi in plants. At present the use of RNAi for disease resistance is limited to engineering transgenic disease resistance plants. RNAi-mediated virus protection by topical application of double stranded RNA (dsRNA), the trigger molecule of RNAi, was once considered infeasible due to a perceived barrier in the form of the plant cell wall. Series of papers have shown that exogenous application of dsRNA can induce RNAi-mediated defence. The major limitation however is the instability of topically applied naked dsRNA on the leaf surface leading to a very short period of protection. BioClay opens the window of opportunity to deliver the same as a sustainable spray application with extended period of protection. We have shown that RNAi effectors delivered as BioClay are stable, do not get washed off and provide protection to the sprayed and unsprayed leaves against the targeted virus for up to 20 days post spray. We have further shown that the clay degrades on the surface of the leaf alleviating any concerns about residues. We are now progressing with exploring BioClay targeting multiple host/pathogen systems and validation in field trials. Real world application of exogenous dsRNA for RNAi-mediated resistance will be governed by factors such as cost effective production of dsRNA and the regulatory landscape.
Grapevine trunk diseases are the most destructive fungal-associated diseases of grapevine in New Zealand and worldwide. Infection by *Eutypa lata* and other fungal pathogens can cause severe symptoms on leaves and trunks, leading to decreases in yield or even plant death. Biocontrol agents have been applied to reduce disease rates for a number of fungal diseases in other crops. We identified *Aureobasidium pullulans*, a biocontrol agent for several tree pathogens, from high throughput sequencing (HTS) of grapevine trunk samples from Marlborough vineyards. Therefore, we undertook to assess the potential of *A. pullulans* to inhibit or protect grapevines against *E. lata* *in silico*, *in vitro* and *in planta*. The Marlborough vineyards comprised six planted in Sauvignon blanc and six in Pinot noir, of which half used herbicide to manage the under-vine ground cover. Statistical analyses of the HTS revealed that vineyard site significantly influenced the microbiome composition; microbiome composition may also be influenced by grapevine cultivar and/or vineyard management method. In addition, the presence of *A. pullulans* correlated negatively to grapevine trunk disease symptoms. *In vitro*, the inhibition rates of *E. lata* by *A. pullulans* ranged from 4% to 21%, depending on which of the four *A. pullulans* strains was used. *In planta* assays assessed the length of staining from the inoculation site for ten treatments and presence of fungal species after 3 months. These included, agar only, *E. lata* only, *A. pullulans* isolates only and combinations of pathogen and potential biocontrol agent. Only one of the four tested *A. pullulans* strains resulted in a reduced average stain size. *Aureobasidium pullulans* is a commercially available biocontrol agent that has potential to protect grapevines from infection of *E. lata*. Further research is required to confirm these preliminary studies.

**Investigation of Actinobacteria as biocontrol candidates against necrotrophic fungal pathogens**

*Dr Katharina Belt*¹, Dr Heng Chooi², Dr Cathryn O’ Sullivan¹, Dr Margaret Roper¹, Dr Karam Singh¹, Dr Louise Thatcher¹

¹CSIRO, Floreat, Australia, ²UWA, Crawley, Australia

*Actinobacteria* present a phylum of gram-positive bacteria, which can be terrestrial or aquatic. They are of great interest in agriculture for their abilities as plant growth promoting agents or production of pathogen inhibiting compounds. Plant beneficial isolates are able to inhabit the plant root system without causing a disease. We have a collection of *Actinobacteria* isolated from south-west Western Australia. Our goal is to identify isolates that can produce antifungal compounds with a focus on protection against economically destructive necrotrophic fungal pathogens like *Sclerotinia*, *Rhizoctonia* and *Leptosphaeria*. Often, beneficial microbes lose their capability of producing certain compounds once isolated from their natural environment. OSMAC (one strain, many compounds) is used to identify optimal growth and environmental conditions for antifungal compound production under lab conditions. Media, temperature, humidity etc. all influence microbial behaviour and trigger certain specialized compound production. By using *in vitro* pathogen growth inhibition assays on agar plates containing different media, strains are screened for bioactivity under different growth conditions. We identified strong candidates with 100% fungal inhibition on agar plates. Extractions of compounds from agar as well as from liquid culture and analysing compound composition using flash chromatography and LCMS are used to identify the antifungal compounds which in the future could be used as biological disease control. In addition, *in planta* infection assays on seed coated Canola is used to investigate beneficial interaction between *Actinobacteria* and plants.
Bacteriophage-mediated control of *Pseudomonas syringae pv. actinidiae* on kiwifruit plants

**Ms Shea Addison**¹, Rebekah Frampton¹, Loreto Hernandez¹, Sandra Visnovsky¹, Sunzanne Warring², Andrew Pitman¹,³, Matt Templeton¹,⁴, Peter Fineran²,³ ¹The New Zealand Institute for Plant and Food Research Limited, Lincoln, New Zealand, ²Department of Microbiology and Immunology, University of Otago, Dunedin, New Zealand, ³Bio-Protection Research Centre, , New Zealand, ⁴The New Zealand Institute for Plant and Food Research Limited, Auckland, New Zealand

*Pseudomonas syringae* pv. *actinidiae* (Psa) and similar bacterial plant pathogens are responsible for devastating crop losses. Bacteriophages (phages) hold promise as environmentally friendly biocontrol agents for plant pathogens. However, the challenge of effective phage application in an orchard or other outdoor setting still remains. In 2011/2012 a collection of over 200 phages with activity against Psa were isolated from New Zealand soil and sewage samples. Host range and suitability for biocontrol were used to select two phages from this collection and the ability of these phages to control Psa on kiwifruit plants was tested. We developed a based assay to assess the effectiveness of phages under controlled conditions. Kiwifruit plantlets were grown on agar growth medium from tissue culture. The plantlets were flooded with Psa culture at approximately three months old. This method of inoculation was used to ensure even coverage of the plantlets. Symptoms, such as leaf lesions, were visible after eight days. Phages were applied to the plantlets by spraying, which resembles the technique that would be used in an orchard setting. Timings and concentrations of phage spraying were tested. Leaf discs were taken from the plantlets and plated to measure Psa and phage numbers. Establishing this plantlet-based assay allowed us to test different factors to better understand the action of phages on plant surfaces. The impact of phage application on Psa numbers and symptom development determined. Both phages were still detected on leaf surfaces two weeks after application but at reduced compared application. We are continuing to optimise the assay conditions to improve the phage stability and effectiveness.

Modes of competition between bacterial pathogens during plant co-colonization

**Ms Hanareia Ehau-Taumaunu**¹, Dr Kevin Hockett¹,² ¹Department of Plant Pathology and Environmental Microbiology, The Pennsylvania State University, University Park, United States, ²The Huck Institutes of the Life Sciences, The Pennsylvania State University, University Park, United States

The exposed nature of agricultural systems can result in the overlap of competing phytopathogens. For *Pseudomonas syringae*, this possibility increases as two or more distantly related strains converge to infect the same host. To explore the modes of competition occurring *in planta*, we performed a series of co-infiltration experiments with strains of *P. syringae* pv. *syringae* (Psy) and *P. syringae* pv. *phaseolicola* (Pph), which are both able to infect and cause disease on *Phaseolus vulgaris* (Common bean) but belong to distinct phylogenetic clades within the species. Importantly, Psy encodes a bacteriocin (a proteinaceous toxin) that inhibits Pph. Populations of each strain were measured over an 8-day period. Interference competition (direct antagonism) via the *Psy* bacteriocins was observed in 1:1 co-infiltration at 4 days postinfiltration (dpi), where *Psy* reduced *Pph* by 100-fold compared to a 10-fold reduction by a bacteriocin-deficient mutant (*Psy* Δbac). Surprisingly, however, at the 1:1 co-infiltration there was no detectable bacteriocin-mediated benefit to *Psy*. Conversely, when *Psy* was co-infiltrated as a minority population (1:9), *Psy* achieved a significantly greater population at 6 dpi than *Psy* Δbac, showing a bacteriocin-mediated benefit. Unexpectedly, co-infiltration with a *Psy* type III secretion system (T3SS) mutant (Ps DHrcC), which is required to suppress plant defenses, resulted in no detectable decrease in the *Pph* population at all dpi. Therefore, T3SS is required for *Pph* suppression by *Psy*. These results indicate that *Psy* employs both direct (bacteriocin-mediated) and indirect (host plant manipulation) modes of competition with *Pph*. As competition forms the basis for most, if not all, biological control strategies, understanding the ecological factors that contribute to strong competition will help in developing robust biological control.
Identification of novel fungal endophytes with bioactivity against *Neonectria ditissima*, the causal agent of European canker of apple

**Ms Lay Lay Nwe**, Dr Seona Casonato, Dr Eirian Jones

1Department of Pest-management and Conservation, Faculty of Agriculture and Life Sciences, Lincoln University, Lincoln 7647, Christchurch, New Zealand

A series of *in vitro* experiments were conducted to investigate the activity of 311 endophytic fungal isolates obtained from apple stem and leaf tissues to reduce the growth of *Neonectria ditissima*, the causal agent of European canker of apple. A preliminary dual-plate assay identified isolates of *Biscogniauxia* sp. (8 isolates), *Chaetomium* sp. (4 isolates), *Xylariaceae* sp. (2 isolates) and *Neosetophoma* sp. (2 isolates) to reduce *N. ditissima* growth. These isolates were tested further for production of volatiles and non-volatile inhibitory metabolites, siderophores and activity of enzymes related to colonisation of fungi in plants. Volatiles produced by the fungal endophytes reduced *N. ditissima* growth by 4.3-28.1%, with 1 *Biscogniauxia* sp. and 1 Xylariaceae sp. isolates reducing growth by over 20%. Agar amended with 50% culture filtrates of 2 *Biscogniauxia* sp. and 2 Chaetomium sp. isolates reduced *N. ditissima* growth by over 10%. Both *Neosetophoma* sp. isolates, 1 Xylariaceae sp. and 4 *Biscogniauxia* sp. isolates were positive for siderophore production on chrome azurol S (CAS) agar plates. Almost all the isolates (15 out of 16) produced at least one of the enzymes assayed; amylase (12/16 isolates), cellulase (8/16 isolates), pectinase (6/16 isolates), protease (12/16 isolates) and xylanase (7/16 isolates). Both *Neosetophoma* sp. isolates were positive for production of all enzymes, with all *Biscogniauxia* sp. and both *Xylariaceae* sp. isolates positive for amylase production. This study indicated that fungal endophytes isolated from apple tissues have the potential for use in sustainable control of *N. ditissima*. These isolates will be tested further *in planta* for their ability to endophytically colonise apple tissue and reduce *N. ditissima* colonisation.

Using indigenous *Trichoderma* as a potential biocontrol of Fusarium Wilt (*Fusarium oxysporum* f.sp. *cubense*) in Australian banana cropping systems

**Mr David East**, Dr Hazel Gaza, Prof Altus Viljoen, Dr Tony Pattison

1Qld Department Of Agriculture & Fisheries, Boogan, Australia, 2Department of Plant Pathology, Stellenbosch University, Matieland, Stellenbosch, South Africa

The confirmation of Fusarium Wilt Tropical Race 4 (TR4) (*Fusarium oxysporum* f.sp. *cubense*) (Foc) near Tully has put at risk the $600 million per year Australian banana industry. To reduce the threat to the wider banana growing industry, the development of management techniques to reduce inoculum and limit disease movement is imperative. Twenty *Trichoderma* isolates were collected from soils in a banana farm with a history of *Foc race 1* (FocR1). The isolates were screened for antagonistic activity against *FocR1*. A *Trichoderma virens* isolate (BRIP65209) consistently suppressed the growth of FocR1. This was confirmed by doing a pseudostem baiting assay. The addition of the *T. virens* isolate to the pseudostem reduced the number of *Foc* conidia and *Foc* chlamydosporation production by two thirds relative to FocR1 only inoculation. The ability of *T. virens* to suppress Fusarium wilt was further evaluated in an *in vivo* bioassay using Ducasse (*Musa* ABB synonym Pisang Awak) banana plants grown in a glasshouse. Three months after inoculation with FocR1, the plants were scored for external and internal disease symptoms. Quantification of *T. virens* and FocR1 in different banana compartments using qPCR was conducted. The results showed that application of *T. virens* caused a 60% reduction in rhizome necrosis. This was due to the reduction in the amount of FocR1 inoculum, which was supported by the qPCR data. There was a significant reduction in FocR1, specifically in the root base, rhizome and pseudostem of bananas when *T. virens* was present. *T. virens* seems to employ mycoparasitism and niche competition as a strategy to suppress FocR1. Further efficacy testing of the *T. virens* isolate is required in the field to confirm suppression of FocR1, but the technique provides promise to limit losses to Fusarium wilt.
A robust quantitative approach using SPME-GC-MS, identified the volatilome of the biocontrol agent, *Aureobasidium pullulans*

**Miss Sashika Yalage Don**, Dr Christopher Steel, Dr Joanna Gambetta, Dr Leigh Schmidtke

1School of Agricultural and Wine Sciences, National Wine and Grape Industry Centre, Charles Sturt University, Locked Bag 588, Wagga Wagga, Australia

Microbial antagonists have been explored as ecofriendly disease management alternatives to synthetic fungicides. Production of antimicrobial volatile organic compounds (VOCs) has become popular due to their biodegradability and activity regardless of a physical contact of the targeted host. Quantitative identification of VOCs is important, as it provides the basis to formulate artificial volatile cocktails, strain selection and growth condition studies to improve VOCs production by biocontrol agents. To our knowledge, a robust automated technique for quantitative analysis of microbial VOCs has not been reported. *Aureobasidium pullulans* is a yeast-like fungus and a potential biocontrol agent. Initial experiments of our study demonstrated a suppressed growth of *Botrytis cinerea* and *Alternaria alternata* by *A. pullulans* VOCs. In this context, we propose a novel approach for the quantitative analysis of *A. pullulans* VOCs by automated solid phase-microextraction-gas chromatography-mass spectrometry (SPME-GC-MS), in an antagonist-pathogen interactive system. *A. pullulans* and either *B. cinerea* or *A. alternata* were grown on two separate PDA layers in a headspace vial. To facilitate accurate quantitation, an internal standard (2-methyl-4-pentanol in methanol) was introduced, through the septum of the screw cap, on to a paper disc glued on a strip of aluminium foil hanging on the wall, before GC-MS analysis. Multivariate Curve Resolution-Alternating Least Squares deconvolution of SPME-GC-MS spectra, enabled the identification of thirteen VOCs from *A. pullulans*. Acetone, 2-heptanone, ethyl butyrate, 3-methylbutyl acetate and 2-methylpropyl acetate were identified as new VOCs from *A. pullulans*. The variables importance in projection scores and selectivity ratio of partial least squares discriminant analysis models identified four compounds; ethanol, 2-methyl-1-propanol, 3-methyl-1-butanol and 2-phenylethanol, as important VOCs that discriminate between *A. pullulans* and pathogens. These four compounds were quantified and ethanol was the highest abundant VOC in *A. pullulans* headspace. Our findings introduce a novel, robust, quantitative approach for microbial VOCs analyses in biocontrol studies.

**Poster Board 63**

Management of Sheath blight disease utilizing Tricho-compost

**Dr Shireen Quazi**

1Bangladesh Rice Research Institute, Gazipur, Bangladesh

Sheath blight disease of rice, caused by *Rhizoctonia solani*, is a devastating rice disease in the rice growing world. Yield loss has been estimated to be approximately 6% in South and South East Asia [1], while in Bangladesh has estimated 14 to 31% under experimental and farmer field conditions [2]. Tricho-compost is an environmental friendly bio-compost and the main compositions are (v/v): Water hyacinth: Cow dung: *Trichoderma inoculum* = 3.0: 1.0: 0.25 and urea solution: 10%. By applying this compost in field during land preparation it can reduce disease to a lower extent and increase yield by 11-32%. In addition, it can supply additional nitrogen 20 kg/ha, phosphorus 5 kg/ha, potash 22.6 kg/ha, sulfur 10.2 kg/ha and zinc 0.04 kg/ha when applied @ 2 t/ha. By adding this additional nutrition and minimizing sheath blight incidence and severity it plays a role on flag leaf length and width increase, panicle length increase and grain weight increase. Thus, all added nutrition contributes to yield increase and *Trichoderma* plays a role to minimize the disease severity index of sheath blight. This technology will be helpful to farmers to fight against the disease. Moreover, increased yield will be added to the national yield and will be able to feed additional people in future.

Green Fluorescent Protein transformation sheds more light on a widespread mycoparasitic interaction

Mr Mark Z. Nemeth1, Dr Alexandra Pintye1, Mr Aron N. Horvath1, Dr Pal Vagi1, Assoc Prof Gabor M. Kovacs1, Dr Markus Gorfer3, Prof Levente Kiss4

1Plant Protection Institute, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary, 2Eotvos Lorand University, Institute of Biology, Department of Plant Anatomy, Budapest, Hungary, 3AIT Austrian Institute of Technology, Tulln, Austria, 4University of Southern Queensland, Centre for Crop Health, Toowoomba, Australia

Powdery mildews, ubiquitous obligate biotrophic plant pathogens, are often attacked in the field by mycoparasitic fungi belonging to the genus Ampelomyces. Some Ampelomyces strains are commercialized biocontrol agents of crop pathogenic powdery mildews. Using Agrobacterium tumefaciens-mediated transformation (ATMT), we produced stable Ampelomyces transformants that constitutively expressed the green fluorescent protein (GFP), to (i) improve the visualization of the mildew-Ampelomyces interaction; and (ii) decipher the environmental fate of Ampelomyces before and after acting as a mycoparasite. Detection of Ampelomyces structures, and especially hyphae, was greatly enhanced when diverse powdery mildews, leaf and soil samples containing GFP transformants were examined with fluorescence microscopy compared to brightfield and DIC optics. We showed for the first time that Ampelomyces can persist up to 21 days on mildew-free host plant surfaces, where it can attack powdery mildew structures as soon as these appear after this period. As a saprobe in decomposing, powdery mildew-infected leaves on the ground, and also in autoclaved soil, Ampelomyces developed new hyphae, but did not sporulate. These results indicate that Ampelomyces occupies a niche in the phyllosphere where it acts primarily as a mycoparasite of powdery mildews. Our work has established a framework for a molecular genetic toolbox for Ampelomyces using ATMT.

Shelf life study of Trichoderma species and their efficacy to control root and basal stem rot disease on mandarin

Mayavira Hahuly1, Julinda Henuk1, Evert Hosang2, Lily Ishaq1, Rita Noveriza3, Dr Agnes Simamora1, Arry Supriyanto4

1Faculty of Agriculture Universitas Nusa Cendana Kupang NTT Indonesia, Kupang NTT, Indonesia, 2Assessment Institute for Agricultural Technologies, Kupang NTT, Indonesia, 3Indonesian Center for Estate Crops Research and Development, Bogor, Indonesia, 4Indonesian Citrus and Subtropical Fruits Research Institute, Malang, Indonesia

Trichoderma is one of the antagonistic fungi that is used as a biocontrol agent because it can suppress the growth of pathogens through competition, antibiosis and mycoparasitism. The successful application of Trichoderma especially in the field is influenced by the availability of nutrients in the formulation ingredients used. The purposes of this study were to obtain the best solid based carrier material capable of storing Trichoderma spp. (T. asperellum, T. hamatum, T. harzianum, T. viride) for two, three, and six months and to test their efficacy in controlling root and basal stem rot disease on mandarin caused by Phytophthora palmivora. The treatment tested was a type of carrier material including husk ash, broken corn, rice granules, and zeolite. Each Trichoderma species was stored in four solid based carrier materials for two, three, and six months in the laboratory bench and each treatment was repeated three times. The results showed that: (a) husk ash, broken corn, rice granules, and zeolite were able to store Trichoderma asperellum, T. hamatum, T. harzianum, T. viride for up to six months; (b) after six months storage, the number of colonies and living spores of T. viride was highest compared to other Trichoderma tested (c) broken corn and rice granules were better carrier materials for storing Trichoderma compared to husk ash and zeolite. In glasshouse and field experiments, T. viride showed markedly greater reduction (40-60%) in both disease incidence and disease severity of root and basal stem rot disease of mandarin.
Arbuscular mycorrhizal fungi drive nodulation by rhizobia and yield of mungbean despite infestation with *Pratylenchus thornei*

**Ms Elaine Tabah**, Dr Kirsty Owen, Dr Rebecca Zwart, Dr Alla Marchuk, Prof John Thompson

*University of Southern Queensland, Toowoomba, Australia*

Mungbean (*Vigna radiata*) is an increasingly important summer grain crop in the sub-tropical grains region of Eastern Australia. However, mungbean is a host to the root-lesion nematode (*Pratylenchus thornei*), which feeds and migrates through crop roots and destroys root cortical tissue resulting in yield loss. Mungbean also forms symbiotic relationships with other soil-borne micro-organisms such as arbuscular-mycorrhizal fungi (AMF) and the nitrogen fixing bacteria *Bradyrhizobium* spp. AMF improve plant uptake of phosphorus and zinc from soil and fertiliser sources, as well as soil water. *Bradyrhizobium* in root nodules converts nitrogen gas from the atmosphere into ammonia for plant use. AMF have been implicated in reducing the damaging effects of *Pratylenchus* spp. and have been promoted as a form of biocontrol. *Pratylenchus* and AMF occupy the same ecological niche of the root cortex. AMF and rhizobia can act synergistically to improve mineral nutrition and plant growth. A glasshouse experiment was undertaken to assess the interaction between *Pratylenchus thornei*, AMF and rhizobia in mungbean in pasteurised vertosolic soil. Cultivar Jade-AU was inoculated with (a) *P. thornei*, (b) a mixture of two AMF strains endemic to the sub-tropical grains region and (c) *Bradyrhizobium* strain CB 1015 in a factorial designed experiment with 4 replications and two sampling times. Despite *P. thornei* inoculation pressure, co-inoculation with AMF and rhizobia resulted in a marked synergistic effect in mungbean compared to either organism alone (*P*<0.001). This synergism increased nodulation, plant biomass and seed yield more than fivefold that achieved with either AMF or rhizobia alone. However, the rate of reproduction of *P. thornei* increased when AMF was present. Understanding the complex multipartite interactions between organisms within the phytobiome of mungbean will lead to greater economic return for growers via management to achieve better nodulation, nitrogen fixation and yield of mungbean crops.
Poster Board 36

Green leafhoppers population as a vector of Tungro virus

Mr Arif Muazam1
1Tungro Disease Research Station, Ministry Of Agriculture, Sidenreng Rappang, Indonesia

Sidrap Regency as the main regency of South Sulawesi producing rice and rice centers is important in Indonesia, in general and eastern Indonesia in particular. Integrated rice cultivation efforts have been carried out as an effort to anticipate the occurrence of tungro virus explosion in endemic areas. This paper discusses the population density of green leafhoppers, predatory insects, and other pests in 3 varieties of rice plantations (Inpari 9 Elo, IR-64, Taichung native 1) in endemic areas.

The study was carried out in a trial garden in Tungro Disease Research Station, using a Complete Random Design (CRD), with 3 treatment plots of varieties, size 10 x 10 m² with 3 replications. With the most common results of adult green leafhopper (Nephotetic verescens) in TN1 varieties the first week and the fourth after planting so that it is significantly different from IR-64 but not significantly different from Inpari 9 Elo. The most nymphs were found on IR-64 in the first week after planting. The highest tungro virus in TN 1 varieties was observed in the last week of observation. The dominant natural predators were observed to fluctuate every week, namely: Agriocnemis spp, Micraspis sp, Conocephalus longipennis, Araenus inustus, Lycosa pseudoannulata, Oxyopes javanacus, and Tetraghenata maxilosa. At 6-7 MST (weeks after planting) Ophionea nigrofasciata species appeared and in 7MST there were species of Anaxipa longipennis.

Poster Board 34

Survey of banana leaf diseases in Southern Lao PDR

Dr Jay Anderson1, Ms Cecilia O’Dwyer2, Prof Andre Drenth2, Ms Sengphet Phanthavong3, Prof Lester Burgess4
1School of Agriculture and Food Sciences, The University of Queensland, St Lucia, Australia, 2Centre for Horticultural Science, Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Dutton Park, Australia, 3Provincial Agriculture and Forestry Office , Pakse, Lao People’s Democratic Republic, 4Sydney Institute of Agriculture, Faculty of Science, The University of Sydney, Sydney, Australia

In February and March 2019 a banana leaf disease survey was undertaken in the provinces of Savannakhet, Salavan, Sekong and Champasak in southern Lao People’s Democratic Republic. The survey was conducted during the dry season to enable ease of access to smallholder farms. Farms were surveyed and symptoms of disease observed on banana leaves, photographed and small sections of symptomatic tissue were excised, placed into paper envelopes and transported to the laboratory for further processing. GPS location data was collected and where possible banana variety names were recorded. Leaf tissue sections were surface sterilized by dipping in 70% ethanol for 2 sec, and plated onto ¼ strength potato dextrose agar amended with cephalaxin. Representative isolates of putative slow-growing leaf pathogens were recovered and deposited in the International Collection of Microorganisms from Plants for later sequencing. Symptomatic leaf tissue was transported to Australia, under import conditions, for DNA extraction and sequencing for identification of leaf disease pathogens.

Banana freckle (caused by Phyllosticta spp.) was the most commonly encountered leaf disease recorded on a range of varieties and in a range of locations. Neocordana musae was commonly observed and Pseudocercospora spp. was noted on some varieties. The smallholder banana production systems in southern Lao PDR are very low input; farmers do not use fungicides and regular de-leafing is not practiced. ‘Kuay Nam’ belonging to the Pisang Awak group (ABB) was the most commonly grown smallholder variety and is known to be resistant to several fungal leaf spot diseases.
Are pathogens responsible for dark staining of pistachio shells?

Dr Belinda Rawnsley

Agxtra, Newton, Australia

The pistachio industry is worth $35.4 million and is dependent on the production of quality pistachios in-shell for export and domestic markets. In 2017, there was a high incidence of dark staining of shells which reduced the marketability of pistachios and caused considerable yield loss (up to 50%). Although the cause of dark staining is unknown, anecdotally it has been associated with fungal infection. This project was established to evaluate the occurrence of dark staining and provide information on the casual agents or other factors associated with the problem to ultimately develop management strategies. Field studies were conducted in Victoria and NSW to assess the development of dark staining at various times in the orchard in accordance with predicted maturity and commercial harvest times. Collections every 5-7 days from fruit ripening to 2 weeks post-harvest showed dark staining occurred predominantly at hull slip when the hull no longer adhered to the shell. Dark staining was first detected 8-10 days prior optimum harvest and the incidence increased after the first harvest shake. Fungal pathogens were isolated from pistachio hull and shell from each sampling period where dark staining was recorded. Alternaria, Fusarium, Penicillium and Rhizopus were isolated from pistachio hulls and dark stained shells. Findings were inconclusive to confirm fungi were solely responsible for dark staining as fungi were also isolated from clean unblemished shells. Fungal isolations from infected fruit were used to inoculate fruit to reproduce dark staining of shells. Dark staining occurred up to 28 days after artificial inoculation, but staining was dissimilar in appearance to the industry grade. Scanning electron microscopy (SEM) has shown decomposition of dark stained shells. Preliminary analysis of polyphenol oxidase (PPO) showed little association of enzyme browning with dark staining of pistachios.

Hidden pathogens in soybean seed detected in the United States and Europe

Dr Kristina Petrović, Dr Febina Mathew, Dr Vuk Đorđević, Dr Svetlana Balešević Tubić, Dr Jegor Miladinović, Dr Zlatica Miladinov, Dr Slobodan Krmanović

Institute of Field and Vegetable Crops, Novi Sad, Serbia, South Dakota State University, Brookings, USA

Diaporthe (Phomopsis) seed decay is a major disease of soybean (Glycine max L.) worldwide. The infected seed typically appear to be small, wrinkled, elongated and occasionally white or chalky. However, seed without symptoms (latent infections) are more common than the typical seed decay symptoms. Since species of Diaporthe exist in seemingly healthy seed, they are capable of spreading greater distances, thus increasing the risk of epiphytotic attack in soybean production areas where these pathogens are unknown. In this study, 45 isolates of Diaporthe were recovered from seed sampled from soybean fields affected by seed decay in eight U.S. states and 117 isolates from seed collected in Serbia, one of the major soybean-producing region in Europe. It was identified ten different Diaporthe species on soybean seed in the U.S. and seven in Serbia based on morphology and phylogenetic analyses of the internal transcribed spacer, the partial translation elongation factor 1-alpha, large subunit and beta-tubulin genes. Diaporthe population on soybean seed is different between these two regions, but there are species that occur in both of them such as D. caulivora, D. longicolla, and D. sojae, while D. longicolla was commonly recovered species. Pathogenicity tests performed with isolates from the U.S. and Europe showed that all of the detected species of Diaporthe negatively affect the soybean seed quality and germination. The incidence of all identified species of Diaporthe in soybean seed was more than 80%. This study clarified the structure and pathogenicity of Diaporthe population present in soybean seed in the U.S. and Europe in order to preserve the effective role that biosecurity agencies play in keeping unwanted phytopathogens out of the U.S. and Europe. Future research should related to epidemiology as well as possible sources of resistance to species of Diaporthe complex.
Leaf spot a possible source of inoculum of dry flower disease in macadamia in Australia

Assoc Prof Olufemi Akinsanmi¹, Prof Victor Galea², Mr Kandeeparoopan Prasannath¹
¹Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Dutton Park, Australia,
²School of Agriculture and Food Sciences, The University of Queensland, Gatton, Australia

Macadamia nut is cultivated commercially in frost-free tropical and subtropical regions worldwide. In Australia, dry flower caused by Pestalotiopsis macadamiae and Neopestalotiopsis macadamiae is one of the biotic constraints leading to significant yield loss in macadamia. Information on dry flower disease cycle and epidemiology is limited. Leaf spot caused by Pestalotiopsis has been reported in macadamia overseas, however, its role as a possible source of inoculum of the dry flower is not known. Preliminary survey of fungal leaf spots on macadamia trees showed two distinct symptoms. Leaves showing circular dark brown spots with yellow halos (type 1) and irregular dark brown spots (type 2) were collected from macadamia orchards in Queensland. Fungal isolates were obtained from 20 infected leaves and were identified by morphology and DNA sequencing as Pestalotiopsis spp. for type 1 spots and Colletotrichum sp. for type 2 spots. To conduct a pathogenicity test, conidia suspension ($10^6$ conidia/mL) was prepared and sprayed onto 10 healthy leaves of a macadamia potted plant, whereas the control was treated with sterile water. The inoculated plants were kept in plastic bags at high relative humidity overnight and thereafter they were incubated on a bench in a shade house at ~28°C. The pathogenicity tests were repeated three times. Leaf spots similar to the respective field disease symptoms were observed on the inoculated leaves for both type 1 and type 2 spots after 7 days, whereas no visible symptoms appeared on the control leaves. Koch’s postulates were fulfilled for the Pestalotiopsis and Colletotrichum species. Hence, the two leaf spots were distinguished as Pestalotiopsis leaf spot (type 1 spots) and Colletotrichum leaf spot (type 2 spots). This results suggest that Pestalotiopsis leaf spot could act as a source of inoculum of dry flower during flowering stage in macadamia.

Validation of weather based paddy blast disease forecasting model

Dr Kuri Sharanappa¹, Dr MK Prasanna Kumar¹, Dr L Vijay Kumar³, Ms LM Netravathi¹, Ms SB Anusha¹, Dr KT Rangaswamy¹, Dr S Rajendra Prasad¹
¹CAAST NGTAA, Department of Plant Pathology, University Of Agricultural Sciences, Bangalore, India

Regression equations were used as empirical models to predict rice blast caused by Magnaporthe grisea at VC Farm Mandya, Karnataka, India. The empirical based pest predict model developed by ICAR-NICRA, as mobile application was used for the validation of the paddy blast disease in percent severity. The real time weather parameters and diseases data of paddy at VC Farm, Mandya district, Karnataka, India from 2011 to 2016 were used for the development of the forecasting model. The data analysis was done by non-linear regression. The analysis revealed that, blast disease severity depends on the minimum and maximum temperature ranging from 10 to 18°C and 28 to 34°C. Hence, minimum and maximum temperatures were the most important weather parameters for the outbreak of blast disease. Furthermore, model evaluation was done by real time observed and simulated (forecasted) paddy blast disease severity percent data for five important paddy cultivars (Jyothi, Gangavathi Sona, Jaya, HR 12 and IR 64) growing in the Karnataka state. The results revealed that the model overestimated the paddy blast disease severity percent for all the cultivars for the rabi season of 2019. The maximum difference of observed and simulated blast severity was found for Gangavathi Sona followed by Jaya, IR 64, HR 12 and Jyothi. This is due to Gangavathi having tolerance to blast disease compared with others. Statistical measures like relative mean error (ME), root mean square error (RMSE), coefficient of residual mass (CRM) and modeling efficiency (EF) were used to evaluate the model. Based on the statistical evaluation, model performance was good except for Gangavathi and Sona cultivars.
Application of predicted weather data to forecast possible occurrence of bacterial grain rot of rice prior to grain infection

Mr Hyo-suk Kim¹, Mr Yong Soon Shin², Mr Joo Hyeon Park², Mr Mun-Il Ahn², Mr Eun Woo Park¹,4,5
¹Department of Agricultural Biotechnology, Seoul National University, Seoul, South Korea, ²Epinet Corporation, Kumgang Penterium IT Tower, Anyang, South Korea, ³Department of Agro-food Safety and Crop Protection, National Institute of Agricultural Sciences, Rural Development Administration, Wanju, South Korea, ⁴Interdisciplinary Program in Agricultural and Forest Meteorology, Seoul National University, Seoul, South Korea, ⁵National Center for Agrometeorology, Seoul, South Korea

Crop growers should be able to implement better tactics for disease management if disease forecast information is available prior to infection by pathogens. This research aimed to forecast possible occurrence of bacterial grain rot (BGR) of rice in advance of grain infection by using weather forecast data as input to the model. The forecast model used in this study was BGRcast, which was previously developed to estimate conduciveness of weather conditions for inoculum buildup and infection by Burkholderia glumae based on daily mean temperature and relative humidity (RH). The predicted temperature and RH data were obtained from the ensemble prediction system (EPS) of Korean Meteorological Administration, which releases 288-hour forecast once a day for 45 locations in South Korea. For 1 Jan. ~ 31 Dec., 2017, predicted daily means of temperature and RH for each of 11 days to the future from the next day of EPS-data release were extracted and compared with observed data for corresponding days. For each day, 16,425 data points (365 days x 45 locations) were included in the calculation. The RMSE of temperature and the regression analysis on RH indicated that the EPS-data were good enough to be used for BGR forecast. As for the performance of BGRcast, the two-way contingency table analysis on disease warnings by BGRcast based on the EPS-data and the observed weather data showed positive output in terms of bias, probability of detection, and false alarm ratio. In conclusion, the EPS-predicted weather data would be useful to forecast possible occurrence of BGR prior to grain infection by the pathogen. By using predicted weather data instead of observed data in disease forecasting, it would be possible to apply protectant pesticides to protect crops effectively, which would help reduce cost for pesticides and possible development of pesticide resistant pathogens.
Poster Board 25

The association of ice nucleating bacteria and frost damage in the Western Australian (WA) broadacre cropping region

Dr Bec Swift1,2, Dr Sarah Jackson1, Ms Lucy DeBrincat1, Prof Dean Diepeveen1,2, Prof Wayne Reeve2, Mr Jaco Zandberg3, Dr Ben Biddulph1

1Department of Primary Industries and Regional Development, South Perth, Australia, 2Murdoch University, Murdoch, Australia

Damage from frost causes serious losses in agricultural crops around the globe and is estimated to cost Australian grain growers around $400 million each year. In WA, the effect of frost is exacerbated after small rainfall events that occur in the afternoon or evening before a frost event. A possibility that has not been explored within the WA cropping system is whether ice nucleation active (INA) bacteria, either present in the rainwater or existing in the canopy and activated by rainfall could be responsible for the increased sensitivity of cereal plants to frost. For instance, up to $10^4$ colony forming units of ice-nucleating bacteria per litre of rainfall have been isolated in the USA [1]. In this study, we have applied a commercial ice nucleating protein isolated from Pseudomonas syringae to wheat in the field and under controlled conditions. We observed an increase in frost damage to the plants that mimics the frost damage we observe in the field under natural conditions. We have isolated P. syringae from frost affected stubble and seed and rainfall from the 2017 cropping season and are using these isolates to develop methods to rapidly screen isolates for the ability to ice nucleate. Results from this work will be presented and discussed. Ultimately, our strategy is to develop the tools to identify and quantify the ice nucleating activity of the bacteria in our field environment and use these to elucidate the potential role in frost damage they may be having.


Poster Board 18

Suitability of New Zealand regions for the establishment of Xylella fastidiosa based on a temperature cut-off model

Ms Virginia Marroni1, Dr Rebecca Campbell2, Dr Rob Beresford2

1The New Zealand Institute for Plant & Food Research Ltd, Christchurch, New Zealand, 2The New Zealand Institute for Plant and Food Research Ltd, Motueka, New Zealand

Xylella fastidiosa is a xylem-limited, Gram-negative bacterium that is vector transmitted and infects a wide range of host plants. High value crops grown in New Zealand including grape, peach, olives and citrus can be severely infected. Plant diseases associated with infection of X. fastidiosa include Pierce’s disease of grapes, citrus variegated chlorosis, olive quick decline syndrome and phony peach disease. Some native New Zealand plants can also be infected by X. fastidiosa. Winter temperature is a key factor in delimiting the areas where X. fastidiosa can persist between growing seasons. The bacterium distribution is limited if the average minimum temperature in the coldest month of the year falls below 4°C and it is rare if it falls below 1.1°C. In the same way, diseases caused by X. fastidiosa, for instance, Pierce’s disease, only occur in areas with a mild winter. In this study, the suitability of the New Zealand climate to support the establishment of X. fastidiosa was determined by an average minimum July temperature cut-off model. Most regions in the North Island of New Zealand have average minimum July temperatures greater than 4.5°C and they would be highly suitable habitats for X. fastidiosa establishment. Regions in the South Island such as Blenheim and Nelson would be less suitable, with average July temperatures between 1.7 and 4.5°C. According to this model, frost-prone regions in the South Island such as Alexandra and Queenstown would prevent or have a lesser risk of X. fastidiosa establishment and development of related diseases.
Methods to standardise the severity of Botryosphaeriaceae infections in experimental grapevine plant materials

Dr Regina Baaijens1, Dr Mark Sosnowski1,2,3, Mr Matthew Ayres2, Assoc Prof Sandra Savocchia1
1National Wine and Grape Industry Centre, Charles Sturt University, Wagga Wagga, Australia, 2South Australian Research and Development Institute, Adelaide, Australia, 3School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, Glen Osmond, Adelaide, Australia

Grapevine nursery plants have been reported with latent infections of Botryosphaeria dieback (BD) pathogens. However, it is unclear if the BD infections in nursery plants contribute to the disease incidence observed in vineyards. Recent studies also showed that water-stress can increase the susceptibility of young vines to BD. However, latent infections have no internal or external symptoms and may be randomly distributed within a vine, thus, accurate quantification of the incidence and severity of infection is difficult. Investigations on the effects of water stress on young vines artificially inoculated with three different conidial concentrations of Neofusicoccum luteum may provide insight on the infection thresholds that result in disease expression in vineyards. A published inoculation method using a vacuum was evaluated for infiltrating 300 (low), 3,000 (moderate) and 30,000 (high) conidia of N. luteum into dormant grapevine canes (cv. Shiraz). Ringers solution was used to vacuum-inoculate control vines. The qPCR analyses showed the vacuum-inoculation was a reliable method, resulting in the pathogen infecting the basal, middle and apical part of the inoculated canes. qPCR analyses also differentiated the low, moderate and high infections with the highest amount of pathogen detected from canes inoculated with 30,000 conidia and the lowest from those inoculated with 300 conidia. No pathogen was detected in any of the canes inoculated with Ringers solution. This study showed that different levels of N. luteum conidia can be vacuum-inoculated into dormant canes without significant impact on plant viability. The method was used to standardise infection levels of N. luteum in Shiraz rootlings in newly established glasshouse and shade house experiments aimed to investigate the effect of water stress on BD symptom expression.

Yield losses associated with Barley yellow dwarf virus in wheat and barley

Ms Narelle Nancarrow1, Dr Mohammad Aftab1, Dr Grant Hollaway1, Dr Brendan Rodoni2, Dr Piotr Trębicki1
1Agriculture Victoria, Horsham, Australia, 2Agriculture Victoria, Bundoora, Australia

Barley yellow dwarf virus (BYDV) is one of the most common and important viruses infecting cereal crops in Victoria, often resulting in significant yield losses. It is transmitted by several aphid species such as the bird cherry-oat aphid (Rhopalosiphum padi) and the corn aphid (R. maidis). A field experiment was conducted in Horsham, Australia to examine yield losses associated with BYDV infection in wheat and barley. The trial consisted of three treatments: early infection, later infection and a non-inoculated control. Randomised replicated plots of wheat and barley were inoculated with BYDV-PAV using viruliferous R. padi. Aphids were contained in cages that covered the plants within the plot to prevent contamination of control plots. After virus inoculation, cages were removed and plants were sprayed with insecticide. Before maturity, plants were tested by tissue blot immunoassay to confirm virus presence. Plants were harvested then plant height, biomass, grain yield and grain count were assessed. Virus infection significantly reduced yield of wheat by 80% and barley by 64%.
Yield losses associated with Turnip yellows virus infection in field peas and lentils

Ms Narelle Nancarrow1, Dr Mohammad Aftab1, Dr Grant Hollaway1, Dr Brendan Rodoni2, Dr Piotr Trębicki1
1Agriculture Victoria, Horsham, Australia, 2Agriculture Victoria, Bundoora, Australia

A number of virus species affect pulse crops in Australia, with many primarily transmitted by insect vectors such as the green peach aphid (Myzus persicae). Turnip yellows virus (TuYV) is one of the most damaging viruses in south eastern Australia and has a wide host range, also affecting canola. In 2018, field trials were established in Horsham, Victoria to examine yield losses associated with TuYV infection in field peas and lentils. Plots (8m x 6 row) of field peas and lentils were sown in a random block design and infected with TuYV early in the growing season. Plants were inoculated by placing green peach aphids which had been feeding on virus infected plants into the plots of lentil and field pea selected for virus treatment. Inoculated and control plots were covered with cages to contain the aphids and prevent contamination of control plots. After the virus inoculation period, cages were removed and the trial was sprayed with insecticide. Plants were monitored for symptom development throughout the season before they were harvested and grain yields were evaluated. Randomly selected plants were sampled and tested for TuYV infection using tissue blot immunoassay. Despite high TuYV infection rates, no obvious symptoms of virus infection were observed in inoculated lentil or field pea at any time throughout the growing season, however yield was significantly reduced in both field pea and lentil due to virus infection. The lack of visible symptoms in lentils and field peas infected with TuYV has implications for crop health assessments. Further epidemiological studies are needed to evaluate the interactions between pulse crops, virus infection and yield losses.

Epidemiology of Pyrenophora tritici repens and Parastagonospora nodorum coinfection of wheat with contrasting host resistance profiles

Dr Chala Turo1, Dr Ayalsew Zerihun1, Prof Mark Gibberd1
1Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Perth, Australia

Pyrenophora tritici repens (Ptr) and Parastagonospora nodorum (Pn) are two of the most damaging foliar fungal pathogens of wheat, collectively causing estimated annual losses of $247M in Western Australia (WA) alone, of which ca. 44% is due to Pn [1]. In the WA wheatbelt, Ptr and Pn are thought to commonly co-infect wheat on the basis of visual assessments, and as such the resultant diseases are referred to as yellow spot-septoria nodorum blotch disease complex [2]. Here, we report on results from extensive longitudinal surveys (>4000 samples) and qPCR quantification of Ptr and Pn infection throughout wheat development (Z12-Z75), over two seasons, from four representative agroecological zones in the WA wheatbelt. The survey included six wheat varieties, with varying degrees of resistance to Ptr and Pn. The multi-season and -location qPCR results showed that with the exception one site in 2017, Pn was a minor component of the disease complex regardless of the host genotype resistance ratings, and more so in the southern regions (contribution to total pathogen load decreased along a north-south latitudinal gradient). In addition to the regional prevalence gradient, there was a clear phenological pattern revealing that Ptr progressively dominated Pn as the crop developed, such that in the all-important grain-filling upper-canopy leaves, Pn was, if present at all, a tiny component of the total Ptr-Pn pathogen load. These results provide very strong imperative for re-evaluation of crop loss attributions due to these pathogens, at least in WA wheatbelt where much of the national crop loss due to these pathogens is thought to occur.

Determining *Peronospora somniferi* genotype diversity and its potential impact on management of systemic downy mildew of opium poppy

**Miss Dharushana Thanabalasingam**, Dr Tamil Thangavel², Mrs Krithika Krishnamoorthy³, Dr Calum Wilson², Dr Suzie Jones¹, Dr Jason Scott¹

¹Tasmanian Institute of Agriculture, University of Tasmania, Burnie, Australia, ²Tasmanian Institute of Agriculture, University of Tasmania, New Town, Australia

Opium poppy (*Papaver somniferum*) is grown for its pharmacologically important opiates (1). Australian production comprises over 50% of the world’s licit production and is primarily based in Tasmania with limited production in mainland Australia. Outbreaks of a new systemic form of downy mildew (SDM) in 2014 raised significant industry concern (1). SDM infections were characterised by stunted and deformed plant growth, often leading to early plant death. *Peronospora somniferi* was identified as the causal organism of SDM (1). The level of diversity within Australian populations of *P. somniferi* is unknown. However, recently an isolate of *P. somniferi* that caused localized lesions rather than a typical systemic infection was noted. This suggests the presence of races in the *P. somniferi* population of Australia. To address this knowledge gap, simple sequence repeat (SSR) markers were developed following construction of a whole genome assembly of a *P. somniferi* individual using Illumina paired end reads. Repeats of tri- and quad-base pair motifs were targeted for further marker development. Primers were developed for screened SSR marker regions and sanger sequencing was used to confirm target region and marker polymorphism. Polymorphic SSR markers were tested against different field *P. somniferi* individuals to identify the level of diversity present, with marker fragments sized by capillary electrophoresis. The outcomes of this study will be presented at the meeting. Studies to examine potential links between pathogen genotype and host symptom response are planned to follow.

Horizontal gene transfer has boundaries: site saturation restricts the movement of an Integrative and Conjugative Element in plant pathogenic ‘Erwinias’

Mr Luciano Nunes-Leite1,2, Dr Peter C. Fineran3, Dr Artemio Mendoza-Mendoza1, Dr Andrew R. Pitman1,4

1Bio-Protection Research Centre - Lincoln University, Lincoln, New Zealand, 2The New Zealand Institute for Plant and Food Research, Lincoln, New Zealand, 3Department of Microbiology and Immunology and Bio-protection Research Centre - University of Otago, Dunedin, New Zealand, 4The Foundation for Arable Research, Christchurch, New Zealand

Horizontal transfer of Mobile Genetic Elements is considered pivotal to the evolution of bacteria as it enables rapid exchange of genetic information between bacteria. Integrative and Conjugative Elements (ICEs) are mobile genetic elements that are transferred largely by conjugation between two bacterial cells. The scarce number of studies concerning the frequency of transfer have been predominantly conducted on highly similar strains or non-related bacterial species, impeding the comprehension of its ecological significance. In this study, the conjugative transfer of Horizontally Acquired Island 2 (HAI2), an ICE that enhances virulence of the potato pathogen Pectobacterium atrosepticum SCRI1043, was investigated by assessing frequency of acquisition into strains of SCRI1043 in which HAI2 had been removed. HAI2 was transferred into engineered recipients confirming it as indeed a functional ICE. Further functional analysis of the island using mutants with deletions in selected core genes of HAI2 demonstrated that the process of conjugation is decoupled from the initial excision of the island from the host genome. To understand whether HAI2 was likely to be transferred to related bacteria within the ecological niche of Pectobacterium atrosepticum SCRI1043, conjugation assays were conducted in vitro and in planta using plant pathogenic ‘Erwinia’ strains belonging to the genera Pectobacterium, Dickeya and Pantoea from New Zealand and overseas. Thirty-two PCR-positive isolates for at least one HAI2-compatible bacterial attachment (attB) site were selected. Surprisingly, HAI2 was not acquired by any of the selected isolates. A screen of the genome sequences of these potential recipients and other publically available ‘Erwinia’ genome sequences revealed that the necessary attachment sites were almost always occupied. A number of different mobile elements is seemingly integrated at these spots in ‘Erwinia’ chromosomes, suggesting that horizontal transfer of ICEs may be restricted by previous acquisition of mobile elements. This work has significant implications for our understanding of the barriers to acquisition of ICEs.
Contrasting genetic diversity and structure among Malagasy *Ralstonia pseudosolanacearum* phylotype I populations inferred by a novel Multilocus Variable Number of Tandem Repeat Analysis scheme

Miss Hasina Ny Aina Rasoamanana¹, PhD Santatra Ravelomanantsoa², PhD Noura Yahiaoui¹, Mr Jean-Jacques Chéron³, Mrs Karine Boyer³, Mr Niry T Dianzinga¹, Mrs Mihaëllosoa-Mirana Gache¹, HDR Olivier Pruvost³, PhD Laurent Costet³, PhD Adrien Rieux³, HDR Isabelle Robène³, PhD Gilles Cellier⁴, PhD Fabien Guérin¹, Prof Stéphane Poussier¹

¹University of La Réunion, Unité Mixte de Recherche, Peuplements Végétaux et Bioagresseurs en Milieu Tropical (UMR PVBMT), Saint-Pierre, France, ²Centre National de la Recherche Appliquée au Développement Rural (CENRADERU/FOFIFA), Antananarivo, Madagascar, ³Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), Unité Mixte de Recherche, Peuplements Végétaux et Bioagresseurs en Milieu Tropical (UMR PVBMT), Saint-Pierre, France, ⁴Agence Nationale de Sécurité Sanitaire de l’Alimentation, de l’Environnement et du Travail (ANSES), Laboratoire de la Santé des Végétaux, Saint-Pierre, France

The *Ralstonia solanacearum* species complex (RSSC), composed of three species and four phylotypes, comprises soilborne bacteria globally distributed with a very broad host range. In 2009, a devastating potato bacterial wilt outbreak was declared in the central highlands of Madagascar, which reduced the production of important crops including potato, eggplant, tomato and pepper. In order to manage the disease, a molecular epidemiology study of RSSC strains was carried out between 2013 and 2017 to identify the *R. pseudosolanacearum* phylotypes I and III and the *R. solanacearum* phylotype II. A previous population biology analysis of phylotypes II and III using two MLVA schemes revealed a clonal narrow epidemic phylotype II, and a diverse endemic phylotype III. In this study, we developed a novel MLVA scheme (RS1-MLVA14) to characterize phylotype I strains with the purpose of understanding their diversity and genetic structure. The collection included strains isolated from 16 fields of different Solanaceae species in the regions of Vakinankaratra and Itasy (highlands) in 2013 (133 strains) and in the region of Atsinanana (lowlands) in 2006 (27 strains). Thirty-one haplotypes were identified, two of them being prevalent: MT7 and MT4 (sequevar I-18). Genetic diversity analysis revealed a contrasting level of diversity according to elevation and sampling region. More diverse at low altitude than at high altitude, the Malagasy phylotype I strains were structured in two clusters, probably resulting from different historical introductions. Moreover, different epidemiological patterns were observed with an epidemic pattern at high elevation and an endemic pattern at low elevation. Interestingly, the most prevalent Malagasy phylotype I strains showed a strong specificity and were genetically distant from worldwide strains. In this work, we demonstrated that the RS1-MLVA14 scheme is highly resolutive from regional to field scales and is thus perfectly suited for deciphering the epidemiology of phylotype I populations.
Poster Session 3 - Evolution & Diversity  
Thursday 28 November 2019, 12:00 PM - 12:30 PM

Poster Board 72

Linking the present to the past: genome sequencing delineates persistent isolates of the skeleton weed biocontrol agent *Puccinia chondrillina* in Australia

**Dr Gavin Hunter¹, Dr Kylie Ireland¹, Dr Mireille Jourdan², Dr Jim Cullen¹, Dr Louise Morin¹**  
¹CSIRO, Canberra, Acton, Australia, ²CSIRO European Laboratory, Montpellier, Montferrier-sur-Lez, France

*Puccinia chondrillina* was the first fungal pathogen released for weed biological control in the world. The fungus was released to specifically target skeleton weed (*Chondrilla juncea*), a deep-rooted perennial native to Europe and Asia, that negatively impacts the Australian grains industry. Three clonal forms of skeleton weed exist in Australia, narrow, intermediate and broad-leaf forms and four isolates of *P. chondrillina* have been released into Australia to control two of these forms. *Puccinia chondrillina* isolate IT32 was released in 1971 to control the narrow-leaf form of skeleton weed, while isolates TU21, IT36 and TU788 were released to control the intermediate-leaf form in 1980, 1982 and 1996 respectively. Since these releases no studies have been undertaken to determine the genetic and phenotypic stability of *P. chondrillina* in Australia nor to confirm which isolates have persisted. To remedy this, genome sequencing of original and contemporary (2007 and 2016) *P. chondrillina* isolates was undertaken. Pathogenicity phenotypes of contemporary isolates were confirmed through cross-inoculation studies while Single Nucleotide Polymorphism (SNP) analyses revealed three genetically distinct clusters. All contemporary *P. chondrillina* isolates from the narrow leaf form of skeleton weed clustered with the original IT32 isolate. However, none of the contemporary *P. chondrillina* isolates collected from the intermediate leaf form clustered with the original isolates TU788, IT36 or TU21 but instead formed a single cluster distant to the others suggesting an undocumented or in lieu intermediate isolate of *P. chondrillina* was released in the past. To date, no evidence of genetic instability of the narrow *P. chondrillina* isolate has been detected, though analyses continue. Results from this study will provide valuable information on the stability of the *P. chondrillina* – *C. juncea* pathosystem in Australia and provide a window into past releases which could not be discerned by a study of pathogenicity phenotypes alone.
Is *Pseudomonas syringae* pv. *actinidiae* (Psa) adapting to kiwifruit?

**Ms Saadiah Arshed**, Ms Lauren Hemara\(^1\,^2\), Ms Magan Schipper\(^3\), Dr Joel L. Vanneste\(^3\), Dr Jay Jayaraman\(^1\), Assoc Prof Matthew D. Templeton\(^1\,^2\)

\(^1\)The New Zealand Institute for Plant and Food Research Limited, Auckland, New Zealand, \(^2\)The University of Auckland, Auckland, New Zealand, \(^3\)The New Zealand Institute for Plant and Food Research Limited, Ruakura, New Zealand

In 2010, the *Pseudomonas syringae* pv. *actinidiae* (Psa) incursion decimated *Actinidia chinensis* var. *chinensis* ‘Hort16A’ kiwifruit plants in New Zealand. The kiwifruit industry has since recovered largely due to the introduction of the Gold3 cultivar (*Actinidia chinensis* var. *chinensis* ‘Zesy002’) in combination with orchard management and Psa control practices such as copper application. However, little is known of whether Psa is evolving and adapting to kiwifruit. In order to determine whether there are signatures of adaptation within Psa genomes, we undertook a high-throughput sequencing survey of twenty Gold3 kiwifruit orchards in the North Island of New Zealand. Over 500 symptomatic leaf tissues were sampled and 192 Psa isolates were whole-genome sequenced over two growing seasons. Additionally, we collected and sequenced Psa isolates from the Actinidiae germplasm in New Zealand, which is a source of novel resistant cultivars important for breeding. The resultant genomes were then mined for changes in the pathogen effector complement and the acquisition of copper resistance conferring integrative conjugative elements (ICEs) or plasmids. We identified changes in the effector complement in a proportion of Psa isolates from the Actinidiae germplasm. Furthermore, we identified an isolate with major effector deletions that appeared to confer increased disease symptoms in *Actinidia arguta*. A proportion of Psa isolates were also identified to have acquired copper resistance conferring ICEs and plasmids. These results highlight the importance of Psa adaptation studies as the appearance of Psa isolates with an expanded host range or increased virulence will provide ongoing challenges for kiwifruit growers. Furthermore, the results from this study are beneficial as they directly inform the strategies used by breeders to improve Psa tolerance in new cultivars.
Genetic characterisation of South African *Pyrenophora teres* isolates using DArTseq™

**Miss Buddhika Dahanayaka**, Dr Niloofar Vaghefi¹, Dr Noel Knight¹, Dr Renée Prins²,³, Dr Lislé Snyman⁴, Dr Anke Martin¹

¹University Of Southern Queensland, Centre for Crop Health, Toowoomba, Australia, ²CenGen (Pty) Ltd, 78 Fairbairn Street, South Africa, ³Stellenbosch University, Department of Genetics, Matieland, South Africa, ⁴Department of Agriculture and Fisheries Queensland, Hermitage Research Facility, 604 Yangan Rd, Warwick, Australia.

Net blotch causes significant yield losses to barley industries worldwide. It occurs as net form of net blotch, caused by the fungus *Pyrenophora teres* f. *teres* (*Ptt*) and spot form of net blotch, caused by *P. teres* f. *maculata* (*Ptm*). Distribution of *P. teres* extends to all barley growing regions of the world. This study aimed to characterise the genetic diversity and structure of *P. teres* stains collected from eight barley fields located in the Western Cape of South Africa. A total of 89 isolates (73 *Ptt* and 16 *Ptm*) were genotyped through Diversity Arrays Technology, which resulted in 7,156 markers after quality filtering. Model based and distance based clustering methods without *a priori* assumptions were implemented to characterise the genetic structure of the population. These analyses clustered the *Ptt* and *Ptm* isolates into genetically distinct groups. Model based and distance based cluster analyses conducted exclusively for *Ptt* isolates detected four and two clusters, respectively. For *Ptm* isolates, both analyses detected two clusters. Analysis of molecular variance and discriminate analysis of principal component analyses indicated no significant genetic variation among isolates when grouped by collection location. The ratio between mating type 1 and 2 for *Ptt* and *Ptm* did not deviate significantly from the 1:1 ratio expected under panmixia. Studying the genetic structure of *P. teres* populations will enable investigation of temporal genetic changes and potential adaptation of the pathogen. This will allow better management of disease incursions and pathogen control through strategic deployment of resistances.
Poster Board 26

Investigating the potential role of ring nematodes (*Mesocriconema xenoplax*) in predisposing plum trees to bacterial canker infection

Ms Khumbuzile Bophela¹, Dr Joyce Jordaan², Dr Yolanda Petersen³, Prof Carolee Bull⁴, Prof Teresa Coutinho¹
¹Centre for Microbial Ecology and Genomics/Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa, ²Department of Statistics, University of Pretoria, Pretoria, South Africa, ³Crop Development Division, Agricultural Research Council, Infruitec-Nietvoorbij, Stellenbosch, South Africa, ⁴Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, State College, USA

The sudden decline of plum trees was reported in production areas of the Western Cape province of South Africa in 2015. The cause of the tree mortality was unknown. A range of factors was thought to be responsible, namely, bacterial canker, drought and ring nematodes, or a combination of the three. The objective of this study was to determine if there was a link between bacterial canker outbreaks and the presence of ring nematodes in plum orchards. Orchard assessments were conducted in March and October 2017 and 2018 in the major plum production areas of the Western Cape. Trees were assessed for symptoms of bacterial canker. Rhizospheric soil samples were collected from plum trees displaying these symptoms. Nematodes were extracted from the soil samples using a centrifugal flotation technique, and ring nematodes were counted per 250ml of soil using a stereo-microscope. The internal transcribed spacer (ITS) region was sequenced for representative ring nematodes, and a phylogenetic tree was constructed using a maximum likelihood analysis. Overall, there was no association between bacterial canker and ring nematode densities. A unit change of ring nematode densities increased the probability of bacterial canker infection by 1% only, and there were no significant differences in the least square means of ring nematode values between asymptomatic and infected plum trees. The majority of the ring nematode specimens were identified as *Mesocriconema xenoplax*. These results support previous reports of *M. xenoplax* as the common ring nematode species present in plum orchards in the Western Cape. The knowledge of the specific species of ring nematodes and relevant information on tolerant rootstocks, cultivars and time of the season of prevalence, can assist in the development of management strategies controlling ring nematode populations in plum orchards.

Poster Board 30

Where does *Austropuccinia psidii* have sex?

Dr Alistair McTaggart¹, Dr Louise Shuey², Dr Stuart Fraser³, Dr Jolanda Roux⁴, Ms Esna du Plessis⁴, Ms Ginna Granados⁶, Dr Irene Barnes⁵, Prof Mike Wingfield⁴, Prof Andre Drenth¹
¹University of Queensland, Brisbane, Australia, ²Queensland Department of Agriculture and Fisheries, Brisbane, Australia, ³SCION, Rotorua, New Zealand, ⁴University of Pretoria, Pretoria, South Africa

*Austropuccinia psidii* is recognized by its prominent urediniospores, the clonal spore stage that infects species of Myrtaceae. Its sexual stage, teliospores, produce gametic basidiospores as the product of meiosis. Two different life cycles of *A. psidii* were hypothesized; either it completes its life cycle on one host, or an alternate stage occurs on an unknown host. Previous studies tested these hypotheses but were inconclusive. We tested the role of basidiospores *in vivo* and in invasive populations to determine whether this spore stage could infect Myrtaceae and whether *A. psidii* reproduces sexually. We amplified five microsatellite loci from pustules on a plant inoculated with basidiospores, and from invasive populations in New Zealand and South Africa. Recombinant genotypes and high genotypic diversity were used as evidence of infection by basidiospores *in vivo*. Presence of a sexual stage, high genotypic diversity and linkage equilibrium were used as evidence for recombination in invasive populations. Our data showed *A. psidii* completes the asexual and sexual parts of its life cycle on Myrtaceae, and meiotic recombination produces basidiospores that infect species of Myrtaceae under controlled conditions and in invasive populations.
Pathogenicity and new records of exotic blue stain fungi on Pinus in Australia

Dr Angus Carnegie, Dr Rosalie Daniel, Fiona Lidbetter, Dr Andrew Daley, Dr Matthew Laurence, Mr Matthew Nagel, Mr David Sargeant, Dr Tuan Dong, Dr Mike Wingfield

1Department of Primary Industries - Forestry, Parramatta, Australia, 2Department of Primary Industries - Plant Biosecurity, Ourimbah, Australia, 3Department of Primary Industries - Plant Biosecurity/EMAI, Cambden, Australia, 4Royal Botanic Gardens, Sydney, Australia, 5University of Pretoria, FABI, South Africa

Species of Ophiostoma and Diplodia are significant pathogens of Pinus worldwide, causing blue stain and in some cases tree mortality. These fungi on Pinus are non-native to Australia. Species in Ophiostomataceae are generally vectored by bark beetles, unlike species of Diplodia. Both O. ips (detected in 1943), vectored by the bark beetle Ips grandicollis, and Diplodia sapinea (detected in 1912) have been associated with significant damage to Pinus plantations in Australia, especially following drought. Despite their importance, there have been few taxonomic studies on these species in Australia. Blue stain associated with Ips bark beetles is generally assumed to be caused by O. ips, or if no bark beetles are present by D. sapinea. During the past several years we have conducted surveys and sampling specifically to detect cryptic Pinus-infecting fungi. Fungi isolated following surveillance throughout NSW were identified using DNA sequencing and phylogenetic inference. We detected four species of Ophiostomataceae new to Australia: O. pallidulum, O. angusticollis, Sporothrix abietina and Graphilbum fragrans. And Grosmania huntii was confirmed from NSW. Following the recent detection of D. scrobiculata from Queensland (Ramsden, Narhung, Tan unpublished), we detected this species in northern NSW. Pathogenicity tests on 18-month-old seedlings of P. radiata and P. taeda revealed significant variation in lesion length after two months. Ophiostoma ips resulted in significantly longer lesions (~16‒19 mm) than the other species of Ophiostomataceae (<10 mm), except one isolate of G. huntii on P. taeda (~15 mm). Diplodia sapinea lesions (~21‒35 mm) were significantly larger than those of D. scrobiculata (~8‒16 mm). There were no significant differences in lesion lengths on the two Pinus species for the different blue stain isolates. Although none of these newly detected fungi were considered feasible or cost-beneficial to eradicate, this work highlights the need for a greater emphasis on biosecurity surveillance targeting cryptic pests.
The Australian almond industry has grown rapidly over the last 15 years, from 5,230 ha in 2001 to 39,662 ha in 2017 and covers different geographic areas and growing practices. To maintain the quality expected by consumers, and the high yields needed by industry, it is necessary for producers to understand the range of economically important diseases present in Australian almond orchards. To accurately determine the most prevalent diseases affecting Australian almonds, extensive sampling was carried out across the almond growing regions of Australia: Sunraysia, Victoria; Riverland and the Adelaide Plains, South Australia; Riverina, New South Wales; and Wheatbelt, Western Australia during the 2017-18 and 2018-19 growing seasons. More than 250 samples were collected and at least 270 isolates of potentially pathogenic organisms obtained. Growers previously identified hull rot and lower limb dieback as their major diseases of concern, and a high incidence of these was observed. In addition, many examples of trunk diseases, leaf spots and fruit rot symptoms were observed. While some diseases can be identified visually e.g. rust, many have overlapping symptoms. Similar symptoms can be caused by different pathogens. For example, hull rot has been attributed to four fungal pathogens in California, and trunk diseases are well known to be caused by pathogen complexes. We are compiling a comprehensive reference collection of potential pathogens isolated from almond disease symptoms. This will provide a resource for further research into pathogenicity, which will inform more accurate diagnosis and management of diseases in Australian almond orchards.

Identification of quantitative trait loci and candidate genes associated with ascochyta blight resistance in the interspecific RIL population

Mr Rama Harinath Reddy Dadu¹, Dr Dorin Gupta¹, Dr Rebecca Ford², Dr Sukhjiwan Kaur³, Dr Ido Bar², Dr Janine Croser⁴, Dr Federico Ribalta⁴, Dr Prabhakaran Sambasivam²

¹University Of Melbourne, Dookie College, Australia, ²Griffith University, Nathan Campus, Australia, ³Agriculture Victoria, Bundoora, Australia, ⁴University of Western Australia, Crawley, Australia

The Australian lentil industry is affected by various biotic stresses where ascochyta blight (AB) caused by Ascochyta lentis is one of the devastating fungal diseases that results in substantial yield losses. Cultivation of AB resistant cultivars remains the preferable long-term environmentally and economically viable strategy. However, the breakdown of AB resistance of some of the major sources (such as Northfield and Nipper) suggests the need for introgression of new and diverse resistance genes to widen the genetic base of cultivars and to improve cultivar stability against the disease. Successful introgression entails an understanding of the genetic basis of resistance. In this context, using a biparental mapping population derived from a cross between a recently identified AB resistant accession ILWL 180 (Lens orientalis) and susceptible cultivar ILL 6002, a genetic linkage map has been constructed using single nucleotide polymorphism (SNP) markers generated using genotyping-by-sequencing transcript (GBS-t) approach. Genetic dissection of the RIL population revealed a QTL associated with resistance to AB on linkage group 5. The identified QTL region stretched 4.93 cM and harbored nine putative candidate defence-related genes linked to AB resistance. Furthermore, three nonsynonymous mutations within coding sequences of three putative candidate genes (Uroporphyrinogen decarboxylase (UROD); Glutathione S transferase DHAR3, chloroplastic (GST-DHAR3; and Protein EXECUTER 2, chloroplastic isoform X1 (PEXE2)) related to defence mechanisms against A. lentis were predicted. The QTL analysis and the candidate gene information are expected to contribute to the development of diagnostic markers and enable marker-assisted selection (MAS) in lentil breeding programs.
Nuclear fibrillarin and coilin are negative regulators of potato plant resistance to biotic and abiotic stresses mediated by salicylic acid

Dr Natalia Kalinina1,2, Miss Antonida Makhotenko1,2, Dr Michael Taliansky1,3
1Pushino Branch Of Shemyakin-Ovchinnikov Institute Of Bioorganic Chemistry Ras, Pushchino, Moscow Region, Russian Federation, 2Belozersky Institute of Physico-Chemical Biology, Lomonosov Moscow State University, Moscow, Russian Federation, 3The James Hutton Institute, Dundee, United Kingdom

Fibrillarin and coilin are nuclear proteins localized mainly in the nucleolus and Cajal bodies, respectively. In addition to their traditional function in biogenesis of various nuclear RNPs, both these proteins have been shown to participate in virus-host interactions and responses to abiotic stress. Here, we demonstrated that fibrillarin or coilin over-expression in transgenic potato plants (cv. Chicago) lead to a significant increase in plant sensitivity to heat stress (manifested as aggravated symptoms) and infection with potato virus Y (PVY) (manifested as enhanced virus accumulation and symptoms). In contrast, a reduction of fibrillarin or coilin in potato plants, achieved by CRISPR/Cas editing, markedly suppressed PVY infection and increased thermotolerance. To provide molecular insights into the functional roles of these proteins in responses to stress, we analysed expression of genes encoding pathogenesis-related (PR) proteins [as markers of salicylic acid (SA)-mediated defence] and heat shock proteins (HSPs). Over-expression of coilin or fibrillarin significantly inhibited the expression of PR-genes in plants infected with PVY at normal (22°C) and particularly at elevated (28°C) temperature. Expression of HSP-genes observed at the elevated temperature was also inhibited by over-production of coilin or fibrillarin. Interestingly, the SA pretreatment subverted the sensitive combined or individual (PVY and heat) stress phenotypes induced in transgenic plants by over-expression of coilin and fibrillarin. These findings suggest that SA-mediated plant defence response against PVY and heat stress may be negatively regulated by a hitherto unrecognised mechanism involving fibrillarin and coilin.

Ascochyta blight resistance in faba bean: marker development and fine mapping

Mrs Levina Pieter1, Dr Ahsan Asif1, Mrs Sara Blake1,2, Dr Jeffrey Paull1, Prof Diane Mather1
1University Of Adelaide, Urrbrae, Australia, 2South Australia Research Development Institute (SARDI), Urrbrae, Australia

Faba bean (Vicia faba L.) is an important crop in Australia, accounting for 10–15% of the annual pulse crop. Ascochyta blight, caused by Ascochyta fabae Speg, is a serious fungal foliar disease that can substantially reduce the yield of faba bean. Recently, a new pathotype of A. fabae emerged in Australia. Some previously resistant cultivars are susceptible to the new pathotype. Differences in resistance between the cultivars Farah (susceptible) and Nura (resistant) have already been genetically mapped at two loci (AB_N1 and AB_N2) in the faba bean genome (1). Molecular markers linked with those loci are of some use in the Australian faba bean breeding program but are not completely diagnostic of ascochyta blight resistance. To provide alternative markers and to fine map AB_N1 and AB_N2, new assays for 16 single nucleotide polymorphisms (8 linked with AB_N1 and 8 linked with AB_N2) were developed. New markers were assayed on resistant and susceptible germplasm and on 168 individual Nura/Farah progeny. Genetically informative progeny were selected, grown in the glasshouse and inoculated at the 3-4 node stage with a spore suspension of a check isolate of the new pathotype. Percent stem area diseased and percent leaf area disease was rated. Comparison of phenotypic and genotypic data should improve the position estimates for the resistance loci. This could lead to the identification of candidate genes and provide useful molecular markers for use in faba bean breeding.

An emerging biosecurity risk: Tomato brown rugose fruit virus

Dr Xuemei Ji, Dr Chandra Warnakula, Dr Neil Grant
1The Department of Agriculture, Canberra, Australia

Australia imports large quantities of seeds annually to produce a wide range of crops, including vegetables. The vegetable seed trade has become globalised and is evolving. In addition, the distribution of seed-borne pathogens are also expanding globally and new risks continually emerge. Tomato brown rugose fruit virus (ToBRFV) is an emerging biosecurity risk to Australian primary producers. This virus naturally infects tomatoes and capsicums resulting in unmarketable fruit—potentially risking Australian industries with an annual production valued at $827 million. The first outbreak of ToBRFV occurred in tomato production in Israel during 2014 and the virus was reported in Jordan (2015), Mexico, Germany, USA-California (2018), Italy, Northern Palestine, Canada and China (2019). Its distribution may be greater than in published records but it is not known to be present in Australia. Global movement via seed is the only credible explanation for the observed intercontinental movement of this virus. Responding to the emerging risk posed by ToBRFV, Australia introduced emergency measures for imported tomato and capsicum seeds for sowing on 5 March 2019. This is a story about implementing effective biosecurity measures against constantly evolving pathogen risks associated with imported seeds, while ensuring the measures are the least trade restrictive. Details of the emergency measures against ToBRFV are on the department’s website:

Colletotrichum: a headache for Australian biosecurity

Dr Vera Andjic, Mrs Doris Mercado-Escueta, Dr Aaron Maxwell
1Department Of Agriculture, Perth, Australia

Colletotrichum (Ascomycota, Sordariomycetes) presents a multitude of problems for Australia’s biosecurity system. It is a destructive pathogen with a wide host range that includes economically important hosts, is often cryptic and taxonomically complex and dependent on multi locus molecular phylogenetic analysis (1). Australia remains free of many economically important Colletotrichum species such as C. acutatum citrus biotype and C. lentis on lentils (2). World-wide there are numerous examples of the introduction of invasive disease as the result of the international plant trade (3). In Australia the Department of Agriculture imposes biosecurity controls on imported plants that include inspection, growth in post entry quarantine, and destruction of diseased consignments. Australia imports approximately 2.85 million ornamental plants each year (DA Nursery stock database, 2018). The following exotic Colletotrichum species were identified from diseased imported plants using multi locus DNA sequencing (ITS, TUB, GAPDH, CAL and GS): C plurivorum (Phalaenopsis), C. orchidearum (Hoya, Phalaenopsis, Zamioculcas), C. cliviae (Clivia) and Colletotrichum sp. nov (Hoya). Species of limited distribution in Australia: C. siamense (Hoya, Sansevieria), C. sansevieriae (Sansevieria). Affected consignments were deep buried and as a consequence Australia remains free of these species.
Assessing testing efficiencies using pospiviroid prevalences in tomato and capsicum seed lots

Dr David Dall\textsuperscript{1}, Dr Lindsay Penrose\textsuperscript{1}, Dr Andrew Daly\textsuperscript{2}, Dr Fiona Constable\textsuperscript{1}, Dr Mark Gibbs\textsuperscript{1}

\textsuperscript{1}Australian Government Dept of Agriculture, Canberra, Australia, \textsuperscript{2}NSW Department of Primary Industries, Elizabeth Macarthur Agricultural Institute, Menangle, Australia, \textsuperscript{3}Agriculture Victoria Research, AgriBio, Bundoora, Australia

Laboratory testing for pospiviroids in tomato and capsicum seed lots proposed for commercial import into Australia, using 12,000 to 40,000 seeds sampled per lot, has enabled the development of empirically-derived distribution curves for viroid prevalences in those commodities. The distribution curves can be linked to statistically-based estimates of detection efficiency that would be realised using smaller sample sizes. Calculations using the binomial distribution show that sample sizes of 3,000 and 9,400 seeds allow detection of viroid prevalences of 0.1\% and 0.032\%, respectively, with 95\% confidence. Applying those calculations to observed viroid prevalences in the least-contaminated one-third of tomato seed lots, it is estimated that use of sample sizes of 3,000 and 9,400 seeds would on average detect 13.5\% and 35.7\%, respectively, of the contaminated seed lots identified with larger sample sizes. In contrast, it is estimated that use of a sample size of 20,000 seeds would detect 59.8\% of those seed lots at the same level of confidence. It is concluded that the imposts that accompany testing of larger sample sizes represent an appropriate investment in agricultural biosecurity for Australia.

Tobamovirus infected tomato and capsicum seed shipments to Australia

Dr David Lovelock\textsuperscript{1}, Mr Ossie Wildman\textsuperscript{2}, Dr Andrew Daly\textsuperscript{2}, Dr Brendan Rodoni\textsuperscript{1}, Dr Fiona Constable\textsuperscript{1}

\textsuperscript{1}Department of Jobs, Precincts and Regions, Bundoora, Australia, \textsuperscript{2}NSW Department of Primary Industry, Menangle, Australia

Infection by the Tobamovirus, tomato brown rugose fruit virus (ToBRFV) can lead to large economic losses in tomato (\textit{Solanum lycopersicum}) and capsicum (\textit{Capsicum} spp) because it causes chlorotic/necrotic spots and deformation on fruit, making them unmarketable. The virus can spread rapidly and disease incidence can reach 95\%. Mechanical transmission of ToBRFV occurs during contact with contaminated tools, hands, plant-to-plant and via bees. It is transmitted through cuttings and grafting. Seed transmission is not verified but is suspected to be a cause of recent outbreaks in Germany, Italy, Israel, Mexico, Saudi Arabia, Turkey, UK and USA after ToBRFV emerged in Jordan 2015. The Australian Department of Agriculture implemented emergency measures on 5\textsuperscript{th} March 2019 and on 1\textsuperscript{st} April, onshore ToBRFV testing of imported tomato and capsicum seeds was commenced, in addition to current requirements for viroid and Pepino mosaic virus testing. Four tests are stipulated for ToBRFV detection including two specific RT-qPCR tests, one specific end-point RT-PCR test and one generic end-point RT-PCR test that detects ToBRFV and closely related Tobamoviruses. Although only one of the four tests are required, Australian labs use both endpoint RT-PCR tests for seed testing. As of 28\textsuperscript{th} June 2019, 47 tomato submissions and 27 capsicum submissions for seed import had been tested for ToBRFV as part of the updated Department of Agriculture testing requirements. So far ToBRFV has not been detected in any imported seed tested in Australia using the two endpoint RT-PCR tests. However, two Tobamoviruses, pepper mild mottle virus (PMMoV) and tomato mosaic virus (ToMV), which occur in Australia, were detected in 1/27 capsicum seed submissions and 2/47 tomato seed submissions respectively with the generic RT-PCR test. The results demonstrate that the additional testing can protect seed importers and the wider growing community from incursions of endemic and exotic Tobamoviruses.
Biosecurity and related governance issues pose significant challenges to minimising incursions of pathogens, pests and weeds in Lao People’s Democratic Republic (PDR) as in many least developed countries. Phytophthora is a good example. *P. palmivora* was identified in 2009 as a significant problem in Champasak province causing dieback of durian and custard apple during an extensive survey of crop diseases. *P. palmivora* is assumed to have been introduced from an adjacent country. Its rapid and devastating spread may have been via equipment used in building the first district power lines as small-holders blamed electricity for the onset of the disease in their well-established symptomless trees. Subsequent local spread would have been facilitated via infected durian seedlings from a key nursery, a problem now resolved. *P. infestans* was also observed in potato crops during these surveys. Over the succeeding five years *P. capsici* was identified as a serious problem in chilli, tomato and eggplant, commonly as a complex with bacterial wilt caused by *Ralstonia pseudosolanacearum*. More recently in Champasak, *P. palmivora* was associated with dieback of papaya and citrus, and *P. cinnamomi* with dieback of avocado. *P. nicotianae* has been associated with dieback of passionfruit, black pepper and roselle (*Hibiscus sabdariffa*) in Sekong province, most likely introduced from an adjacent country via infected planting material, as the area had previously been forested. It is proposed *P. nicotianae* was then spread to adjacent farms by vehicles, motor bikes and local farm workers walking to and from their villages to work. Thus movement of pathogens in planting material, soil attached to equipment or footwear pose challenges both at regional and local level where the resources for implementing biosecurity measures are limited. It takes much more than training and legislation to meet these challenges.

**Phytophthora: a scourge of vegetable, fruit, and field crops in southern Lao PDR – biosecurity issues**

**Poster Board 7**

**Prof Lester Burgess**, Nicholas Pain, Sengphet Phanthavong, Phitsamay Phitsanoukane, Diane White, Treena Burgess, Bevan Weir, Andrew Daly, Kylie Ireland, Sophia Callaghan, Adam Williams, Somlit Vilavong

1 Sydney Institute of Agriculture, University of Sydney, Sydney, Australia, 2CSIRO Agriculture and Food, Floreat, Australia, 3Agriculture Section, Provincial Agriculture and Forestry Office, Thaluang Village, Pakse, Lao PDR, 4Murdoch University, Western Australia, 5Elizabeth Macarthur Agricultural Institute (EMAI), Menangle, Australia, 6CSIRO Health and Biosecurity, Black Mountain Science & Innovation Park, Australia, 7Landcare Research, Auckland, Australia

Phytosanitary “Systems Approaches” comprise two or more independent, phytosanitary measures to reduce the risk of pest and pathogen movement through trade. They are increasingly being used to access domestic and international markets for fresh fruit and vegetables. A risk framework was recently developed to assess the robustness of active systems approach protocols and used to create new effective protocols. The four risk reduction objectives are: i) minimising exposure to pests when fruit are vulnerable, ii) minimising host vulnerability, iii) reducing infestation rate and iv) reducing establishment likelihood. Its applicability to preventing movement of high-risk plant pathogens managed by a systems approach was tested. Of the publicly-available, active systems approach protocols reviewed, 30% included plant pathogens. They utilized significantly more risk reducing mechanisms than the average insect and mite protocol. The protocols emphasized Good Agricultural Practices (GAPs) and orchard hygiene more frequently. Foliar pathogens were primarily controlled under systems approach pest management; none of the protocols were designed for systemic pathogens. The risk framework maintains its ability to assess the quality of active systems approach trade protocols and can aid in designing future trade protocols involving biosecurity pathogens while accommodating a variety of management technique unique to plant pathogens. The risk framework can also act as the basis for pathogen risk assessments and risk management proposals.

**Poster Board 10**

**Systems approach risk framework for biosecurity pests: plant pathogen case study**

**Dr Kate Fiedler**, Dr Rieks Van Klinken

1CSIRO, Dutton Park, Australia

Phytosanitary “Systems Approaches” comprise two or more independent, phytosanitary measures to reduce the risk of pest and pathogen movement through trade. They are increasingly being used to access domestic and international markets for fresh fruit and vegetables. A risk framework was recently developed to assess the robustness of active systems approach protocols and used to create new effective protocols. The four risk reduction objectives are: i) minimising exposure to pests when fruit are vulnerable, ii) minimising host vulnerability, iii) reducing infestation rate and iv) reducing establishment likelihood. Its applicability to preventing movement of high-risk plant pathogens managed by a systems approach was tested. Of the publicly-available, active systems approach protocols reviewed, 30% included plant pathogens. They utilized significantly more risk reducing mechanisms than the average insect and mite protocol. The protocols emphasized Good Agricultural Practices (GAPs) and orchard hygiene more frequently. Foliar pathogens were primarily controlled under systems approach pest management; none of the protocols were designed for systemic pathogens. The risk framework maintains its ability to assess the quality of active systems approach trade protocols and can aid in designing future trade protocols involving biosecurity pathogens while accommodating a variety of management technique unique to plant pathogens. The risk framework can also act as the basis for pathogen risk assessments and risk management proposals.
Plant diseases such as Citrus canker, Sudden Oak Death and those caused by Xylella fastidiosa, have the potential to destroy the viability and competitiveness of Australian horticultural industries. The Post Entry Quarantine (PEQ) facility at Mickleham, Victoria, is the only Commonwealth-operated facility for high-risk plant imports and is home to state-of-the-art glasshouses and laboratories – all designed to keep exotic plant diseases out of Australia while supporting our horticultural industries and protecting our unique environment. The science team based at PEQ Mickleham conduct plant pathology and molecular diagnostics for hundreds of plant pathogens on a wide range of imported temperate, sub-tropical and tropical hosts, to ensure that plants released from PEQ are free of exotic diseases. Likewise the plant pathologists based at the Melbourne Airport precinct, test goods intercepted at the border for plant pathogens, inspect plant samples at medium risk Approved Arrangements (AAs) PEQ facilities, provide risk management advice and develop and deliver training packages for biosecurity inspectors. Tens of thousands of diagnostic tests are conducted each year by our team to protect Australian plant health.

The Plant Innovation Centre at Post Entry Quarantine (PIC@PEQ) is a newly established group in the Australian Government, Department of Agriculture. The team conduct applied, innovative trials to address operational issues and service delivery challenges for both internal and external stakeholders. PIC@PEQ assists in the implementation of operational changes and is establishing collaborative links with the research community and education sector, including hosting and co-supervising Honours and Post-Graduate students at the world-class PEQ Facility in Melbourne. Several case studies are presented of where PIC@PEQ has trialled new approaches to champion change in biosecurity practices, resulting in improved outcomes for industry, importers and regulators including:
- Developing and validating molecular diagnostics for emerging plant pathogens
- Conducting alternative herbicide treatments for imported cut-flowers and new methods for verifying treatment of imported cut-flowers
- Engaging in a project using next-generation sequencing (NGS/HTS) as a validated, standardised tool for plant pathogen PEQ diagnostics*
- Investigating rapid, low-level gamma irradiation for effective phytosanitary treatment of various commodities
- Exploring alternative sterilisation treatments for seeds and horticultural tools
- Completing laboratory and field trials of various smart-phone disease and invertebrate identification apps

Queries from industry, government and academia are welcomed to collaborate on future trials to further improve biosecurity outcomes in Australia as well as potential collaboration on student projects related to biosecurity. * see presentation by Roberto Barrero for more details about this project
Poster Board 4

**Mitogen-activated protein kinase phosphatase 1 reduces the replication efficiency of Bamboo mosaic virus in** *Nicotiana benthamiana*

**Prof Menghsiao Meng**<sup>1</sup>, **Dr Cheng-Cheng Lee**<sup>1</sup>

<sup>1</sup>National Chung Hsing University, Taichung, Taiwan

In plants, the mitogen-activated protein kinase (MAPK) cascades are the central signaling pathways of the complicated defense network triggered by the perception of pathogen-associated molecular patterns to repel pathogens. The Arabidopsis MAPK phosphatase 1 (AtMKP1) negatively regulates the activation of MAPKs. Recently, the AtMKP1 homolog of *Nicotiana benthamiana* (NbMKP1) was found in association with the bamboo mosaic virus (BaMV) replication complex. This study aimed to investigate the role of NbMKP1 in BaMV multiplication in *N. benthamiana*. Silencing of NbMKP1 increased accumulations of the BaMV-encoded proteins and the viral genomic RNA, although the same condition reduced the infectivity of *Pseudomonas syringae* pv. *tomato* DC3000 in *N. benthamiana*. On the other hand, overexpression of NbMKP1 decreased the BaMV coat protein accumulation in a phosphatase activity-dependent manner in protoplasts. NbMKP1 also negatively affected the in vitro RNA polymerase activity of the BaMV replication complex. Collectively, the activity of NbMKP1 seems to reduce BaMV multiplication, inconsistent with the negatively regulatory role of MKP1 in MAPK cascades in terms of warding off fungal and bacterial invasion. In addition, silencing of NbMKP1 increased the accumulation of foxtail mosaic virus but decreased potato virus X. The discrepant effects exerted by NbMKP1 on different pathogens foresee the difficulty to develop plants with broad-spectrum resistance through genetically manipulating a single player in MAPK cascades.

Poster Board 6

**Status of papaya phytoplasma diseases in far north Queensland**

**Dr Nandita Pathania**<sup>1</sup>, **Dr Natalie Dillon**<sup>1</sup>, **Ms Louise Hucks**<sup>1</sup>, **Mrs Grace Sun**<sup>2</sup>, **Mrs Jodie Cheesman**<sup>1</sup>, **Mr Lynton Vawdery**<sup>1</sup>

<sup>1</sup>Department of Agriculture and Fisheries, Mareeba, Australia, <sup>2</sup>Department of Agriculture, Melbourne Airport, Australia

Economic losses (15-80%) to papaya production in far north Queensland have been attributed to an increased incidence of phytoplasma diseases (‘Candidatus Phytoplasma’). A survey of commercial plantations conducted between June 2014 and November 2018 showed that phytoplasma infected plants exhibit an array of symptoms including stunting, yellowing, low sap flow, bunchy top and plant dieback. Gene sequencing (16S rRNA) of 118 phytoplasma positive samples from papaya plants, weeds and insects identified pathogens from the 16Sr II group; ‘Ca. P. australasia’ (Papaya yellow crinkle and mosaic), ‘Ca. P. aurantifolia’ (Australian lucerne yellows) and 16Sr XII group of phytoplasma ‘Ca. P. australiense’ (Papaya dieback). Pairwise sequence analysis of a few papaya samples showed 100% similarity to Peanut witches broom (MPLDRRI); Pigeon pea witches broom (GenBank Accession No. AB741637), *Celotia argentea* (GenBank Accession No. KX426374), *Corchorous aestuans* (GenBank Accession No. KX645865), Sweet potato little leaf (GenBank Accession No. JQ868446) and *Vigna unguiculata* phytoplasma (GenBank Accession No. KU170535). A 16Sr II group phytoplasma was also detected in leafhoppers *Orosius orientalis* (Cicadellidae) and a lace bug (*Tingidae* family). This is the first report of phytoplasma detection from the *Tingidae* family and requires further ecological and transmission studies to confirm whether they are a vector of papaya yellow crinkle and mosaic disease. This research reveals that in Australia, greater genetic diversity exists among papaya phytoplasma strains than previously thought and further validation is required to determine pathogenic variations within the different groups/subgroups based on ecologically separated populations.
Poster Board 5

**Molecular responses of *Nicotiana glutinosa* to infection with lettuce necrotic yellows virus subgroups**

*Miss Shweta Shinde*, Dr Gardette Valmonte-Cortes, Dr Colleen Higgins

1School of Science, Auckland University Of Technology, Auckland, New Zealand

The most scrutinised species of the genus *Cytorhabdovirus* is *Lettuce necrotic yellows virus* (LNYV) which causes serious disease in lettuce. This virus appears to be endemic in Australia and New Zealand and has been categorised into two subgroups; subgroups I and II. A study in 2016, suggested that apparent extinction of subgroup I in Australia maybe due to subgroup II outcompeting subgroup I, which has yet to happen in New Zealand. It is possible that subgroup II is more efficient at infecting the plant host. To date, host molecular responses to infection by LNYV, and infection by each of the subgroups, has not been studied. Understanding host responses may help determine the reason why subgroup II has rapidly dispersed compared to subgroup I and support the idea that subgroup II is outcompeting subgroup I. Relative quantification of mRNA accumulation is being studied by RT-qPCR in the model host plant *Nicotiana glutinosa* infected with either subgroup I or II. Target genes have been identified from studies of another virus infected *Nicotiana* species. In parallel, suitable reference genes are also being identified. Since there is no published *N. glutinosa* genome, primers for each gene were designed using orthologous sequences from published *Nicotiana* genomes. These primers amplify the expected products from *N. glutinosa* and analysis of mRNA accumulation in LNYV infected plants is underway. Host metabolomic responses are also being studied. A pilot study showed accumulation of few metabolites that differed between subgroup I and subgroup II infected *N. glutinosa*. This study will be expanded to confirm these findings. Alteration in gene expression and metabolic pathways may help identify how LNYV subgroup II rapidly spreads compared to subgroup I.
ZnO nanoparticles can be used to manage white mold of french bean

Dr Himadri Kaushik, Dr Pranab Dutta
1Assam Agricultural University, Jorhat, Assam, Jorhat, India

Nanotechnology is a new and fascinating science that understands and controls the matter at the nanoscale ranging from 1-100 nm. Of all nanoparticles (NP), ZnO NPs are gaining more popularity as they possess superior durability, greater selectivity and heat resistance as compared to organic materials. Presently, the protocol for synthesis of ZnO NPs is standardized with a Surface Plasmon Resonance (SPR) band of 350 nm, a size of 33.4 nm, a Polardispersity Index (PDI) of 0.697, negatively charge, a zeta potential of -2.34 mV, crystalline and chemically pure and an irregularly spherical shape. Fourier-transform infrared spectroscopy (FTIR) spectra indicated that ZnO NPs were in the range of 463.51-902.99 cm⁻¹. In vitro bioassays showed that ZnO NPs at 100 and 225 ppm caused complete inhibition of radial growth and sclerotial germination of Sclerotinia sclerotiorum. Electron microscopy showed ZnO nanoparticles caused deformation, followed by lysis and complete breakdown of hyphal cells. Seed treatment with ZnO NPs at 225 ppm decreased the incidence of white mold to 6.66%. Major antioxidant, non-enzymatic compounds like total soluble sugar, total soluble protein, phenols, flavonoids, alkaloids and total chlorophyll content were found in highest concentration in plants raised from seed treated with ZnO NPs at 225 ppm, along with activities of antioxidant enzymes (POX, PPO and PAL). Concentrations of N, P, K, Ca, S, Fe, Mn and Cu were also highest in plants raised from seed treated with ZnO NPs at 100 ppm. However, concentrations of Mg and Zn in plants were highest in seeds treated with ZnO NPs at 225 ppm. The highest uptake of N, P, K Ca, Mg, S, Fe, Mn, Zn and Cu were observed in seed treated with ZnO NPs at 100 ppm, followed by 225 ppm in the tested crops.

Effect(s) of compost tea on plant growth promotion and antifungal activity

Dr Sang-mi Yu, Mrs Weon Jung Song
1Nakdonggang National Institute Of Biological Resources, Sangju-si, South Korea, 2Sangju Agricultural Technology Center, Sangju-si, South Korea

Compost tea, a microbial culture, is prepared by injecting oxygen into high quality compost. It is an inoculum of useful microorganisms that also serves as a water-soluble fertilizer. In this study, the effect(s) of compost tea obtained from bark composts was evaluated when applied to pepper plants. In field, an increase was noted in the total production, branch index and fruit number, by 18.5%, 21.1%, and 38.5%, respectively, as compared to the control. An increment in the yield was observed to be related with an increase in fruit number per plant, whereas the weight of the single fruit was unaffected by the treatment. The microorganisms isolated from compost tea were tested for antifungal activity against 5 plant pathogens, resulting in selection of 5 microbial isolates. Three isolates were identified as Bacillus sp. and 2 were identified as Pseudomonas sp., based on their bio-chemical characteristics using the Biolog system and by 16S rDNA gene sequence analysis. The results demonstrated the effectiveness of compost tea application in significantly improving the yield performances of pepper crops under a greenhouse organic system. However, we plan to further investigate the function(s) of microbes derived from compost tea in future studies.
Integrated use of *Aureobasidium pullulans* strain CG163 and acibenzolar-S-methyl for management of bacterial canker in kiwifruit

**Mr Huub de Jong**1,2, Dr Tony Reglinski1, Dr Philip Elmer1, Dr Kirstin Wurms1, Dr Joel Vanneste1

1Plant and Food Research, Hamilton, New Zealand, 2University of Auckland, Auckland, New Zealand

An isolate of *Aureobasidium pullulans* (strain = CG163) and the plant defence elicitor acibenzolar-S-methyl (ASM) were investigated for their ability to control leaf spot in kiwifruit (*Actinidia chinensis* var. *deliciosa* 'Hayward') caused by *Pseudomonas syringae* pv. *actinidiae* biovar 3 (Psa). Clonal kiwifruit plantlets were treated with ASM, CG163 or ASM+CG163 at 1 and 7 days before inoculation with Psa. ASM (0.2 g/L) was applied either as a root or foliar treatments and CG163 was applied as a foliar spray containing 2x107 colony forming units/mL. Leaf spot incidence was significantly reduced by all treatments compared with the control. The combination of ASM+CG163 had greater efficacy (93%) than either ASM (79%) or CG163 (64%) alone. Extending the interval to 21 days between treatment and pathogen challenge did not adversely affect disease control, even though CG163 populations on the phylloplane significantly declined over the same period. Treatment efficacy correlated positively with the expression of defence-related genes: pathogenesis-related protein 1 (PR1), β-1,3-glucosidase, Glucan endo 1,3-β-glucosidase and Class IV chitinase, with greater gene upregulation and disease control in plants treated with ASM+CG163 than by the individual treatments. Expression of PR1 and β-1,3-glucosidase were significantly elevated in CG163 treated plants 24 hours after inoculation with Psa, compared with the control, suggesting that CG163 operates in part by 'priming' the host defence response. Pathogen population studies indicated that CG163 had significant suppressive activity against epiphytic populations of Psa. Whilst, endophytic populations were significantly reduced by the combination of ASM+CG163 but not by the individual treatments, and by 96-144 hours after inoculation, were significantly lower than the control. These findings suggest that ASM+CG163 have complementary modes of action that contribute to greater control of Psa leaf spotting than either treatment alone.

Successful establishment of a dieback biocontrol event in a population of *Parkinsonia aculeata* using a fungal bioherbicide

**Prof Victor Galea**1, Mr Peter Riikonen2, Dr Ammar Abdul Aziz1, Ms Fathin Azizan1

1The University of Queensland, Gatton, Australia, 2BioHerbicides Australia, Gatton, Australia

Australia’s first woody weed bioherbicide (Di-Bak Parkinsonia™) gained APVMA registration in December 2018. The product, commercialised by the University of Queensland and BioHerbicides Australia, utilises the endophytic fungi *Lasiodiplodia pseudotheobromae*, *Macrophomina phaseolina* and *Neoscytalidium novaehollandiae* to induce dieback in the host plant. Di-Bak Parkinsonia is formulated as a capsule which is inserted and sealed into the tree stem using a purpose engineered In-Jecta® applicator. An isolated infestation of Parkinsonia (*Parkinsonia aculeata*) located at Corporal Dam, Alexandria Station (Barkly Tablelands, Northern Territory S18° 59’ 14.7” E137° 39’ 27.3”) was selected for treatment with this product in August 2016. The infestation consisted of two discreet areas of 1.95 and 11.2 ha on naturally treeless Mitchell grass plains country. The smaller northern area consisting of approximately 2,000 parkinsonia trees was heavily treated with all trees (1,095 in total) of suitable size (stem diameters at least 30 mm) injected with a single dose. The larger southern area (11.2 ha) was partially treated at its south-western most end with 705 trees treated while the remaining majority were left un-treated. Assessment of the trial site was conducted at 10, 15 and 37 months after treatment (MAT). Visual inspection of 200 trees in the northern area where an injection site could be verified allowed them to be rated for health condition using a 0-5 rating scale. Similarly, 200 trees in the un-treated area were also assessed for comparison. Georeferenced drone flight imagery was used to pinpoint areas of interest in both treated and non-treated areas of similar target plant density. Six-monthly satellite data views of the selected areas were accessed using PlanetScope (www.planet.com) to access Normalized Difference Vegetation Index (NDVI) data sets at 3 metre resolution to determine vegetation health changes as a result of treatment.
Concurrent Session 5 – Biocontrol
Thursday 28 November 2019, 1:15 PM - 2:45 PM

Profiling volatile organic compounds produced by Bacillus species with biocontrol properties against Leptosphaeria maculans

Ms Sana Hanif, Dr Benjamin Stodart, Dr Sandra Savocchia, Prof Gavin Ash
1School of Agricultural and Wine Sciences, Charles Sturt University, Wagga Wagga, Australia, 2Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, Australia, 3National Wine and Grape Industry Centre, Charles Sturt University, Wagga Wagga, Australia, 4Centre for Crop Health, University of Southern Queensland, Toowoomba, Australia, 5Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan

Antifungal volatile organic compounds (VOCs) produced by Bacillus species have demonstrated their efficacy in a number of pathogen systems. Strains of Bacillus spp. were selected based on their antagonistic potential toward previously characterised virulence strains of Leptosphaeria maculans in vitro. VOCs produced by the Bacillus strains were assessed for their efficacy against L. maculans. HS-SPME-GCMS was used to profile the two best performing strains, both of which were later identified as Bacillus amyloliquefaciens based on multigene analysis. A less effective strain of B. subtilis was also used for comparison and detection of key VOCs responsible for antagonistic ability of the potential biocontrol agents. Gas chromatographic (GC-MS) studies revealed the presence of antagonistic VOCs from a range of classes, including alcohols, aldehydes, hydrocarbons and variety of ketones. Detected compounds included 2-Pentanone, 3-methyl, 2-Hexanone, 5-methyl-1, Pyrazine, 2,5-dimethyl, 2-heptanone 5-methyl, 2-heptanone Benzaldehyde, 2,5-bis[(trimethylsilyl)oxy]-, 2-Hexadecanol, 2,5-Cyclohexadiene-1,4-dione, 2,6-bis(1,1-dimethylethyl), 2-Decanone, 2-Decanol Cyclohexane, [(1-methylpropyl)thio]-, 6-methyl, 2-heptanone, 3-Octanone, 2-ethyl, 1-Hexanol, 2-Nonanone. Based on the correlation matrix, multivariate analysis was carried out using principle component analysis to identify strain differences in the production of VOCs and to determine the relatedness among the potential biocontrol strains of B. amyloliquefaciens. Additional compounds such as ethanol and hexadecane were only detected in the head space of cultures containing both the selected Bacillus strains and L. maculans, which established that the profile of VOCs differs in the presence of the fungal pathogen. In planta assays of bacterial volatiles produced by selected strains reduced disease severity by 75-85%. It is expected that profiling of VOCs from selected bacterial species may provide the opportunity to develop new tools for integrated management of blackleg disease of canola.

Characterization of bacteriophage for biocontrol of Pseudomonas syringae, causative agent of canker in Prunus spp.

Dr Moigan Rabiey, MS Shyamali Roy, Mr Billy Quilty, Mr Ryan Creeth, Prof George Sundin, Prof Robert W Jackson
1University Of Reading, Reading, United Kingdom, 2Michigan State University, East Lansing, USA

Bacterial canker is a major disease of Prunus species such as cherry (Prunus avium). It is caused by Pseudomonas syringae species including P. syringae pv. syringae (Pss) and P. syringae pv. morsprunorum race 1 (Psm1) and race 2 (Psm2). Concerns over the environmental impact of, and developing resistance to, copper controls call for alternative approaches to disease management. One method of control could be achieved using naturally occurring bacteriophage (phage) infective to the bacterial pathogens. Phage were isolated from soil, leaf and bark of cherry trees in five locations in the South East of England. The phage were assessed for their host range against strains of Pss, Psm1 and Psm2. The phage exhibited a differential ability to infect and lyse different Pss and Psm isolates as well as some other P. syringae pathovars. However, the phage were unable to infect beneficial bacteria such as Pseudomonas fluorescens. A subset of 18 of these phage were further characterised genetically (RAPD-PCR fingerprinting and sequencing) and using electron microscopy. The phage are tentatively identified as belonging to the order Caudovirales and the families Myoviridae, Podoviridae and Siphoviridae, with genetic material being dsDNA. Future research will fully sequence the phage genomes and investigate the efficacy of the phage, both individually and in cocktails, to reduce disease progression in vivo to understand the potential for practical use of these phage as biocontrol agents.
Plant defense-bioreporters and combined microbial omics approaches facilitates the discovery of new Actinobacteria biofungicide candidates

Dr Louise Thatcher1, Dr Katharina Belt1, Dr Cathryn O’Sullivan2, Dr Donald Gardiner2, Dr Jonathan Anderson1, Dr Karam Singh1, Dr Margaret Roper1
1CSIRO Agriculture And Food, Floreat, Australia, 2CSIRO Agriculture And Food, St Lucia, Australia

Actinobacteria play important roles in soil and rhizosphere ecology with many members of the phylum contributing to plant health. This includes for example, production of phytopathogen inhibiting compounds, induction or priming of plant immunity, or plant growth promotion (1,2). The combined properties of beneficial Actinobacteria may offer new opportunities for the control of economically destructive fungal pathogens where management options in agriculture can be limited due to the lack or complexity of host resistance, or ineffective and/or harmful chemical controls. To address these limitations and concerns we curated a collection of beneficial soil and plant endophyte Actinobacteria isolated from the biodiversity hotspot of south-west Australia (3) and initiated disease suppressive screening via two platforms:
1) Combining omics approaches with traditional microbial fermentation processes and in vitro and in planta screening across a fungal pathogen diversity panel for pathogen suppressive isolates/compounds. This platform is also being exploited to “awaken” hidden chemical potential, such as the production of new biofungicides. Genome sequencing indicates a limited number of compounds are expressed under standard laboratory conditions but that many more compounds may be produced through genome-predicted silent or cryptic biosynthetic gene clusters (4).
2) Using plant defense-bioreporters to screen Actinobacteria in planta for their ability to potentiate plant immunity or manipulate plant defence signalling responses. This way, tripartite plant-Actinobacteria-pathogen interactions can be monitored in real-time through non-destructive imaging. Combined, these tools are facilitating the discovery of Actinobacteria isolates and their compounds with powerful disease suppressive properties.

Clarifying the taxonomy of a fungus being investigated as a potential biocontrol agent for an invasive plant of beaches in Australia

Miss Isabel Zeil-Rolfe1, Dr Gavin Hunter1, Dr Louise Morin1
1CSIRO, Canberra, Acton, Australia

A fungus that causes significant leaf and stem blight on sea spurge (Euphorbia paralias) in France has been investigated as a potential biocontrol agent for this invasive plant in Australia. Sea spurge is a significant environmental weed that invades beaches on the southern Australian coastline. The fungus was previously identified in 2010, based on morphology, as Passalora euphorbiae. Due to recent taxonomic revisions within the fungal family Mycosphaerellaceae, including Passalora sensu lato, we sought to clarify the taxonomy of this potential biocontrol fungus. The LSU, ITS and EF-1α gene regions of P. euphorbiae were sequenced and its infection process on sea spurge leaves investigated in detail. Phylogenetic analyses of DNA sequence data revealed that P. euphorbiae groups in the genus Venturia within the Venturiaceae. Infection studies of the pathogen corroborated the DNA sequence identification and showed that P. euphorbiae follows an infection process similar to other Venturiaceae species. Germinating conidia directly penetrated the leaf cuticle and formed characteristic ameboid primary hyphae at 7 days post inoculation. Young subcuticular hyphae spread from ameboid primary hyphae extending through the leaf forming dense fungal mats. At 12 days post inoculation subcuticular fungal stroma were observed leading to eventual formation of fasciculate conidiophores rupturing through the cuticle to produce abundant conidia. This infection process differs to that of Passalora and other Mycosphaerellaceae species. Results from this study therefore support the combination of P. euphorbiae into Venturia.
Turnip yellows virus in winter canola crops in Victoria: prevalence and incidence over multiple years

Dr Mohammad Aftab¹, Ms Narelle Nancarrow¹, Dr Piotr Trebicki³
¹Agriculture Victoria, Horsham, Australia

In the last five years, Turnip yellows virus (TuYV) has emerged as the most economically important virus of canola crops in Australia. In 2014, there was an outbreak of TuYV in canola in South Australia causing widespread crop failure. During the outbreak, over one thousand diagnostic samples were tested for virus in Victoria and TuYV incidence was high in all south eastern states. Canola crops in Victoria continue to be assessed for viruses, including TuYV. From 2015-2018, 8,300 samples were randomly collected from 83 canola crops across different climatic regions (Mallee, Wimmera and South West) of western Victoria. Samples were blotted onto nitrocellulose membrane and tested for viruses using tissue blot immunoassay. Overall from 2015-2018, TuYV was detected in 88% of crops with a mean incidence of 20% and a maximum incidence of 89%. Prevalence and incidence varied between years and regions but were highest in 2015 and 2017 and lowest in 2018. TuYV infection showed severe symptoms including chlorosis, purple, red or yellow leaf discoloration and stunting in most of the cultivars tested. Some cultivars exhibited non-symptomatic virus infection. Prevalence and incidence of TuYV in winter canola crops in Victoria will be presented and infection drivers discussed.

Investigating the impact of huanglongbing in Lao PDR

Dr Nerida Donovan¹, Ms Anna Englezou¹, Mr Grant Chambers¹, Miss Seng Phanthavong², Ms Sally Cowan³, Dr Hang Dao⁴, Dr Lester Burgess⁵
¹NSW Department of Primary Industries, Elizabeth Macarthur Agricultural Institute, Menangle, Australia, ²Champasak Provincial Agriculture and Forestry Office, Pakse, Lao PDR, ³Plant Protection Centre, Vientiane, Lao PDR, ⁴Plant Protection Research Institute, Hanoi, Vietnam, ⁵Sydney Institute of Agriculture, Faculty of Science, University of Sydney, Sydney, Australia

Huanglongbing (HLB) is the most significant threat to global citrus production. It is widespread throughout South-East Asia and is causing serious losses in the United States and South America. HLB is caused by an endogenous, phloem limited, α-Proteobacterium. The most common and devastating species reported in Asia is ‘Candidatus Liberibacter asiaticus’ (‘Ca. L. asiaticus’), spread by the Asian citrus psyllid (ACP), Diaphorina citri. Commercial citrus growing areas and backyard citrus are found throughout the Lao People’s Democratic Republic (PDR). Widespread decline of citrus trees has been observed in the major growing areas by the authors and both ACP and ‘Ca. L. asiaticus’ have been reported in Lao PDR. However there is a lack of available information on disease issues faced by citrus farmers in Lao PDR with little evidence on the distribution or impact of HLB and potential vectors. Such information is important for government planning, policy development and promotion of horticultural crops. During surveys of citrus in southern Lao PDR we observed symptoms consistent with HLB including asymmetric leaf mottle, poor fruit production, twig and tree dieback and tree death in four of the five most southern provinces; Savannakhet, Salavan, Champasak and Sekong. ‘Ca. L asiaticus’ was detected in 42 leaf mid-rib samples collected from all four provinces. ACP was also recorded in Champasak province up to an altitude of between 700 and 900 m in three districts. Other diseases were detected in a limited number of samples but it is likely that HLB is the major contributor to the decline of citrus trees in southern Lao PDR. HLB is considered the biggest threat to the Australian citrus industry. Knowledge and positive controls gained through work in Lao PDR forms part of a collaborative effort to prepare Australia for an incursion of HLB.
Increased incidence of cereal viruses in western Victoria and detection of exotic Barley virus G in Australia

Ms Narelle Nancarrow, Dr Mohammad Aftab, Dr Linda Zheng, Dr Solomon Maina, Dr Angela Freeman, Dr Merrin Spackman, Dr Brendan Rodoni, Dr Piotr Trębicki

1Agriculture Victoria, Horsham, Australia, 2Agriculture Victoria, Bundoora, Australia, 3NSW Department of Primary Industries, Wagga Wagga, 2650

Wheat, barley and oats are among the most economically important cereals in Australia and worldwide. A number of cereal virus species are present in western Victoria with varying prevalence and incidence, often resulting in significant yield losses. Barley and cereal yellow dwarf viruses are common in Victoria and are mainly transmitted by the bird cherry-oat aphid (Rhopalosiphum padi) and the corn aphid (R. maidis). Wheat streak mosaic virus (WSMV) and High Plains wheat mosaic virus (HPWMoV) are also present in Australia and are transmitted by the wheat curl mite (Aceria tosichella). The prevalence and incidence of three yellow dwarf virus (YDV) species in cereal crops across western Victoria were assessed in September/October for four successive years (2014-2017). Plant samples were randomly collected from each crop and tested using tissue blot immunoassay (TBIA). Samples were also tested for WSMV in 2015 and 2017. During 2014-2017, yellow dwarf viruses were more prevalent and had higher incidence in Victoria than had previously been reported. YDVs were detected in 75% of crops with a maximum incidence in an individual crop of 58%. WSMV was not detected in 2015 but low levels were detected in 2017. In April 2018, aphids and virus symptoms including leaf yellowing and streaking discoloration were observed on volunteer cereal plants in Horsham, Victoria, then tested for virus presence using TBIA. A number of samples were positive for WSMV, HPV and luteoviruses but only a small percentage were positive for one of the yellow dwarf luteovirus species typically found in the Horsham region. A subset of samples was further tested by RT-PCR and amplicons were sequenced which confirmed the presence of WSMoV, HPV and the exotic Barley virus G. The importance, increased occurrence and epidemiology of cereal viruses will be discussed.
Virus diseases of watermelon in southern Lao PDR and associated challenges for training on integrated disease management

Mr Nicholas Pain¹, Dr Lester Burgess³, Dr Lucy Tran-Nguyen², Dr Maxine Piggott², Ms Kaisone Sengsoulichanh⁴, Ms Sengphet Phanthavong⁵

¹CSIRO Agriculture and Food, Floreat, Australia, ²Northern Territory Department of Primary Industries, Darwin, Australia, ³Sydney Institute of Agriculture, Sydney, Australia, ⁴Provincial Agriculture and Forestry Office, Savannakhet, Lao PDR, ⁵Provincial Agriculture and Forestry Office, Pakse, Lao PDR

Small-holder farmers in southern Laos who have access to water from farm dams or irrigation water during the dry season (November to March) commonly grow watermelons as a cash crop which contributes significantly to poverty alleviation. The farmers sell their produce to local traders, or in simple roadside stands. In 2014 there was a high incidence of virus-like symptoms which led to losses of up to 100% in many crops. There were continuing losses associated with these virus-like symptoms in subsequent years. In 2017 we carried out an extensive disease survey across watermelon farms in western Savannakhet province to again monitor disease problems with a focus on viruses. Leaf samples with virus-like symptoms were collected from three farms and sent to Agdia in the United States for molecular analysis where they determined that at least one virus was present, zucchini yellow mosaic virus (ZYMV). The RNA samples were then forwarded to the Northern Territory Department of Primary Industries where two additional viruses, melon yellow spot virus (MYSV) and watermelon silver mottle virus (WSMoV) were detected, with one sample containing both ZYMV and WSMoV. These viruses represent a serious challenge to small-holder farmers. It is challenging for small-holder farmers to understand the nature of infectious diseases and viruses, and to implement effective management strategies. In cooperation with the local Provincial Agriculture and Forestry Office staff, volunteers from the Australian Volunteer Program and with the support of an Australia-ASEAN Council grant and the Crawford Fund, we have initiated basic training workshops for farmers on the nature and importance of diseases, pests and weeds. The workshops were popular and there was excellent farmer engagement. It is imperative that further training be provided for government staff and farmers, and that researchers work together with the farmers to determine feasible IDM strategies for these viruses.
Long-term pathogenicity surveys of *Puccinia triticina* underpin sustained genetic control of leaf rust in Australian wheat crops

**Prof Robert Park**, Dr Jingqin Wu

1. The University Of Sydney, Cobbitty, Australia

The wheat leaf rust pathogen *Puccinia triticina* has been present in Australia since at least European colonisation. It does not undergo sexual recombination here because the alternate host *Thalictrum* is absent. Australia-wide surveys of pathogenicity in *P. triticina* began in 1921. They involve the identification of pathotypes from field collected samples in greenhouse assays using wheats carrying different resistance genes. Critical surveys of *P. triticina* from 1980-2018 identified over 6,000 isolates of 80 pathotypes, preserving representative isolates in an historic collection of isolates dating back to the 1920s. These surveys provided strong evidence of 6 exotic incursions (1981, 1984, 1996, 2006 (2), 2014), each of which acting as a founding isolate and giving rise to clonal lineages through mutation to virulence on resistance genes.

We used long-read sequencing to generate haplophased genomes and annotations for 3 isolates of *P. triticina*. Genetic dissection based on these high-quality phased genomes, along with short-read sequencing of 27 additional isolates supported an exotic origin for the 6 putative incursions and provided the first demonstration of somatic hybridisation and parasexuality in a rust pathogen. The incursions of 6 exotic *P. triticina* isolates since 1981 is of concern given that only two other incursions of wheat rusts were detected since then. The origin of each, the means by which they were introduced, and why so many *P. triticina* incursions have occurred are unknown. Also of interest is that while a local mutation to virulence for *Lr13* has not been detected, 5 of the 6 incursions carry virulence for this gene. Gene *Lr13* is common in Australian wheats, and prior to 1981 was effective. Following 1981, combinations of *Lr13* with genes such as *Lr1*, *Lr17b*, *Lr24*, *Lr26* and *Lr37* remained effective but eventually succumbed either as a result of subsequent incursions or pathogen mutation.
Industry-wide survey of diseases in Australian almond orchards

Dr Tonya Wiechel1, Brittany Oswald2, Simone Kreidl1, Peta Faulkner3, K Giri1, Dr Len Tesoriero4, Dr Suzanne McKay2, Dr Mark Sosnowski5,6, Dr Jacky Edwards1,6

1Agriculture Victoria Research, AgriBio Centre for AgriBiosciences, Bundoora, Australia, 2South Australian Research & Development Institute, GPO Box 397, Australia, 3Agriculture Victoria Research, DJPR, Mildura, Australia, 4NSW Department of Primary Industries, Ourimbah, Australia, 5School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, Australia, 6School of Applied Systems Biology, La Trobe University, Bundoora, Australia

In 2017, the Australian almond industry had an estimated farm-gate value of approximately $1 billion with $429 million of this destined to export markets. Australian almonds are grown in five production regions: Sunraysia, Vic; Riverland and the Adelaide Plains SA; Riverina, NSW; and the Wheatbelt, WA. Industry considers hull rot and lower limb dieback/trunk diseases the main diseases of economic concern, but accurate knowledge of the prevalence and impact of the diseases affecting this rapidly expanding industry is lacking. An extensive disease survey was designed and conducted in 2018-19. Growers were asked via questionnaire for perceptions of their disease issues and details of their agronomic practices. Orchard disease surveys were carried out in spring and repeated in late summer. 2,104 trees were assessed from 10,179 ha orchards across all regions. The main varieties included the industry standard Nonpareil, plus Carmel, Monterey, Price, Vella and Peerless. The most prevalent diseases were shot hole, lower limb dieback (LLD), hull rot and trunk diseases (which included Phytophthora). Grower perceptions were different to the survey results; eg, growers rated anthracnose, rust and bacterial spot highly, but they were not commonly observed this season. Regional differences were evident with rust and anthracnose rarely observed in the eastern states, while in WA, LLD and hull rot were rare, and rust was common. Hull rot is a late season disease and the summer surveys were timed to assess hull rot as close to Nonpareil harvest as possible. As a result, Nonpareil contributed most to the hull rot incidence observed, followed by Price. Correlation analyses are being conducted to explore regional and agronomic factors that may influence disease expression. The surveys will be repeated during 2019-20 season. This research is being conducted as part of a national project investigating integrated disease management practices for the Australian almond industry.
The emergence of bacterial diseases of Eucalyptus due to host range expansions

Prof Teresa Coutinho, Ms Nomakula Zim1, Ms Khumbuzile Bophela1
1Centre for Microbial Ecology and Genomics/Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

Bacterial plant pathogens can be highly specialised and infect only a single plant species or colonise a few or a considerable number of hosts, which can belong to different plant families. However, new diseases can emerge when pathogens evolve the capacity to colonise novel host species that are either closely (host shift) or distantly (host jumps) related to their present hosts. Xanthomonas species usually cause disease in only a few host species and are regarded as highly adapted to their hosts. This is unlike Erwinia where the majority of species have broad host ranges, infecting members of the same plant family. In Eucalyptus, there are three examples of host range expansions, which led to the emergence of new bacterial diseases. In the case of a host shift, Erwinia psidii, a known pathogen of guava (Psidium guajava), now infects several Eucalyptus spp. and a E. grandis x E. urophylla hybrid in South America, and more recently in Malaysia. Xanthomonas vasicola was recently shown to have jumped hosts from sugarcane to a single E. grandis clone in South Africa. X. perforans, a pathogen responsible for black spot of tomato and pepper, was shown to have jumped to E. pellita in Indonesia. The latter two events are interesting in that host jumps are considered to rarely occur as the host specificity barriers are difficult to bypass. These three examples will be used to discuss the expansion of the host ranges of bacterial plant pathogens to Eucalyptus species.

Biology of aerial Phytophthora in New Zealand’s plantation forests

Ms Judy Gardner1, Dr Stuart Fraser1, Dr Nari Williams1, Dr Rebecca McDougal1
1Scion, Rotorua, New Zealand

Phytophthora pluvialis and Phytophthora kernoviae have been associated with needle disease in New Zealand plantation forests since 2008. Plantation forestry is a valuable export industry and Pinus radiata (radiata pine) makes up 90% of all planted forest, followed by Pseudotsuga menziesii (Douglas fir). Both species of Phytophthora cause needle loss in radiata pine, but only P. pluvialis is known to also cause needle loss in Douglas fir. Phytophthora pluvialis has also been recorded in Oregon and Washington, USA and Phytophthora kernoviae in the United Kingdom and Chile. Analysis of pathogen populations suggest that P. kernoviae is native to New Zealand and P. pluvialis is native to the United States of America. Susceptibility screening of native New Zealand plants supports this hypothesis for P. kernoviae. To enable control of these diseases it is important to understand the epidemiology of the two pathogens, including their occurrence in relationship to the other two important needle diseases of radiata pine, dothistroma needle blight and cyclaneusma needle cast and the interplay of Swiss needle cast and P. pluvialis in Douglas fir. Other important areas of research that have helped improve our understanding of the behavior of these two pathogens include the development of diagnostic tools, morphological and molecular. The later has been used to investigate the presence of the pathogens in old herbarium samples. Results indicate that it is likely that P. kernoviae was the cause of, what was formerly known as ‘physiological needle blight’, a disease sporadically observed since at least the 1980s. Research has also investigated variation in resistance and chemical control. This work has important implications for our understanding of the relationship between hosts and pathogens, as well as the management of the disease caused by these two Phytophthora.
Ceratocystis manginecans in Indonesia

Heru Indrayadi1,2, Morag Glen1, Jeremy Brawner2, Anto Rimbawanto4, Caroline Mohammed1
1Tasmanian Institute of Agriculture, University of Tasmania, Sandy Bay, Australia, 2PT Arara Abadi, Perawang, Riau, Indonesia, 3Plant Pathology Department, University of Florida, Gainesville, United States, 4Centre for Forest Biotechnology and Tree Improvement, Indonesia

Ceratocystis manginecans was first described from mango trees in Oman and Pakistan (1). Shortly afterwards it was detected infecting, and killing, Acacia mangium trees in Indonesian plantations (2). It had such an impact on productivity and profitability that plantings of Acacia mangium were greatly reduced and replaced with Eucalyptus pellita and Eucalyptus hybrids. An ACIAR-funded project (FST 2014-068) is focussing on the development of resistant or tolerant Acacia germplasm. More recently, C. manginecans has been isolated from eucalypts, though tolerance in eucalypts is greater than in Acacias. Other hosts include West Indian locust (Hymenaea courbaril) and a range of fruit trees, including duku (Lansium parasiticum), mango (Indica mangifera), and avocado (Persea americana). The same species was found in Thailand, infecting bullet wood, Mimusops elengii (3). A cross-inoculation trial, using isolates from Acacia, eucalypts, mango and locust, is in progress to better understand the virulence of isolates from different hosts on a range of forestry, amenity and horticultural tree species. In addition to informing disease management in Indonesia, the results will clarify the biosecurity threat posed by C. manginecans to horticulture, forestry and the environment in neighbouring countries, including Australia.


An investigation into the role of almond trunk disease pathogens in lower limb dieback syndrome

Miss Brittany Oswald1, Dr Susanne. F. McKay1, Dr Jacqueline Edwards2,3, Dr Mark. R. Sosnowski1,4
1South Australian Research And Development Institute, Urrbrae, Australia, 2Agriculture Victoria Research, AgriBio Centre for AgriBiosciences, Bundoora, Australia, 3School of Applied Systems Biology, La Trobe University, Bundoora, Australia, 4School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, Urrbrae, Australia

Lower limb dieback (LLD) and trunk diseases are emerging issues throughout the almond production regions in California and Spain, and more recently in Australia. LLD is characterised by the dieback of smaller diameter branches on lower scaffolds of the tree. Symptoms include chlorotic leaves in spring, dying shoots, and dieback of branches, typically after warm weather events. Trunk diseases are potentially lethal perennial diseases of almond trees that can have a high impact on orchard longevity and profitability. Trunk disease symptoms can include gummosis, dieback and internal necrosis of woody tissues. A disease survey of Australian almond orchards in 2018-19 revealed that LLD and trunk diseases occur in all regions. The aetiology of LLD is unknown, but there are currently multiple hypotheses as to what the causal or exacerbating factors of LLD may be. These include scale infestations, water management, light interception, herbicide drift or fungal pathogens associated with cankerous trunk diseases. To investigate the possible role of trunk disease pathogens in LLD, the pathogenicity of seven key species isolated from symptomatic plant material was tested. These species were Diplodia seriata, Eutypa lata, Colletotrichum acutatum, Pleurostoma richardsiae, Collophora rubra, Collophora hispanica. and Cytospora diatrypelliodea. Agar plugs with mycelia from the seven species were inserted into pre-drilled holes on branches of potted almond trees, cv. Carmel. Blank agar plugs were used as the controls. At 3 and 6 months after inoculation, the length of necrotic staining within the woody tissue was measured and the inoculated organisms were reisolated to fulfil Koch’s postulates and to determine the distance of colonisation. Results confirmed that E. lata, D. seriata, C. rubra, C. acutatum and P. richardsiae are pathogenic to almond, cv. Carmel. Future research will investigate the susceptibility of almond varieties to the most pathogenic species and evaluate the efficacy of fungicides for their control.
Araucaria dieback—A threat to native and plantation forests

Dr Louise Shuey, Dr Ken Pegg, Dr Sarah Dodd, Dr Andrew Manners, Ms Diane White, Professor Treena Burgess, Mr Stuart Johnson, Dr Geoff Pegg

1 Department of Agriculture and Fisheries, Dutton Park, Australia, 2 Department of Environment and Science, Toowoomba, Australia, 3 Murdoch University, Perth, Australia

Two economically, environmentally and culturally important Australian native tree species, Araucaria cunninghamii (hoop pine) and A. bidwilli (bunya pine) are rapidly declining in the Bunya Mountains national park. Some of the affected bunya pines are estimated to be more than 600 years old. Symptoms include yellowing of the crown and rapid dieback, which is consistent with infection by Phytophthora, a fungal- like oomycete. Aerial surveys have shown that symptomatic trees of both species are spread throughout the national park. Phytophthora multivora, a pathogen associated with dieback of Eucalyptus gomphocephala and Pinus radiata in Western Australia, was isolated from the rhizosphere of symptomatic bunya pines. Phytophthora multivora has also been associated together with P. cinnamomi in the dieback of wollemi pine (Wollemia nobilis) in New South Wales, and kauri pine (Agathis australis) in New Zealand. Both pathogens have wide host ranges that include agriculturally and environmentally important plant species. DNA meta-barcoding analysis of the soil detected both pathogens at high numbers. Pathogenicity testing of the organisms is currently being conducted on bunya and hoop pine to confirm aggressiveness. Additional surveys and testing need to be conducted to confirm how wide spread the problem is, and to implement control measures to prevent future damage to the national park and surrounding softwood plantations. From initial observations of the symptoms, spread patterns and environmental history of the affected trees, P. multivora is the most likely causal agent of the dieback.

New Zealand provenance Leptospermum scoparium (mānuka) expresses three resistance phenotypes to the pandemic biotype of Austropuccinia psidii, the causal pathogen of myrtle rust

Grant Smith, David Chagné, Beccy Ganley, Jayanti Nadarajan, Ranjith Pathirana, Julie Ryan, Elise Arnst, Roanne Sutherland, Julia Soewarto, Gary Houlston, Alby Marsh, Emily Koot, Angus Carnegie, Louise Shuey, Geoff Pegg

1 The New Zealand Institute for Plant and Food Research Limited, Lincoln, New Zealand, 2 The New Zealand Institute for Plant and Food Research Limited, Palmerston North, New Zealand, 3 The New Zealand Institute for Plant and Food Research Limited, Te Puke, New Zealand, 4 Manaaki Whenua Landcare Research, Lincoln, New Zealand, 5 Scion Limited, Rotorua, New Zealand, 6 New South Wales Department of Primary Industries, Sydney, Australia, 7 The Queensland Department of Agriculture and Fisheries, Brisbane, Australia

Three resistance phenotypes to the pandemic biotype of the invasive fungal biotrophic pathogen Austropuccinia psidii were identified in artificially inoculated New Zealand provenance Leptospermum scoparium (mānuka) plants grown from seed collected from mother trees growing in different locations within New Zealand. The first two resistance phenotypes, putatively a constitutive response and a hypersensitive response, were leaf resistance phenotypes. On the lateral and main stems a putative constitutive stem resistance was also observed in the trials. Mānuka is the first myrtaceous species where consistent infection of stems in trials was observed, resulting in the development of a new disease severity assessment scale. No individual plants demonstrated both leaf resistances: c. 18% of plants showed both stem resistance and one of the leaf resistances; however c. 26% plants showed either a leaf or a stem resistance but not both, and the remainder of the plants tested (56%) were susceptible, with some plants showing extensive symptom expression. Plant and seed family analysis revealed limited genetic linkage between the putative constitutive leaf and stem resistances suggesting two independent resistance mechanisms. The locale from where the seed were collected was important, as the proportion of leaf and/or stem resistance plants grown from the independent seed families varied by seed provenance.
Genome-wide association mapping for adult plant resistance to powdery mildew in common wheat

Ms Yichen Kang¹, Dr Angela Merry¹, Prof Meixue Zhou¹, Dr Xuechen Zhang², Dr Fangbing Cao², Dr Karen Barry¹
¹Tasmanian Institute Of Agriculture, University of Tasmania, Launceston, Australia, ²Department of Agronomy, Zhejiang University, Hangzhou, China, ³Tasmanian Institute of Agriculture, University of Tasmania, Hobart, Australia

Common wheat (Triticum aestivum L.) is globally the most traded and third produced cereal crop, but is constantly threatened by diseases, particularly fungal pathogens. Blumeria graminis f. sp. tritici, the causal agent of wheat powdery mildew disease, can occur at all stages of the crop and reduces yield ranging from 13-34%. Genetic improvement of wheat for powdery mildew resistance is required, and this can be facilitated through genome-wide association studies (GWAS). Assisted by GWAS, many loci responsible for traits related to improved disease resistance and productivity in wheat have been characterised. We performed GWAS on a total set of 330 wheat varieties obtained from different origins, with the aim of discovering powdery mildew resistance associated SNPs (single-nucleotide polymorphisms) markers that can benefit marker-assisted selection (MAS) for resistance breeding. These wheat materials were genotyped using wheat 90K SNP array, and evaluated for their resistance against powdery mildew in both field or glasshouse conditions from 2016 to 2018. To correct for population structure and relatedness among individuals, principal component analysis and kinship matrix were incorporated into an association model. Resistance associated SNPs have been detected, and to further identify potential candidate genes, alignment of those SNPs onto wheat physical map IWGSC RefSeq v1.0 will be carried out for candidate gene exploration and their gene annotations. Also a BLAST search will be performed in NCBI (National Center for Biotechnology Information) database to identify orthologs of candidate genes in close species. Finally, result from our study will be compared with previously reported powdery mildew resistance loci, and present in integrated mapping plot.

Resistence mechanisms and expression of disease resistance-related genes in sugarcane to Sporisorium scitamineum infection

Mrs Nurul Hidayah¹,², Dr Meredith McNeil³, Dr Shamsul Bhuiyan¹,⁴, Prof Victor Galea¹, Dr Karen Aitken³
¹School of Agriculture and Food Sciences, The University Of Queensland, Gatton, Australia, ²Indonesian Agency for Agricultural Research and Development, Jakarta, Indonesia, ³CSIRO Agriculture and Food, St Lucia, Australia, ⁴Sugar Research Australia, Woodford Station, Woodford, Australia

Resistance of sugarcane to smut infection caused by Sporisorium scitamineum is generally believed to be driven by two resistance mechanisms, external and internal. Development of sugarcane varieties containing both resistance mechanisms promises to achieve a sustainable resistance against smut infection. Two experiments were conducted to identify the resistance mechanism of two full-sib clones, QBYN04-26258, which was susceptible to smut and QBYN04-26006 which was highly resistant to smut infection. The first experiment was through histopathological screening of the infection site using trypan blue staining of the pathogen at different stages of plant growth. The second experiment determined the relative expression of ten disease resistance-related genes in the same two progenies using RT-qPCR. Microscopic observation of the two sugarcane genotypes revealed that the fungal hyphae were only present in the meristem of the susceptible genotype. The RT-qPCR results demonstrated different expression levels of genes within QBYN04-26258 and QBYN04-26006. Genes related to defence mechanisms were up-regulated in QBYN04-26006 and down-regulated in QBYN04-26258. While the genes related to whip development were up-regulated in QBYN04-26258, they were down-regulated in QBYN04-26006, confirming that QBYN04-26258 contained neither external nor internal resistance to smut infection and QBYN04-26006 contained both mechanisms. Interestingly, the HCT1-gene which is a precursor of the phenylpropanoid pathway and is involved in lignin biosynthesis, was up-regulated with a 50-fold change in the susceptible genotype. This result suggested that this gene has a different role in resistance and susceptibility to smut in sugarcane.

275
Harnessing genetics, genomics and pan-genomics to understand cyst nematode resistance in wheat and barley

Prof Diane Mather1, Dr Kelvin Khoo1, Ms Kara Levin1, Mr Bart Van Gansbeke1, Assoc Prof Matthew Tucker1, Assoc Prof Ken Chalmers1, Mr John Lewis2
1School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, Adelaide, Australia, 2South Australian Research and Development Institute, Urrbrae, Australia

Cereal cyst nematodes (CCN, Heterodera spp.) can cause significant yield loss in wheat (Triticum aestivum L.), barley (Hordeum vulgare L.) and other cereal crops. Much of this can be prevented through the use of resistant varieties, which limit the build-up of CCN populations in soils. In Australia, breeding for resistance against the Ha 13 pathotype of CCN (H. avenae) has been very successful, but requires ongoing work to ensure that new varieties are resistant. Elsewhere in the world, there are cereal production regions for which no effective resistance is available. Key CCN resistance loci have been genetically mapped and diagnostic DNA markers are available, but the actual resistance genes have not yet been isolated and functionally analysed. Our research on the Rha2 and Rha4 resistance loci of barley and the Cre8 resistance locus of wheat has narrowed the search to small (< 1 cM and < 1 Mb) regions of the host plant genomes. Given the limited understanding of CCN resistance mechanisms, it is not obvious which predicted genes from the reference genomes should be considered candidates. There is little similarity in gene content among Rha2, Rha4 and Cre8 regions, indicating that the causal genes and resistance mechanisms may differ among these loci. New variety-specific genome assemblies from pan-genome projects are being used to evaluate varietal differences in the presence, sequence and copy number of predicted genes. Several predicted genes have been selected as candidates for functional analysis.

Investigating the genetics underpinning Adult Plant Resistance (APR) to Tan Spot (Pyrenophora tritici repentis) in wheat (Triticum aestivum)

Ms Tamaya Peressini1,2, Dr Eric Dingalasan1,2, Ms Belinda Worland2, Dr Lee Hickey2, Prof Ian Godwin1,2, Dr Caroline Moffat3
1University Of Queensland, School of Agriculture and Food Science, Brisbane, Australia, 2QAAFI Crop Science, Brisbane, Australia, 3School of Molecular Life Sciences, Curtin University, Perth, Australia

Tan Spot is a major foliar disease of wheat (Triticum aestivum) crops in Australia. It is caused by the necrotrophic pathogen Pyrenophora tritci repentis (Ptr), which uses necrotrophic effectors (NE) to elicit disease in the host. The NE ToxA is the major virulence factor causing disease in wheat with the host sensitivity gene Tsn1. In Australia, there are few known resistance genes in germplasm material and many elite cultivars carry Tsn1. Hence, it is important to investigate other race non-specific sources of resistance such as adult plant resistance (APR) to incorporate into breeding germplasm. Recent screening of the Vavilov wheat collection identified several accessions that exhibit APR despite carrying Tsn1. This study aims to identify the genomic regions conferring APR. A recombinant inbred line (RIL) population fixed for Tsn1 derived from the resistant Vavilov landrace WLA036 (APR+) and the susceptible Australian cultivar Banks (APR-) was phenotyped for disease severity in the field. Using 1062 polymorphic DArTseq markers, mapping analyses revealed two resistance QTL (LOD score >3.0): qRL313.YS-2B and qRL313.YS-5B. A QTL for flowering time (qRL313.Mat-2B) co-located with the photoperiod gene Ppd-B1 and was in weak linkage disequilibrium with the resistance QTL qRL313.YS-2B (r² = 0.11-0.23). Each resistance QTL individually reduced disease severity but the combination did not provide an advantage. To investigate the resistance mechanism associated with qRL313.YS-2B, lines differing in allelic status at the qRL313.YS-2B region but carrying identical susceptibility alleles for qRL313.YS-5B were selected for a time-course disease assay examining the expression of Tsn1 during infection. Expression of Tsn1 decreased for the resistant line in the first 24 hours compared to the susceptible line that had no change in expression; suggesting the qRL313.YS-2B region could be involved in the recognition pathway for ToxA-Tsn1. Investigations to identify candidate genes in qRL313.YS-2B region and quantifying effectiveness of this APR to other races of Ptr will enhance our understanding of the pathosystem and provide genomic tools for wheat breeders in Australia.
Fine mapping towards cloning of barley leaf rust resistance gene Rph5

Mr Chris Rothwell1, Dr Matthias Jost2, Dr Evans Lagudah1, Dr Davinder Singh1, Dr Robert Park1, Dr Chunhong Chen2, Dr Peter Dracatos1

1University Of Sydney, Sydney, Australia, 2Commonwealth Scientific and Industrial Research Organisation, Black Mountain, Australia

Leaf rust of barley (Puccinia hordei) is an economically significant disease, however sustainable disease control can be achieved through the use of genetic resistance. Rph5 is an all-stage resistance gene conferring a near immune response to most Australian P. hordei pathotypes. While Rph5 virulence exists in Australia, its frequency is generally low and the gene remains useful for breeders for gene pyramiding. We aimed to determine the molecular basis of the Rph5 resistance using a map based cloning and mutational genomics approach. Previous studies have determined that Rph5 maps near the telomeric region of chromosome 3HS. To fine map the Rph5 locus, 780 F2 individuals derived from the cross Peruvian (rph5) x Quinn (Rph5) were genotyped using EST (expressed sequence tag) derived markers flanking an 8cM region on 3HS to identify recombinants. Further iterative mapping was conducted utilising the Morex reference genome (2017) using insertion-deletion and SNP markers. Rph5 was localised to the telomere of chromosome 3HS and a marker was identified that both co-segregated with the Rph5 resistance and was predictive when validated across a Magnif 104 (Rph5) x Prosa (rph5) doubled haploid population. Due to the lack of sequence information for Rph5 resistance donor accessions, we are currently using a mutational genomics approach to identify the causal gene by comparing wild type with multiple independent knockout mutants. We developed Sodium Azide mutant populations in two backgrounds (Bowman + Rph5 and Magnif 104) and rust tested more than 3,000 M2 spikes in the greenhouse for Rph5 knockouts. Progeny tests confirmed at least six different knockout mutants from each background and we are now analysing candidate genes in the Rph5 region. Our overall aim is to generate a high quality sequence scaffold between Magnif 104 and the Morex barley reference genome to understand the gene space around the Rph5 locus.

Characterisation of genes involved in the sensitivity of barley to Pyrenophora teres f. teres toxins

Dr Abolfazl Sarpeleh1, Dr Haipei Liu1, Prof Amanda Able1

1Department of Agricultural Science, School of Agriculture, Food and Wine, The University of Adelaide, Adelaide, Australia

Pyrenophora teres f. teres (Ptt) causes net form of net blotch (NFNB), a destructive foliar disease of barley worldwide. Despite intensive breeding efforts, disease resistance to NFNB has been breaking down via the evolution of new pathogen races. We have previously showed that Ptt induces disease symptoms through a number of host-specific proteinaceous toxins that potentially target host proteins in susceptible barley cultivars. We have previously identified that significant quantitative trait loci (QTL) associated with toxin sensitivity are located on chromosomes 7H and 5H with 512 and 311 genes underlying each of these QTL respectively. In this study, forty six candidates from the 7H and 38 candidates from the 5H region, selected based on their function and Likelihood Ratio Score, were further analysed for their expression dynamics in response to toxin extracted from a highly virulent isolate of Ptt. Gene expression was measured at 6, 12, 24, 48, 72, 96 and 120 hours post treatment with toxin for all 84 candidates in sensitive barley varieties, Harrington and Mundah, and insensitive varieties, Skiff and Keel. Eight candidates from the 7H and five from the 5H QTL that were consistently differentially expressed between sensitive and insensitive varieties were then profiled in the sensitive and insensitive tails of the Harrington/Skiff and Mundah/Keel mapping populations. The association with toxin sensitivity/insensitivity was confirmed for three genes from the 7H QTL [a putative disease resistance RPP-13-like protein, protein enhanced disease resistance 2-like protein and probable leucine rich repeat receptor-like protein kinase (LRR-RLK)] and two genes from the 5H QTL [nitrate/peptide transporter (NRT1/PTR) and receptor-like protein kinase HSL1]. Analysis of the gene sequences revealed haplotypic variation associated with sensitivity for LRR-RLK from 7H and NRT1/PTR from 5H. These genes, therefore, are potential candidates for developing molecular markers for future resistance strategies for NFNB disease of barley.
Grapevine red blotch surveillance in New Zealand: working in partnership to detect an unwanted pathogen

Ms Sophie Badland¹, Dr Edwin Massey¹
¹New Zealand Winegrowers, Blenheim, New Zealand

Grapevine red blotch virus (GRBV) is the causal agent of red blotch disease in *Vitis vinifera*. Although GRBV was first identified and described in the Napa Valley, California in 2008, studies show it is not of recent origin. Due to symptom variability and similarities with grapevine leaf roll-associated virus, it likely went undetected by viticulturists in the USA for many years. It has since been detected in other grape growing areas of North America, as well as in Korea and India. GRBV poses a biosecurity threat to the wine industry in New Zealand, where quarantine testing for this pathogen did not commence until 2013. While New Zealand does not import large amounts of germplasm from North America and is free from the key Californian vector *Homalodisca vitripennis*, there is a low risk that GRBV may have been imported prior to quarantine testing commencing. This presentation examines the potential risk of GRBV to the New Zealand wine industry and outlines the combined response from the industry, the Vine Nursery Association and the Ministry for Primary Industries to manage this potential risk. The presentation highlights that the establishment of a GRBV surveillance and testing programme required parties to work together and communicate transparently. Without this sense of partnership, it would have been more difficult to confirm the disease is not yet present in New Zealand.

The ever increasing spread of tropical plant pathogens

Prof Andre Drenth¹
¹The University of Queensland, Brisbane, Australia

Over the last century many plant pathogens have significantly increased their geographic ranges. Increases in global travel and trade combined with the global movement of planting material have fuelled this ever-increasing number of new invasions by plant pathogens. Managing these invading pathogens is often troublesome and in many cases caused major consequences in plant based industries and/or disastrous effects on the natural environment. Invasions can take on truly epidemic proportions due to the polycyclic nature of pathogens, their ability to produce large numbers of different spore types increasing their ability for successful establishment and spread and host plants grown in monoculture with little or no resistance. Many pathogens invading new environments often cause higher levels of disease than they do in their centre of origin. Using bananas as an example, the spread of several pathogens across the globe was tracked with the conclusion the “Bridgehead effect” often applies to these invasive pathogens. Thus invasive populations once established, act as novel source populations for new invasions. Realizing the presence and importance of the “Bridgehead effect” has implications for biosecurity and efforts aimed at managing invasive pathogens.
Filling in the gaps: preparing Australia for the arrival of a new biosecurity threat

Mr Craig Elliott\textsuperscript{1,2}  
\textsuperscript{1}Wine Australia, Adelaide, Australia, \textsuperscript{2}Hort Innovation, Sydney, Australia

The plant bacteria \textit{Xylella fastidiosa} is listed as Australia’s number one plant biosecurity threat. Since its first detection, as Pierce’s Disease in California in the 1880’s, Xylella has now established a global footprint through the Americas, in Southern Europe, the Middle East and Taiwan in addition to detections in a number of other countries. The evolution and increased genetic diversity of the bacteria presents a major risk to agricultural systems and ecosystems. The known host range now exceeds 560 plant species and includes grape, olives, citrus, summer fruits, almonds, apple, cherries, coffee and a range of ornamental and Australian native species. It is anticipated that the plant host range, and the likely insect vectors, will continue to increase and the pathogen-host-vector relationship creates a complex biosecurity risk management issue. In the Australian context, this complexity is further complicated by ambiguity; as it is unknown what the full extent of the local host range is and how the bacteria and its potential vectors may behave if Xylella enters the country. In recognition of the emerging threat and the diversity of interests at risk in Australia, Wine Australia and Hort Innovation have collaborated to support a national preparedness role in Australia to coordinate efforts across industry and support government to improve preparedness for a Xylella detection. This presentation outlines the current situation globally for Xylella and the approach taken to develop this preparedness program. This includes outlining the knowledge gaps and research priorities for Xylella in Australia that exist at the various stages of a biosecurity incursion - pre-entry, upon detection, during a response and for recovery - as well as preparing for ongoing management in the event that the eradication of a Xylella outbreak isn’t feasible.

Improving biosecurity outcomes through the establishment of a plant pest surveillance network in Australian botanic gardens

Mr David Gale\textsuperscript{1}, Dr Sharyn Taylor\textsuperscript{1}, Ms Alexandra Lucchetti\textsuperscript{1}, Mr Greg Fraser\textsuperscript{1}  
\textsuperscript{1}Plant Health Australia, Deakin, Australia

Australia has over 150 botanic gardens and arboreta that hold a range of native and introduced plant species. Botanic gardens and arboreta are visited by millions of people each year and can be one of the first sites visited by overseas travellers after they enter the country. As a result, botanic gardens represent both a risk for establishment of new pests or diseases entering on clothing or footwear of travellers and an opportunity for the early detection before exotic pests and diseases become widely established. With coordination and support, existing resources are being leveraged and new capabilities mobilised to provide data on plant pest status. These data will be used to help safeguard plant health on a local and regional scale and globally through the International Plant Sentinel Network (IPSN). This paper presents preliminary outcomes of two related pilot biosecurity programs in participating gardens. The first program engaged staff of botanic gardens in Western Australia, South Australia, Victoria, Tasmania, New South Wales and the Australian Capital Territory to undertake surveillance and provide data on pest absence (or any potential suspected presence) of five target pests using sentinel plants in their gardens. Pests have been selected as they are highly visible and either exotic or confined to localised areas. The second initiative involved ‘Friends of Botanic Gardens’ in Sydney, Melbourne and Canberra. Many gardens are reliant on their Friends of Botanic Gardens group for hands-on help with horticultural care, research, outreach, fundraising and advocacy. To assist each Friends group in general surveillance, a Community of Practice (CoP) is being established on the extensionAUS\textsuperscript{TM} platform to connect biosecurity and surveillance experts with Friends across botanic gardens.
Using honey bees for plant virus surveillance

Dr John Roberts, Dr Kylie Ireland, Dr Wee Tek Tay, Dr Liz Milla, Dr Dean Paini
CSIRO, Canberra, Australia

Early detection of plant viruses is critical for effective biosecurity because it enables growers to respond quickly and limit their spread. Current surveillance methods operate at limited scale, relying on targeted testing of plant material that is usually showing signs of disease and by then the virus is often widespread. We have recently shown that when using high throughput sequencing (HTS) of honey bees collected from commercial hives across Australia for surveillance of honey bee viral pathogens that many plant viruses could also be detected. Using this approach we found two plant viruses that were considered exotic at the time of sampling; cucumber green mottle mosaic virus (CGMMV) and tomato ringspot virus (ToRSV). Importantly, these honey bee samples were collected before either virus was detected from diseased plant material. This indicates that honey bee hives could provide a unique area-wide early detection system for plant viruses that occur in the pollen and nectar collected by honey bees and when combined with HTS deliver a powerful system for untargeted plant virus surveillance at a far lower cost that current approaches. One way to use this approach is to use sentinel bee hives that are already positioned at major Australian ports for the detection of exotic bee pests and pathogens. HTS of samples from sentinel hives foraging around these ports of entry may achieve early detection of an exotic virus before it spreads further. To investigate this, Illumina RNA sequencing of bees and pollen from sentinel hives was used for virus detection and metabarcoding of pollen used to identify the host range of foraging bees around port areas.

Phytophthora palmivora: potential threat to Elaeis guineensis Jacq and the ensued mitigation measures

Dr Shamala Sundram, Ms Intan Nur Ainni Mohamed Azni, Dr Maizatul Suriza, Dr Idris Abu Seman, Dr Mohd Hefni Rusli
Malaysian Palm Oil Board, Bandar Baru Bangi, Malaysia

Oil palm cultivation occupies a large planting area in Malaysia and is one of the most profitable commercial crops contributing to unprecedented socio-economic development in the country. The crop planted along the equatorial belt is susceptible to a number of diseases. Diseases affecting oil palm have been confined according to the region where they have established. Oil palm planted in South East Asia is devastated by the deadly white rot fungus, Ganoderma spp. while in Africa, Fusarium oxysporum spp. causes the catastrophic Vascular Wilt. Yield losses reported by these diseases are higher than the losses caused by other pests in the crop. In the South American industry, bud rot is considered to be the worst disease due to the speed of the spread and its economic impact. Initial reports associated abiotic factors to the outbreak but after extensive studies, researchers from Colombia proved a biotic agent is responsible for the disease. Phytophthora palmivora was identified as the causal agent although the finding is still being challenged. The pathogen has a cosmopolitan distribution recording significant disease damages in other commodity crops in Malaysia including cocoa, durian, jackfruit, papaya and black pepper. A biosecurity alert was initiated in Malaysia resulting in various activities to assess and reduce the potential threat presented by the pathogen. Although phylogenetic analysis of the local P. palmivora isolates showed the isolates are closely related to the Colombian isolates based on ITS region, pathogenicity tests with the local isolates on oil palm resulted in negative infection. This paper reviews the disease, potential risk involved to the multibillion dollar industry and outlines mitigating steps to avoid accidental introduction to the country.
Dispersal patterns of grapevine trunk disease pathogen spores in Australian vineyards

**Dr Regina Baaijens**, Assoc Prof Sandra Savocchia, Mrs Meifang Liu, Mr Matthew Ayres, Mr Simon McDonald, Dr Mark Sosnowski. 1 National Wine and Grape Industry Centre, Charles Sturt University, Wagga Wagga, Australia, 2 Spatial Data Analysis Network (SPAN), Research Office, Charles Sturt University, Wagga Wagga, Australia, 3 South Australian Research and Development Institute, Adelaide, Australia, 4 School of Agriculture, Food and Wine, The University of Adelaide, Glen Osmond, Adelaide, Australia

Eutypa dieback (ED) and botryosphaeria dieback (BD) are important grapevine trunk diseases causing significant yield reduction and threatening the sustainability of Australian vineyards. The spores (ascospores and conidia) of these pathogens are dispersed by rain splash and wind and infect primarily through pruning wounds resulting in cankers, dieback and eventually death of vines. Understanding the spore dispersal patterns of these pathogens will assist in determining the critical times of the year when spores are abundant in Australian vineyards and will also assist growers in making decisions on optimal timing of pruning and the application of wound protection treatments. The spore dispersal patterns of ED (Diatrypaceae) and BD (Botryosphaeriaceae) pathogens were investigated over 3 years in four wine growing regions in Australia. From 2014-2016, four Burkard spore traps were deployed in South Australia (Barossa Valley and Coonawarra) and in New South Wales (Hunter Valley and Griffith). The spore trap tapes were collected and replaced monthly at each site and analysed by qPCR using group-specific primers for Diatrypaceae and Botryosphaeriaceae spores. ED and BD pathogens spores were released all year round but numbers and species varied between regions, season and year. The ED and BD pathogen spores in South Australia were primarily detected in late winter and in early spring while a high number of spores were trapped over summer in New South Wales. Spores were generally detected during or immediately after rain but not all rain events resulted in spore detection. The spore numbers and frequency of detection varied between years with 2016 having the highest number of spores being recorded, particularly for Diatrypaceae species. Preliminary computer modelling of data showed very weak correlation between other weather factors (temperature, relative humidity, dew point, wind speed), indicating that the spore release may be difficult to predict for these pathogens.

Decision Apps for managing disease in Canola, Wheat and Mungbean

**Dr Art Diggle**, Dr Steve Marcroft, Dr Grant Hollaway, Dr Adam Sparks, Dr Jean Galloway. 1 DPIRD WA, Kensington, Australia, 2 Marcroft Grains Pathology, Horsham, Australia, 3 Agriculture Victoria, Horsham, Australia, 4 University of Southern Queensland, Centre for Crop Health, Toowoomba, Australia, 5 DPIRD WA, Northam, Australia

New decision apps have been developed for managing blackleg and sclerotinia of canola, stripe rust of wheat, and powdery mildew of mungbean. The apps include seasonal risk factors, expected yield, and economics. They give the decision maker the range of possible outcomes that can arise from any management decision, customised for each paddock and season. They are based on all available knowledge from national pathology research projects. They will be updated each year with the latest research findings so that new information can be utilised by industry as soon as possible. The apps are designed for quick and efficient use with clients in the field. They will allow users to make the most profitable decisions about disease management in their crops. The apps are delivered for use on iPads or Android tablets. They have a straight-forward user interface that asks for inputs that can be readily estimated by agronomic specialists. We envisage that the main use case for these apps is as an aid to conversations about disease management between growers and their advisors, and that these conversations typically occur in the field. The BlacklegCM and SclerotiniaCM apps for management of blackleg and sclerotinia of canola are available to be downloaded at no cost from the iTunes store or Google Play. The apps for management of stripe rust of wheat and powdery mildew of mungbean have been field tested this year and will be available for use in the coming growing season.
Modelling long-distance dispersal of wheat rusts: towards early-warning systems

Prof Christopher Gilligan¹
¹Department of Plant sciences, University of Cambridge, United Kingdom

Emerging strains of wheat stem rust and stripe rust pose major threats to wheat production world-wide. Using a combination of meteorological and epidemic modelling it has been possible to identify major patterns of dispersal throughout Southern and East Africa, the Middle East, and the South Asia. The results allow seasonal forecasting to identify principal areas at risk when a new race appears. The models, which track the movement of many billions of spores, are also used to identify low-probability: high-risk events with evidence of the risk of spore transmission from Southern Africa to Australia. I also briefly describe a pilot study of a near-real time, early-warning system for wheat rusts in Ethiopia in which we are coupling spore dispersal models with weather-forecast data to provide small-holder farmers with a window of three weeks in which to deploy fungicides to prevent epidemic development.

An archaeological contribution to 40+ years investigation into a ‘new’ disease of Australian grapes

Mr Peter A Magarey¹, Dr Nuredin Habili², Mrs Carla C Magarey³
¹Magarey Plant Pathology, Loxton, Australia, ²Australian Wine Research Institute, Urrbrae, Australia

In 1967, 2 years prior to the formation of APPS, Japanese investigators first reported mycoplasma-like organisms (MLO) in ‘yellows-diseased’ plants. This was prior to PCR diagnosis of these important plant pathogens. In 1976, 7 years after APPS formed, South Australian investigators first reported a yellows-disease of unknown aetiology in Australian viticulture. Thus began a long-term investigation that required newly learned techniques in diagnosing plant-based MLO disease. Likewise, a saga began with intrigue, corporate inertia, inter-organisational red-tape, national biosecurity, science, pseudo-science, high drama, worn-out boot-leather, and Eastern European international politics. All this amid a rapidly developing technology applied in Australia and New Zealand ...and despite long-term uncertainty about the disease which, later known as Australian Grapevine Yellows (AGY), had incorrectly been thought an environmentally induced disorder of cool-climate grapevine cultivars. In the late-1970s, diagnosis of MLO-diseases relied on attempting graft-indexing; transmission to indicator plants; the injection of antibiotics; and epifluorescent and electron (EM) microscopy especially if insects such as leafhoppers, were implicated as vector. Indexing studies proved negative but fluorescence microscopy of the phloem and the injected antibiotic Terramycin® but not Penicillin G® had implicated AGY with Gram-negative bacteria or MLO. But what next? A recent ‘archaeological dig’ has revealed long-forgotten and not-yet-published archived papers. They were from Japanese Dr T Hatta at the Waite Institute in the early-1980s. Disregarded EM micrographs of thin-sections of AGY-diseased stems had shown presence of MLO but it seems now that Dr Hatta’s work rightly constitutes the first EM record of phloem-based MLO (phytoplasma-like organisms) associated with AGY. The subsequent development and application of PCR-analyses and other tools by Australasian investigators led to significant new understandings as to the aetiology of AGY confirming it as native to Australia and thus likely to have native plant hosts and perhaps a native leafhopper vector. Investigations continue.
Diversity and economic impact of bacterial soft rot pathogens (*Pectobacterium* spp. and *Dickeya* spp.) on potato production in the Columbia Basin, USA

Jessie Brazil¹, Dr Hannah Rivedal¹, Dr Kenneth Frost¹
¹Oregon State University, Hermiston, United States

The Columbia Basin growing region of Oregon and Washington accounts for 57% of the United States’ potato production, valued at over $2 billion dollars (farm gate). This region is conducive to high yielding potato production and is impacted by bacterial soft rot pathogens like *Pectobacterium* spp. and *Dickeya* spp. In this region, the diversity of these pathogens has not recently been characterized nor has their economic impact on potato production been quantified. Initially, to examine the diversity of soft rot bacteria, a multiplex PCR protocol was used to identify three common pectinolytic soft rot bacteria, *Pectobacterium atrosepticum* (Pba), *P. carotovorum* subsp. *carotovorum* (Pcc), and *Dickeya* spp., from 132 diseased potato samples that were submitted to the Oregon State University plant diagnostic clinic in Hermiston, OR. Pba accounted for 77% of submitted samples, Pcc accounted for 19%, and 3% were positive for *Dickeya* spp. In 14% of samples, infection by both Pba and Pcc were detected. The phylogenetic relationships of these isolates is currently being examined by sequencing bacterial housekeeping genes and, eventually, through whole genome sequencing. To evaluate the economic impact of soft rot infested seed pieces on overall yield, two species of soft rot bacteria, *P. carotovorum* subsp. *carotovorum* and *D. chrysanthemi*, were vacuum infiltrated into seed pieces of susceptible (Lamoka) and resistant (Russet Burbank) potato varieties. Inoculated seed pieces were mixed with clean pieces at rate of 0%, 5%, 10%, 20% and 30% of total seed. Plants in each of the resulting twenty treatments were evaluated for emergence, disease severity, and yield in 2018 and 2019. The susceptible cultivar Lamoka had lower emergence and emergence was correlated with percent infested seed. This work suggests that it will be important to further develop new diagnostic tests that can detect more of the soft rot pathogens than may be present.

Epidemiological characterisation of pasture dieback in eastern Australia

Dr Anthony Young¹, Ms Melody Thomson¹, Dr Ammar Abdul Aziz¹, Ms Fathin Ayuni Azizan¹, Dr Ike Sari Astuti¹, Mr Hank Xu¹, Adjunct Assoc Prof Graham Stirling¹, Dr Shane Campbell¹
¹The University Of Queensland, Gatton, Australia

Pasture Dieback (PD) is a devastating condition that leads to death of a range of introduced and native pastures throughout Queensland. Commencing with yellowing and reddening of leaf blades of plants along the spreading margins of affected pastures, it results in complete plant death and subsequent proliferation of broadleaf weeds. PD was temporally mapped using satellite imagery, and hyperspectral data were collected in patches along scales of metres to hundreds of metres. A range of potentially pathogenic fungi were isolated from roots of affected plants from sites in south-east and central Queensland. These included species belonging to *Gaeumannomyces*, *Fusarium*, *Periconia*, *Marasmius*, *Leptosphaeria* and *Curvularia*. Inoculation of these isolates onto healthy creeping blue grass cv. Bisset (*Bothriochloa insculpta*) did not result in symptom expression. Parasitic nematodes belonging to *Pratylenchus*, *Xiphinema*, *Rotylenchus*, *Rotylenchulus*, *Meloidogyne* and *Helicotylenchus* were encountered, but not consistently among different PD sites. Although mealy-bugs, which have been reported to cause PD, have been observed at some sites, high numbers of the white ground pearl, *Margarodes australis* (Hemiptera: Margarodidae), have been observed infesting PD affected grass in multiple sites. The infestation density has been positively correlated with the severity of foliar symptoms, as measured by hyperspectral analysis. Being a cryptic organism resilient to conventional control strategies, and belonging to a group with well-documented impacts on other grass species, the potential role of ground pearls in PD needs to be investigated as a priority.
Phylogenetic relationship between the Australian *Fusarium oxysporum* isolates and resolving the species complex using the multispecies coalescent model

**Mrs Saidi Achari**¹,², Dr Jatinder Kaur², Dr Quang Dinh², Dr Ross Mann², Dr Tim Sawbridge¹,², Prof Brett Summerell³, Dr Jacqueline Edwards¹,²

¹La Trobe University, Bundoora, Australia, ²AgriBio, Centre for AgriBioscience, Bundoora, Australia, ³Royal Botanic Gardens & Centennial Parklands, Sydney, Australia

*Fusarium oxysporum* is a ubiquitous fungal species readily isolated from agroecosystem and natural ecosystem soils which include important plant and human pathogens. Studies have indicated that it is a species complex with pathogenic and putatively non-pathogenic isolates. In 2012, phylogenetic analysis of 45 isolates from Australian natural ecosystems resulted in the formation of five clades. Later in 2014, two phylogenetic “species” were identified using Genealogical Concordance Phylogenetic Species Recognition (GCPSR) analysis. In 2017, GCPSR analysis of 61 European isolates from agroecosystems identified three clades in the complex representing three phylogenetic “species” based on 10 complete gene and mitochondrial genome sequences. However, in 2019, eight clades containing 21 phylogenetic “species” were identified from four partial gene sequences of 91 isolates from the CBS culture collection of the Westerdijk Fungal Biodiversity Institute (WFBI). In this study, the phylogenetic relationships between 99 Australian *F. oxysporum* isolates from both natural and agricultural ecosystems were determined using three datasets: whole-genome sequence data, nuclear genes, and mitochondrial genome sequence data. The phylogenies were concordant except for the three isolates. There were three concordant clades from the phylogenies of all the three datasets, suggesting similar evolutionary history for mitochondrial genome and nuclear genes for the isolates in these three clades. The number of species within FOSC was determined using the multispecies coalescent model. The three concordant clades were designated as three species. There was 100% posterior probability support for the formation of three species within the FOSC using the nuclear gene dataset. This is the first report of using the multispecies coalescent model to estimate species within the *F. oxysporum* species complex. Phylogenetic analyses using three different gene datasets from 99 Australian *F. oxysporum* isolates have all supported the formation of three major clades which delineated into three species. Species 2 (Clade 3) may be called *F. oxysporum*. 
A story of an evolving crop pathogen - population structure and evolution of pathogenicity in the Australian Ascochyta rabiei

Dr Ido Bar1, Prabhakaran Sambasivam1, Robert Lee2, Rebecca Ford1
1Environmental Futures Research Institute, School of Environment and Science, Griffith University, Nathan, Australia, 
2Centre for Crop and Disease Management, School of Molecular and Life Sciences, Curtin University, Bentley, Australia

Ascochyta blight disease, caused by the necrotrophic fungus Ascochyta rabiei, is one of the major biotic constraints to chickpea production in Australia and worldwide. Thanks to continuous monitoring efforts in the past 5 years, a comprehensive collection of A. rabiei isolates was collected from the major Australian production regions, representing a broad range of phenotypes and pathogenicity levels. Over these years, representative isolates from each collection year, growing region and pathogenicity level were genetically characterised using a range of methodologies, from microsatellite markers and mating-type PCR assays, to genome-by-sequencing and whole-genome-sequencing. The genotypic data obtained was used to infer population structure and genotype-phenotype associations. Overall, the Australian A. rabiei population displays low genetic diversity (average Nei’s gene diversity of 0.047) when compared to other populations worldwide [1], which can be explained by the presence of just a single mating-type in Australia, MAT1-2, limiting its reproduction to a clonal mode. However, despite this low diversity, the fungal isolates seem to adapt well to the cultivating regimes and resistant chickpea cultivars that are being used, with the emergence of highly aggressive isolates able to overcome the most resistance cultivars at an increasing rate [1]. A temporal pattern was revealed from haplotype analysis, suggesting that at each year, new isolates emerge and then spread across the growing regions, rather than following a within-region evolution pathway. These results emphasize the need for continuous monitoring of the A. rabiei populations and their genetic structure for breeding material screening, along with strict farm and “clean seed” management practices to avoid dispersal of the pathogen.


Xanthomonas campestris pv. campestris – a genomic analysis of Australian historical isolates

Dr Toni Chapman1, Len Tesoriero1, Aaron Darling2, Tracey Berg3, Michael Liu2, Daniel Bogema1
1Nsw Department Of Primary Industries, Narellan, Australia, 2University of Technology Sydney, Sydney, Australia, 
3University of Wollongong, Wollongong, Australia

Xanthomonas campestris pv campestris is the causative agent of Black rot, one of the most devastating diseases to brassica crops world-wide. This seed-borne pathogen is favoured by warm humid conditions and persistent leaf wetness. Black rot is a systemic vascular disease typically identified by the classical V-shaped lesions originating on the leaf margin. To understand the genetic diversity of this pathogen in Australia, we sequenced 221 isolates in our collection using an Illumina MiSeq, with the earliest isolate dating back to 1969. The isolates were assembled with A5-miseq and then phylogenetically compared using marker gene (Phylosift) and core-genome SNP methods. Phylosift was best able to separate the true Xanthomonas campestris pv. campestris isolates from other X. campestris isolates within the collection. Core-genome SNP analysis was more effective at comparing isolates within the X. campestris pv. campestris group, and categorized isolates into at least eight major phylogenetic groups with strong branch support. Genomes from Races 3 (ATCC33913) and 9 (8004) clustered within the same phylogenetic group, while other Races (Race 1: CFBP1869/B100; Race 4 CFBP5817) clustered separately. The Type III secretion system is believed to play an integral role with pathogenicity. With this in mind, we have investigated each major pv. campestris group to determine correlations between effector presence, pv. campestris group and brassica host. Future analysis of these sequences will examine gene content, genomic islands and horizontal gene transfer. The next phase of this work will also examine the genomics of Xanthomonas campestris pv. campestris isolates that are currently being collected during brassica crop surveys as part of a vegetable project (VG16086).
Elucidation of diversity of Barley yellow mosaic virus by RNA-seq analysis

Dr Youko Oono1, Dr Kohei Mishina1, Dr Tetsuo Oikawa1, Mr Tsuneo Kato1, Mr Arihiro Handa1, Dr Hiroomi Kai2, Dr Yuhi Haraguchi2, Dr Emiko Aoki1, Dr Takashi Yanagisawa1, Prof Dr Kazuhiro Sato9, Prof Dr Takao Komatsuda1

1Institute of Crop Science, National Agriculture And Food Research Organization, Tsukuba, Ibaraki, Japan, 2Wheat & Barley Research Center, Tochigi Prefectural Agricultural Experiment St., Utsunomiya, Tochigi, Japan, 3Team of barley breeding, Agricultural Department, Fukuoka Agriculture and Forestry Research Center, Chikusino, Fukuoka, Japan, 4Group of Genome Diversity, Institute of Plant Science and Resources, Okayama Univ., Kurashiki, Okayama, Japan

Barley yellow mosaic virus (BaYMV) causes several symptoms in barley such as long, thin scaly spots appear on the leaves, and the leaves and stems become yellow and atrophy. It is a domestic and foreign agronomic problem that causes yield decline when barley is infected. BaYMV is mediated by plant parasitic protozoan Polymyxa graminis in the rhizosphere. The virus-poisoned Polymyxa can become dormant spores and can survive in the soil for a long time, so that an infected field causes a virus disease for a long time. Therefore, pesticides and cultivar control are difficult, and virus resistance breeding is the only practical method to overcome the problem. Barley yellow mosaic virus belong to Bymovirus genus and composed of two types of single-stranded RNA (RNA-1, -2) with poly-A and a coat protein. Nucleotide sequencing has been performed for some virus strains, but number of those strains is little. Understanding of exact virus type in the infected fields and its relationship with resistance genes in barley can contribute to the barley breeding. Since it is necessary to elucidate the relationship between the BaYMV and the resistance gene of barley for resistance breeding, in this project virus nucleotide sequences are collecting by RNA-seq analysis of root of susceptible barley growing in the infected field located in several parts of Japan. We elucidated the different infection level of BaYMV among varieties and among individuals. We will discuss the diversity of BaYMV.

What can we learn from population genomics studies of Curtobacterium flaccumfaciens pv. flaccumfaciens, the cause of tan spot on mungbean?

Dr Niloofar Vaghefi1, Dr Dante Adorada1, Ms Encarnacion Adorada1, Ms Lisa Kelly1,2, Dr Anthony Young3, Dr Adam Sparks1

1University Of Southern Queensland, Toowoomba, Australia, 2Department of Agriculture and Fisheries, Toowoomba, Australia, 3The University of Queensland, Gatton, Australia

The bacterium Curtobacterium flaccumfaciens pv. flaccumfaciens (Cff) is the cause of tan spot (in some regions known as ‘wilt’) on mungbean (Vigna radiata) and other legumes worldwide. The pathogen was first reported in mungbean paddocks in Queensland in 1984, and subsequently in New South Wales in 1986, causing yield losses of up to 25% in hot and dry seasons. No chemical control is available, and disease management relies on pathogen exclusion, through the use of clean seed, and deployment of moderately susceptible varieties. Breeding programs are currently working to incorporate better resistance into new mungbean varieties. The success of breeding programs depends on a thorough understanding of the genetic diversity and evolution of the pathogen population(s). This project was designed to elucidate the genotypic diversity of Cff population(s) and investigate sources of inoculum that contribute to tan spot epidemics in the northern grains region (Queensland and northern New South Wales). Whole genome re-sequencing of 100 Cff isolates detected moderate genotypic diversity, with a narrower genetic background compared to the global Cff population. One highly adapted clonal lineage was found to dominate the population with a frequency of 45%. This study showcases how population genomics studies can be used to test hypotheses relating to disease epidemiology and provide useful information for resistance breeding programs. The results provide insights on Cff population structure and epidemiology, and have direct application for breeding programs by providing a set of Cff isolates that represent the genetic diversity of the pathogen population(s) in the northern grains region.
Indonesia is one of the largest potato producers in southeast Asia. Late blight caused by *Phytophthora infestans* is a major constraint to profitable potato production in Indonesia. The genetic structure of *P. infestans* populations is dynamic and new genotypes with different epidemiological characteristics are constantly emerging due to migration, mutation, and sexual recombination. To address this challenge, the USAID FtFBPP is working to transform potato cv. Granola, a popular Indonesian variety, with multiple *P. infestans* resistance Rpi genes. To evaluate the potential durability of the three-gene stack in Indonesia, it is important to understand the genetic diversity of *P. infestans* strains in Indonesia. Very little is known about the genetic composition of *P. infestans* isolates in Indonesia. In this study, 148 samples were collected from infected potato leaves on FTA cards from 15 locations in the main potato growing regions on the island of Java from 2016 - 2019. Cards were transported back to the lab at the University of Idaho Aberdeen R&E center in Idaho. Nucleic acids (DNA) were extracted from the FTA cards using QIAamp DNA Investigator Kit (Qiagen) or FTA cards were purified using FTA purification reagent (GE Healthcare). Various different analyses were carried out using DNA isolated from the cards. Allelic diversity was characterized using one-step multiplex markers (12 SSR markers) and cleaved amplified polymorphisms (CAPS) markers were used to determine mating type. A total of 131 multilocus genotypes were determined out of 146 isolates. Cluster population analysis of data revealed that most of the isolates were unique to Indonesia. However, some of the isolates clustered with European isolates EU_2A1, EU_4A1 and EU_13A2. Eighty percent of the samples that amplified with the CAPS markers were determined to be the A1 mating type.
**Genome-based phylogeny of phytoplasmas in coconut and banana**

*Dr Lilia Carvalhais¹*, Ms Cecilia O’Dwyer¹, Dr Alistair McTaggart¹, Dr Paul Dennis², Dr Vivian Rincon-Florez¹, Ms Jane Ray², Prof Andre Drenth¹

¹Centre For Horticultural Science, Queensland Alliance For Agriculture And Food Innovation, University of Queensland, St Lucia, Australia, ²School of Earth and Environmental Sciences, University of Queensland, St Lucia, Australia

Phytoplasmas are insect-vectored bacteria that affect many plant species, causing devastating yield losses in crops worldwide. Their transmission occurs through insects, planting material and possibly seeds. In 2011, a phytoplasma was associated with the Bogia coconut syndrome, a disease responsible for decimating coconut plantations in the Madang province in Papua New Guinea (PNG) since the late 1970s. In 2012, a new disease, known as Banana Wilt Associated Phytoplasma (BWAP), was reported in banana plants from the same location. It has spread in PNG and recently it was reported from the Solomon Islands. In PNG, 87% of the total population live in rural areas, with bananas and coconuts being the second and third most important commodities. Phytoplasmas associated with banana and coconut diseases were classified as belonging to the same taxon based on their near-identical sequence of the 16S rRNA gene region. Whether these phytoplasmas belong to the same taxa or have jumped from coconut palms to banana have not been comprehensively investigated. Using comparative genomics, we sought to test: (i) the hypothesis that phytoplasmas from banana and coconut are two different species and (ii) if there is a genetic basis for host adaptation. Phytoplasmas are non-culturable, have small genomes and they require part of the machinery in cells of their hosts (plant and insect) for multiplication. For this reason, we adopted a genome-centric metagenomics approach that uses a hybrid of high throughput and long read sequencing to assemble whole genomes from the DNA of infected plant material. The obtained genome sequences of the banana and coconut phytoplasmas were compared to each other and to publicly available genomes of phytoplasmas from other hosts. Our results showed gene gains and losses across the group, and refined the evolutionary relationships between species of phytoplasma based on a phylogenomic analysis.

**How phytoplasmas modulate plant architecture and promote their own spread via insect vectors**

*Prof Hogenhout lab¹*

¹Department of Crop Genetics, John Innes Centre, Norwich, United Kingdom

Phytoplasmas are obligate intracellular bacterial parasites of plants that induce dramatic changes in plant architecture, including for instance, proliferation of stems and branches (witches’ brooms) and the reversion of flowers into leaf-like structures (phyllody). These bacterial parasites cause economic losses of a diverse range of crops worldwide and predominantly depend on sap-feeding insects for transmission to plants. The ubiquitous Aster Yellows Witches’ Broom phytoplasma (AY-WB) produces the three effectors SAP05, SAP11, SAP54 that promote the degradation of plant SPL, GATA, TCP and MADS-box transcription factors, leading to changes in shoot formation timing and numbers, plant aging, branching, and leaf and flower development. The insect vectors of AY-WB are polyphagous *Macrosteles* leafhopper species. Interestingly, the three AY-WB SAPs also convert plants into more attractive hosts for egg laying and reproduction of *M. quadrilineatus*. Thus, phytoplasmas produce specific effectors that interfere with key plant developmental processes leading to dramatic changes in plant architecture. Moreover, these effectors promote insect vector reproduction rates thereby increasing the number of insects, which then transmit the obligate phytoplasmas to new host plants.
Dancing with the stars: *Botrytis cinerea* and a novel, mechanically transmitted DNA mycovirus that it hosts mutually regulate each other’s replication rates

Dr Mahmoud Khalifa$^{1,2}$, Dr Robin MacDiarmid$^{2,3}$

$^1$Botany and Microbiology Department, Faculty of Science, Damietta University, Damietta, Egypt, $^2$The New Zealand Institute for Plant & Food Research Limited, Auckland, New Zealand, $^3$School of Biological Sciences, The University of Auckland, Auckland, New Zealand

Among the 73 recognised species of the *Genomoviridae* ssDNA virus family, a lone species has been isolated from a fungal host, *Sclerotinia sclerotiorum*. Research to identify the viral hosts for the other ‘orphaned’ (‘sequence-only’) virus species is aimed at expanding the known host range of mechanically transmissible, hypovirulence-conferring ssDNA mycoviruses. Here, we present a proof-of-concept that broadens the range of known hosts of these ssDNA mycoviruses to include a second cosmopolitan fungus, *Botrytis cinerea*. We report a new-to-science ssDNA mycovirus tentatively named botrytis gemyardayirivirus 1 (BGDaV1). The mycovirus is 1701 nt long and has three open reading frames (ORFs). Of the three ORFs, only ORF I, which codes for a replication initiation protein (Rep), shared identity with other proteins in GenBank. This finding increases the diversity of genomoviruses, as it represents the type species of a novel genus, *Gemydayirivirus*. BGDaV1 is infective as cell-free purified particles and confers hypovirulence on its natural host by reducing the rate of fungal growth. As a counter defence, the BGDaV1 is a target for RNA silencing and genomic DNA methylation, keeping the virus at very low titre. The discovery of BGDaV1 expands our knowledge of the diversity of genomoviruses and their interaction with fungal hosts.

High throughput detection of Australian Pea seed-borne mosaic virus populations and its molecular properties

Dr Solomon Maina$^1$, Dr Linda Zheng$^2$, Dr Wycliff Kinoti$^2$, Dr Mohammad Aftab$^1$, Ms Narelle Nancarrow$^1$, Dr Peter Trebecki$^1$, Mr Shane King$^1$, Dr Fiona Constable$^2$, Dr Brendan Rodoni$^2$

$^1$Agriculture Victoria Research, Horsham, Australia, $^2$Agriculture Victoria Research, AgriBio, Bundoora, Australia

*Pea seed-borne mosaic virus* (PSbMV; Family *Potyviridae*, Genus *Potyvirus*) mainly infects field pea (*Pisum sativum*) along with other crops belonging to the leguminous group worldwide. PSbMV can be spread through sowing infected field pea seed stocks which produce infected plants that then act as the main source of inoculum for crop-to-crop spread by aphid vectors in a non-persistent manner throughout the growing season. In Australia, weather conditions such as wind-mediated contact transmission early in the growing season have been found to spread PSbMV. Virus infection can cause substantial seed yield and quality losses in field pea, especially when the seed sown has infection levels > 0.5%. PSbMV isolates are classified biologically into four pathotypes based on resistance genes. Some pathotypes have different levels of virulence and some decrease yield despite not showing any virus-like symptoms. In Australia, most studies on PSbMV have focussed on coat protein genes. A high throughput sequencing method was implemented to test the overall hypothesis that there is a relationship between the phylogenetic grouping of PSbMV genomes in Australia and their biological properties. Leaf samples from field peas with virus-like symptoms were collected from different parts of Australia. RNA libraries were prepared using the TruSeq stranded Ribozero-plant method. Bioinformatics analysis followed by a subsequent recombination study revealed that a common recombination event occurred within Australian pathotypes at the 3'UTR region. Phylogenetic analysis of complete PSbMV genomes reveals that two introductions have occurred in Australia. This is the first study that describes PSbMV genomes and their pathotype recombination in Australia.
Characterisation of ‘Candidatus Liberibacter brunswickensis’, a novel candidate Liberibacter species identified in Australia

Ms Jacqueline Morris1,2,3, Dr Rachel Mann2,3, Dr Rebekah Frampton3,4, Dr Jason Shiller2, Mr Angage Sanka Perera2, Mr Sorn Norng2, Dr Mallik Malipatil1,2, Dr Alan Yen1,2,3, Dr Grant Smith3,4, Dr Brendan Rodoni1,2,3

1 La Trobe University, Bundoora, Australia, 2 Agriculture Victoria, Bundoora, Australia, 3 Plant Biosecurity Cooperative Research Centre, Bruce, Australia, 4 The New Zealand Institute for Plant & Food Research Limited, Lincoln, New Zealand

The incursion of exotic Liberibacter phytopathogens, in particular ‘Candidatus Liberibacter asiaticus’ (CLas) and ‘Candidatus Liberibacter solanacearum’ (CLso) are of major concern to Australian agricultural crop production in the Rutaceae, Solanaceae and Apiaceae families. Species of the Liberibacter genus are phloem-limited, gram-negative, alpha-proteobacteria that are predominantly vectored by psyllids. Although Australia is a centre for psyllid diversity, phytopathogenic or endophytic Liberibacter species had not been detected in mainland Australia prior to this study.

‘Candidatus Liberibacter brunswickensis’ (CLbr) was detected in an initial survey of the eggplant psyllid, Acizzia solanicola collected from metropolitan Melbourne, Victoria, Australia. CLbr was identified using novel generic Liberibacter genus primers followed by a novel metagenomic multi-locus sequence analysis (MLSA) mapping approach. Further characterisation determined that CLbr can be transmitted by A. solanicola to eggplant, replicate, move and persist in eggplant and be acquired from eggplant by CLbr-negative A. solanicola individuals. Findings also strongly suggest that CLbr movement in planta follows the source to sink relationship as previously described for CLas and CLso. CLbr does not cause disease of eggplant during the early stages of host colonisation and is unlikely to be a pathogen of eggplant. The draft genome of CLbr was assembled and included in the largest and most diverse Liberibacter comparative genomics study to date, providing new insights into the Liberibacter genus and species within. The phylogeny of the core Liberibacter genome and average nucleotide identity supports the current taxonomical separation of species. A small number of carbohydrate active enzymes and putative effectors were common to all Liberibacter genomes analysed and are likely to be important for host colonisation (plant and psyllid). Prophage elements common to all Liberibacter species were also identified for the first time that will improve our understanding of the evolution of Liberibacter species within this genus.
Grapevine leafroll-associated virus 3: symptoms, suppression and seasonal movement

Miss Roshni Rohra$^{1,2}$, Dr Karmun Chooi$^2$, Dr Robin MacDiarmid$^{1,2}$

$^1$The New Zealand Institute for Plant and Food Research Limited, Auckland, New Zealand, $^2$School of Biological Sciences University of Auckland, Auckland, New Zealand

Grapevine (Vitis vinifera) is susceptible to infections from nearly 70 viruses and virus-like organisms, of which Grapevine leafroll-associated virus 3 (GLRaV-3) is one of the most economically destructive. Infection of GLRaV-3 causes grapevine leafroll disease, creating characteristic symptoms of leaf rolling and chlorosis or leaf reddening, depending on the grapevine cultivar. Previous studies have indicated GLRaV-3 is known to accumulate differentially depending on season and plant tissue. However, differences in symptomology, titre and spread over a growing season between GLRaV-3 genetic variants has yet to be understood. A comprehensive understanding of the temporal-spatial movement of Group I, VI and X genetic variants of GLRaV-3 has been undertaken using RT-qPCR quantification of viral titre. The findings of this research will lead to an effective sampling and detection regime for improved disease management, as well as further insight into the underlying molecular processes of symptom development caused by GLRaV-3. Understanding the pathogenicity factors of GLRaV-3 is a crucial area of research to correlate symptom expression and severity with genetic variants of GLRaV-3. Currently, the key virulence factors of GLRaV-3 are proteins that function as viral suppressors of RNA silencing (VSRs), which inhibit the hosts defence response, RNA silencing (RNAi). Using Agrobacterium-mediated transient expression assay in Nicotiana benthamiana, two VSRs of GLRaV-3 have been identified and characterised from Group I, VI and X variants of GLRaV-3. Based on these results, VSRs of weak virulence have been identified because of genetic changes of the protein coding genes. These findings will aid in obtaining a mild strain of GLRaV-3 which results in weak viral infection and symptoms. Overall, this work has correlated symptom expression to temporal-spatial analysis of Group I, VI and X relative titre within grapevines and the role of VSRs in the processes of virus movement, accumulation and symptom expression.
Optimisation of cold plasma to manage *Fusarium* species in postharvest wheat grain

Mrs Maninder Kaur¹, Dr Daniel Huberli², **Dr Kirsty Bayliss**¹

¹Murdoch University, Murdoch, Australia, ²Department of Primary Industries and Regional Development, South Perth, Australia

*Fusarium* species are one of the most common pathogens found in wheat grain, both in the field and in postharvest storage. Some *Fusarium* are also associated with the production of mycotoxins that are carcinogenic and mutagenic to humans and animals. Cold plasma is an ionised gas that can be used to treat a range of microorganisms. In this study conditions were optimised for cold plasma treatment of pure cultures of *Fusarium* spp. and infested wheat grain. Isolates of *Fusarium graminearum* were selected as these represent the most mycotoxic species found in stored grain in Western Australia. Actively growing cultures were exposed to cold plasma for different time intervals and from varying distances. To determine the effect of cold plasma on culture media, uninoculated plates were also exposed to cold plasma, which were then inoculated with the *Fusarium* isolates. After each treatment, radial colony growth was measured and compared to the untreated control. In addition, different volumes of *Fusarium*-infested grain were exposed to cold plasma. Treated grain was analysed to assess any phytotoxicity of cold plasma to the grain and inhibition of *Fusarium*. Results demonstrated that cold plasma could significantly inhibit the growth of *F. graminearum* isolates, and also had a positive influence on treated grain, increasing germination by more than 10%. The results of these experiments will be presented in the context of cold plasma as a postharvest grain treatment.

Influence of seaweed bioformulations in the management of fungicidal stress and blast disease in rice

**Dr MK Prasannakumar**¹, Dr Banakar Sahana N¹, Dr Sri Sailaja Nori², Dr Shrikumar Suryanarayan², Dr Girish TR², Mr Punith ME¹

¹Department of Plant Pathology, University of Agricultural Sciences, Bangalore, India, ²Sea6 Energy Pvt Ltd, Centre for Cellular and Molecular platforms, NCBS-TIFR, Bangalore, India

Rice is an important, staple and mainstay crop for billions of livelihoods. Rice crops experience a wide range of environmental perturbances during development that could limit its productivity. When rice is grown under suboptimal environmental conditions, a yield gap is observed and thus the actual average yield obtained is much lower than the maximum yield potential. Biotic and abiotic stresses are the main constraints in rice production. This study was focused on managing fungicidal stress (abiotic) and blast disease (biotic) using tropical red seaweed (*Kappaphycus alvarezii*) bioformulations (SPE1 and SPE2). Foliar application of fungicides alone resulted in negative physiological and biochemical changes viz., extended stomatal closure, increased leaf temperature and higher ROS production. However, these were improved in combination with fungicide and seaweed bioformulations. Further biochemical analysis revealed application of seaweed bioformulations act by inducing the activity of antioxidants (APX, CAT, GR, POD, SOD) and plant minerals (Ca⁺ and K⁺). Rice plants that were primed and inoculated with the rice blast pathogen *Magnaporthe oryzae* (MG01) showed increased expression levels of OsPR1#012, OsPR1#021, OsPR1#022, OsPR1#074, OsPR1#121, PAL-6, PR1-5 and PR-15 transcripts with relative expression of 5.60, 7.86, 2.93, 4.13, 2.61, 3.86, 7.33 and 3.18 at 24 hpi respectively. Expression of the stress related genes clearly showed the short-term stress in plants treated with fungicides. Level of expression of different transcripts viz., E2F, HSFA2A, HSFB2B, HSFB4C, HSFC1A and ZIP12 was lower in case of combination treatments compared to sole application of fungicides. Application of fungicides alone led to higher expression levels of stress genes. In the field conditions, seaweed bioformulation SPE2 was on par with tricyclazole in curtailing the blast disease. Another bioformulation SPE1 increased the growth parameters which directly impacted on straw and grain yield. The study suggests that the seaweed bioformulations acts as antistress agents in relieving both biotic and abiotic stress by regulating stress related genes.
Exploring the interactions between bacterial endophytes and trunk disease pathogens of grapevine

Ms Jennifer Niem1,2, Dr Regina Billones-Baaijens1, Dr Benjamin Stodart3, Dr Sandra Savoccia1,2
1National Wine and Grape Industry Centre, Charles Sturt University, Mambarra Drive, Wagga Wagga, Australia, 2School of Agricultural and Wine Sciences, Charles Sturt University, Boorooma Street, Wagga Wagga, Australia, 3Graham Centre for Agricultural Innovation (Charles Sturt University and NSW Department of Primary Industries), School of Agricultural and Wine Sciences, Charles Sturt University, Boorooma Street, Wagga Wagga, Australia

In recent years, the use of microbials to manage plant disease has gained popularity driven in part by safety concerns posed by synthetic fungicides for humans and the environment. Anecdotal evidence indicates that some endophytic bacteria of grapevines including Pseudomonas species suppress the growth of grapevine trunk disease (GTD) pathogens in vitro. To understand the interactions between bacterial endophytes isolated from grapevine and GTDs, we investigated: a) the bacterial endomicrobiome associated with grapevine wood using next-generation sequencing (NGS); and b) the potential of Pseudomonas spp. as a biocontrol agent for GTDs. Metagenomic characterisation of the grapevine endomicrobiome was conducted using 16S rDNA primers with DNA extracted from GTD symptomatic and asymptomatic grapevine wood collected from Harden and Hunter Valley, NSW. Pseudomonas spp. predominated the bacterial community in the asymptomatic grapevine tissue from both locations, comprising 56-74% of the total population. In contrast, the Pseudomonas population in grapevine wood symptomatic for GTD were significantly lower representing 29% (Harden) and 2% (Hunter Valley). Targeted isolation of fluorescent Pseudomonas was undertaken followed by dual culture assays against nine Botryosphaeria dieback (BD) and three Eutypa dieback (ED) pathogens. From the 47 fluorescent isolates obtained, 10 exhibited antagonism towards the pathogens. In detached cane assays, three isolates reduced the infection of Neosicoccum luteum up to 90% compared to controls (100% infection). One isolate (BCA 17) was further found to reduce BD infection by 80% in potted grapevines. A rifampicin-resistant strain of this Pseudomonas isolate was inoculated on potted vines and was found to colonise and persist in the grapevine tissues for up to 6 months. The presence and abundance of Pseudomonas spp. in grapevine tissues indicates its ability to colonise the host tissue with the potential to suppress GTD infections.

Using microwave radiation to destroy macroconidia of the cereal pathogen Fusarium pseudograminearum: a hot solution?

Mrs Toni Petronaitis1,4, Mr Clayton Forknall2, Dr Graham Brodie3, Dr Steven Simpfendorfer1, Dr David Backhouse4
1New South Wales Department of Primary Industries, Tamworth, Australia, 2Department of Agriculture and Fisheries, Toowomba, Australia, 3University of Melbourne, Dookie, Australia, 4University of New England, Armidale, Australia

Cereal production in Australia is impacted by stubble-borne diseases such as crown rot, caused by the fungus Fusarium pseudograminearum (Fp). The disease can be difficult to manage, as Fp can survive within crop residues as macroconidia or mycelium across multiple seasons. Microwave radiation may offer a rapid and chemical-free approach to destroying Fp inoculum within stubble. The energy required to kill Fp macroconidia using microwave radiation was therefore investigated in a microwave dose response experiment. Suspensions of macroconidia of Fp (2.6 x 10⁴ macroconidia/mL) were microwaved in a conventional 1100 W microwave oven for 0, 4, 5, 6, 7, 8, 9 and 10 seconds. Viability after microwaving was assessed by counting colony forming units (CFU) following dilution plating on ¼ potato dextrose agar plus novobiocin. Conidial viability declined as the energy applied increased. Significant reductions in viability (>90% reduction in CFU) were achieved after 7 seconds of microwave treatment, or 131 Jg⁻¹ of energy. Macroconidia were completely non-viable following microwave treatment times of 8 seconds or longer. The minimum mean energy and temperature requirements to achieve total death were therefore 172 Jg⁻¹ of energy and 62.5°C, respectively. Thus, microwave radiation can be used to destroy Fp macroconidia using a relatively small energy dosage. This method could be used for assessing the susceptibility of other plant pathogens to microwave radiation, and potentially adapted for treating inoculum in soil and stubble for crown rot management under field conditions.
RNA sprays to combat plant pathogenic fungi

Dr Anne Sawyer\textsuperscript{1,2}, Dr Louise Shuey\textsuperscript{2}, Dr Ken Pegg\textsuperscript{3}, Dr Lindy Coates\textsuperscript{3}, Prof Bernie Carroll\textsuperscript{1}, Prof Neena Mitter\textsuperscript{2}

\textsuperscript{1}School of Chemistry and Molecular Biosciences, The University Of Queensland, St Lucia, Australia, \textsuperscript{2}Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Australia, \textsuperscript{3}Department of Agriculture and Fisheries, Ecosciences Precinct, Dutton Park, Australia

RNA interference (RNAi)-inducing sprays are a new non-toxic, non-transgenic, environmentally friendly strategy that has the immediate potential to revolutionise crop protection against insect-transmitted plant viruses, and facilitate a transition away from the use of chemical insecticides in agriculture. The approach, which involves spraying plants with virus-specific dsRNA, triggers and augments systemic RNAi, the plant’s natural defence mechanism against viruses. When applied in combination with stabilising nanoclay, in the formulation known as BioClay, dsRNA can provide virus protection to plants for more than 20 days, making a single spray a commercially feasible and lasting approach to protect crops from viruses. The aim of the present work is to develop BioClay-based RNA sprays to protect avocados, pineapples and Australian Myrtaceae species from pre- and post-harvest fungal diseases. This will lead to clean green safe produce from pre- to post-harvest, from field to supermarket trolley, safeguarding Queensland horticulture and ecosystems.
Achari Saidi 284
Addison Shea 234
Adorada Dante 198
Aftab Mohammad 115, 267
Ahmad Waqas 83
Aldaoud Ramez 101, 209
Andersen Mark 118
Anderson Jay 160, 239
Andjic Vera 257
Arshed Saadijah 250
Aylward Janneke 77, 210
Badland Sophie 278
Balandres Mark Angelo 181
Bar Ido 285
Bariana Harbans 222
Barroso Roberto 80
Bayliss Kirsty 292
Bellard Stanley 160
Belt Katharina 266
Bennett Sarita 222
Besselma Noureddine 170
Bhuiyan Md Abdulahil Baki 208
Bilkiss Marzia 208
Billones-Baaijens Regina 244, 281
Birt Henry W.G. 186
Black Amanda 76
Blake Sara 216
Bothma Sheryl 203
Bowen Joanna 219
Bradshaw Rosie E. 84, 186
Brain Linda 85
Bull Carolee 231
Burgess Lester 161, 184, 185, 259
Buyoyu Peter 175
Callaghan Sophia 97, 183
Candresse Thierry 146
Carnegie Angus 102, 253
Carvalhais Lila 288
Chapman Toni 285
Chng Sooie 223
Choi Kar Mun 81, 176
Cobon Jennifer 98
Coutinho Teresa 252
Coutinho Teresa 272
Covarelli Lorenzo 165, 166, 176, 205
Crump Nigel S. 122, 177
Cui Wei 192
Cutajar Jennifer 196
Dadu Rama Harinath Reddy 255
Dagvadorj Bayantes 133
Dahanayaka Buddhika 251
Dall David 258
Darling Toni Louise 180
Darma Reynald 157
Davenport Bryant 179
Davis Richard 153
De Boer Rudolf 99
De Jong Huub 264
De Silva Awalikara 124
Demers Michelle N. K. 157
Dennis Paul 212
Diggie Art 281
Dinh Xuan Hoan 223
Dinsdale Adrian 260
Donovan Nerida 267
Dravitzki Cordelia 190
Drayton Gabrielle 182
Drenth Andre 278
Dron Nicole 195
Dundore-Arias JP 138
East David 235
Edwards Jacqueline 210, 225
Ehau-Taumaunu Hanareia 234
Elliott Craig 279
Esthe Beye 153
Evans Margaret 204
Evans Margaret 216
Fabian Belinda 187
Fiedler Kate 259
Filardo Fiona 81
Frampton Rebekah 169
Gale David 279
Galea Victor 264
Gambley Cherie 147
Garcia-Ceron Donovan 219
Gardner Judith 272
Gaza Hazel 205
Gilligan Christopher 282
Gozar Hossein 196
Gozar Hossein 197
Gomez Apollo 121
Gomez Apollo 206
Gomez Apollo 207
Gough Elaine 238
Grant Neil 257
Grice Kathy 102
Gul Sumnia 136
Hahn Bum-Soo 129
Halvorson Jessica 164
Hanif Sana 265
Hansen Bryan 168
Harper Lincoln 71
Harris Kellyanne 74
Harvey Paul 171, 212
Hayden Helen 162
Henderson Caitlin 177
Hidayah Nurul 131, 275
Hidayat Sri 217
Hill Erin 191
Hogenhout Saskia 288
Hong Toan 213
Horlock Christine 144
Hu Fang-Yu 172
Huberli Daniel 140
Hunter Gavin 249
Idnurn Alexander 148
Ifikhar Sehrish 71
Innes Roger 105
Ismail Ismail 72
Jacott Catherine 220
Jeff-Ego Olumide 202
<table>
<thead>
<tr>
<th>Name</th>
<th>Index</th>
<th>Name</th>
<th>Index</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jin</td>
<td>Hailing</td>
<td>106</td>
<td>Mitter</td>
</tr>
<tr>
<td>John</td>
<td>Evan</td>
<td>134</td>
<td>Mk</td>
</tr>
<tr>
<td>Johnson</td>
<td>Shakira</td>
<td>111</td>
<td>Mohamed</td>
</tr>
<tr>
<td>Jones</td>
<td>Darcy</td>
<td>158</td>
<td>Cassim</td>
</tr>
<tr>
<td>Jooste</td>
<td>Anna</td>
<td>142, 217</td>
<td>Mohammed</td>
</tr>
<tr>
<td>Jorgensen</td>
<td>Dorthe</td>
<td>199</td>
<td>Monk</td>
</tr>
<tr>
<td>Kalinina</td>
<td>Natalia</td>
<td>86</td>
<td>Montagna</td>
</tr>
<tr>
<td>Kamoun</td>
<td>Sophien</td>
<td>70</td>
<td>Montagna</td>
</tr>
<tr>
<td>Kang</td>
<td>Yichen</td>
<td>275</td>
<td>Montagna</td>
</tr>
<tr>
<td>Kant</td>
<td>Pragya</td>
<td>150</td>
<td>Morin</td>
</tr>
<tr>
<td>Kaur</td>
<td>Jatinder</td>
<td>143</td>
<td>Morris</td>
</tr>
<tr>
<td>Kaushik</td>
<td>Himadri</td>
<td>263</td>
<td>Mostert</td>
</tr>
<tr>
<td>Kelly</td>
<td>Lisa</td>
<td>114</td>
<td>Mostowfizadeh-Ghalamfarsa</td>
</tr>
<tr>
<td>Khambalkar</td>
<td>Pravin</td>
<td>220</td>
<td>Muazam</td>
</tr>
<tr>
<td>Khan</td>
<td>Mohamed</td>
<td>87, 164</td>
<td>Mulholland</td>
</tr>
<tr>
<td>Khangura</td>
<td>Ravjit</td>
<td>87</td>
<td>Mwape</td>
</tr>
<tr>
<td>Khudhair</td>
<td>Mohammed</td>
<td>190</td>
<td>Nair</td>
</tr>
<tr>
<td>Kim</td>
<td>Hyo-Suk</td>
<td>242</td>
<td>Nancarrow</td>
</tr>
<tr>
<td>Kinoti</td>
<td>Wycliff</td>
<td>218</td>
<td>Neilsen</td>
</tr>
<tr>
<td>Kiss</td>
<td>Levente</td>
<td>225, 237</td>
<td>Ngle</td>
</tr>
<tr>
<td>Knight</td>
<td>Noel</td>
<td>77</td>
<td>Niem</td>
</tr>
<tr>
<td>Kreidl</td>
<td>Simone</td>
<td>254</td>
<td>Noble</td>
</tr>
<tr>
<td>Kroese</td>
<td>Duncan</td>
<td>120, 170</td>
<td>Nogarotto</td>
</tr>
<tr>
<td>Kularathna</td>
<td>Manjula</td>
<td>141</td>
<td>Norman</td>
</tr>
<tr>
<td>Kumari</td>
<td>Safaa</td>
<td>150</td>
<td>Nunes Leite</td>
</tr>
<tr>
<td>Kusch</td>
<td>Stefan</td>
<td>94</td>
<td>Nunn</td>
</tr>
<tr>
<td>Ladja</td>
<td>Fausiah</td>
<td>151</td>
<td>Nurlita</td>
</tr>
<tr>
<td>Le</td>
<td>Khoa</td>
<td>99</td>
<td>Nwe</td>
</tr>
<tr>
<td>Le</td>
<td>Duy</td>
<td>218</td>
<td>O'Donnell</td>
</tr>
<tr>
<td>Leach</td>
<td>Jan</td>
<td>229</td>
<td>O'Dwyer</td>
</tr>
<tr>
<td>Lehwala</td>
<td>Ruvini</td>
<td>78</td>
<td>Ogaji</td>
</tr>
<tr>
<td>Lim</td>
<td>Fook Hwa</td>
<td>193</td>
<td>Oke</td>
</tr>
<tr>
<td>Liu Heang</td>
<td>Winnie</td>
<td>127</td>
<td>O'Neill</td>
</tr>
<tr>
<td>Longmuir</td>
<td>Amy</td>
<td>188</td>
<td>Oono</td>
</tr>
<tr>
<td>Lovelock</td>
<td>David</td>
<td>259</td>
<td>Oswald</td>
</tr>
<tr>
<td>Lux</td>
<td>LeAnn</td>
<td>122</td>
<td>Outram</td>
</tr>
<tr>
<td>MacDiarmid</td>
<td>Robin</td>
<td>88, 289</td>
<td>Owen</td>
</tr>
<tr>
<td>Magarey</td>
<td>Robert</td>
<td>88</td>
<td>Pain</td>
</tr>
<tr>
<td>Magarey</td>
<td>Peter</td>
<td>123, 282</td>
<td>Park</td>
</tr>
<tr>
<td>Maina</td>
<td>Solomon</td>
<td>289</td>
<td>Parkinson</td>
</tr>
<tr>
<td>Mair</td>
<td>Wesley</td>
<td>147</td>
<td>Pathania</td>
</tr>
<tr>
<td>Malseed</td>
<td>Nellie</td>
<td>143</td>
<td>Pathrose</td>
</tr>
<tr>
<td>Mann</td>
<td>Rachel</td>
<td>103</td>
<td>Pattemore</td>
</tr>
<tr>
<td>Mann</td>
<td>Ross</td>
<td>213</td>
<td>Pattison</td>
</tr>
<tr>
<td>Marroni</td>
<td>Virginia</td>
<td>243</td>
<td>Perera</td>
</tr>
<tr>
<td>Marsh</td>
<td>Alby</td>
<td>74</td>
<td>Peressini</td>
</tr>
<tr>
<td>Martin</td>
<td>Anke</td>
<td>158</td>
<td>Petronaitis</td>
</tr>
<tr>
<td>Martin</td>
<td>Juliet</td>
<td>200</td>
<td>Petrović</td>
</tr>
<tr>
<td>Masino</td>
<td>Andrea</td>
<td>111, 113</td>
<td>Pieter</td>
</tr>
<tr>
<td>Maso</td>
<td>Winnie</td>
<td>180</td>
<td>Plummer</td>
</tr>
<tr>
<td>Mather</td>
<td>Diane</td>
<td>139</td>
<td>Prabhakaran</td>
</tr>
<tr>
<td>Mather</td>
<td>Diane</td>
<td>276</td>
<td>Prasannath</td>
</tr>
<tr>
<td>Matthews</td>
<td>Andrea</td>
<td>138</td>
<td>Purushotham</td>
</tr>
<tr>
<td>Mccarthy</td>
<td>Hannah</td>
<td>135</td>
<td>Quade</td>
</tr>
<tr>
<td>McGeare</td>
<td>Brogan</td>
<td>159</td>
<td>Quazi</td>
</tr>
<tr>
<td>McNeil</td>
<td>Meredith</td>
<td>94</td>
<td>Rabbidge</td>
</tr>
<tr>
<td>McRoberts</td>
<td>Neil</td>
<td>75</td>
<td>Rahaman</td>
</tr>
<tr>
<td>McTaggart</td>
<td>Alistair</td>
<td>226, 252</td>
<td>Rai</td>
</tr>
<tr>
<td>Melloy</td>
<td>Paul</td>
<td>72</td>
<td>Ransom</td>
</tr>
<tr>
<td>Meng</td>
<td>Menghsiao</td>
<td>261</td>
<td>Rasoamanana</td>
</tr>
<tr>
<td>Michael</td>
<td>Pippa</td>
<td>163</td>
<td>Rawsley</td>
</tr>
<tr>
<td>Minton</td>
<td>Sharl</td>
<td>204</td>
<td></td>
</tr>
</tbody>
</table>
INDEX

Ray Jane 155
Raza Waqas 112
Reglinski Tony 73, 120
Regmi Roshan 159
Ridgway Hayley 215
Rigano Luciano 82
Rincon Florez Vivian 152
Rivedal Hannah 283
Roberts John 280
Robinson Neil 201
Rodrigues Jardim Bianca 227
Rogoni Bethany 140
Rohra Roshni 291
Rose Jade 113
Rothwell Chris 277
Rozano Lina 137
Sarker Suchana Rani 91, 126
Sarpeleh Abolfazl 277
Sawyer Anne 294
Schroeter Barry William 95
Scott Eileen 145
See Pao Theen 135
Sharma Anjana 148
Sharma Rudrakshi 189
Sheedy Jason 202
Shin Mee-Yung 100
Shinde Shweta 262
Shuey Louise 274
Siddika Asfakun 173
Silva-Campos Matias 125
Simamora Agnes 237
Smith Reannon 228
Smith Grant 274
Solomon Peter 221
Sperschneider Jana 96
Steele Visnja 200
Summerell Brett 69
Sundin George 230
Sundram Shamala 280
Swift Bec 243
Tai Elaine 107
Takács András 174
Talliansky Michael 86
Tan Kar-chun 86
Tang Tianyi 233
Taylor Andrew 91, 107
Taylor Andrew 107
Taylor Paul 156
Thanabalasingam Abharushana 246
Thangavel Tamilarasan 92
Thatcher Louise 266
Todd Cathryn 115
Toome-Heller Merje 183
Tran Nga 79, 128
Trevorrow Peter 121
Trollip Conrad 103
Ulloth Margaret 104
Vaghefi Niloofar 286
Vance Megan 152
Vanga Bhanupratap 93
Vanneste Joel L. 149
Waipara Nick 76
Wang Weixia 209
Warren Rachael M 149
Weeraratne Nirodha 165
Wei Haochen 96
Weir Bevan 163
Wharton Phillip 177, 287
Wiechel Tonya 271
Williams Simon 221
Wilson Hayley 167
Wong Percy 116
Wood Shona 197
Woolley Rebecca 114, 127
Yalage Don Sashika 236
Young Shelby 100
Young Anthony 283
Yu Sang-Mi 263
Zaveri Anjali 254
Zeil-Rolfe Isabel 266
Zerihun Ayalsew 119, 245
Zheng Linda 181
Zulak Katherine G. 73