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Welcome

On behalf of the North Island branch of the Australasian Plant Pathology Society and the Conference organising committee, I would like to welcome you to the 19th Biennial Australasian Plant Pathology Conference.

We have made a concerted effort to put together an exciting programme on “protecting our crops and native flora”, with excellent keynote speakers, offered papers and posters. Our eight themes are designed to cover every aspect of plant pathology, and to include talks and posters from nematologists, mycologists, bacteriologists and virologists so that we can learn from progress made in each other’s sub-disciplines. We thank the members of our society who are organizing eight workshops, including two field studies, to further facilitate interaction and learning.

We trust you enjoy the City of Sails, Auckland, and get a chance to experience this first hand after the conference on the numerous cruises, charter yachts and ferries that criss-cross the Waitemata Harbour, as well as other sources of scenic beauty in Auckland and throughout New Zealand.

Kerry Everett
APPS 2013 Conference Convenor
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Prosperity from trees

Scion is a Crown Research Institute (CRI) that specialises in research, science and technology development for the forestry, wood product, wood-derived materials, and other biomaterial sectors.

We are New Zealand’s leading CRI in forest biosecurity and risk management. Our pathology group specialises in diseases that affect New Zealand’s planted, conservation and urban forests.

www.scionresearch.com
The 19th Australasian Plant Pathology Conference

Plant & Food Research and the APPS are proud to present the 19th Australasian Plant Pathology Conference

Venue

The University of Auckland
Owen G Glenn Building
Level 0 (level below ground level)
12 Grafton Road
Auckland

Level 0

Owen G Glenn Building

Level 1: Entrance from Grafton Rd
Level 0: Registration

Central Elevators
Stairs to Level 1

Lecture Theatre
OGGB 4

Case Rooms
Case Room 1
Case Room 2
Case Room 3
Case Room 4

Rest rooms
Sponsor’s profiles

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**CRC Plant Biosecurity**

The Plant Biosecurity Cooperative Research Centre (PBCRC) was established in recognition of the need to strengthen the plant biosecurity scientific capacity of Australia.

The PBCRC aims to develop and deploy scientific knowledge, tools, resources and capacity to safeguard Australia, its plant industries and regional communities from the economic, environmental and social consequences of damaging invasive plant pests and diseases.

Through 27 participant organisations, the PBCRC coordinates plant biosecurity scientific research across the country and internationally through its international participants, providing linkages, participation, resources and science.

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**Grains Research & Development Corporation**

The Grains Research and Development Corporation (GRDC) is one of the world’s leading grains research organisations, responsible for planning, investing in and overseeing research, development and extension to deliver improvements in production, sustainability and profitability across the Australian grains industry.

The GRDC’s primary objective is to drive the discovery, development and delivery of world-class innovation to benefit growers and the wider community. In consultation with industry, Regional Panels and Regional Cropping Solutions Networks, The GRDC invests over $150 million a year in RD&E activities to deliver productivity and profitability gains to Australian grain growers.

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**SCION**

Scion is a Crown Research Institute (CRI) specialising in research, science and technology development for the forestry, wood product, wood-derived materials, and other biomaterial sectors.

We are New Zealand’s leading CRI in forest biosecurity and risk management. Our pathology group specialises in diseases that affect New Zealand’s trees.

We offer capabilities to support the health of all forest types: planted, conservation and urban forests.

Our capabilities include:

- Biosecurity, surveillance and diagnostics
- Chemical control of forest pathogens
- Biological control using fungi and viruses
- Site manipulation to reduce disease
- Inducing resistance and improving growth in trees through micro-organisms or genetic selection

www.scionresearch.com
Sponsor’s profiles

Exhibitor

Australasian Plant Pathology Society

The Australasian Plant Pathology Society is dedicated to the advancement and dissemination of knowledge of plant pathology and its practice in Australasia. Australasia is interpreted in the broadest sense to include not only Australia, New Zealand and Papua New Guinea, but also the Indian, Pacific and Asian regions. Although the Society’s activities are mainly focused on the Australasian region, many of the activities of our members are of international importance and significance.

Each member of APPS is an associate member of the International Society for Plant Pathology. Through the International Society, APPS is a member of the International Union of Biological Sciences (IUBS), the International Union of Microbiological Societies (IUMS), in liaison with the UN Food and Agriculture Organization (FAO), and the International Council for Science (ICSU).

Exhibitor

Conviron

Headquartered in Canada and with a global sales, distribution, and service network – Conviron is the world leader in the design, manufacture and installation of controlled environment systems for plant science research. Conviron controlled environments provide precise, uniform, and repeatable control of temperature, light, humidity, dehumidification, CO2, and other environmental conditions. All environmental parameters can be remotely programmed, monitored and analyzed with unparalleled accuracy and convenience.

From small reach-in chambers, to large walk-in rooms, the Conviron Growth House™, the Conviron Research Greenhouse, and customized designs - Conviron controlled environments can be found in small start-up facilities to many of the world’s largest and most prestigious universities and research facilities in over 90 countries.

Learn more at www.conviron.com or contact us at info@conviron.com
Organising Committee

Local organising and scientific committee:

Kerry Everett
Chair, Plant & Food Research

Bénédicte Lebas
Ministry for Primary Industries

Mike Pearson
The University of Auckland

Nick Waipara
Auckland Council

Peter Johnston
Landcare Research

Robin MacDiarmid
Plant and Food Research

Yvonne McDiarmid
Plant & Food Research
Social Programme

Welcome Reception
Monday 25th November | 6m – 7.30pm
The evening reception will be held at the University’s Fale Pasifika, the spiritual home of the University’s Pacific community.
Follow signs from the Registration Desk.

Venue:
The University of Auckland
Fale Pasifika
Wynard Street
Auckland

Wine & Cheese Poster Session
Tuesday 26th November | 6pm - 7pm

Rugby Club BBQ
Tuesday 26th November | 7pm - 10.30pm
This is an opportunity to mix and mingle at a traditional “kiwi BBQ” at the Teachers Eastern Rugby Football Club, once the rugby home of Andy Dalton (All Black’s Captain 1982-85).
Buses will depart from outside of Owen Glen at 7pm sharp.

Venue:
Teachers Eastern Rugby Football Club
Reihana Stret
Tamaki
Auckland

Gala Dinner
Wednesday 27th November | 7pm - 12pm
The conference dinner to be held in the Squadron Ballroom and Dinghy Locker, at the Royal New Zealand Yacht Squadron.
Buses will depart from outside of Owen Glen at 7pm sharp.

Venue:
Royal New Zealand Yacht Squadron
Westhaven Drive
Auckland
The McAlpine Lecture

The invitation to present the 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 is named after Daniel McAlpine, considered to be the father of plant pathology in the Australasian region. His most notable contributions were to study wheat rust following the 1889 epidemic, to classify and describe Australian smuts, and to recognise *Ophiobolus graminis* (now *Gaumannomyces graminis*) as the cause of wheat take-all. He also collaborated with Farrer on resistance to rust in wheat (John Randles 1984, Stanislais Fish 1976).

In 2013, the McAlpine Lecture will be delivered by Dr Shaun Pennycook from Landcare Research, New Zealand.

PREVIOUS MCALPINE LECTURERS

<table>
<thead>
<tr>
<th>Year</th>
<th>Lecturer</th>
<th>Institution</th>
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<tbody>
<tr>
<td>1976</td>
<td>Dr Lilian Fraser</td>
<td>Department of Agriculture, NSW</td>
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<tr>
<td></td>
<td></td>
<td>Disease of citrus trees in Australia- the first hundred years</td>
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<tr>
<td>1978</td>
<td>Dr David Griffin</td>
<td>Australian National University, ACT</td>
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<tr>
<td></td>
<td></td>
<td>Looking ahead</td>
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<tr>
<td>1980</td>
<td>Mr John Walker</td>
<td>Department of Agriculture, NSW</td>
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<tr>
<td></td>
<td></td>
<td>Taxonomy, specimens and plant disease</td>
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<tr>
<td>1982</td>
<td>Professor Richard Matthews</td>
<td>The University of Auckland, NZ</td>
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<td></td>
<td></td>
<td>Relationships between plant pathology and molecular biology</td>
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<tr>
<td>1984</td>
<td>Professor Bob McIntosh</td>
<td>University of Sydney, NSW, and Dr Colin Wellings, Department of Agriculture, NSW</td>
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<tr>
<td></td>
<td></td>
<td>Wheat rust resistance: the continuing challenge</td>
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<tr>
<td>1986</td>
<td>Dr Allen Kerr</td>
<td>Waite Agricultural Research Institute, SA</td>
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<tr>
<td></td>
<td></td>
<td>Agrobacterium: pathogen, genetic engineer and biological control agent</td>
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<tr>
<td>1989</td>
<td>Dr Albert Roveria</td>
<td>CSIRO Division of Soils, SA</td>
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<td></td>
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<td>Ecology, epidemiology and control of take-all, rhizotomies bare patch and cereal cyst nematode in wheat</td>
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<tr>
<td>1991</td>
<td>Mr John Walker</td>
<td>Department of Agriculture, NSW</td>
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<td></td>
<td></td>
<td>Plants, diseases and pathologists in Australasia- a personal view</td>
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<tr>
<td>1993</td>
<td>Dr John Randles</td>
<td>University of Adelaide, SA</td>
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<td></td>
<td></td>
<td>Plant viruses, viroids and virologists of Australasia</td>
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<tr>
<td>1995</td>
<td>Dr Ron Close</td>
<td>Lincoln University, NZ</td>
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<td></td>
<td></td>
<td>The ever changing challenges of plant pathology</td>
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<tr>
<td>1997</td>
<td>Professor John Irwin</td>
<td>CRC Tropical Plant Pathology, Qld</td>
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<tr>
<td></td>
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<td>Biology and management of <em>Phytophthora</em> spp. attacking field crops in Australia</td>
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<tr>
<td>1999</td>
<td>Dr Dorothy Shaw</td>
<td>Department of Primary Industries, Qld</td>
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<tr>
<td></td>
<td></td>
<td>Biology and management of <em>Phytophthora</em> spp. attacking field crops in Australia</td>
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<tr>
<td>2001</td>
<td>Dr Alan Dube</td>
<td>South Australian Research and Development Institute, SA</td>
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<tr>
<td></td>
<td></td>
<td>Long-term careers in plant pathology</td>
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<tr>
<td>2003</td>
<td>Dr Mike Wingfield</td>
<td>University of Pretoria, South Africa</td>
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<tr>
<td></td>
<td></td>
<td>Increasing threat of disease to exotic plantation forests in the southern hemisphere</td>
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<tr>
<td>2005</td>
<td>Dr Gretina Weste</td>
<td>University of Melbourne, Vic</td>
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<tr>
<td></td>
<td></td>
<td>A long and varied fungal foray</td>
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<tr>
<td>2007</td>
<td>Dr Graham Stirling</td>
<td>Biological Crop Protection, Qld</td>
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<tr>
<td></td>
<td></td>
<td>The impact of farming systems on soil biology and soil-borne diseases: examples from the Australian sugar and vegetable industries, the case for better integration of sugarcane and vegetable production and implications for future research</td>
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<tr>
<td>2009</td>
<td>Assoc. Prof. Phil Keane</td>
<td>La Trobe University, Vic</td>
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<tr>
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<td>Lessons from the tropics- the unfolding mystery of vascular-streak dieback of cocoa, the importance of genetic diversity, horizontal resistance, and the plight of farmers</td>
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<tr>
<td>2011</td>
<td>Honorary Professor Lester Burgess</td>
<td>University of Sydney, NSW</td>
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<tr>
<td></td>
<td></td>
<td>A love affair with Fusarium</td>
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<tr>
<td>2013</td>
<td>Dr Shaun Pennycook</td>
<td>Landcare Research, NZ</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Fungal Names in Flux</td>
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</tbody>
</table>
McAlpine Lecturer 2013

Shaun Pennycook

Shaun began his working life with 10 years on high country sheep stations in the South Island mountains, before enrolling for a BSc in Botany at the University of Auckland. He was recruited by DSIR Plant Diseases Division (PDD), and in 1974 completed his PhD on the phylloplane microflora of unsprayed apple trees. During his years as a PDD plant pathologist, Shaun specialised in diseases of fruit crops. He made significant pioneering studies of the emerging diseases of kiwifruit, including a taxonomic study of Botryosphaeria pathogens, which clarified species differences and described two new species. His work on botrytis storage-rot of kiwifruit formed the basis for recommendations that reduced disease incidence without using chemicals, so that post-harvest botrytis rots are no longer a commercial significant problem for the New Zealand industry. One of his major legacies was the 1989 publication of a three volume book, “Plant diseases recorded in New Zealand”, a valued resource for New Zealand plant pathologists to this day. Subsequently, as a mycologist at Landcare Research, Shaun focussed on fungal nomenclature and taxonomy, rather than phytopathology, but continued to contribute to the electronic databasing of plant disease records. He “retired” in 2009, but remains active as a Research Associate at Landcare Research; as Nomenclature Editor of Mycotaxon (the International Journal of Fungal Taxonomy & Nomenclature); and as a member of the IAPT Nomenclature Committee for Fungi and the Sub-committee on Governance of the Code with Respect to Fungi.

Allen Kerr Postgraduate Prize

The Allen Kerr Postgraduate Prize commemorates the significant contribution to research in plant pathology made by Professor Allen Kerr AO, recipient of the inaugural Australia Prize. The award is made at the APPS biennial conference and is open to postgraduate student members of APPS undertaking original research relevant to Australasia. The prize is awarded by the Society for the best piece of original research by a postgraduate student in the field of plant pathology. The prize is normally awarded on the basis of publication in refereed journals.
Keynote Speakers

The Right Honourable James Brendan Bolger, ONZ

The Right Hon. James Bolger was Prime Minister of New Zealand from October 1990 to December 1997. During his 25-year career in politics he led the National Party for almost 12 years, was a Minister for 16 years and had three consecutive terms as the country’s head of government.

Under his leadership the New Zealand economy was transformed from having the lowest growth rate among the 29 OECD nations to one of the strongest.

On 31 December 1997 Mr Bolger was appointed a member of the Order of New Zealand (ONZ), New Zealand’s highest honour.

From June 1998 to January 2002 Mr Bolger was New Zealand’s Ambassador to the United States.

Since 2002 Mr Bolger has been Chairman of the International Board of the World Agricultural Forum, St Louis, USA.

Today Mr Bolger is the Chancellor of the University of Waikato, Chairman of the Board of Directors of the Ian Axford Fellowships in Public Policy, Chairman of the Gas Industry Company Limited, Chairman of Trustees Executors Limited and Chairman of Mt Cook Alpine Salmon Ltd. He is also a Trustee of the Rutherford Trust and President of the NZ/US Council. In August 2009 he became Patron of the New Zealander of the Year Awards.

In 2010 Mr Bolger was elected Distinguished Fellow of the New Zealand Institute of Directors. He was previously Chairman of NZ Post, Kiwibank and KiwiRail among other companies.

In 1983 he was elected President of The International Labour Organisation in Geneva.

Prior to entering national politics in 1972, he was a dairy, beef and sheep farmer and he still chairs the family’s farm company, Hollow Lands Ltd.

In 1963 he married Joan Riddell whose work in public life was recognised in 1997 when she was honoured with the award Companion of New Zealand Order of Merit (CNZM). Jim and Joan have 9 children and 13 grandchildren.

Neil McRoberts (UC Davis)

In the Quantitative Biology and Epidemiology Lab of the Department of Plant Pathology, epidemiology encompasses elements of biology, social sciences, economics, computer modelling techniques and applied mathematics and statistics. I am interested in how pathogens and hosts interact at the plant level; how those interactions result in the reproduction and dispersal processes of pathogens, driving disease epidemics at field and larger scales; how the required management decisions are reached and how the consequences of management actions feed back into the dynamics of the epidemics over short and long time scales; and how all of those interactions contribute to the sustainability of food production and its environmental impact.
Keynote Speakers

**Jen Sheen**

Jen Sheen grew up in a sugarcane plantation community in a rural area next to the city Pinton in southern Taiwan. The sweet scent in the air and the lush tropic plants in her parents’ gardens are important childhood influence for her choice of studying botany as an undergraduate at National Taiwan University. She started her own research group in the Department of Molecular Biology at Massachusetts General Hospital in 1987 after obtaining her PhD degree at Harvard, and is currently professor in Genetics at Harvard Medical School. Her laboratory is probing plant life by developing simple and powerful tools and strategies to unravel plant signal transduction pathways extending from sensors/receptors to signalling cascades and target genes and proteins that are central to energy and metabolic homeostasis, innate immunity, hormonal regulation, stress adaptation, cell fate specification, plant shape and architecture determination. The investigations are guided by curiosity and the desire to promote the use of green plants as a versatile and fascinating model system for discovering fundamental principles in the regulatory networks of living organisms.

**Margaret Dick**

Margaret Dick joined the Forest Research Institute, Rotorua (now trading as ‘Scion’) in 1972, as one of only five forest pathologists in the country at that time. She specialised in the diagnosis of disorders of forest trees from nursery age to maturity, and although the focus was on exotic plantation species there was always a strong interest in indigenous woody plants. The urban forest was also a component of the programme with time spent on diseases such as the decline of Albizia julibrissin and of Schinus molle. She has been a long-term member of the Dutch elm disease Advisory Committee that has successfully contained Dutch elm disease within Auckland.

Evaluation of potential threats posed by overseas pathogens to the New Zealand’s forest estate has also been a component of the work. She was involved in the early detection of Fusarium circinatum (cause of pitch canker disease of pines) in quarantine material in 2003, which prevented the introduction of this unwanted forest fungus into New Zealand.

In recent years there has been an increasing focus on diseases of trees caused by members of the genus Phytophthora. This included the study and description of two new Phytophthora species that were unusual in living high up in the crowns of eucalypts. Margaret is a member of the Kauri Dieback Joint Agency Response Technical Advisory Group that is responding to the disease of kauri associated with Phytophthora taxon Agathis.

In 2012 Margaret was very honoured (and surprised) to be the recipient of the New Zealand Plant Protection Society Medal.
Keynote Speakers

David Guttman
Dr. Guttman received his Ph.D. in microbial evolutionary genetics from Stony Brook University in 1994, followed by postdocs in molecular evolution and molecular plant pathology at the University of Chicago. He started his faculty position at the University of Toronto in 2000, and is currently a Professor with joint appointments in the Departments of Cell & Systems Biology (CSB) and Ecology & Evolutionary Biology. He is also the Associate Chair for Research in CSB and founder and Director of the University of Toronto Centre for the Analysis of Genome Evolution & Function.

Dr. Guttman runs a highly diverse research program with three major foci: (1) the evolution of host specificity and virulence in plant pathogenic bacteria; (2) plant and microbial comparative genomics; and (3) studies of the human and plant-associated microbiome. He is best known for elucidating evolutionary and mechanistic processes that determine the course and fate of microbial infections, and characterizing the impact of natural genetic variation on the balance between disease and immunity. These studies have led to numerous awards and honors, including a Canada Research Chair in Comparative Genomics, the Chair of the American Society for Microbiology Division for Evolutionary and Genomic Microbiology, and membership on the editorial boards of prestigious journals such as PLoS Pathogens and PLoS Genetics.

Virginia Stockwell
Virginia Stockwell is a research faculty member in the Department of Botany and Plant Pathology at Oregon State University. She obtained her Bachelors degree in Biology from Rutgers University and her Doctorate in Plant Pathology from Colorado State University. She has an active research program on the management of several bacterial diseases of plants, including crown gall of stone fruits and bacterial blight of lilac and blueberry caused by *Pseudomonas syringae*.

Virginia has focused primarily on management of fire blight of pear and apple trees caused by *Erwinia amylovora*. Fire blight is the most damaging bacterial disease of pear and apple. Fire blight was controlled with antibiotic sprays during bloom until antibiotic-resistant populations of the pathogen emerged. Virginia’s research on fire blight is focused on the development of bacterial biological control agents for disease control, with the long-term goal of identifying sources of variability associated with biological control that impacts efficacy. Currently, her research is aimed at identifying genetic factors that are essential for the pathogen and/or biological control agents to colonize flowers, a key stage in biocontrol and pathogenesis. To better understand the pathogen, she is participating in a collaborative project using next generation sequencing to examine genetic diversity in populations of *E. amylovora*. Virginia has been active in addressing concerns about the use of antibiotics for disease prevention in plant agriculture, monitoring development of resistance of bacterial plant pathogens to antibiotics, and conducting research on integrated control measures to encourage prudent use of antibiotics and to hinder emergence of antibiotic-resistant populations of bacterial plant pathogens.
Keynote Speakers

Angus Carnegie
Dr Angus Carnegie is a Principal Research Scientist with Biosecurity NSW in the NSW Department of Primary Industries. His main roles include managing and conducting forest health surveys and overseeing and improving pest and disease management programs. His areas of expertise include forest health (pests and diseases), forest health surveillance, leaf spot fungi of eucalypts, research on improving pest and disease management strategies, and forest biosecurity. He has collaborative links and research projects with numerous Australian and international colleagues. Dr Carnegie’s involvement in the emergency response to the recent incursion of an exotic disease in Australia (myrtle rust) has strengthened his expertise in biosecurity at the operational, strategic and policy levels. Current research projects include the impact of myrtle rust on key industries and the native environment in Australia and on new and emerging pest and disease issues.

Saskia Hogenhout
Research in the Hogenhout lab is aimed at gaining a better understanding of the molecular basis of plant-microbe-insect interactions. Hogenhout’s PhD thesis research ( Wageningen University and Research Centre, The Netherlands) focused on molecular aspects of luteovirus-aphid interactions (1994-1999). Hogenhout became an independent Project Leader (Assistant Professor) at The Ohio State University (OSU), USA, after receiving her PhD degree in 1999. At OSU, she started new research projects on leafhopper and planthopper transmission of phytoplasmas and rhabdoviruses, and obtained tenure as Associate Professor in 2005. Hogenhout commenced her Project Leader position at JIC, UK, in June 2007 where she received tenure in October 2012. She received the Derrick Edward Award from The International Organization of Mycoplasmology (IOM) for outstanding research in mycoplasmology comprising global research on human, animal and plant-associated mycoplasma and mycoplasma-like (including phytoplasma) pathogens. Hogenhout’s discoveries include phytoplasma virulence factors (effectors), which interact with conserved plant transcription factors to promote the vegetative growth of plants, thereby encouraging phytoplasma and insect vector colonization. She also established genomic analysis tools for aphids that are used towards understanding the molecular basis of plant-insect interactions and improving plant resistance to insects. Hogenhout has established many fruitful collaborations within the UK and worldwide.
Keynote Speakers

**Thierry Candresse**

Initially trained as an agronomical engineer of INA Paris-Grignon, Thierry Candresse got his PhD on the enzymology of plant viruses replication from the University of Bordeaux 2 in 1984. This was followed by a postdoc on viroids in the laboratory of TO Diener at USDA-ARS in Beltsville, USA. He started his work at INRA Bordeaux in 1986 and is currently director of the Joint Research Laboratory on Fruit Biology and Pathology of the University of Bordeaux and INRA, the French national institute for agronomical research. He is also group leader of the Bordeaux Plant Virology team in this laboratory.

His research interests are wide ranging but mostly address two areas of plant virology. The first concerns the study of molecular interactions between viruses and their host plants and, in particular, those controlling the success of viral infection (host susceptibility and genetic resistance, virus resistance-breaking). The second topic, on which he has been most active in recent years, concerns the development of detection and characterization techniques for plant viruses, with practical applications in detection and diagnosis, taxonomy, epidemiology, and more recently on studies on viral communities (metagenomics). These projects have been carried out on a wide range of viruses, with particular emphasis on potyviruses (virus-host interactions) and on fruit tree viruses (virus characterization and diagnosis). In the past few years he has devoted an important part of his activity to the harnessing of next generation sequencing technologies for virus identification and plant virus metagenomics studies.

**Neil Boonham**

Neil currently heads the novel diagnostics team at the Food and Environment Research Agency, and has a background in Plant Virology and Molecular Biology. The research of the team is focused on the development of detection, identification and diagnostic tools for use in centralised laboratory facilities as well as in the field by non-specialist users. Current research focuses in two areas, firstly on the use of next generation sequencing techniques for the detection and characterisation of unknown disease causing agents and secondly in the development and deployment of novel molecular techniques with non-specialists in the field or point of decision making. Neil maintains a keen interest in Virology in particular the interaction between viruses and plant hosts and the evolution of virus species.
Poster Sessions

Tuesday 26th November
6pm - 7pm – Wine & Cheese Poster Session

Wednesday 27th November
1.30pm - 2.30pm | Poster Session 1
Application of New Technologies, Biosecurity, Disease management, Population Genetics

Thursday 28th November
1.30pm - 2.30pm | Poster Session 2
Epidemiology, New and emerging diseases, Plant-pathology interactions, Biological interactions and plant diseases
### Summary programme

#### Monday 25th November 2013

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8.30 am - 4.30 pm</td>
<td>Workshop/Tours</td>
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<tr>
<td>2 pm - 5 pm</td>
<td>Registrations Open (Foyer, Owen G Glenn Building)</td>
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<tr>
<td>2 pm - 6 pm</td>
<td>Poster Placement (Foyer, Owen G Glenn Building)</td>
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<tr>
<td>6 pm - 7.30 pm</td>
<td>Welcome Reception at Fale Pasifika</td>
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<tr>
<td>7.30 pm - 9.30 pm</td>
<td>APPS Council Meeting. Dr Elaine Davison. Room 317.</td>
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#### Tuesday 26th November 2013

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8 am - 8.30 am</td>
<td>Poster Placement (Foyer, Owen G Glenn Building)</td>
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<tr>
<td>8 am - 6 pm</td>
<td>Registrations Open</td>
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<tr>
<td>8.30 am - 9 am</td>
<td>Plenary 1: The Right Honourable Jim Bolger, ONZ (Opening Speaker)</td>
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<tr>
<td>9 am - 9.30 am</td>
<td>Plenary 2: Dr Elaine Davison (Presidential Address)</td>
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<tr>
<td>9.30 am - 10.30 am</td>
<td>Concurrent Sessions (1A, 3A, 7A)</td>
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<tr>
<td>10.30 am - 11 am</td>
<td>Morning Tea</td>
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<td>11 am - 11.30 am</td>
<td>Plenary 3: Prof Jen Sheen</td>
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<tr>
<td>11.30 am - 12.30 pm</td>
<td>Concurrent Sessions (2A, 4A, 6A)</td>
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<tr>
<td>12.30 pm - 1.30 pm</td>
<td>Lunch</td>
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<tr>
<td>12.30 pm - 1.30 pm</td>
<td>Capability Survey (with lunch)</td>
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<tr>
<td>1.30 pm - 2 pm</td>
<td>Plenary 4: The Ross Beever Memorial Lecture</td>
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<tr>
<td></td>
<td>Dr Saskia Hogenhout</td>
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<tr>
<td>2 pm - 2.30 pm</td>
<td>Plenary 5: Dr Margaret Dick</td>
</tr>
<tr>
<td>2.30 pm - 3.30 pm</td>
<td>Concurrent Sessions (2B, 4B, 8A)</td>
</tr>
<tr>
<td>3.30 pm - 4 pm</td>
<td>Afternoon Tea</td>
</tr>
<tr>
<td>4 pm - 4.30 pm</td>
<td>Plenary 6: Dr Neil Boonham</td>
</tr>
<tr>
<td>4.30 pm - 6 pm</td>
<td>Concurrent Sessions (3B, 5A, 7B)</td>
</tr>
<tr>
<td>6 pm - 7 pm</td>
<td>Wine &amp; Cheese Poster Session</td>
</tr>
<tr>
<td>7 pm - 10.30 pm</td>
<td>Social Dinner - Teachers’ Eastern Rugby Football Club</td>
</tr>
</tbody>
</table>
# Summary programme

## Wednesday 27th November 2013

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>8 am - 6 pm</td>
<td>Registrations Open</td>
</tr>
<tr>
<td>7.30 am - 8.30 am</td>
<td>Presidential Breakfast</td>
</tr>
<tr>
<td>8.30 am - 10 am</td>
<td>Concurrent Sessions (2C, 4C, 6B)</td>
</tr>
<tr>
<td>10 am - 10.30 am</td>
<td>Plenary 7: Dr Thierry Candresse - sponsored by School of Biological Sciences</td>
</tr>
<tr>
<td>10.30 am - 11 am</td>
<td>Morning Tea</td>
</tr>
<tr>
<td>11 am - 11.20 am</td>
<td>Plenary 8: MacAlpine Book Dr Doug Parbery</td>
</tr>
<tr>
<td>11.20 am - 12.30 pm</td>
<td>Plenary 9: MacAlpine Lecture Dr Shaun Pennycook</td>
</tr>
<tr>
<td>12.30 - 1.30 pm</td>
<td>Lunch and Editors’ lunch</td>
</tr>
<tr>
<td>1.30 pm - 2.30 pm</td>
<td>Poster Session 1</td>
</tr>
<tr>
<td>2.30 pm - 3.30 pm</td>
<td>Concurrent Sessions (3C, 5B, 8B)</td>
</tr>
<tr>
<td>3.30 pm - 4 pm</td>
<td>Afternoon Tea</td>
</tr>
<tr>
<td>4 pm - 4.30 pm</td>
<td>Plenary 10: Ass. Prof. Virginia Stockwell</td>
</tr>
<tr>
<td>4.30 pm - 6 pm</td>
<td>Concurrent Sessions (4D, 6C, 7C)</td>
</tr>
<tr>
<td>6 pm - 7 pm</td>
<td>APPS General Meeting</td>
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<tr>
<td>7 pm - 11.30 pm</td>
<td>Conference Dinner - Royal NZ Yacht Squadron</td>
</tr>
</tbody>
</table>

## Thursday 28th November 2013

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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</thead>
<tbody>
<tr>
<td>8 am - 6 pm</td>
<td>Registrations Open</td>
</tr>
<tr>
<td>7.30 am - 8.30 am</td>
<td>APPS Executive Breakfast Meeting</td>
</tr>
<tr>
<td>8.30 am - 9.30 am</td>
<td>Concurrent Sessions (2D, 6D, 8C)</td>
</tr>
<tr>
<td>9.30 am - 10.30 am</td>
<td>Plenary 11: Getting the Word Out (1) Ruby Andrew, Nick Waipara and Robin Nitschke</td>
</tr>
<tr>
<td>10.30 am - 11 am</td>
<td>Morning Tea</td>
</tr>
<tr>
<td>11 am - 12 pm</td>
<td>Plenary 11: Getting the Word Out (2) Ass. Prof. Mike Pearson, Melissa Cook, Cherie Gambley</td>
</tr>
<tr>
<td>12 pm - 12.30 pm</td>
<td>Plenary 12: Prof. David Guttman</td>
</tr>
<tr>
<td>12.30 pm - 1.30 pm</td>
<td>Lunch</td>
</tr>
</tbody>
</table>
Summary programme

12.30 pm - 1.30 pm  
Student Mentor Lunch - Invitation only

1.30 pm - 2.30 pm  
Poster Session 2

2.30 pm - 3 pm  
Plenary 13: Ass. Prof. Neil McRoberts

3 pm - 3.30 pm  
Plenary 14: Dr Angus Carnegie - sponsored by Ministry for Primary Industries

3.30 pm - 4 pm  
Afternoon Tea

4 pm - 5 pm  
Concurrent Sessions (1B, 2E, 7D)

5 pm - 5.30 pm  
APPS Awards

5.30 pm - 5.40 pm  
The CRC Plant Biosecurity Student Awards
The Springer Student Awards

5.40 pm - 5.50 pm  
The Allen Kerr Award

5.50 pm - 6.10 pm  
Invitation to Forthcoming Conferences

6.10 pm - 6.20 pm  
Acknowledgements and Conference Close

6.20 pm -  
Regional Councillors Informal Dinner meeting

Friday 29th November 2013

8.30 am - 4.30 pm  
Workshops/Tours

APPs Biennial Conference
September 2015
Perth Western Australia

For further information or to register for alerts
see the conference website:
## Programme

### Monday 25th November 2013

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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</thead>
<tbody>
<tr>
<td>8.30 - 16.30</td>
<td>Workshops/Tours</td>
</tr>
<tr>
<td>14.00 - 17.00</td>
<td>Registration Open (OGG building foyer)</td>
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<tr>
<td>14.00 - 18.00</td>
<td>Poster placement (OGG building foyer)</td>
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<tr>
<td>18.00 - 19.30</td>
<td>Welcome Reception / Official Opening</td>
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<td>Welcome by Convenor and Powhiri Maori welcome at Fale Pasifika</td>
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### Tuesday 26th November 2013

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<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>8.00 – 8.30</td>
<td>Poster placement (OGG Building Foyer)</td>
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<tr>
<td>8.00 – 18.00</td>
<td>Registration Open (OGG Building Foyer)</td>
</tr>
<tr>
<td>8.30 - 9.00</td>
<td>PLENARY 1: OPENING SPEAKER</td>
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<tr>
<td></td>
<td>Speaker: The Right Honourable Jim Bolger ONZ</td>
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<td>Chair: Kerry Everett</td>
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<tr>
<td>9.00 - 9.30</td>
<td>PLENARY 2: APPS PRESIDENTIAL ADDRESS</td>
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<tr>
<td></td>
<td>Speaker: Dr Elaine Davison, President of the APPS</td>
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<td>Chair: Kerry Everett</td>
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<tr>
<td>9.30 - 10.30</td>
<td>Concurrent Oral Sessions (15 mins/talk including questions)</td>
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<tr>
<td>9.30 - 9.45</td>
<td>SESSION 7A: PLANT PATHOGEN INTERACTIONS</td>
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<tr>
<td></td>
<td>Chairs: Barry Scott &amp; Alicia Greenhill</td>
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<td></td>
<td>THEATRE: OGGB3</td>
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<tr>
<td>9.45 - 10.00</td>
<td>SESSION 1A: APPLICATION OF NEW TECHNOLOGIES</td>
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<tr>
<td></td>
<td>Chairs: Giles Hardy &amp; Trudy Paap</td>
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<tr>
<td></td>
<td>THEATRE: OGGB4</td>
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<tr>
<td>9.30 - 9.45</td>
<td>Detection of potato potyviruses in aphids caught in water and</td>
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<td>propylene glycol trap solutions.</td>
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<td></td>
<td>Ron van Toor, The New Zealand Institute for Plant &amp;</td>
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<td>Food Research Limited</td>
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<tr>
<td>9.45 - 10.00</td>
<td>Identification of trapped insects and associated</td>
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<td>microbes by next generation sequencing.</td>
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<td>Simon Bulman, The New Zealand Institute for Plant &amp;</td>
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<td>Food Research Limited</td>
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<td>Hyperspectral leaf response of plant infected with</td>
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<td>Phytophthora cinnamomi.</td>
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<td>Zoe-Joy Newby, The Royal Botanic Gardens and Domain Trust, Australia</td>
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<tr>
<td>9.45 - 10.00</td>
<td>Increasing the genetic diversity of sugarcane</td>
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<td>germplasm through continuous introduction of disease-free</td>
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<td>foreign varieties.</td>
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<td>Fe Dela Cueva, University of the Philippines, Los Banos</td>
</tr>
</tbody>
</table>
## Programme

### 10.00 - 10.15

**Phytophthora root rot of avocado - why are some rootstocks more resistant?**
Merran Neilsen, Queensland Alliance for Agriculture and Food Innovation, Australia

**Citizen science and a smartphone application to monitor the incidence and severity of Quambalaria diseases in Western Australian marri, Corymbia calophyllina.**
Cielito Marbus, Murdoch University, Australia

**Defining core pan-genomes of species in “Candidatus” Liberibacter for the development of new diagnostic tools.**
Grant Smith, The New Zealand Institute for Plant & Food Research Limited

### 10.15 - 10.30

**Investigating the role of strigolactones in pea (Pisum sativum) interactions with soilborne fungal pathogens.**
Sara Blake, University of Tasmania, Australia

**Field evaluation of a bioherbicide for control of parkinsonia (Parkinsonia aculeata) in Australia.**
Victor Galea, The University of Queensland, Australia

**Fusarium vascular infection of oil palm: Epidemiology, genetic diversity and molecular diagnostic tools.**
Mohd Hefni Rusli, Malaysian Palm Oil Board

### 10.30 - 11.00

Morning Tea (OGG building foyer)

### 11.00 - 11.30

**PLENARY 3: PLANT PATHOGEN INTERACTIONS**

**THEATRE: 098**

**Speaker:** Prof Jen Sheen, Harvard Medical School, USA
**Chair:** Robin McDiarmid

### 11.30 - 12.30

**Concurrent Oral Sessions (15 mins/talk including questions)**

<table>
<thead>
<tr>
<th>SESSION 4A: DISEASE MANAGEMENT</th>
<th>SESSION 6A: NEW AND EMERGING DISEASES</th>
<th>SESSION 2A: BIOLOGICAL INTERACTIONS AND PLANT DISEASES</th>
</tr>
</thead>
<tbody>
<tr>
<td>THEATRE: OGGB3</td>
<td>THEATRE: OGGB4</td>
<td>THEATRE: 098</td>
</tr>
</tbody>
</table>

**11.30 - 11.45**

**Big achievement from a handful of high performing varieties: a concept in the context of crop health for wheat in Western Australia.**
Moin Salam, Department of Agriculture and Food Western Australia

**Opium poppy mosaic virus, a new member of Umbravirus isolated from Papaver somniferum and Tropaeolum majus in New Zealand.**
Bénédicte Lebas, Ministry for Primary Industries, New Zealand

**What makes Trichoderma rhizosphere competent: A molecular analysis.**
Artemio Mendoza, Bio-Protection Research Centre, Lincoln University, New Zealand

<table>
<thead>
<tr>
<th>11.45 - 12.00</th>
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<tbody>
<tr>
<td><strong>Control of crown canker of passion fruit (Passiflora edulis Sims.) an acute disease problem for New Zealand passion fruit growers.</strong></td>
</tr>
<tr>
<td>Pia Rheinländer, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<tr>
<td><strong>Forest trials testing phosphate for control of kauri dieback.</strong></td>
</tr>
<tr>
<td>Ian Horner, The New Zealand Institute for Plant &amp; Food Research Limited</td>
</tr>
<tr>
<td><strong>Species- and strain- specific identification and quantification of root disease suppressive Trichoderma inoculants in cropping soils.</strong></td>
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<tr>
<td>Belinda Stummer, CSIRO, Australia</td>
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<td>Time</td>
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<tr>
<td>12.00 - 12.15</td>
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<td>12.15 - 12.30</td>
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<td>14.30 - 15.30</td>
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<td>14.30 - 14.45</td>
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<td>14.45 - 15.00</td>
</tr>
</tbody>
</table>

**Recent emergence of Fusarium dieback of tea (*Camellia sinensis*) in Sri Lanka and its potential link with Tea Shot Hole Borer (*Eucallptea fomicatae*). Pradeepa Liyanage, Tea Research Institute of Sri Lanka**

**Dissecting the molecular crosstalk between endophytic fungi and their host plants: *Trichoderma* as fungal model system. Artemio Mendoza, Bio-Protection Research Centre, Lincoln University, New Zealand**

**The disease cycle of alternaria leaf blotch and fruit spot of apple. Dalphy Harteved, University of Queensland, Australia**

**Identification of a naturally occurring, mild isolate of Tamarillo mosaic virus. Arnaud Blouin, The New Zealand Institute for Plant & Food Research Limited**

**Population structures of Neosfusioccum species from nurseries and vineyards indicate movement and origins of infection. Regina Billones-Baaijens, Lincoln University, New Zealand**

**Myrtle rust in *Eucalyptus grandis* identification and expression of host defence genes. David Guest, University of Sydney, Australia**
Programme continued

15.00 - 15.15
Managing Ganoderma basal stem rot of oil palm: Innovative approach through endophytic microorganism application.
Shamala Sundram, Malaysian Palm Oil Board

Germination and bioactivity of Trichoderma atroviride affected by culturing and storage conditions.
Amir Daryaei, Bio-Protection Research Centre, Lincoln University, New Zealand

Development of a multiplexed microsatellite library for a population genetics study of Stagonosporopsis tanaceti the cause of ray blight disease of pyrethrum in Australia.
Niloofar Vaghefi, The University of Melbourne, Australia

15.15 - 15.30
Optimising pruning wound protection for management of eutypa dieback in grapevine.
Matthew Ayres, South Australian Research and Development Institute

Effect of Aureobasidium isolates on mycelium growth of three major bunch rot pathogens of grapes.
Sujeewa Rathnayake, Charles Sturt University, NSW, Australia

Simple sequence repeat markers (SSRs) for understanding population structure of Colletotrichum coccodes infecting potato in Australia.
Jiang Chang, The University of Melbourne, Australia

15.30 - 16.00
Afternoon Tea (OGG building foyer)

16.00 - 16.30
PLENARY 6: APPLICATION OF NEW TECHNOLOGIES
THEATRE: 098
Speaker: Dr Neil Boonham, FERA, York, UK
Chair: Bénédicte Lebas

16.30 - 16.45
The effect of postharvest hot fungicidal dip and exogenous ethylene gas application on the incidence of dendritic spot & stem end rot in Kensington Pride (KP) Mangoes.
Asian Qureshi, The University of Queensland, Australia

Development of real-time PCR assays for the detection of the myrtle rust fungus Puccinia psidii.
Jeyaseelan Baskarathivan, Ministry for Primary Industries, New Zealand

Botryosphaeriaceae fungi as a potential mycoherbicide for prickly acacia.
Ahsanul Haque, The University of Queensland, Australia

16.45 - 17.00
The incidence of Huanglongbing (HLB) on 2-3 year old tangerine trees (Citrus reticulata) grown from disease free nursery stock.
Angsana Akarapisan, Chiang Mai University, Thailand

Eradication of Chestnut blight in Victoria Australia.
Martin Mebalds, DEPI Biosecurity, Victoria, Australia

Profiles of Fusarium species and mycotoxin on white corn varieties in the Philippines.
Cecilia Pascual, Philippine Phytopathological Society

16.30 - 18.00
Concurrent Oral Sessions (15 mins/talk including questions)

SESSION 5A: EPIDEMIOLOGY
Chairs: Robert Beresford & Kaori Itagaki
THEATRE: OGGB3

SESSION 3B: BIOSECURITY
Chairs: Lisa Ward & Agnes Simamora
THEATRE: OGGB4

SESSION 7B: PLANT PATHOGEN INTERACTIONS
Chairs: Matt Templeton & Honour McCann
THEATRE: 098
### Programme continued

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Speaker(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>17.00 - 17.15</strong></td>
<td>Seed tuber incidence and pathogenicity of <em>Verticillium</em> species infecting potatoes in Australia.</td>
<td>Prakash Vijayamma, Ramakrishnan Nair, The University of Melbourne, Australia</td>
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<tr>
<td></td>
<td>Diversity and classification of <em>Phellinus noxius</em> in Queensland and New South Wales.</td>
<td>Louise Shuey, Queensland Department of Agriculture, Fisheries and Forestry, Australia</td>
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<td></td>
<td>Manipulating the Boom and Bust cycle of blackleg disease of canola saves Australian farmers $20 million in 2012.</td>
<td>Angela Van de Wouw, School of Botany, University of Melbourne, Australia</td>
</tr>
<tr>
<td><strong>17.15 - 17.30</strong></td>
<td>Seasonal variations in hull rot incidence in almonds.</td>
<td>Chin Gouk, Department of Environment and Primary Industries, Australia</td>
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<td></td>
<td>Checklists, Quarantine and Trade - continuing challenges for developing countries.</td>
<td>Lester Burgess, University of Sydney, Australia</td>
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<td>Phyllosphere microbes influence Succinate dehydrogenase activity in mitochondria of tomato.</td>
<td>P K Paul, Amity University Uttar Pradesh, India</td>
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<tr>
<td><strong>17.30 - 17.45</strong></td>
<td>Stemphylium grey leaf spot infection of lupins favoured on seedlings in wet and warm conditions.</td>
<td>William MacLeod, Department of Agriculture and Food, Western Australia</td>
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<td></td>
<td>A new era for government and industry partnerships on biosecurity in New Zealand.</td>
<td>Lois Ransom, Government Industry Agreement Secretariat, New Zealand</td>
</tr>
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<td></td>
<td>Mechanisms by which dual NB-LRR genes confer disease resistance in <em>Arabidopsis</em>.</td>
<td>Kee hoon Sohn, Massey University, New Zealand</td>
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<tr>
<td><strong>17.45 - 18.00</strong></td>
<td>The effect of elevated temperature on the titre of <em>Barley yellow dwarf virus-PAV</em> in wheat.</td>
<td>Narelle Nancarrow, Department of Environment and Primary Industries, Australia</td>
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<td></td>
<td>Stripe smuts of grasses: one lineage or high levels of polyphyly.</td>
<td>Kryrylo Savchenko, University of Haifa, Israel</td>
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<td></td>
<td>Unravelling the cause of Black Pod Syndrome of narrow-leaved lupin: Survey data, satisfying Koch's postulates, and next generation sequencing of virus isolates.</td>
<td>Monica Kehoe, University of Western Australia</td>
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<tr>
<td><strong>18.00 - 19.00</strong></td>
<td>Wine and cheese Poster session</td>
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<tr>
<td><strong>19.00 - 22.30</strong></td>
<td>Social dinner at the Teachers Eastern Rugby Football Club</td>
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</table>
### Programme continued

**Wednesday 27th November 2013**

<table>
<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>8.00 – 18.00</td>
<td>Registration Open (OGG building foyer)</td>
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<tr>
<td>7.30 - 8.30</td>
<td>Presidential Breakfast (past Presidents and Incoming)</td>
<td>CAFETERIA</td>
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<td></td>
<td>Dr Greg Johnson on ISPP and Task Force on Food Security</td>
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<tr>
<td>8.30 - 10.00</td>
<td>Concurrent Oral Sessions (15 mins/talk including questions)</td>
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<td></td>
<td><strong>SESSION 4C: DISEASE MANAGEMENT</strong></td>
<td><strong>SESSION 6B: NEW AND EMERGING DISEASES</strong></td>
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<tr>
<td></td>
<td>Chairs: Mark Sosnowski &amp; Zoe-Joy Newby</td>
<td>Chairs: Barbara Hall &amp; Sunil Singh</td>
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<td>THEATRE: OGGB3</td>
<td>THEATRE: OGGB4</td>
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<td></td>
<td><strong>SESSION 2C: BIOLOGICAL INTERACTIONS AND PLANT DISEASES</strong></td>
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<td>Chairs: Hayley Ridgeway &amp; Philippa Child</td>
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<td>THEATRE: OGGB5</td>
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<tr>
<td>8.30 - 8.45</td>
<td>Containment and eradication of <em>Phytophthora cinnamomi</em> in natural ecosystems.</td>
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<td>Bill Dunstan, Murdoch University, Australia</td>
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<tr>
<td>8.45 - 9.00</td>
<td>Impact of fungicide resistance in <em>Venturia inaequalis</em> on control of apple scab in New Zealand.</td>
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<td></td>
<td>Robert Beresford, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<tr>
<td>9.00 - 9.15</td>
<td>Heat and chemical treatments to reduce systemic infection of tissue culture derived boysenberry plants by the downy mildew pathogen <em>Peronospora sparsa</em>.</td>
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<td>Anusara Herath Mudiyanseilage, Ecology Department, Lincoln University, New Zealand</td>
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<td>Françoise Poliakoff, ANSES - Plant Health Laboratory - France</td>
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<td><strong>Emergence of Pestalotiopsis species as the causal agent of raceme blight and dieback of macadamia</strong></td>
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<td>Femi Akinsanmi, QAAFI, The University of Queensland, Australia</td>
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<td><strong>Biological interactions of mites and microbes associated with gall formation in Scotch Broom <em>Cytisus scoparius</em></strong></td>
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<td>Chantal Probst, Landcare Research, New Zealand</td>
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**Session Titles:**

- **SESSION 4C: DISEASE MANAGEMENT**
- **SESSION 6B: NEW AND EMERGING DISEASES**
- **SESSION 2C: BIOLOGICAL INTERACTIONS AND PLANT DISEASES**
<table>
<thead>
<tr>
<th>Time</th>
<th>Session Title</th>
<th>Speaker</th>
<th>Institution</th>
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<tbody>
<tr>
<td>9.30 - 9.45</td>
<td>Application of the PBcast model for timing fungicide sprays to control Phytophthora blight of pepper.</td>
<td>Eunwoo Park, Seoul National University, Korea</td>
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<td>Biological and molecular characteristics and geographic spread of the different biovars of Pseudomonas syringae pv. actinidiae.</td>
<td>Joel Vanneste, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<td>Transcriptome analysis of the beneficial fungus Trichoderma virens during interaction with Zea mays.</td>
<td>Robert Lawry, Lincoln University, New Zealand</td>
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<tr>
<td>9.45 - 10.00</td>
<td>Protection of apple budding wounds from European canker.</td>
<td>Reiny Scheper, The New Zealand Institute for Plant and Food Research Ltd</td>
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<td></td>
<td>Phytophthora pluvialis and its relation to red needle cast disease of Pinus radiata in New Zealand.</td>
<td>Nari Williams, SCION - New Zealand Forest Research Institute</td>
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<td>Identifying targets for sustainable control of Sclerotinia diseases.</td>
<td>Alicia Greenhill, La Trobe University, Australia</td>
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<tr>
<td>10.00 - 10.30</td>
<td>PLENARY 7: APPLICATION OF NEW TECHNOLOGIES</td>
<td>Speaker: Dr Thierry Candresse, INRA, Bordeaux, France</td>
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<td>Chair: Mike Pearson</td>
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<tr>
<td>10.30 - 11.00</td>
<td>Morning Tea (OGG building foyer)</td>
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<td>11.00 - 11.20</td>
<td>PLENARY 8: MACALPINE BOOK</td>
<td>Speaker: Dr Doug Parbery</td>
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<td>Chair: Kerry Everett</td>
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<tr>
<td>11.20 - 12.30</td>
<td>PLENARY 9: MACALPINE LECTURE</td>
<td>Speaker: Dr Shaun Pennycook, Landcare Research, Auckland, New Zealand</td>
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<td>Chair: Kerry Everett</td>
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<td>12.30 - 13.30</td>
<td>Lunch (OGG building foyer)</td>
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<td>12.30 - 13.30</td>
<td>Editors Lunch</td>
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<td>13.30 - 14.30</td>
<td>POSTER SESSION 1</td>
<td>Application of new technologies, Disease management, Epidemiology, Population genetics</td>
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<tr>
<td>14.30 - 15.30</td>
<td>Concurrent Oral Sessions (15 mins/talk including questions)</td>
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<td>14.30 - 14.45</td>
<td>The development of an elsinoe infection risk model for apple in New Zealand.</td>
<td>Peter Wood, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<td>Keeping one step ahead of invasive species: Using an integrated framework to screen and target species, for detailed biosecurity risk assessment.</td>
<td>Sunil Singh, CSIRO Ecosystem Sciences, Australia</td>
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<td>Phylogeny and Secreted In Xylem (SIX) gene characterisation of Fusarium oxysporum.sp. canariensis in Australia.</td>
<td>Matthew Laurence, The Royal Botanic Gardens and Domain Trust, Australia</td>
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<td>Time</td>
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<td>14.45 - 15.00</td>
<td>Temperature and moisture content stimulate the growth of fungi on healthy stored grain over time.</td>
<td>Kirsty Bayliss, Murdoch University, Australia</td>
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<td>Recent changes in Colletotrichum taxonomy.</td>
<td>Bevan Weir, Landcare Research, New Zealand</td>
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<td>Next Generation Sequencing reveals unexplored Phytophthora diversity in Australian soils.</td>
<td>Treena Burgess, Murdoch University, Australia</td>
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<td>15.00 - 15.15</td>
<td>Sensitivity analysis and uncertainty in a species distribution model.</td>
<td>Hossein Narouei Khandan, Lincoln University, New Zealand</td>
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<td>Dutch elm disease in New Zealand: From eradication to management.</td>
<td>Beccy Ganley, SCION - New Zealand Forest Research Institute</td>
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<td>An expanded AvrLm6-like gene family in scab fungi.</td>
<td>Jason Shiller, La Trobe University, Australia</td>
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<td>15.15 - 15.30</td>
<td>Modeling the impact of disease resistance on rice yields in the Philippines and Indonesia.</td>
<td>Adam Sparks, International Rice Research Institute, Philippines</td>
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<td>Mango malformation in the Northern Territory of Australia.</td>
<td>Lucy Tran-Nguyen, Department of Primary Industry and Fisheries, NT, Australia</td>
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<td>Dynamics of Dasheen mosaic virus population structure in evolutionary space and time.</td>
<td>Wee-Leong Chang, Auckland University of Technology, New Zealand</td>
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<tr>
<td>15.30 - 16.00</td>
<td>Afternoon Tea (OGG building foyer)</td>
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<td>16.00 - 16.30</td>
<td>PLENARY 10: DISEASE MANAGEMENT THEATRE: 098</td>
<td>Speaker: Ass. Prof. Virginia Stockwell, USDA, Oregon State, USA</td>
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<td>Chair: Nick Waipara</td>
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<td>16.30 - 18.00</td>
<td>Concurrent Oral Sessions (15 mins/talk including questions)</td>
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<td>16.30 - 16.45</td>
<td>SESSION 7C: PLANT PATHOGEN INTERACTIONS THEATRE: OGGB3</td>
<td>Kieren Arthur, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<td>Quantitative measurement of the impacts of virus infection in Arabidopsis thaliana.</td>
<td>Fiona Giblin, University of the Sunshine Coast, Australia</td>
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<td>Heat and dessication kills Pseudomonas syringae pv. actinidiae on kiwifruit pollen.</td>
<td>Kerry Everett, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<tr>
<td>16.45 - 17.00</td>
<td>SESSION 6C: NEW AND EMERGING DISEASES THEATRE: OGGB4</td>
<td>Duy Le, The University of Queensland, Australia</td>
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<td>In search of resistance to grapevine trunk diseases.</td>
<td>Mark Sosnowski, South Australian Research and Development Institute</td>
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<td>Pathogenicity of Pythium spp. isolated from ginger fields in Australia.</td>
<td>Eirian Jones, Lincoln University, New Zealand</td>
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<td>17.00 - 17.15</td>
<td>SESSION 4D: DISEASE MANAGEMENT THEATRE: 098</td>
<td>Rebekah Fuller, The University of Auckland, New Zealand</td>
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<td>Variable disease resistance to Sclerotinia solani.</td>
<td>Treena Burgess, Murdoch University, Australia</td>
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<td>Selection and characterisation of Trichoderma isolates for suppression of Pratylenchus in wheat roots.</td>
<td>Mark Braithwaite, Bio-Protection Research Centre, Lincoln University, New Zealand</td>
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### Programme continued

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<tr>
<th>Time</th>
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<th>Presenters</th>
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<tr>
<td>17.15 - 17.30</td>
<td>Characterisation of toxins from <em>Pyrenophora teres</em> f. <em>teres</em> in net form net blotch disease of barley.</td>
<td>Amanda Able, The University of Adelaide, Australia</td>
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<td>A new Phytophthora disease from nurseries in Western Australia.</td>
<td>Agnes Simamora, Murdoch University, Australia</td>
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<td></td>
<td><em>Pratylenchus teres</em> Western Australia's home grown root lesion nematode (RLN).</td>
<td>Sarah Collins, Department of Agriculture and Food Western Australia</td>
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<tr>
<td>17.30 - 17.45</td>
<td>Internal movement of <em>Pseudomonas syringae</em> pv. <em>actinidiae</em> through symptomless kiwifruit tissues.</td>
<td>Joy Tyson, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<td>Blackberry decline along the Warren and Donnelly Rivers: a major disease of <em>Rubus anglocandicans</em> in south-west Australia.</td>
<td>Giles Hardy, Murdoch University, Australia</td>
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<td>Management of <em>Grapevine leafroll-associated virus</em> 3 in New Zealand.</td>
<td>Daniel Cohen, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<tr>
<td>17.45 - 18.00</td>
<td>Crop growth enhancement and disease control using nursery-inoculated <em>Trichoderma</em> root endophytes isolated from local healthy plants.</td>
<td>Robert Hill, Bio-Protection Research Centre, Lincoln University, New Zealand</td>
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<td></td>
<td>First report of &quot;<em>Candidatus Liberibacter solanacearum</em> in carrot in France.</td>
<td>Françoise Poliakoff, ANSES - Plant Health Laboratory-France</td>
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<tr>
<td></td>
<td>Effects of susceptible and resistant cultivars on populations of the potato cyst nematode <em>Globodera rostochiensis</em> Ro1 and on potato yields in Victoria, Australia.</td>
<td>Rudolf de Boer, Department of Environment and Primary Industries, Victoria, Australia</td>
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<td>18.00 - 19.00</td>
<td><strong>APPS GM</strong></td>
<td><strong>THEATRE: 098</strong></td>
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<td>19.00 - 23.30</td>
<td><strong>Conference Dinner at the Squadron Ballroom and Dinghy Locker, at the Royal New Zealand Yacht Squadron</strong></td>
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### Thursday 28th November 2013

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<tr>
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<tr>
<td>8.00 – 18.00</td>
<td>Registration Open (OGG building foyer)</td>
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<tr>
<td>7.30 – 8.30</td>
<td>APPS Executive Breakfast Meeting (current and incoming Management Committees)</td>
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<tr>
<td>8.30 – 9.30</td>
<td>Concurrent Oral Sessions (15 mins/talk including questions)</td>
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<tr>
<td><strong>SESSION 2D: BIOLOGICAL INTERACTIONS AND PLANT DISEASES</strong></td>
<td>Exotic pests and pathogens detected by general surveillance in Victoria – 2010 to 2013.</td>
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<tr>
<td>Chairs: Amanda Able &amp; Robert Lawry</td>
<td><strong>SESSION 6D: NEW AND EMERGING DISEASES</strong></td>
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<tr>
<td><strong>THEATRE: OGGB3</strong></td>
<td>Robert Holmes, Department of Environment and Primary Industries Victoria(DEPI), Australia</td>
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<tr>
<td>8.30 – 8.45</td>
<td>A study of Botrytis Virus X transmission and vegetative incompatibility in <em>Botrytis cinerea</em>.</td>
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<tr>
<td>Gregor Kolbe, The University of Auckland, New Zealand</td>
<td><strong>SESSION 8C: POPULATION GENETICS</strong></td>
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<tr>
<td>8.45 – 9.00</td>
<td>Exotic pests and pathogens detected by general surveillance in Victoria – 2010 to 2013.</td>
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<tr>
<td>Robert Holmes, Department of Environment and Primary Industries Victoria(DEPI), Australia</td>
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<tr>
<td>9.00 – 9.15</td>
<td>Drought tolerance in endophyte-infected ryegrass – a transcriptomics study.</td>
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<td>Yanfei Zhou, Institute of Fundamental Sciences, Massey University, New Zealand</td>
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<td>9.15 – 9.30</td>
<td>Species and subclade composition of <em>Leptosphaeria</em> spp. populations causing blackleg in brassica crops in New Zealand.</td>
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<td>Suhaizan Lob, Lincoln University, New Zealand</td>
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<td>Kar Mun Chooi, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<td>Celeste Linde, The Australian National University</td>
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<td>Andrew Pitman, The New Zealand Institute for Plant &amp; Food Research Limited</td>
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<tr>
<td>10.30 – 12.00</td>
<td>Genetic diversity and genetic structure of <em>Fusarium oxysporum</em> f. sp. ubter the causal agent of yellows and wilt of sesame in Fars Province in Iran by using IGS-RFLP.</td>
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<td>Seddiqe Mohammadi, Shiraz Islamic Azad University, Iran</td>
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<td>12.00 – 13.00</td>
<td>PLENARY 11: GETTING THE WORD OUT</td>
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<td>Speaker on “Science-to-grower communications in the wine industry – a case study”: Ruby Andrew, New Zealand Winegrowers</td>
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<td>Speaker on “The importance of the role of communication in science when industry is faced with a crisis”: Robin Nitschke, Manager of the Tamarillo Growers’ Association</td>
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<td>Speaker on “How we use science communication to increase public engagement and behaviour change – lessons learnt from the management of kauri dieback”: Nick Waipara, Auckland Council</td>
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<td>Chair: Robin MacDiarmid</td>
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10.30 – 11.00  Morning Tea (OGG building foyer)

11.00 – 12.00  **PLENARY 11 (CTD): GETTING THE WORD OUT**  
THEATRE: 098  
Speaker on “Science to Science”: Ass. Prof. Mike Pearson, PestNet  
Speaker on Plant Pathology International Development: A Year in the Kingdom of Tonga: Melissa Cook, Tonga  
Speaker on Area wide management of *Tomato yellow leaf curl, Potato leafroll* and *Tomato spotted wilt viruses* in Bowen, Australia: Cherie Gambley, Department of Agriculture, Fisheries and Forestry, QLD, Australia  
Chair: Robin MacDiarmid

12.00 – 12.30  **PLENARY 12: POPULATION GENETICS**  
THEATRE: 098  
Speaker: Prof. David Guttman, University of Toronto, USA  
Chair: Rob Taylor

12.30 – 13.30  Lunch (OGG building foyer)

12.30 – 13.30  **HAL Student Mentor Lunch**  
PRESENTATION OF HAL AWARDS  
DECIMA GLENN, ROOM 310

13.30 – 14.30  Poster Session 2 (OGG building foyer)  
Biosecurity, New and emerging diseases, Plant pathogen interactions, Biological interactions & plant diseases

14.30 – 15.00  **PLENARY 13: EPIDEMIOLOGY**  
THEATRE: 098  
Speaker: Ass. Prof. Neil McRoberts, University of California, Davis, USA  
Chair: Wellcome Ho

15.00 – 15.30  **PLENARY 14: BIOSECURITY**  
THEATRE: 098  
Speaker: Dr Angus Carnegie, Department of Primary Industries, New South Wales, Australia - Sponsored by Ministry for Primary Industries  
Chair: Wellcome Ho

15.30 – 16.00  Afternoon Tea (OGG building foyer)

16.00 – 17.00  Concurrent Oral Sessions (15 mins/talk including questions)

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<tr>
<th>SESSION 7D: PLANT PATHOGEN INTERACTIONS</th>
<th>SESSION 2E: BIOLOGICAL INTERACTIONS AND PLANT DISEASES</th>
<th>SESSION 1B: APPLICATION OF NEW TECHNOLOGIES</th>
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<td>THEATRE: OGGB5</td>
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16.00 – 16.15  Role of OASTL-A1 in plant immunity and interaction with NBS-LRR immune receptor. Jibran Tahir, Massey University, New Zealand

Three diseases of potato plants caused by *Spongospora subtomentosa* powdery scab on tubers, galls on roots, zoosporangia in root cells (root malfunction). Richard Falloon, New Zealand Institute for Plant & Food Research Limited

Can a single genomic difference result in a better biocontrol agent? Claudia Lange, Bio-Protection Research Centre, Lincoln University, New Zealand
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<th>Time</th>
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<tr>
<td>16.15 – 16.30</td>
<td>Secretome analysis identifies conserved putative effectors of the fungal pathogen <em>Ciborinia camelliae</em>.</td>
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<td><strong>Matt Denton-Giles, Massey University, New Zealand</strong></td>
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<td>Protecting commercial Australian potato genotypes from Verticillium wilt through identification of sources of resistance.</td>
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<td><strong>Veradina Dharjono, The University of Melbourne, Australia</strong></td>
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<td>Application of viability PCR for the selection detection of live pathogens in a quarantine setting.</td>
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<td><strong>Robert Taylor, Ministry for Primary Industries, New Zealand</strong></td>
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<td>16.30 – 16.45</td>
<td>Towards a molecular tool for identifying virus infected plants.</td>
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<td><strong>Sonia Lilly, The New Zealand Institute for Plant &amp; Food Research Limited</strong></td>
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<td>Insects as vectors of <em>Quambalaria piteka</em> the significant shoot, flower and bud blight pathogen of <em>Corymbia calophylla</em> in southwest Western Australia.</td>
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<td><strong>Briony Williams, Murdoch University, Australia</strong></td>
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<td>The detection of brassica-infecting viruses in the aphids <em>Myzus persicae</em> and <em>Brevicoryne brassicae</em>.</td>
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<td><strong>Sarah Thompson, The New Zealand Institute for Plant &amp; Food Research Limited</strong></td>
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<td>16.45 -17.00</td>
<td>Analysis of the accessory genome of the kiwifruit pathogen <em>Pseudomonas syringae pv. actinidiae</em>.</td>
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<td><strong>Matthew Templeton, The New Zealand Institute for Plant &amp; Food Research Limited</strong></td>
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<td>Friends don’t eat friends: loss of endophyte mutualism triggers activation of host degradation.</td>
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<td><strong>Carla Eaton, Massey University, New Zealand</strong></td>
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<td>Preliminary results on the use of electronic nose for the early diagnosis of bacterial canker of kiwifruit.</td>
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<td><strong>Francesco Spinelli, University of Bologna, Italy</strong></td>
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<td>17.00 – 17.30</td>
<td>APPS Awards: Fellows and honorary members</td>
<td>THEATRE: 098</td>
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<td>Chair: Professor Eileen Scott</td>
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<td>17.30 – 17.40</td>
<td>The CRC Plant Biosecurity Student Awards</td>
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<td>Chair: Dr Michael Robinson</td>
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<td></td>
<td>The Springer Student Awards</td>
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<td>17.40 – 17.50</td>
<td>The Allen Kerr Award</td>
<td>THEATRE: 098</td>
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<td>Chair: Professor Eileen Scott</td>
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<td>17.50 – 18.10</td>
<td>Invitation to Forthcoming Conferences</td>
<td>THEATRE: 098</td>
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<td>Dr Phil O’Brien</td>
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<td>18.10 – 18.20</td>
<td>Acknowledgements and Conference Close</td>
<td>THEATRE: 098</td>
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<td>18.20 -</td>
<td>Regional Councillors Informal Dinner meeting</td>
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<td>Dr Christine Horlock</td>
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**Friday 29th November 2013**

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<tr>
<td>8.30 – 16.30</td>
<td>Workshops/Tours</td>
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**THEATRE: 098**
Don’t forget the plants!

Dr Elaine Davison
e.davison@curtin.edu.au
Department of Environment and Agriculture, Curtin University, Perth, GPO Box U1987, Western Australia 6845

The plant disease triangle is one of the fundamental concepts that underlie the understanding and management of plant disease. It presupposes knowledge of the host, the pathogen and the environment, how these interact, and how they can be modified to minimise the risk of severe disease developing. Agricultural crops are well known; plant pathologists have access to an extensive literature on their structure, physiology, nutritional requirements and genetics all of which feed into practical control measures. Native plants in natural ecosystems, however, are a different proposition because so little is known about them. How can we understand a diseased plant without a detailed knowledge of a healthy one? This is the situation confronting me when starting to work on jarrah dieback, so that I have spent some time investigating jarrah (Eucalyptus marginata) in addition to working with the introduced soil-borne pathogen Phytophthora cinnamomi. This journey has been full of surprises.

Plant innate immune signaling networks

Prof Jen Sheen
sheen@molbio.mgh.harvard.edu
Department of Genetics, Harvard Medical School, Department of Molecular Biology and Center for Computational & Integrative Biology, Massachusetts General Hospital, Boston, MA, USA

Plant innate immunity is triggered by broadly conserved microbe-associated molecular patterns (MAMPs) and specific pathogenic effectors, which confer tolerance or resistance to a broad spectrum of microbes and pathogens. MAMPs are perceived by cell-surface pattern recognition receptors (PRRs) encoded by receptor-like kinases (RLKs) or receptor-like proteins (RLPs), whereas pathogenic effectors are delivered into plant cells and detected by intracellular NB-LRRs (NLRs) immune sensors. Despite the receptor diversity in MAMP and effector perception evolved to capture the potentially infinite invaders, the intracellular signaling mechanisms appear to converge and establish differential transient or prolonged plant protection against infection. It remains unknown how MAMP-PRR signaling and effector-NLR signaling are intertwined or distinguished in the dynamic and complex plant innate immune signaling networks. I will present our efforts in developing integrated approaches, which enabled detailed molecular, chemical, biochemical, genetic and genomic dissection of signal transduction mechanisms underlying plant innate immune responses. Novel insights into the dynamic and differential calcium signaling in PTI (pattern-triggered immunity) and ETI (effector-triggered immunity) will be highlighted.
PLENARY SPEAKERS

Insect vectors and vector-borne disease agents of plants - the surprising dynamics of interactions among three unrelated organisms

Dr Saskia A. Hogenhout
saskia.hogenhout@jic.ac.uk
Department of Cell and Developmental Biology, John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK

Insects are the main consumers of plants and are responsible for an estimated 15% of global crop losses. In addition, particularly sap-feeding insects such as aphids, whiteflies and leafhoppers, transmit a variety of pathogens and hence may be viewed as the mosquitoes of plants. Remarkably, more than 80% of the insect species are regarded as specialists with less than 10% feeding on plants in more than 3 plant families. Thus, most plants are resistant to most insect herbivores. Research in my laboratory has demonstrated that insects modulate plant processes to efficiently colonize plants. We have identified virulence proteins (effectors) in aphid saliva that promote aphid colonization on plants. Intriguingly insect-vectored pathogens often assist in the modulation of plant processes to the benefit of both the insect vectors and the pathogens. The obligate leafhopper-transmitted phytoplasmas have effectors that promote leafhopper colonization thereby increasing the chance of phytoplasma transmission to other plants. Phytoplasma effector protein SAP11 destabilizes TCP transcription factors resulting in increased stem production and altered leaf development and reduced jasmonate (JA) synthesis, while effector protein SAP54 destabilizes MADS-box transcription factors leading to the conversion of flowers into leaves and delayed plant senescence. Leafhoppers feed and lay eggs on green plant tissues and are sensitive to JA. Both phytoplasma effectors promote leafhopper feeding and reproduction contributing to a 60% increase in the number of insect vectors on phytoplasma-infected plants. Thus, both insects and insect-transmitted pathogens produce effectors that promote insect colonization on plants. Overall this research will lead to a greater understanding of plant defence mechanisms to insect herbivores that can be used towards approaches to improve crop resistance to insects.

New diseases of woody plants – a New Zealand perspective

Dr Margaret Dick
margaret.dick@scionresearch.com
Scion, New Zealand Forest Research Institute Ltd., Rotorua, New Zealand

Plant communities have evolved in association with cohorts of potentially pathogenic microorganisms which generally cause little or no damage to their hosts. However introduction of these microorganisms to another part of the world, where different host species with no resistance are exposed to a pathogen may lead to a new, sometimes devastating, disease. The movement of organisms into new environments also provides the opportunity for the formation of hybrids, new species or subspecies that are potentially pathogenic to new host species or host genera. Hybridisation between long-established related species may also, though rarely, result in a new pathogen. Climate change presents another avenue for altering virulence patterns of existing pathogens, whether by altering host response mechanisms or by affecting expression of virulence genes. Mutation or recombination of genetic material during meiosis can affect pathogenicity of microorganisms, likewise the acquisition of new effector proteins. The plant-based component of New Zealand’s economy is currently dependent on exotic plant species whether the industry be forestry, agriculture or horticulture. New diseases that have had a marked effect in New Zealand in recent decades have fallen into the categories of both known and undescribed organisms. Measures to prevent entry of causal agents of known diseases of these hosts that occur in overseas countries are embedded in import legislation. Notwithstanding regulations incursions happen and sometimes with devastating impact e.g. the bacterial disease of kiwifruit caused by Pseudomonas syringae pv. actinidiae. The urban forest has also been affected, particularly in Auckland (New Zealand’s primary gateway for people traffic and imports). Indigenous plants have been largely unaffected to date though they are not exempt, with the Phytophthora root disease of Agathis australis (kauri) as the current high-profile example. Ways in which ‘new’ pathogens and new diseases emerge will be discussed and illustrated with examples, primarily from the New Zealand experience and with a focus on woody plants.
Contrasted patterns of phytoviral metagenomes in wild and agricultural environments

Dr Thierry Candresse

Contrasted patterns of phytoviral metagenomes in wild and agricultural environments

Dr Thierry Candresse

tc@bourdeaux.inra.fr

T. Candresse1,2, A. Marais1,2, C. Faure1,2, S. Then1,2, L. Svanella-Dumas1,2, S. Carrere3,4, B. Bergey1,2, C. Couture1,2, Y. Laizet1,2

1) INRA, UMR 1332 BFP, BP 81, 33883 Villenave d’Ornon cedex, France.
2) Université de Bordeaux, UMR 1332 BFP, BP 81, 33883 Villenave d’Ornon cedex, France.
3) INRA, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR 441, F-31326 Castanet-Tolosan, France.
4) CNRS, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR 2594, F-31326 Castanet-Tolosan, France.

The development of novel sequencing techniques allows an unprecedented access to viral metagenomes and, in particular, to the yet poorly studied communities of phytoviruses in plant populations. We have studied two very different ecological settings, agricultural plots in south western France and the uncultivated Kerguelen Islands, the second most isolated archipelago on earth. The results obtained in the Kerguelen Islands demonstrate a very low diversity of single-stranded RNA (ssRNA) viruses and a large diversity of novel double-stranded RNA (dsRNA) viruses belonging to the families Totiviridae, Partitiviridae and Endornaviridae and the recently proposed Amalgamaviridae family. A similar diversity of novel dsRNA viruses was observed in SW France with, in addition, a wide range of both known and novel ssRNA viruses (Alpha- and Betaflexiviridae, Bromoviridae, Closteroviridae, Luteoviridae, Potyviridae, Secoviridae, Tombusviridae…). Remarkably, at the sampling intensity used, close to half of the weed species were found to be free of infection by ssRNA viruses while the number of novel ssRNA agents remained roughly comparable to the number of known ones, suggesting that in the studied agricultural ecosystem a significant proportion of ssRNA viruses has already been described through classical approaches. Simultaneous presence of viruses in crops and in neighboring weeds was observed, suggesting viral spillover from crop to weeds but not allowing to draw conclusions on potential reservoir roles. These first efforts illustrate the potential of these approaches to analyze the phytoviral diversity as a first step towards the identification of the drivers shaping this diversity and the resulting viral communities.

Application of New Technologies

Dr Neil Boonham

neil.boonham@fera.gsi.gov.uk

The Food and Environment Research Agency, Sand Hutton, York, North Yorkshire. YO41 1LZ. UK

Detection and identification of plant pathogens relies upon a broad range of techniques and skills, combining traditional culture and taxonomic skills with modern molecular based methods. Whilst usually delivered as a laboratory service methods that can be performed in the field are starting to reach maturity. The challenge for many laboratories is selecting an from a plethora of methods which all have equally high performance, in addition deciding if the biggest benefits can be gained from delivering testing in the field or in the laboratory. Delivering services in the field offers obvious advantages in terms of speed of analysis and potentially reduced costs in terms of overheads if not individual analysis. However, pushing testing into the field may directly or inadvertently serve to reduce the size of laboratory services. These staff are important knowledge custodians when there are new pest incursions, equally centralised testing laboratories are capable of testing the vast numbers of samples generated during outbreaks. This provides a policy conundrum and a delicate balance needs to be reached between retaining expertise deployed during times of crisis and delivery of more cost effective day-to-day screening services. Concurrent with the maturation of field testing technologies is the rapid pace at which Next Generation Sequencing technologies are developing and the potential they bring in delivering generic approaches in the first instance for the investigation of new or intractable diseases. The developments though may be more far reaching, cost per nucleotide is a new currency and as it drops it brings with it the potential for ultra-high throughput, very low cost per sample testing which would have been unheard of even five years ago when we started exploring the potential of NGS.
Fungal names in flux

Dr Shaun Pennycook
PennycookS@LandcareResearch.co.nz
Research Associate, Manaaki Whenua Landcare Research, Private Bag 92 170, Auckland 1142, New Zealand

A discourse is presented on fungal nomenclature: its origin, history, and governance; its utility; how names should be formed and cited; why names change; the type principle; the priority principle; invalid and illegitimate names; sanctioned names; and the dual nomenclature of anamorphic and teleomorphic names. The major changes affecting fungal nomenclature as a consequence of emendments to the International Code of Nomenclature (ICN), ratified at the XVIIIth International Botanical Congress, Melbourne 2011, are described; in particular, the revolutionary abolition of dual nomenclature (“one fungus, one name”) is discussed, with consideration and speculation on the possible composition of the lists of “accepted” and “rejected” names being prepared by special sub-committees for each group of fungi.

Management of bacterial diseases of plants: successes and challenges

Ass Prof Virginia Stockwell
stockwev@science.oregonstate.edu
Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97330 USA

Control of bacterial diseases of plants is difficult, in part, because there are few effective materials to suppress growth of bacterial pathogens on plants. Antibiotics are effective preventatives for a few plant diseases, but emergence of resistance and regulatory constraints threaten their long-term use. Biological control is an attractive alternative. Agrobacterium radiobacter K84 (and its derivative K1084) has been used with noteworthy success for prevention of crown gall of stone fruit rootstocks in nurseries. Adoption of other biocontrol systems by growers is hampered, in part, due to unexplained variation in efficacy. We study factors that impact efficacy of the biological control agents Pseudomonas fluorescens A506 and Pantoea vagans C9-1 for fire blight of apple and pear flowers caused by Erwinia amylovora. A506 and C9-1 suppress disease by pre-emptive exclusion and production of peptide antibiotics, respectively. Combining A506 and C9-1 did not improve efficacy compared to single strains. We found that an extracellular protease of A506 inactivated the peptide antibiotic of C9-1. Biological control of fire blight was improved by altering a single factor (protease production) mediating the outcome of interactions between C9-1 and A506 and the pathogen. Because microbial interactions are complex and rarely determined by a single factor, we are now using genomics-enabled approaches to characterize interactions between the biocontrol agents and the pathogen on flowers. Identifying factors shaping interactions between microorganisms in agroecosystems may lead to methods to improve the efficacy, consistency, and adoption of biological control for management of bacterial diseases of plants.
**Dissecting the Co-Evolutionary Arms Race between Bacterial Effectors and the Plant Immune System**

Prof David S. Guttman  
david.guttman@utoronto.ca  
Department of Cell & Systems Biology, University of Toronto, Toronto, Ontario Canada

The YopJ/HopZ family of type III secreted effector proteins is evolutionarily diverse and widely distributed among both plant and animal pathogens. We have previously shown that the family diversified in the plant pathogenic bacterium *Pseudomonas syringae* via both mutational processes during vertical descent from the ancestral *P. syringae*, as well as through horizontal transfer from ecologically similar pathogens into five distinct allele groups. We also have shown that the most ancestral allele (HopZ1a) is consistently recognized by the plant resistance protein, ZAR1, and that this interaction induces ETI. Here we discuss genetic screens and heterologous assays to identify virulence targets of HopZ1. We first show that HopZ1a interacts with the plant microtubule network, and demonstrate that it is an acetyltransferase that acetylates itself and tubulin. Furthermore, HopZ1a requires its acetyltransferase activity to disrupt the Arabidopsis microtubule network and the secretory pathway as well as to suppress cell wall-mediated defense. We also demonstrate that HopZ1a directly interacts with and acetylates a previously uncharacterized protein kinase (ZED1), which is encoded within a tandemly arrayed family of related kinases, and which also directly interacts with and is required for ZAR1 activation.

**The Structure of Diagnostic Information**

Ass Prof Neil McRoberts  
nmcroberts@ucdavis.edu  
G. Hughes(1), N. Mcroberts(2)

(1) Crop and Soil Systems, SRUC, West Mains Road, Edinburgh, EH9 3JG, UK  
(2) Plant Pathology Department, University of California, Davis, Davis CA 95616-8751, USA

Diagnosis is characterized as an exercise in classification, where the task is to assign a crop to a risk group as a basis for evidence-based crop protection decision making. Underlying the process of diagnostic decision making is Bayesian updating of probabilities. Alongside updating of probabilities, assessments of diagnostic information allow further description of the characteristics of diagnostic tests, and of the predictions made on the basis of test outcomes. To this end, the paper demonstrates potential uses of the information quantities entropy, expected mutual information, specific information and relative entropy. The applications are described analytically, graphically (by means of iso-information contour plots and information graphs) and by discussion of example epidemiological scenarios. Some conjectures are also offered on how information quantities might be used to provide a formal means to analyze resistance to adoption of decision aids among groups of decision makers who are recipients of support by extension workers.
PLENARY SPEAKERS

**Puccinia psidii (myrtle rust): preparing for an invasion**

Dr Angus J. Carnegie
angus.carnegie@dpi.nsw.gov.au

Biosecurity NSW, NSW Department of Primary Industries, PO Box 242, Parramatta, NSW 2124, Australia.

*Puccinia psidii* (guava/eucalyptus/myrtle rust) is an invasive rust with a host range encompassing over 350 species in 65 genera of Myrtaceae. Described in Brazil over a century ago, it slowly invaded countries in South and Central America, and in the mid-1970s reached Florida (USA). Over the past decade it has invaded Hawaii (2005), China and Japan (2009), Australia (2010) and South Africa and New Caledonia (2013). Rust spores can be moved internationally via infected plant material and commonly on clothes of international travellers as well as on cargo; the former mode of transport can be regulated, thus restricting the highest risk of invasion. However, it is only a matter of time before *P. psidii* reaches New Zealand. Early detection is essential in any potential eradication attempt. Lessons learnt from the invasion of myrtle rust into Australia will be discussed in light of the threat of *P. psidii* to New Zealand. A speedy and well resourced and coordinated program is required for any eradication attempt. Staff (e.g. biosecurity, pathologists, botanists) need to be identified, as well as systems in place to access them. Strong links with industry bodies and interest groups are required. Assume all species of Myrtaceae are a host. Don’t assume that symptoms of *P. psidii* are obvious to find. The potential impact of *P. psidii* is real: myrtle rust has now spread along the eastern seaboard of Australia and in less than 3 years has caused significant impact to key Myrtaceae and threatened species.
Area wide management of *Tomato yellow leaf curl*, *Potato leafroll* and *Tomato spotted wilt viruses* in Bowen, Australia

Dr Cherie Gambley  
Department of Agriculture, Fisheries and Forestry, QLD  
cherie.gambley@daff.qld.gov.au

Cherie Gambley(1), Rebecca Roach(1), Denis Persley(1), Murray Sharman(1)

(1)Department of Agriculture, Forestry and Fisheries, QLD

*Tomato yellow leaf curl virus* (TYLCV; Begomovirus) and *Potato leafroll virus* (PLRV; Polerovirus) are emerging concerns for tomato production in the Bowen region of north Queensland. Both viruses were confirmed present in Bowen in 2011 with high incidences recorded for some crops in 2012. TYLCV is transmitted by the Silverleaf whitefly (SLW) and PLRV by several aphid species, including the Green peach aphid (GPA). GPA has, in recent seasons, developed large populations in the Bowen district and has proven difficult to control. *Tomato spotted wilt virus* (TSWV; Tospovirus) is an ongoing concern for the district and due to recent switches to the use of non-TSWV resistant varieties, either to combat TYLCV or due to unavailability of seed, economic losses to this virus also increased. A recent workshop on the epidemiology and management of whitefly-transmitted viruses held in Brisbane (October 2012) demonstrated the effectiveness of area wide management of insects both as pests and virus vectors. Local research has provided valuable information on the use of biological control agents to control virus vectors, levels of insecticide resistance within vector populations and how vectors move within the landscape. This local knowledge combined with that from overseas researchers provides an excellent basis to attempt area wide management of viruses in the Bowen region. The first phase of this work is to generate base line data on the distribution and prevalence of the viruses and the vectors in early, mid and late season. Results from these surveys will be presented and includes the prevalence of TYLCV, PLRV and TSWV within crops across the district. The presentation will also include the prevalence of SLW within crops across the district and the proportion of those populations which are identified as TYLCV positive vectors. This phase of work also includes investigation of alternative hosts for TYLCV and PLRV, including both weed species and other crops. The cotton industry periodically experiences outbreaks of Cotton bunchy top disease (CBT) which is also caused by a polerovirus. Although CBT is present in most cotton crops each season, large outbreaks of the disease are rare. Similarly, PLRV is thought to occur in many tomato growing regions but only causes significant disease in Bowen. Potential similarities in environmental conditions between outbreaks of CBT and PLRV will be discussed.

Plant Pathology & International Development: A Year in the Kingdom of Tonga

Ms Melissa Cook  
Ministry of Agriculture, Food, Forest & Fisheries, Tonga  
melissajanecook@gmail.com

Melissa Cook  
Plant Pathology Department, Ministry of Agriculture, Food, Forest & Fisheries Research Station, Vaini, Kingdom of Tonga

My recent Australian Youth Ambassador for Development (AYAD) assignment in the Kingdom of Tonga, as a Plant Pathologist for the Ministry of Agriculture, Food Forest and Fisheries (MAFFF), was an incredibly rewarding yet challenging role. The Kingdom of Tonga is an archipelago of over 70 islands. The largest and most densely populated island, Tongatapu, is almost half the total land area of the whole archipelago. As Tongatapu is relatively low lying (the highest elevation is 65m in the south-east) groundwater contamination issues have risen over the last few decades, due in part to the overuse of pesticides and commercial fertilizer for high value export crops. High levels of rainfall and humidity, especially between November and April, also contribute to high fungal disease incidence and severity on many crops in Tonga. Increased government interest in IPDM practices and sustainable agricultural methods has lead to multiple projects in Tonga aiding subsistence and cash crop farmers to address these issues sustainably. My presentation will focus on my experiences as a early career plant pathologist working in the challenging field of international development, as well as projects and initiatives that could be implemented in the Kingdom of Tonga.
Detection of potato potyviruses in aphids caught in water and propylene glycol trap solutions

Dr Ron van Toor
Plant and Food Research
Ronald.vanToor@plantandfood.co.nz
Ron van Toor(1), Gaynor Malloch(2), Brian Fenton(2)
(1)Bioprotection Technologies, The New Zealand Institute for Plant & Food Research Limited, Lincoln, Canterbury, NZ
(2)James Hutton Institute (formerlySCRI), Invergowrie, UK

Yellow-bowl traps containing water-detergent are used extensively in Scotland to monitor virus risk in potatoes from aphid virus vectors, which is calculated by multiplying the number of aphids in a weekly trap catch by a virus efficiency factor specific to each species. The proportion of aphids carrying viruses can also be measured directly using molecular diagnostic techniques, but it is not known how long the non-persistent potyviruses, potato virus A (PVA) and potato virus Y (PVY), remain detectable in water, or if they transfer in solution between aphids, thereby negating estimates of virus incidence. We compared water with a solution of 50% propylene glycol/water (PG50), both containing 1% detergent, to support PVA and PVY detection in the aphid Myzus persicae. Virus presence was diagnosed by RT-PCR/nested PCR and the products analysed on gels. There was no change in the proportion of alatae carrying PVA and PVY from 0 to 9 days in both solutions under laboratory conditions. In the field, the proportion of alatae carrying PVY in traps containing either solution declined from 94% at 0 days to 65% after 7 days in the presence of insect by-catches. As nucleases released by the decaying insects in the by-catch may have inhibited virus detection, activated charcoal and bentonite nucleases adsorbents, were evaluated as PG50 additives. In the presence of decaying insects, all solutions were effective in preserving PVY after 7 days in the laboratory, but in a tunnel house where air temperatures exceeded 35 °C, the proportion of alatae in water carrying PVY declined to half the initial levels, and lesser amounts in the PG50 solutions, with no benefit from charcoal or bentonite. Under summer field conditions in traps refreshed weekly the proportion of aphids carrying PVA tended to decline over the 7 days in the trap solution, while the proportion of aphids carrying PVY remained similar to when they were placed in solution. On rare occasions in extremely high summer temperatures PVY appeared transmissible from PVY-carrying alatae to virus-free aphids in both solutions. However, under normal temperatures, solutions containing detergent and water or PG50 appear suitable for monitoring the incidence of potyviruses in aphids caught in yellow-bowl traps.

Hyperspectral leaf response of plant infected with Phytophthora cinnamomi

Ms Zoe-Joy Newby
The Royal Botanic Gardens and Domain Turst
zoejoy.newby@rbgsyd.nsw.gov.au
Zoe-Joy Newby(1), Richard Murphy(2), David Guest(3), Daniel Ramp(4), Edward Liew(5)
(1)PDDU, Royal Botanic Gardens, Mrs Macquaries Rd, Sydney, 2000, Australia
(2)A11- Edgeworth David Geology, The University of Sydney, NSW 2006, Australia
(3)CB1 - Biomedical Building, The University of Sydney, NSW 2006, Australia
(4)School of the Environment, University of Technology, Sydney.4.5.60A, Broadway, NSW, 2007, Australia

Remote sensing is routinely applied within environmental management to assess vegetation health and plant productivity. Recent developments in the use of hyperspectral remote sensing (HRS) have demonstrated numerous examples of its application to quantify foliar disease in agricultural, horticultural and forestry industries. Here we report on the ability of HRS to quantify Phytophthora cinnamomi infection in plants of native Australian ecosystems in an attempt to identify a more efficient and effective method of disease identification. A glasshouse trial investigated how leaf reflectance in species with different susceptibilities to P. cinnamomi changed in response to infection, and if this change could be distinguished from changes caused by a lack of water. Leaf reflectance in the wavelength region of 350-2500nm was measured fortnightly using a hand held spectroradiometer over four months. Data were imported into ENVI, spectra were smoothed and the first and second derivative spectra were calculated. Water features were identified within the spectra and the effect of inoculation and water stress on their size was assessed using ANOVA. A number of vegetation indices (VIs) which assess changes in leaf pigments, water content and general plant health were calculated and again analysed using ANOVA. Reflectance in the UV-NIR region (350-900nm) was assessed using principal component analysis (PCA). Infection could be identified in the water features although the response between species was not universal. A unique combination of two to three VIs could be used to identify infection in most species and these typically included reflectance in the green (530-550nm) and red regions (650-680nm), and the anthocyanin reflective index. The PCA showed treatment separation of the first derivative data within the visible and NIR region and explained more than 95% of the data variation in three components. Unique spectral signatures outside the visible range (400-700nm) were identified in two of the species suggesting the detection of P. cinnamomi infection is possible in asymptomatic species or before visually symptoms are evident when using HRS. Disease detection was more difficult in the field resistant species and once water stress became severe, changes in reflectance due to infection were often no longer significantly different from controls. If the response of individual species to P. cinnamomi infection is understood, real-time and presymptomatic disease detection may be possible with HRS. This has implications on greatly improving disease management decision making.
Citizen science and a smartphone application to monitor the incidence and severity of Quambalaria diseases in Western Australian marri *Corymbia calophylla*

Cielito Marbus
Murdoch University
g.hardy@murdoch.edu.au

Cielito Marbus(1), Treena Burgess(1), Trudy Paap(1), Briony Williams(1), Pieter Poot(2), Erik Veneklaas(2), Giles Hardy(1)

(1)State Centre of Excellence for Climate Change, Woodland and Forest Health, School of Veterinary and Life Sciences, Murdoch University, Murdoch, 6150, Western Australia,
(2)School of Plant Biology, University of Western Australia, Crawley, 6009, Western Australia

The incidence and severity of cankers caused by *Quambalaria coyrecup* and *Q.piterika*, the cause of shoot, flower and fruit blight in marri (*Corymbia calophylla*), have increased significantly since the early 1990s in the south-west of Western Australia. Marri is an iconic overstorey forest tree with an extensive range in a number of diverse forest ecosystems. It plays a major role as a food source, habitat tree and refugium for numerous vertebrate and invertebrate fauna including the endangered Carnaby’s cockatoo (*Calyptrhyynchus laterostris*), as well as being a key species providing pollen and nectar for apiarists. Consequently, the impact of these pathogens on marri is causing increasing concern across the community for a wide range of reasons. We have developed a smartphone marri application that works across Android and IPhone mobile platforms that can be used by interested members of the public, local government agencies, foresters and scientists to capture location (GPS), incidence and severity of cankers and shoot blight on trees, and lodge photographs and other critical site information to a central server. To fully inform users, the smartphone marri application also supplies detailed photographic information and text on what cankers and shoot blight look like at different stages of development, and how to differentiate these from other similar biotic and abiotic symptoms. Importantly, it also provides information on how to establish and monitor fungicide and other treatment trials that will be statistically robust and informative for scientific purposes across the marri range. The development and use of the ‘marri app’, together with the strengths and weaknesses associated with using citizen science to help drive research will be discussed.

Field evaluation of a bioherbicide for control of parkinsonia (*Parkinsonia aculeata*) in Australia

Dr Victor Galea
The University of Queensland
v.galea@uq.edu.au

Victor Galea, Ken Goulter,
School of Agriculture and Food Sciences, The University of Queensland, Gatton, QLD 4343 Australia

Parkinsonia *Parkinsonia aculeata* L., is a serious weed of Australia’s rangelands affecting more than 3.3 million ha with the potential to invade 70% of the mainland (March 2009). This highly invasive thorny weed is a major impediment to cattle production and a threat to wetlands. A bank of fungal isolates from dieback affected parkinsonia collected across northern Australia has been evaluated under laboratory and glasshouse conditions to select isolates aggressive against this woody weed host. A selection of isolates drawn from fungal genera including *Lasiodiplodia*, *Macrophomina* and *Neoscytalidium* showed great promise as potential bioherbicides and are currently undergoing commercial development. A field experiment was established among naturally occurring parkinsonia on Stradbroke Station (near Duchess, western Queensland) to evaluate the performance of three isolates singly, or combined together in their ability to cause infection and subsequent mortality in adult trees. Isolates were formulated into gelatine capsules as individual isolates or as a blend (equal parts) of all three. Control capsules contained sterile carrier media only. Trees were inoculated in April 2011 by introducing single capsules into 10 mm diameter holes drilled into the stem (30 mm depth) at 200 mm above ground level. Inoculation holes were sealed with domestic roof & gutter silicone sealant. Trial assessments conducted at six monthly intervals over a 2 year period assessed plants for attributes such as inoculation success, presence of stem lesions and or discoulouration, and degree of overall tree morbidity / mortality expressed as the proportion of canopy showing dieback. First signs of infection became obvious at the 12 month assessment as evidenced by branchlet death and general morbidity across all fungal treatments. At the 18 month assessment, all fungal treatments demonstrated signs of significant dieback symptoms including stem discoulouration, major branch death, and in some cases main stem death. There was little evidence of further progression of dieback at the 24 month assessment. The outcomes of this trial clearly demonstrates the viability of this (patented) inoculation method to initiate a dieback event among naturally growing parkinsonia trees and shows great promise as an additional tool to employ in the management of woody weeds.
Can a single genomic difference result in a better biocontrol agent?

Ms Claudia Lange  
Bio-Protection Research Centre, Lincoln University  
claudia.lange@lincolnuni.ac.nz  
Claudia Lange(1) , Richard Weld(2) , Murray Cox(1) , Rosie Bradshaw(2) , Alison Stewart(3) , Johanna Steyaert(4)  
(1)Bio-Protection Research Centre, Lincoln University, PO Box 85084, Lincoln 7647, New Zealand  
(2)Lincoln AgriTech Ltd, PO Box 69133, Lincoln 7640, New Zealand  
(3)Institute of Fundamental Sciences, Massey University, Palmerston North 4442, New Zealand  
(4)Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA

The filamentous fungus Trichoderma atroviride is used widely for biological control of major plant diseases. Biocontrol activity is linked to a wide range of parameters and we have limited knowledge of what specific attributes make certain strains particularly effective as a biocontrol agent (BCA). In this study, we report on molecular differences between two closely related T. atroviride isolates and the implications they might have on biocontrol activity. Two T. atroviride isolates (LU132 and LU140) were isolated from the same onion paddock in New Zealand as potential BCAs against onion white rot. The isolates were phenotypically distinct and extensive studies found that LU132 was an excellent BCA and achieved better control than LU140 of a variety of plant pathogens. Direct comparison of a wide range of phenotypic characteristics of the two isolates found that the biggest difference between the isolates is LU132’s faster growth rate. Attempts were made to design an isolate-specific molecular marker for LU132, but it was impossible to distinguish it from LU140, suggesting high genetic similarity. Sequencing of the genomes of both isolates revealed only 2 single nucleotide polymorphisms (SNPs). The SNPs were associated with 3 genes similar to: 1) a hypothetical gene, conserved in fungi; 2) predicted Small EDRK-rich Factor H4F5 (SERF), conserved in animals and fungi; 3) Proliferating Cell Nuclear Antigen (PCNA), conserved in eukaryotes and archaea. No expression differences of these 3 genes could be identified but cDNA sequencing revealed a gene annotation error in SERF. While the published annotated genome of T. atroviride describes SERF as having 2 exons and one intron, it actually has an additional exon in LU132 and LU140. One of the SNPs is located in the 3rd exon of SERF where it changes the amino acid sequence in LU132. Bioinformatic analysis suggests that the amino acid change creates a MAPK docking motif on the LU132 SERF protein that is not present in the LU140 protein. To study the function of the gene it was knocked-out in both isolates via Agrobacterium-mediated transformation and the mutants were subjected to phenotypic examinations. We will present first results from the gene function analysis and discuss potential implications for biocontrol activity in this important species.

Application of viability PCR for the selection detection of live pathogens in a quarantine setting

Mr Robert Taylor  
Ministry for Primary Industries  
robert.taylor@mpi.govt.nz  
Robert Taylor (1) , Stephanie FitzGerald (1) , Suzanne Keeling (2) , Brett Alexander (3)  
(1)Plant Health and Environment Laboratory, Ministry for Primary Industries, PO Box 2095, Auckland, New Zealand  
(2)Science and Risk Assessment, Ministry for Primary Industries, PO Box 2526, Wellington, New Zealand

Molecular diagnostics utilising polymerase chain reaction (PCR) techniques are now routinely used for the detection and identification of regulated organisms in quarantine and biosecurity. However, one limitation of PCR technology has been the inability to differentiate positive results originating from live or dead cells. Correlating positive PCR results with diseased crops can be relatively straightforward. However, interpreting the biological risks of PCR positives in asymptomatic nursery stock, pollen, fresh produce and other environmental items can be very difficult. Biosecurity decision makers are faced with the challenge of balancing PCR positive results with the time needed to demonstrate viability of the organism, assuming it can be grown using traditional culturing techniques. One recent approach to address this problem has been the use of nucleic acid intercalating dyes, such as propidium monoazide (PMA) and ethidium monoazide (EMA), prior to DNA extraction to selectively inhibit the PCR amplification of DNA derived from dead cells. PMA and EMA are unable to penetrate viable cells with intact membranes but will penetrate dead cells with compromised membranes. Exposure to light allows cross-linking of these dyes to DNA which inhibits PCR amplification. In this study we assessed the applicability of such an approach by using PMA or EMA in conjunction with existing real-time PCR assays to detect viable cells of biosafety risk organisms. The development, application and some of the practical limitations of this technology to detect viable pathogen cells in a quarantine setting are discussed.
The detection of brassica-infecting viruses in the aphids *Myzus persicae* and *Brevicoryne brassicae*

Ms Sarah Thompson  
The New Zealand Institute for Plant and Food Research Ltd  
sarah.thompson@plantandfood.co.nz

Sarah Thompson, Sandi Keenan, John Fletcher, David Teulon, Simon Bulman  
The New Zealand Institute for Plant and Food Research Ltd, Lincoln, New Zealand

Viruses can significantly reduce brassica crop yield and quality. They are vectored between crops by sap-sucking insects – the key vectors in New Zealand being the aphids *Myzus persicae* and *Brevicoryne brassicae*. Monitoring the presence of the aphid vectors is currently seen as the major determinant for virus risk and can lead to spraying regardless of actual virus presence. Aphid monitoring is often carried out by attracting flying aphids to yellow bowl traps (YBTs) containing a trapping solution. The aim of this study was to develop techniques to directly monitor viruses in field captured aphids to aid farmers in decision-making about risk to crop. qPCR assays based on coat protein gene were developed for *Turnip mosaic virus* (TuMV) and *Turnip yellows virus* (TuYV). An internal control assay based on the elongation factor 1α gene was also designed for detecting the aphids *M. persicae* and *B. brassicae*. Propylene glycol (PG) is a candidate medium for trapping insects while at the same time preserving nucleic acids. Virus-carrying *M. persicae* were stored in PG for up to four weeks with individuals insects removed and tested weekly for virus levels. Both viruses could still be detected in the aphids after four weeks of storage in PG although TuMV was nearing the limit of detection; levels of TuYV were always substantially greater than for TuMV. TuMV is a stylet-borne *Potyvirus* and had a substantially lower titre in fresh aphids than the persistent, circulative *Luteovirus* TuYV. To test whether these qPCR tests translated to field conditions, virus-carrying aphids were spiked into yellow bowl traps and incubated under field conditions for up to 2 weeks. Virus could still be detected in these aphids after this period. Subsequently, individual wild aphids flying in rape fields were screened for TuYV and TuMV. It was demonstrated that both viruses could be detected in wild aphids caught in YBTs. PG, a relatively cheap and non-toxic medium, was confirmed to be effective at preserving aphids in YBT’s for testing of virus load. In time, such detection and quantification of viruses in insects could become a semi-automated process allowing relatively cheap monitoring of virus levels in the field. This would allow farmers to make informed decisions about spraying regimes, thus reducing costs.

Preliminary results on the use of electronic nose for the early diagnosis of bacterial canker of kiwifruit

Dr Francesco Spinelli  
Department of Agricultural Sciences, Alma Mater Studium - University of Bologna  
Francesco.spinelli3@unibo.it

Francesco Spinelli(1), Antonio Cellini(2), Giampaolo Buriani(3), Irene Donati(4), Valenito Giacomuzzi(5), Maria Teresa Rodriguez-Estrada(3), Stefano Savioli(3), Brian Farrenqi(6), Franco Biasioli(6), Simona Cristescu(6), Guglielmo Costa(7), Joel Vanneste(8)

(1)Department of Agricultural Sciences, Alma Mater Studium -University of Bologna, viale Fanin 46, 40127 Bologna - Italy  
(2)Faculty of Science and Technology, Free University of Bolzano, piazza Università 5, 39100 Bolzano - Italy  
(3)Department of Food Science and Technology, Alma Mater Studium -University of Bologna, viale Fanin 40, 40127 Bologna - Italy  
(4)Food Quality and Nutrition Department, Research and Innovation Centre - Fondazione Edmund Mach, Via E. Mach 1, 38010 S. Michele all’Adige (TN) - Italy  
(5)Radboud University, Institute of Molecules and Materials, Heyendaalseweg 135, 6525AJ Nijmegen - The Netherlands  
(6)Plant & Food Research, Ruakura, Private Bag 3123, Waikato Mail Centre, Hamilton, 3240 - New Zealand

One of the major constrain in plant disease diagnosis is the sampling procedure that needs to be carefully designed to detect reliably the presence of a pathogen. Therefore, even thought DNA-based protocols are the golden standard for the diagnosis, they may produce false negative results if the sampled material is not contaminated. On the other hand, volatiles-based diagnosis can be performed on the whole plant thus minimizing the risk of false negative. Nowadays, techniques such as gas chromatography-mass spectroscopy (GC-MS) and proton-transfer time of flight mass spectroscopy (PTR-TOF-MS) constitute a powerful method to characterize volatiles emitted by infected plants and to identify possible disease-specific markers. However, these techniques are very expensive, time-consuming and require trained personnel. Electronic nose may represent a sensitive, accurate and operator-friendly alternative for rapid and reliable screening of volatiles produced by asymptomatic infected plants. In the present study, the analysis of volatile compounds is used for the diagnosis of bacterial canker of kiwifruit (*Pseudomonas syringae pv. actinidiae*) on propagation material. The profile of volatiles emission was initially performed by GC-MS and PTR-TOF-MS. In addition, two different electronic noses, EOS507 (Sacmi Srl, Imola, Italy) and PEN3 (Airsense Analytics GmbH, Schwering, Germany), both based on metal oxide semiconductors, were used for diagnosis. The results show that electronic-nose might be adapted to be used in practical conditions, such as nurseries or customs, to screen large quantity of asymptomatic plant material in order precisely steer molecular diagnosis.
What makes *Trichoderma* rhizosphere competent: A molecular analysis

Dr Artemio Mendoza Mendoza
Bio-Protection Research Centre
artemio.mendoza@lincoln.ac.nz

Johanna Steyaert(1), Damian Bienkowski(1), Jessica Yardley(1), Mark Braithwaite(1), Kirstin McLean(1), Alison Stewart(1), Artemio Mendoza-Mendoza(1)

1) Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647
2) Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647
3) Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA

Establishment of root symbiosis has been reported as one of the key drivers of biocontrol success for members of the fungal genus *Trichoderma*. This root symbiosis is described as a two-step process, whereby *Trichoderma* isolates colonise the soil surrounding the root (rhizosphere) and then penetrate the root tissue and establish an endophytic relationship. The ability to colonise and then proliferate over time within the rhizosphere is termed rhizosphere competence, and there have been numerous reports of *Trichoderma* biocontrol strains which persist within the rhizosphere over the growing season of the crop plant. In this study, we are exploring the genetic basis of rhizosphere competency in *Trichoderma atroviride* LU132, which is a commercial biocontrol agent. Analysis of the transcriptome of LU132 proliferating in the rhizosphere of maize revealed a major down-regulation of genes when compared with *Trichoderma* free-living in soil. These findings are currently being explored through over-expression of selected genes and assessment of presence and proliferation of mutants within the rhizosphere. Analysis of nucleic acids from soil samples can be time consuming and not necessary amenable to large scale trials, therefore we are analysing the validity of using a root exudate assay from both maize and wheat plants to generate rhizosphere transcriptomes from *Trichoderma*. Results from these experiments will be discussed.

Species- and strain- specific identification and quantification of root disease suppressive *Trichoderma* inoculants in cropping soils

Dr Belinda Stummer
CSIRO
Belinda.Stummer@csiro.au

Belinda Stummer(1), Qingxia Zhang(2), Rosemary Warren(1), Hetong Yang(2), Paul Harvey(3)

1) CSIRO Ecosystem Sciences, Waite Campus, PMB 2 Glen Osmond, 5064, South Australia
2) College of Horticulture and Plant Protection, Yangzhou University, Yangzhou, 225009, Jiangsu, China
3) Biology Research Institute, Shandong Academy of Sciences, Jinan, 250014, Shandong, China

Inoculation of wheat and barley field trials in southern Australia with *Trichoderma harzianum* (Tr904, LTR-2) and *T. koningiiopsis* (Tr905) have significantly suppressed (P < 0.05) root disease severity caused by *Rhizoctonia solani* and *Pythium irregulare*. The aim of this study was to develop *Trichoderma* species- and strain- specific quantitative assays (qPCR) to define the rhizosphere dynamics and soil persistence of these disease suppressive inoculants. Primers for *Trichoderma* qPCR were designed from the internal transcribed spacer region of the 5.8S rRNA (ITS-5.8s rDNA) and sequences of DNA fragments (AFLP) diagnostic for each inoculant. The minimum detection threshold (MDT) of each qPCR assay was determined via inoculation (10^3 – 10^7) and recovery (microbiology) in 2 contrasting soils; an alkaline sand (pH 8.9, Warramboo, SA) and an acidic loam soil (pH 6.0, Temora, NSW). *Trichoderma* were quantified (microbiology and qPCR) immediately after inoculation (T0) and at 28 (T28) days. MDT’s of the qPCR assays varied between 10^3 (LTR-2) and 10^4 (Tr905) conidia per gram of soil (c g^-1 soil), with the maximum detected being 10^8 c g^-1 soil. Both the minimum and maximum qPCR DT’s were independent of soil type. At *Trichoderma* inoculum levels above the qPCR MDT’s, there was a strong correlation (r^2 = 0.969) between culture dependent (microbiology) and independent (qPCR) quantification methods. Significant differences (P < 0.001) in soil colonisation and persistence (microbiology, qPCR) were observed between species of *Trichoderma* inoculants over a 56 day incubation period. In acid and alkaline soils, *Trichoderma harzianum* LTR-2 and Tr904 increased 100 fold from 10^3 – 10^5 by T28 and maintained these levels for the remainder of the experiment. *T. koningiiopsis* Tr905 however, increased 30 fold (to 3 x 10^6 c g^-1 soil) in both soils by T28, but only continued to proliferate in the acidic soil, reaching 10^7 c g^-1 by T56. There was no significant change in Tr905 inoculum in alkaline soil between T28 and T56. In controlled environment wheat bioassays (acidic loam soil) by T28 post-emergence (tillering), all 3 inoculants actively colonised rhizosphere and bulk soils to a depth of 20cm. Root colonisation was however, restricted to 0-10 cm. By T56 (late anthesis), Tr904 and LTR-2 root and soil inoculum had persisted, whereas those of Tr905 were below the qPCR MDT. In summary, these *Trichoderma* qPCR assays can be applied to monitor rhizosphere competence of inoculants and their roles in suppression of root diseases.
Dissecting the molecular crosstalk between endophytic fungi and their host plants: *Trichoderma* as fungal model system

Dr Artemio Mendoza Mendoza
Bio-Protection Research Centre
artemio.mendoza@lincoln.ac.nz

Mendoza-Mendoza A(1), Lawry R(1), Nieto-Jacobo M F(2), Brown C(2), Salazar-Badillo F(1), Greenwood D(1), Schnable P(1), Braithwaite M(1), Jimenez-Bremenont JF(1), Alison Stewart(1)

(1)Bio-Protection Research Centre, P.O. Box 84, Lincoln University, Canterbury, New Zealand
(2)Biochemistry Department and Genetics, University of Otago P.O. Box 56, 710 Cumberland St, Dunedin 9054, New Zealand

Symbioses, including fungal endophytes in plants, are one of the most remarkable interactions in nature. Endophytes improve plant growth, disease resistance, nutrient availability and abiotic stress tolerance, while the fungi themselves obtain nutrients. Despite directly benefiting from this symbiosis, plants still react to colonization from endophytes by activating their innate immune system which has evolved to recognize common features of microorganisms, termed microbe-associated molecular patterns (MAMPs). Plants translate this recognition into a defence response that is specifically directed against the invader encountered. *Trichoderma* spp. are soil-borne filamentous fungi which enter the roots of higher plants and form symbiotic relationships (endophytism). The relationship between endophytes and their respective hosts requires constant communication between the organisms involved.

For example, the fungal-derived phytohormone indole acetic acid (IAA) plays an important role in cross-communication between *Trichoderma* and *Arabidopsis thaliana*. However, we have shown that IAA derivatives are a complex mixture of molecules which are isolate dependent. Interestingly, we observe no correlation between IAA/IAA-derivatives production and root promotion in *A. thaliana*. This finding suggests that additional, currently unknown molecular signals may be even more important in the interaction between *Trichoderma* and plants. A comprehensive knowledge of the gene expression changes in both the fungus and the plant is required. Using Hi-Throughput RNA-Seq technology, we analysed the transcriptomes of maize and *Trichoderma* during *T. virens* root colonization. Our results suggest that diverse signalling cascades related to plant immunity are differentially regulated in the plant colonization. Additionally, we found that of 50 fungal transcripts encoding secreted proteins at 3, 5 and 7 days of interaction were upregulated. An additional 103 transcripts encoding for secreted proteins were upregulated at only the 3 day time point. Our current work is focused on the functional characterization of these proteins and their relationship to plant colonization. A comprehensive analysis of our findings will be discussed in this conference.

Identification of a naturally occurring, mild isolate of *Tamarillo mosaic virus*

Mr Arnaud Blouin
The New Zealand Institute for Plant & Food Research Limited
arnaud.blouin@plantandfood.co.nz

Katrin Pechinger(1), Arnaud G Blouin(1), Samantha J Edwards(1), Kar M Choo(1), Daniel Cohen(1), Robin M MacDiarmid(1)(2)

(1)Plant & Food Research Mt Albert, Private Bag 92169, Auckland, 1142, New Zealand
(2)School of Biological Sciences, The University of Auckland, PO Box 92019, Auckland 1142, New Zealand

*Tamarillo mosaic virus* (TamMV, *Potyvirus*), a tamarillo isolate of *Potato virus A* (PVA), is the most damaging virus that infects tamarillo, resulting in low plant vigour, poor yield and discolouration of fruit. Most orchards grown in New Zealand are infected with the virus. In this study a branch of a TamMV-infected tree that bore leaves and fruit that had no or few virus symptoms was identified in a commercial orchard; the branch tested positive for potyvirus infection by ELISA. The rest of the plant was showing typical symptoms of the virus. This plant, named LL, was the core of this research. Three tamarillo genotypes were screened with two virus isolates in order to identify differences in susceptibility to virus infection. The tamarillo genotypes selected were the seedling from the LL plant, cuttings from a tamarillo labelled #23 and selected from a different commercial orchard for its apparent resistance to the virus (#23 being the only non infected plant present in a block over a period of 8 years), and Mulligan Round, a commercial cultivar known to be susceptible to the virus. The two virus isolates selected were LL6 from the symptomless branch of the LL tamarillo and B14, from a plant showing strong symptoms typical of the virus. When infected with the B14 TamMV strain, the three tamarillo genotypes were found to be susceptible, demonstrating that the genotype of the tamarillo plant did not confer resistance to TamMV. The infection rate was comparable between the genotypes and most plants expressed typical TamMV symptoms. When infected with the LL6 virus isolate, most replicates of all the tamarillo genotypes were symptomless, only giving mild symptoms to less than 5% of the infected plants. Information from deep-sequencing of the genome sequences of both the mild and severe isolates will be presented. The mild strain of TamMV is closely related to previously published sequences of TamMV and PVA but has at least some differences in the HC-Pro suppressor of silencing gene. The discovery of this naturally occurring, mild isolate of TamMV was made possible by the close working relationship between orchardists and scientists. Please refer to Samantha Edwards’ poster for an update on the ability of the mild isolate of TamMV to cross-protect against severe isolates.
Optimization, formulation and stabilisation of the biocontrol yeast *Rhodotorula glutinis* for controlling strawberry blight

Wafaa Haggag  
National Research Centre  
wafaa_haggag@yahoo.com  
Wafaa M. Haggag (1), Fareed Abd El-Kreem (2)  

(1) Department of Plant Pathology, National Research Centre, Dokki, Egypt

Biocontrol agents represent an alternative or supplement to chemicals for disease control. *Rhodotorula glutinis* was evaluated for its activity in reducing gray mold and blight diseases of strawberry caused by *Botrytis cinerea* and *Phomopsis obscurans*, respectively, in vitro and in vivo. Spore germination of pathogens in PDB was greatly controlled in the presence of living cell suspensions. In order to standardize the mass and metabolite production, some cultural conditions like different incubation time in hours, pH, carbon sources and concentrations and nitrogen source were determined. Yeast was produced biopolymers (polysaccharide-peptide mixture) when grown in a medium with excess fructose as carbon source and soybean as nitrogen source. The stabilization techniques were evaluated using liquid formulations. Preharvest application of liquid formulation of certain microbial isolates provided an effective control of leaves blight as well as fruit gray mould disease pre and protect fruit during storage than the tested fungicide at the recommended levels.

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**Incidence of Tomato Leaf Curl Virus (ToLCV) in the Philippines and Development of an Infectious DNA Clone for Virus Resistance Screening in Tomato**

Ms Lolita Dolores  
University of the Philippines Los Banos (UPLB)  
lpmdolores@gmail.com  

Lolita Dolores (1), Shamdee Nahar (1), Araceli Alcachupas (1), Hayde Galvez (1), Melquiades Reyes (1), Alma Canama (1)  

(1) Crop Science Cluster, Institute of Plant Breeding, College of Agriculture, University of the Philippines Los Banos, College, Laguna, Philippines

Survey and collection of virus infected tomato was done primarily, to determine the incidence and distribution of the Philippine tomato leaf curl virus (ToLCV-P), a whitefly transmitted begomovirus. Tomato samples with and without virus symptoms were collected and subjected to ELISA and PCR for virus detection. The tomato leaf curl Philippine virus (ToLCV-P) was found to be the most predominating virus with an incidence of 82%. The other viruses that were detected included TMV, CMV and ToMV in decreasing order of virus incidence. Majority of the samples came from plants with multiple virus infections exhibiting varying symptoms of mosaic, mottle, leaf curl, leaf distortion, leaf clustering, yellowing and stunting while some samples came from plants with mild or apparently healthy appearance. Most of the representative symptomatic samples collected from the different regions were found positive for ToLCV generating a 1.1kB DNA fragment with ToLCV specific primers. A total of 50 ToLCV virus isolates were obtained and are being characterized. Meanwhile, the full length DNA-A of ToLCV—Laguna isolate was cloned and inserted into a Ti plasmid vector and made infectious through Agrobacterium-mediated inoculation. A. tumefaciens LBA 4404 was used to agroinoculate healthy seedlings of tomato with bacterial suspension harboring the ToLCV—DNA-A using a syringe needle, made to penetrate the base of the stem and the whole plant with at least ten injections. Symptoms of chlorotic spots and leaf curling were observed 2 weeks after inoculation. The efficacy of this technique in ToLCV resistance screening in tomato and its practical application in breeding for resistance is also discussed.
Germination and bioactivity of 
*Trichoderma atroviride* affected by 
culturing and storage conditions

Mr Amir Daryaei  
Bio-Protection Research Centre  
amir.daryaei@lincolnuni.ac.nz  
Amir Daryaei(1), Richard E Falloon(1), Travis R Glare(1), Eirian Jones(1),  
Hossein Alizadeh(2), Alison Stewart(2)  
(1)Bio-Protection Research Centre, Lincoln University, Lincoln 7647,  
Canterbury, New Zealand  
(2)Marrone Bio Innovations, Davis, California 95618, USA

Identification of the production and storage factors that affect conidial germination and bioactivity (fitness) will assist the success of biological control agents. Effects of culturing conditions on conidial fitness of *Trichoderma atroviride* LU132 were examined in different storage conditions over time. Abiotic factors (temperature, nutrients, water activity, pH) during production were studied. Conidia from the culturing regimes which resulted in greatest and least bioactivity against *Rhizoctonia solani* in dual culture were selected to assess effects of storage condition on conidial fitness. Fitness of the test conidia was examined after storage at 30°C and at 0 or 50% relative humidity (RH) over 6 months. Fitness declined over time, and the decline was greater for 50% RH than 0% RH. The greatest number of conidia and germination percentage resulted from conidia produced at 25°C, but greatest bioactivity resulted from those produced at 30°C. Different C to N ratios (5:1 or 160:1) did not affect these parameters. However, fewer conidia were produced at 30°C, and the least germination and bioactivity resulted from conidia produced at 20°C. Conidia can be divided into two groups: those adapted to extreme culturing conditions (e.g. high temperature), and those protected by nutrients during storage. However, environmental factors are not independent. For example, conidial production at 30°C is probably accompanied by water stress, oxidation, and rapid pH change which may also affect fitness.

Effect of *Aureobasidium* isolates on mycelium growth of three major bunch rot pathogens of grapes

Ms Sujeewa Rathnayake  
Charles Sturt University  
rathnayake@csu.edu.au  
RM Sujeewa P Rathnayake, Sandra Savocchia , Leigh M Schmidtke ,  
Christopher C Steel  
National Wine and Grape Industry Centre, School of Agricultural and  
Wine Sciences, Charles Sturt University, Wagga Wagga, NSW 2678

Currently, fungicide treatments represent the primary method for the control of bunch rot disease of grapes. But chemical control methods have consequences with social and environmental perspectives. Public concerns about fungicidal residues in grapes and development of fungicidal resistant strains of the pathogens have promoted the search for alternative means, less harmful to environment and human health. Recently, considerable success has been achieved by utilizing the microbial antagonists to control post and pre-harvest diseases of fruits. *Aureobasidium pullulans*, an important cosmopolitan yeast-like fungus, colonize on the surfaces of many fruits and vegetable is a potential biocontrol agent for plant pathogens. In this experiment, different *Aureobasidium* isolates were isolated from surfaces of Chardonnay grapes collected from four different berry development stages during 2012 vintage. Altogether 27 *Aureobasidium* isolates were screened against the three major bunch rot pathogens of grapes such as *Botrytis cinerea*, *Colletotrichum acutatum* and *Greeneria uvicola* under in-vitro condition. According to the results, *Aureobasidium* isolates showed high level of suppression on mycelium growth of the fungus *Greeneria uvicola* when compared to the other tested two pathogens *Colletotrichum acutatum* and *B. cinerea*. 
Trichoderma koningiopsis (Tr905) suppression of a barley root disease complex alters the species composition and intra-specific genetic structure of pathogen populations

Rosemary Warren
CSIRO
Rosemary.Warren@csiro.au

Rosemary Warren(1), Jingli Yu(2), Belinda Stummer(3), Li Jinhua(4), Xiuyun Lu(5), Paul Harvey(6)

(1)CSIRO Ecosystem Sciences, Waite Campus, PMB 2 Glen Osmond 5064, South Australia
(2)College of Environment and Resources, Inner Mongolia University, Hohhot 225009, Inner Mongolia, China
(3)Bio-protection Research Centre, Lincoln University PO Box 85084 Lincoln 7647 Canterbury New Zealand
(4)Institute of Plant Protection, Hebei Academy of Agricultural and Forestry Sciences, Baoding, Hebei 071000, China

Patches of poor barley growth, characteristic of Pythium and Rhizoctonia root rot, were observed in disease suppressive inoculant field trials at Urania and Bute in South Australia. At 12 weeks post-emergence, plots inoculated with Trichoderma koningiopsis Tr905 were observed to have improved crop growth, compared to the unoinculated plots. The aims of this study were to determine i) the incidence of a Pythium-Rhizoctonia root disease complex at the 2 trial sites; ii) the root disease suppressive efficacies of Tr. koningiopsis Tr905 and iii) the relationships between Tr905-induced disease suppression and the genetic structure of pathogen populations. Pathogen root isolation frequencies were used to quantify disease incidence and Tr905 disease suppression, the latter also including changes in soil-borne pathogen inoculum. Taxonomic identities of isolates were determined by morphology and species-specific PCR. At Urania, Pythium disease incidence (66 %) was significantly greater than Rhizoctonia (8 %). Incidences of Pythium and Rhizoctonia at Bute were 78 % and 27 % respectively. Tr905 significantly reduced root disease incidence of Rhizoctonia (Bute -50 %) and P. irregulare (Bute -33 %, Urania -24 %). Inoculant-induced suppression of root disease and rhizosphere inoculum was comparable to or better than that achieved with the chemical seed treatment (difenoconazole + metalaxyl-M). AFLP analyses resolved significant genetic differentiation between geographical (Bute vs Urania) populations of Rhizoctonia and P. irregulare. Significant intra-specific genetic differentiation between untreated and Tr905-treated populations of these pathogens was also observed at both trial sites. This was most evident in the Rhizoctonia disease complex at Urania, where the taxonomic compositions of untreated and Tr905-treated pathogen populations were dominated by R. oryzae and R. solani AG-8 genotypes, respectively. Genetic differentiation was also observed at Urania between P. irregulare and Rhizoctonia populations isolated from inside and outside of disease patches. In summary, Tr905 significantly decreased the frequency of Rhizoctonia and Pythium root infection, resulting in disease suppression and significant shifts in the genetic structure of the pathogen populations.
Seasonal and regional variation of Botrytis in New Zealand vineyards

Dr Peter Johnston
Landcare Research
johnstonp@landcareresearch.co.nz

Peter Johnston, Paula Wilkie, Karyn Hoksbergen, Duckchul Park
Landcare Research, Private Bag 92170, Auckland, New Zealand

Genetic diversity of Botrytis in New Zealand vineyards was surveyed over the period 2008 to 2012 from five wine growing regions. Isolates were gathered from symptomless flower buds immediately prior to flowering and, from the same vines, from diseased fruit at harvest. The isolates collected in spring represent the total genetic diversity of Botrytis associated with fruit in the vineyard, whereas the isolates collected in autumn comprise only that part of the Botrytis population that is associated with disease at harvest. Both B. cinerea and B. pseudocinerea were present, with B. cinerea being the most common species. Within B. cinerea, isolates containing both the Flipper and Boty transposons were more common than those with only one transposon, or with neither. Despite the fact that Botrytis produces huge numbers of air-borne spores, strong seasonal variation in the vineyard Botrytis diversity. Even in those vineyards where B. pseudocinerea, Boty-only and Flipper-only isolates were common at flowering, they were rarely detected in association with diseased fruit at harvest. These observations suggest that B. pseudocinerea, and isolates with one or both of the Flipper and Boty transposons missing, are less capable of causing disease than B. cinerea or isolates with both transposons present. Results will be presented from pathogenicity tests carried out to test this explanation.

Biological interactions of mites and microbes associated with gall formation in Scotch Broom Cytisus scoparius

Dr Chantal Probst
Landcare Research
probstc@landcareresearch.co.nz

Chantal Probst(1), Nilish Anand(2), Vansha Malal(3), Daniel Thar(3), Zhi-Qiang Zhang(3), Sarah Dodd(3), Quentin Paynter(3), Hugh Gourtlay(4), Stanley Bellgard(1), Simon Fowler(1),

(1) Landcare Research, Private Bag 92170, Auckland 1142, New Zealand
(2) School of Biological Sciences, The University of Auckland, Private Bag 92019, Auckland 1142, New Zealand
(3) BioDiscovery New Zealand Limited, 24 Balfour Rd, Parnell, Auckland, New Zealand
(4) Landcare Research, PO Box 69040, Lincoln 7640, New Zealand

Originally from western and central Europe, Scotch broom (Cytisus scoparius) was introduced to New Zealand as an ornamental plant, and has become a significant weed in pastures, commercial plantations and native ecosystems. Biocontrol is being attempted using a suite of introduced arthropods including the entophytid broom gall mite (Aceria genistae), which was first released in 2008 and originated from France. Aceria genistae causes abundant galls on broom which can lead to the death of whole branches and plants. In the absence of this biocontrol agent, smaller galls have been observed. Scanning electron microscope images of A. genistae revealed spores of unknown microbial species adhering to its integument. It has been hypothesised that a synergistic relationship between gall mites and another pathogen was responsible for the formation of extensive galls on C. scoparius. This study was designed to investigate the relationship between mites and pathogens in broom by inoculating microbial gall isolates to broom, screening the microbial endophytes from New Zealand and French C. scoparius stems and galls, and determining the effects of miticide and fungicide treatments on mite and microbial populations and broom morphology. No significant differences were observed between broom seedlings inoculated with spores from microbial gall isolates and the controls, suggesting that these microorganisms were not detrimental to the plant. Morphologically distinct isolates recovered from broom tissues were identified by sequencing the ITS gene region and identifying the closest sequence match in a GenBank Blastn search. In total, 105 genetically unique endophytic fungi and 29 bacteria were isolated from broom tissues. Among the endophytic fungi, 17 belonged to the Basidiomycota and 88 to the Ascomycota phyla. Species of Phoma and Alternaria were predominantly isolated from plant tissue with 90.3 and 43.0% isolated from New Zealand plants, respectively and 91.2 and 47.1% isolated from French plants, respectively. Sequence alignments of fungal DNA from New Zealand and France showed 11 common fungal genera with at least 7 genera specific to France and 25 to New Zealand. The results indicate an unexpected diversity of endophytes associated with an invasive plant species in its exotic range. Significantly higher gall numbers were observed on plants without miticide treatments than on those with miticide applications, with no effect in the fungicide treatments. Endophyte diversity and abundance varied with time and treatments, resulting in a complex network among the biocontrol agent, microbial endophytes and predators.
Transcriptome analysis of the beneficial fungus Trichoderma virens during interaction with Zea mays.

Mr Robert Lawry
Lincoln University
Robert.Lawry@lincolnuni.ac.nz

Robert Lawry(1), Maria Fernanda Nieto-Jacobo(1), Chris Brown(2), Alison Stewart(2), Artemio Mendoza-Mendoza(1)

(1)Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, Robert.Lawry@lincolnuni.ac.nz, nietojam@lincoln.ac.nz, artemio.mendoza@lincoln.ac.nz
(2)Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA, artemio.mendoza@lincoln.ac.nz
(3)Biochemistry Department School of Medical Sciences, University of Otago, New Zealand. chris.brown@otago.ac.nz

Trichoderma spp. are ubiquitous soil fungal species that are able to form endophytic (mutualistic) relationships with a number of plant species. Plant colonization by Trichoderma is thought to occur in three main stages: 1) physical penetration of the host plant 2) modulation of the innate plant immune response and 3) modulation of the R protein mediated immune response. Our current hypothesis is that during plant root interaction, Trichoderma modulates plant immunity in a similar manner to biotrophic plant pathogenic fungi, which utilize an array of proteins to counter the hosts immune response. However, very little is known about this beneficial interaction. To understand the plant-Trichoderma interaction a comprehensive understanding of the gene expression changes in both the fungus and the plant is required. We used RNA sequencing to determine the expression profiles at 3, 5 and 7 days of interaction between T. virens and Zea mays. Reads were mapped to publicly available genomes of T. virens Gv29.8 and Mo-17 maize using the junction mappers Bowtie2 and TopHat2. To identify proteins relevant to plant colonization Cufflinks and Cuffdiff were used to show differential expression levels at different time points. Transcripts highly up-regulated in Trichoderma during plant interaction were then identified and confirmed using qRT-PCR. A number of proteins similar to those involved in pathogenicity were identified, adding support to the theory that mutualists survive in plants in a manner similar to that of pathogens. A detailed analysis will be discussed in this presentation.

Identifying targets for sustainable control of Sclerotinia diseases

Ms Alicia Greenhill
La Trobe University
algreenhill@students.latrobe.edu.au

Alicia Greenhill(1), Ian Porter(2), Ulla Benny(2), Jeffrey Rollins(2), Kim Plummer(2)

(1)Botany department, La Trobe University, Melbourne, Australia
(2)Department of Primary Industries, Victoria, Australia
(3)University of Florida, Florida, USA

Sclerotinia diseases cause over A$100M loss to vegetable crops annually in Australia, with significant losses worldwide. Disease control is severely impeded by the pathogen’s ability to produce sclerotia; highly melanised structures crucial to the pathogen’s propagation, reproduction and survival. There are many genes known to be involved in sclerotial formation and maturation, however the exact pathway and contribution of different genes is not yet elucidated. This research used both a targeted and de novo approach to identify genes that may contribute to the formation and maturation of sclerotia in Sclerotinia. Melanin is vital to the robustness of sclerotia and may represent a target for sustainable control. Sclerotinia sclerotiorum produces melanin via the 1,8-Dihydroxynaphthalene (DHN) pathway. In vitro chemical inhibition and gene silencing were both used to reduce the amount of melanin produced by Sclerotinia. A silencing vector targeting a gene (tetrahydroxynapthalene reductase (4HNR), Ss1G_11315.3) on the DHN melanin biosynthetic pathway was stably transformed into S. sclerotiorum. Transformed isolates show variant phenotypes, and characterisation of these silenced isolates has been undertaken. In the second approach a number of Sclerotinia sclerotiorum mutants with sclerotia-minus or -aberrant phenotypes were characterised. These mutants were created via Agrobacterium-mediated transformation. In this process a short DNA sequence (T-DNA) is inserted randomly into the fungal genome. As the sequence of this T-DNA tag is known, the gene or region into which it has been inserted can be determined. T-DNA insertion points have been identified in a number of these mutants and the interrupted genes examined to determine their potential role in sclerotial formation.
A study of *Botrytis Virus X* transmission and vegetative incompatibility in *Botrytis cinerea*

Mr Gregor Kolbe  
The University of Auckland  
gkol700@aucklanduni.ac.nz  
Gregor Kolbe(1), Matt Templeton(2), Mike Pearson(1)  
(1) School of Biological Sciences, University of Auckland, Private bag 92019, Auckland, New Zealand  
(2) The New Zealand Institute for Plant & Food Research Ltd, Private bag 92169, Auckland, New Zealand  

*Botrytis cinerea*, commonly known as grey mould, is a necrotrophic ascomycete fungus which infects more than 200 crops and horticultural species worldwide. A conservative estimate from 2012 places global cost of *B. cinerea* control worldwide at ~1 billion euro per annum. Currently, control of *B. cinerea* relies heavily on the use of fungicides since there are few host crops where resistant cultivars are available. There are several concerns with the use of fungicides including the emergence of fungicide resistant strains and fungicide residue on the edible part of the crop which is often consumed without further processing. These factors are making biological control agents an attractive candidate to add to the *B. cinerea* control tool-box. *Botrytis virus X* (BVX) has some potential as a biocontrol agent for *B. cinerea* as it has been shown to reduce host pathogenicity under certain circumstances. However, the only known mode of horizontal transmission of mycoviruses is via hyphal anastomosis and *B. cinerea* has many genetically determined vegetative incompatibility (VI) groups, making it unlikely that two given isolates are able to successfully complete hyphal anastomosis. VI is a potential barrier to virus transmission, although it is suppressed in some fungi when anastomosis occurs during very early stages of germination. In order to determine whether conidial anastomosis provided a mechanism for the transmission of BVX in *B. cinerea* a conidial anastomosis assay was optimized for imaging with fluorescence microscopy, in order to study anastomosis of incompatible strains expressing different nuclear localized fluorescent proteins. Six strains from four different compatibility groups and differing BVX status were all able to perform conidial anastomosis. An expression vector system optimized for *B. cinerea* with multiple antibiotic resistances and fluorescent protein markers was modified for nuclear localization by engineering a histone-GFP fusion protein using a bacterial in-vivo cloning system. The fluorescent markers enable differentiation between incompatible strains during the imaging of conidial anastomosis and recognition of the outcome of anastomosis between compatible and incompatible strains. The different antibiotic resistances also provide a means to re-isolate individual strains from a mixed sample which can be tested for BVX transmission using an established RT-PCR based method. Results of conidial anastomosis between incompatible strains will be discussed.

Drought tolerance in endophyte-infected ryegrass - a transcriptomics study

Mr Yanfei Zhou  
Institute of Fundamental Sciences, Massey University  
Y.Zhou1@massey.ac.nz  
Yanfei Zhou(1), Jan Schmid(1), Richard D. Johnson(1), David E. Hume(2), Murray Cox(1), Pierre-Yves Dupont(1), Rosie E. Bradshaw(1)  
(1) Bio-Protection Research Centre, Institute of Fundamental Sciences, College of Sciences, Massey University, Private Bag 11-222, Palmerston North 4442, New Zealand  
(2) AgResearch, Grasslands Research Centre, Private Bag 11008, Palmerston North 4442, New Zealand  

Infection of the pasture ryegrass *Lolium perenne* by the endophytic fungus *Neotyphodium lolii* enhances grass performance, but its benefit on grass drought tolerance is influenced by host genotype. However, little is known regarding how the endophyte improves grass drought tolerance and why this effect varies among grass genotypes. Knowing this would help us to make better use of endophytes, such as selecting and applying specific endophyte strains on grasses growing in arid areas; it would also increase our knowledge of this very important plant-microbe symbiosis. We selected a drought sensitive (DS) and a tolerant (DT) *N. lolii* infected ryegrass genotype from the same cultivar (Nine O One) in a glasshouse experiment. Endophyte-free grasses were generated from these and drought tolerance experiments involving genetically identical pairs of endophyte-infected (E+) and -free (E-) grasses were conducted in a controlled environment growth chamber, and both physiological and transcriptome analyses were done. Physiological parameters (including relative water content, osmotic potential, Fv/Fm and biomass) were determined and grass tissue (leaf, sheath, and root) was collected under two soil moisture conditions: 75% FC (field capacity) and 15% FC (maintained for one week to simulate drought conditions). The physiological results showed that endophyte enhanced drought tolerance in DT but not in DS plants. RNA was extracted from grass sheath and duplicate cDNA libraries for each grass in each condition were sequenced using Illumina next generation sequencing. More than 36 million 100 bp reads were obtained for each sample. Analysis of endophyte genes showed that 2,205 and 2,054 genes were differently expressed (> 2 fold) between endophyte in DT and DS grass respectively, under drought conditions. Analysis of grass genes showed an increase in numbers of endophyte induced differently expressed genes in both DSE+ and DTE+ grasses under drought conditions (3,359 and 1,626 respectively) compared to well watered conditions (2,862 and 799 respectively). Initial functional analysis indicates that endophyte genes, involved in photosynthesis, lipid biosynthesis and sucrose-starch metabolism were differently expressed. Further detailed analysis is in progress.
Biological control of black rot of Brassica by a potential biocontrol agent- *Paenibacillus* sp.

Ms Hoda Ghazali-Biglar  
Bio-Protection Research Centre  
hoda.ghazalibiglar@lincolnuni.ac.nz

Hoda Ghazali-Biglar (1), John Hampton (1), Eline van Zijll de Jong (1), Andrew Holyoake (1), Alison Stewart (2)

(1) Bio-Protection Research Centre, Lincoln University, Lincoln 7647, New Zealand
(2) Marrone Bio Innovations Incorporation, California 95618, USA

Black rot is a widespread disease of brassicas caused by the seed-borne pathogen *Xanthomonas campestris pv. campestris* (Xcc). The aim of this research was to investigate the use of *Paenibacillus* for biological control of black rot on cabbage following application as a seed treatment, and to determine its effect on cabbage growth. Based on a dual culture assay, 24 isolates of *Paenibacillus* were categorized for their interactions with Xcc. Nine of these isolates with different bioactivity in suppression of Xcc *in vitro* were then screened for their capacity to reduce black rot symptoms on cabbage in pot trial assays. From these results one *Paenibacillus* isolate (P16), at concentration of 5×10^7 CFU/ml was selected as a potential biocontrol agent (BCA). To investigate if the disease control was provided via plant growth promotion, the BCA was co-applied with Xcc as a seed treatment. In the presence of Xcc, BCA-treated seedlings had significantly (P<0.05) greater growth than the control. However, there was no significant difference in plant growth parameters between these treatments in the absence of the pathogen. To determine whether this BCA is rhizosphere competent and/or endophytic, cabbage seedlings grown from BCA-treated (1.5×10^7 CFU/seed) seeds were tested for the presence of BCA by real-time PCR using a specific primer pair based on the gyrB gene. Standard curves were generated for soil and plant samples, and the detection limit (1×10^2 CFU/g) determined. In rhizosphere soil, BCA density had decreased from 9.9×10^9 to 1.1×10^5 CFU/g by 11 days after sowing (DAS), and thereafter it was below the limit of detection. BCA population in the bulk soil was only detected up to 6 DAS, and was not recorded in plant samples, indicating either that the BCA is not endophytic or its density in the plant was below the detection limit. Overall, this BCA is rhizosphere competent only during early cabbage seedling growth, and is most probably not endophytic. However, it appears that the BCA, by reducing Xcc infection, better enables the seedlings to survive and grow.

Evolution of *Rhynchosporium commune* on barley grass

Dr Celeste Linde  
The Australian National University  
celeste.linde@anu.edu.au

Celeste Linde  
Research School of Biology, Evolution, Ecology and Genetics, Bldg 44, Daley Rd, The Australian National University, Canberra, ACT 0200, Australia

Scald caused by *Rhynchosporium commune* is commonly found on barley as well as barley grass (*Hordeum leporinum*) in Australia, where barley grass is a common weed. Wild hosts of cereal diseases could play a significant role in the epidemiology and evolution of diseases. Disease evolution is significantly affected by population size and heterogeneity of the host. Although susceptible barley would harbour large population sizes of scald favouring increased pathogen evolution on barley, barley grass is genetically more diverse than cultivated barley and most likely harbour more resistance genes than barley. This heterogeneity could select for a pathogen population that is also genetically diverse with virulences that could render newly introduced resistance genes in barley ineffective. To investigate the effect of barley grass on the evolution of scald, pathogenicity of scald isolates from barley and barley grass was assessed on both hosts. Seed of barley grass in conspecific and heterospecific interactions was collected and increased to represent single mother lines. Twenty isolates each from barley and barley grass were inoculated onto 20 barley grass lines and 20 barley differentials. No significant difference in leaf area affected on barley was observed for isolates from barley and barley grass, thus isolates from barley grass are equally likely to affect barley than barley grass. In contrast, isolates from barley resulted in a significantly smaller percentage of leaf area infected on barley grass lines. This suggests that scald populations from barley rarely infects barley grass, however scald populations from barley grass has a high potential for gene flow to barley populations. Local adaptation of isolates from barley grass was noted as conspecific infections resulted in significantly higher levels of virulence than heterospecific infections. Barley grass therefor successfully acts as an ancillary host to scald harbouring highly virulent scald populations.
Three diseases of potato plants caused by Spongospora subterranea: powdery scab on tubers, galls on roots, zoosporangia in root cells (root malfunction)

Prof Richard Falloon
New Zealand Institute for Plant & Food Research Limited
richard.falloon@plantandfood.co.nz

Richard Falloon(1)(2), Ueli Merz(2), Ros Lister(1), Denis Curtin(1), Ruth Butler(2)
(1) New Zealand Institute for Plant & Food Research Limited, PB 4704, Christchurch 8140, New Zealand
(2) Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand
(3) Plant Pathology, ETH Zürich, Universitätsstr. 2, CH-8092 Zürich, Switzerland

The plasmodiophorid pathogen Spongospora subterranea f. sp. subterranea causes powdery scab of potato tubers, a long-recognised and economically important disease (“a disturbance that interferes with normal growth and development”). Powdery scab results from S. subterranea infection of host stolons (which develop into tubers). Each powdery scab lesion contains many sporosori, which are conglomerates of resting spores, and resting spores are the perennation life cycle stage of the pathogen. This tuber disease severely reduces the quality of potatoes for processing and fresh market sale, and causes down-grading or rejection of seed potatoes because infested seedlines are responsible for pathogen transmission to future crops. Spongospora subterranea also causes a second disease, galls (hyperplasia) on host roots. These are at first creamy-white, and later mature to dark brown as they become filled with sporosori. Galls on roots of potato and solanaceous weed hosts are responsible for inoculum build-up and long-term survival of the pathogen in soil. Field surveys have shown that Spongospora root galls occur commonly in potato crops, particularly where cool, moist (irrigated) soil conditions predominate. Zoospores of S. subterranea infect host roots to cause a third disease. Zoosporangia develop in root epidermis cells from zoospore infections, and release secondary zoospores to initiate subsequent cycles of root infection. Evidence is accumulating that zoosporangia in roots harm plant growth and productivity (shoot dry matter, tuber number and weight). Controlled experiments have demonstrated that inoculation with S. subterranea caused disrupted root function (water and nutrient uptake). Some potato cultivars that are highly resistant to powdery scab have been shown, nevertheless, to be very susceptible to zoosporangium infection and root hyperplasia. Spongospora subterranea is therefore responsible for three diseases of host plants; root malfunction (from zoosporangium infections), root hyperplasia and powdery scab on tubers. All three diseases have practical and economic importance for potato crop productivity (yield and quality).

Protecting commercial Australian potato genotypes from Verticillium wilt through identification of sources of resistance

Ms Veradina Dharjono
The University of Melbourne
v.dharjono@student.unimelb.edu.au

Veradina Dharjono (1), Paul Taylor (1), Tonya Wiechel (2), Nigel Crump (3)
(1) Department of Agriculture and Food System, Melbourne School of Land and Environment, The University of Melbourne, Victoria 3010, Australia
(2) Department of Environment and Primary Industries, Agribio Centre, Bundoora, Victoria 3083, Australia
(3) VIC SPA, 1015 Myers Creek Road, Toolangi, Victoria 3777, Australia

Verticillium dahliae is a major and persistent soil pathogen known to cause Verticillium wilt in potato (Solanum tuberosum L.). Host resistance remains as one of the most economical, environmental and efficient management practices for this disease. Prior to screening for resistance, a glasshouse bioassay was developed to optimise the inoculum density that would differentiate resistant genotypes in a glasshouse screening trial. Inoculum density was important in symptom expression as high inoculum level (10^6 spores/ml) was shown to kill potato plants. Tissue culture seedlings of Russet Burbank, a susceptible potato genotype, were established in sand in a glasshouse. After four weeks, the roots were dipped in water as a control and in six different inoculum concentrations 10^6, 10^5, 10^4, 5x10^3, 10^3, and 10^2 spores/ml for five minutes, followed by transferring plants to pasteurised potting mix. Severity of foliar symptoms in growing plants was assessed and determined using a 0-5 visual qualitative scale. Results showed that an inoculum threshold level of around 10^5 spores/ml was required before the onset of wilt symptoms, although V. dahliae could be isolated from petiole and crown root tissue plants inoculated at 10^2 spores/ml. Seedlings of 13 commercial potato genotypes were subsequently inoculated with an inoculum level of 5x10^3 spores/ml using root dipped technique. Host reaction was determined at 10 weeks after inoculation based on visual symptoms and petiole or crown root tissue infection. Many genotypes exhibited typical symptoms of V. dahliae with infection of either petiole or crown root tissues, rendering them to be susceptible. Genotype Catani produced mild symptoms and was considered as moderately resistant. Two genotypes, Denali and Kennebec only produced slight symptoms and hence were considered as resistant. These potential resistant genotypes are undergoing further glasshouse trials and may be used as part of an integrated disease management practice to control Verticillium wilt.
Insects as vectors of *Quambalaria pitereka*, the significant shoot, flower and bud blight pathogen of *Corymbia calophylla* in south-west Western Australia

Briony Williams
Murdoch University
brionymwilliams@hotmail.com
Briony Williams(1), Trudy Paap(1), Cielito Marbus(1), Giles Hardy(1), Treena Burgess(1)
(1) State Centre of Excellence for Climate Change, Woodland and Forest Health, School of Veterinary and Life Sciences, Murdoch University, Murdoch, 6150, Western Australia

Marri (*Corymbia calophylla*) is a keystone species in forests of the south-west of Western Australia, providing fauna such as the critically endangered Carnaby’s Cockatoo (*Calyptorhynchus latirostris*) with food and shelter, and pollen and nectar for honey bees. The primary pathogen *Quambalaria pitereka* was introduced to Western Australia from the eastern states in the early 1990s and has since spread across most of the *C. calophylla* range. This pathogen causes leaf, flower and shoot blight in Marri, and as its incidence and severity increases, it is likely to deeply impact the ecosystem services that Marri provides. Little is known about how the pathogen is disseminated. The present study has shown that a range of insect species are associated with infected foliage, flowers and fruit and are likely to act as vectors of the pathogen. *Quambalaria cyanescens*, a non-pathogenic species which grows in close association with *Q. pitereka*, was isolated onto selective agar from bees, ants, weevils and flies collected from Marri showing symptoms of the blight. Insects have not previously been shown to be vectors of *Quambalaria* species. Since *Q. cyanescens* outgrows *Q. pitereka* on isolation media, molecular analysis was conducted to confirm the presence of *Q. pitereka* on these insects. To do this, specific primers were developed for *Q. pitereka*, *Q. cyanescens* and other *Quambalaria* species. Insects shown to carry *Q. pitereka* and *Q. cyanescens* spores are now being used in pathogenicity experiments to determine their ability as vectors in the disease syndrome. This study may open up avenues for the management and control of the disease. Further studies will look at potential biocontrol agents that could potentially be disseminated by the insect vectors, such as the honeybee.

Friends don’t eat friends: loss of endophyte mutualism triggers activation of host degradation

Dr Carla Eaton
Massey University
c.j.eaton@massey.ac.nz
Carla Eaton(1), Pierre-Yves Dupont(1), Murray Cox(1), Aiko Tanaka(2), Barry Scott(1)
(1) Institute of Fundamental Sciences and The Bio-Protection Research Centre, Massey University, Palmerston North, New Zealand
(2) Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya 464-8601, Japan

Associations between the fungal endophyte *Epichloe festucae* and perennial ryegrass require signalling between the fungus and its host in order to regulate fungal growth *in planta* and maintain these beneficial associations. In recent years, a number of fungal pathways essential for this signalling have been identified, including the NADPH oxidase/reactive oxygen species signalling pathway, stress-activated MAP kinase pathway, and cell integrity pathway. Disruption of these pathways leads to a dramatic switch from mutualistic to pathogenic-like association with perennial ryegrass. Infected plants display severe stunting and prematurely senesce only weeks after inoculation, in comparison to the generally asymptomatically wild-type associations. To identify the molecular mechanisms underlying this symbiotic switch we pioneered the novel approach of using high through-put mRNA sequencing to identify plant and fungal gene expression differences between the mutualistic wild-type symbiotum and pathogenic-like ΔsakA stress-activated MAP kinase mutant symbiotum. This resulted in identification of a putative symbiotic gene set of 1202 genes. In this study, we take this approach further in order to narrow this symbiotic gene set. To this end, we performed mRNA sequencing of two additional symbiotic mutants, the main catalytic component of the NADPH oxidase, noxA, and C6 zinc finger transcription factor, *proA*. Comparison of the genes differentially expressed among these three symbiotic mutants identified a core symbiotic gene set of 181 genes. The majority of these genes (79%) were up-regulated in the symbiotic mutants relative to wild-type, suggesting they may play a role in promoting the switch towards pathogenesis. In support of this, a number of putative transporters and plant cell wall-degrading enzymes were identified. Interestingly, around 10% of the core gene set had no homologues in the NCBI non-redundant protein database, implying that these may be unique to the *Clavicipitaceae*. Interrogation of 11 additional *Clavicipitaceae* genome sequences revealed that 13 of these genes are unique to the *Epichloe* endophytes. Of these, seven were predicted to encode secreted proteins smaller than 200 amino acids. These are two hallmarks of fungal effector proteins, raising the possibility that *Epichloe* endophytes produce effectors to evade host defenses and establish systemic colonization.

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(1) Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya 464-8601, Japan

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(2) Institute of Fundamental Sciences and The Bio-Protection Research Centre, Massey University, Palmerston North, New Zealand

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(1) State Centre of Excellence for Climate Change, Woodland and Forest Health, School of Veterinary and Life Sciences, Murdoch University, Murdoch, 6150, Western Australia
Identification of trapped insects and associated microbes by next generation sequencing

Simon Bulman
Plant & Food Research
simon.bulman@plantandfood.co.nz

Simon Bulman, Sam Beard, Ian Scott, Grant Smith
The New Zealand Institute for Plant & Food Research Limited, Gerald Street, Lincoln 7068, New Zealand

Increased global movement of people and produce is accompanied by heightened threats from insect pests. The arrival of new pests and associated pathogens can have severe consequences for agriculture, as demonstrated by the incursion of the tomato potato psyllid into New Zealand. Simple, reliable detection systems could provide early discovery or delineation of outbreaks, allowing eradication or enhanced management. However, there are few systems for routine untargeted surveillance of insect incursions anywhere in the world; monitoring and identifying insects is expensive. We have set out to use next generation sequencing to rapidly and simply identify mixed insects and the microbes that they carry. Known combinations of sap-sucking insects (psyllids, aphids, whiteflies, thrips) were assembled and DNA extracted. Amplicons were generated from these mixtures with a range of conserved PCR primers for the cytochrome oxidase I gene. The amplicons were subject to barcoded 454 FLX pyrosequencing. Although all primer pairs were shown to be effective against individual DNAs, comparable detection of insects within mixtures was not obtained and high levels of bias were instead evident. Aphids were detected by all primer combinations with the mtd6/HCO2198 primers almost exclusively favouring detection of aphids. C1-U1709/HCO2198 favoured the psyllid Bactericera cockerelli largely to the exclusion of aphids and the thrips Frankliniella occidentalis. This result suggested that insect biomass was not the key determinant of detection. In general, we saw surprisingly little improvement after introducing degeneracy into the conserved primers to make them match a broader selection of the insects. Modification of mtd6 led to better detection of thrips and psyllids, but it remained poor for whitefly. Inclusion of the HCO2198 primer appeared important to broaden detection of insect genera. In addition to the simple insect mixtures, larger combinations of 20 insects captured in yellow bowl traps (in propylene glycol) in the field were also examined. DNA sequences from these mixtures were again dominated by sequences from only a few of the insects. Overall, it appears that detecting a wide range of insects with such PCR-based techniques will require the use of more than one primer combination. Ribosomal 16S bacterial amplicons have recently been generated from the DNA mixtures. Pyrosequence data from these amplicons is being processed with the aim of detecting and identifying bacteria carried by the insects.

Increasing the Genetic Diversity of Sugarcane Germplasm through Continuous Introduction of Disease-Free Foreign Varieties

Dr Fe Dela Cueva
University of the Philippines Los Banos
fmdcueva@yahoo.com

Fe M. Dela Cueva(1), David B. Cristobal(2), Chona R. Untal(2), Rosalyn T. Luzaran(2), Merle B. Palacpac(2)

(1)Institute of Plant Breeding, CSC, CA, UPLB, Laguna
(2)Philippine Sugar Research Institute Foundation, Inc.,Victorias City, Negros Occidental
(3)Plant Quarantine Service, Bureau of Plant Industry, San Andres, Manila

Introduction of foreign sugarcane varieties is an indispensable step in the continuous development for new sugarcane breeds. These introduced varieties provide a wide array of ingredients for breeders to craft superior canes. Sugarcane varietal exchange among Southeast Asian countries was strengthened in 2001 when Common Fund for Commodities (CFC) funded a project with Philsirin and UPLB. The genetic base of the Philippine sugarcane germplasm collection was widened through the project. Realizing the importance of varietal exchange, efforts was made to expand this endeavour to other sugarcane producing countries even after the project ended in 2006. To prevent incursion of new strains of pathogens or pathogens that are unrecorded in the country, strict post-entry quarantine actions through routine disease detection and monitoring was implemented through collaborative efforts of PHILSURIN, IPB, and BPI. To date, more than 300 elite varieties had been introduced to the Philippines. These varieties came from Thailand, Indonesia, Malaysia, Bangladesh, Japan, China, Australia, France, USA, Vietnam, Pakistan and Mauritius. All the materials had undergone the routine disease indexing scheme at the post-entry quarantine glasshouse for two years, and another year under the open field quarantine. Both antibody- and nucleic acid-based disease detection techniques are being employed to ensure the release of disease-free varieties either commercially or for breeding purposes. At present, three varieties are being used by sugarcane planters, three varieties are being tested in 11 locations across the country. Some varieties are being used in local hybridization. Key words: sugarcane, varieties, diseases, quarantine, disease detection
Defining core pan-genomes of species in ‘Candidatus’ Liberibacter for the development of new diagnostic tools

Dr Grant Smith
The New Zealand Institute for Plant & Food Research Limited
grant.smith@plantandfood.co.nz

Sarah Thompson (1)(2), Chris Johnson (2), Ashley Lu(2), Rachel Mann(2)
(1), Rebekah Frampton(1), Mark Fiers(3), Andrew Pitman(3), Ian Scott(3),
Neil Gudmestad(3), Brendan Rodoni(4), Grant Smith(1)
(1)The New Zealand Institute for Plant & Food Research Limited, Gerald Street, Lincoln 7068, New Zealand
(2)Plant Biosecurity Cooperative Research Centre, Canberra, ACT 2617, Australia
(3)Department of Plant Pathology, North Dakota State University, Fargo 58108, USA
(4)Biosciences Research Division, Department of Primary Industries, AgriBio, La Trobe University, Bundoora, Victoria, 3083, Australia.

The ‘Candidatus’ Liberibacter genus contains five unculturable α-proteobacteria species (asiaticus, americanus, africansus, solanacearum and europeaus). A sixth species Liberibacter crescens is cultivable, and is thus not categorised as ‘Candidatus’. The first three species are implicated as the causal agents of Huanglongbing (HLB) of citrus, which is generally regarded as the most serious and destructive disease of citrus in the world. Ca. L. solanacearum is considered to be the causal agent of Zebra Chip disease of potato (and causes pathology on a range of other solanaceous plants). The remaining two species are considered to be endophytes of pear/ scotch broom and papaya respectively. All five Ca. Liberibacter species are associated with, and vectored by, a range of species of phloem-feeding psyllids (Hemiptera:Psyllidae or Hemiptera:Trioziidae). L. crescens has no known insect vector. Four haplotypes of Ca. Liberibacter solanacearum (CLsoI) have been described based on SNPs in the rRNA, intergenic spacer or ribosomal protein regions. The genome of CLsoI haplotype B has been published revealing a genome of approximately 1.25 Mbp. Draft genome assemblies of haplotype A from one USA source and two independent New Zealand sources have revealed significant changes between the haplotype A and B genomes. The three CLsoI haplotype A draft genomes have significant colinearities with the exception of the prophage domains. In these regions, the two NZ domains are similar to each other, and different from the USA prophage region sequence. The three haplotype A genomes also have a greater number of SNPs relative to the haplotype B genome. The origin of CLsoI in New Zealand is believed to be via incursions of the tomato potato psyllid (Bactericera cockerelli) from the USA. The genetic similarity of the current assemblies of the two NZ CLsoI genomes (from diverse solanaceous sources) may suggest a limited incursion of the genetic diversity of this bacterium into NZ. As more Liberibacter genome data are gathered this preliminary hypothesis can be robustly challenged. Further CLsoI genomes are being sequenced to contribute to a pan-genome for this species. To define a wider Ca. Liberibacter pan-genome, and provide a context for a CLsoI pan-genome, sources of Ca. L. asiaticus and other species from a wide range of plant/insect hosts and geographic regions are currently being sequenced. Together this data will facilitate the development of robust molecular-based diagnostic tools for the detection of Liberibacter species and its haplotypes.

Fusarium vascular infection of oil palm: Epidemiology, genetic diversity and molecular diagnostic tools

Dr Mohd Hefni Rusli
Malaysian Palm Oil Board
mohd.hefni@mpob.gov.my

Mohd Hefni Rusli, Richard Cooper, Alan Wheals, Idris Abu Seman
(1)Malaysian Palm Oil Board (MPOB). No. 6, Persiaran Institusi, Bandar Baru Bangi, 43000 Kajang Selangor, Malaysia
(2)Department of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK

Vascular wilt disease caused by Fusarium oxysporum f. sp. elaeidis (Foe) causes a devastating disease of oil palm in West and Central Africa. However, this disease has not been reported in South East Asia, in spite of long term importation for breeding purposes of African seed and pollen, known to be often contaminated with Foe. Malaysia is the second largest palm oil producer in the world and Foe remains a major threat to this industry, especially as this study shows four current palm genotypes grown there are susceptible. This research was conducted in order to help Malaysia avoid and/or be prepared for this potential problem. Disease epidemiology was studied in plantations in Ghana. Statistical analysis showed the disease mainly occurred in clusters, implying root-root transmission rather than aerial spread by spores. Many Foe isolates were obtained for genetic analysis from diseased palms, including 10 per cent from 21 symptomless trees. This shows that visual disease surveys are flawed. The only practical, sustainable approach to controlling Fusarium is by breeding disease resistant palm lines. The success of this strategy depends on the variability of Foe isolates. Resistance should be stable because this analysis showed Foe isolates have a monophyletic origin. Molecular diagnostic tools were developed for (1) rapid detection and quantification of Foe in seed and pollen for quarantine purposes in order to prevent transcontinental spread of Foe, (2) to test efficacy of putative disease resistant or tolerant palm genotypes, and (3) to facilitate epidemiological studies involving palm tissues and soils. Primers were designed for detecting the species F. oxysporum, based on the translation elongation factor gene (TEF-1α), superior to the existing ones used currently at quarantine. The first Foe-specific primers to be developed were based on a virulence effector gene that excluded 70 other phylogenetically closely related Fusarium species from various hosts and origins.
Development of real-time PCR assays for the detection of the myrtle rust fungus *Puccinia psidii*

Dr Jeyaseelan Baskarathevan  
Ministry for Primary Industries  
jeyaseelan.baskarathevan@mpi.govt.nz  

Jeyaseelan Baskarathevan, Robert Taylor, Wellcome Ho, Brett Alexander  
Plant Health and Environment Laboratory, Ministry for Primary Industries,  
PO Box 2095, Auckland1140, New Zealand

Myrtle rust (*Puccinia psidii*) is expected to arrive into New Zealand in the near future. Early detection of *P. psidii* would be important to determine biosecurity options to prevent further spread as this pathogen can be spread quickly by airborne spores. Thus it is important to have a fast and accurate method to detect the *P. psidii* at the early stages of infection. Currently, only a conventional species-specific nested PCR assay is available for the detection of *P. psidii*. In this study, multiple sets of primers and TaqMan probes were designed using conserved sequences of the internal transcribed spacer (ITS) region and the beta-tubulin (*βt*) gene of *P. psidii*. A total of seven TaqMan real-time PCR assays, including three targeting the ITS region and four targeting the *βt* gene, were developed for the detection of *P. psidii*. These TaqMan assays were able to detect the genomic DNA of all 13 *P. psidii* isolates obtained from Brazil, Hawaii, and Australia. High specificity of these assays were confirmed by testing these assays against seven other closely related *Puccinia* species and DNA extracted from 13 healthy myrtaceous plant species commonly found in New Zealand. The sensitivity of all three ITS real-time PCR assays were at least 100 times more sensitive than the *βt* real-time PCR assays. Among the three ITS real-time PCR assays, the assay with the highest sensitivity was able to detect *P. psidii* DNA down to 100 fg, which is approximately the amount of DNA from a single spore. This ITS real-time PCR assay was selected for further validation and was shown to be able to detect *P. psidii* from symptomatic as well as non-symptomatic leaf samples collected from an infected host in Australia. The newly developed ITS real-time assay takes around one and a half hours to run and has proven to be four times faster than the conventional nested PCR assay.

Eradication of Chestnut blight in Victoria Australia

Martin Mebalds  
Department of Environment and Primary Industries Victoria  
Martin.Mebalds@depi.vic.gov.au  

Martin Mebalds, Patrick Sharkey, William Washington, Brendan Ralph  
1 Department of Environment and Primary Industries Victoria, Biosecurity Victoria, Knoxfield Centre, Private Bag 15, Ferntree Gully DC, VIC 3156, Australia  
2 Department of Environment and Primary Industries Victoria, Great Alpine Road, Ovens, VIC 3737

Chestnut blight (*Cryphonectria parasitica*) was first detected in Eurobin, north east Victoria in September 2010. A survey of 322 commercial groves and 158,000 chestnut and oak trees defined the extent of the incursion to 9 groves in the Ovens Valley. All host trees within 100m of an infected tree were removed and burnt. A four year surveillance program was initiated to detect any properties with newly emerging infections and to collect evidence for a declaration of eradication. A further two infected groves were subsequently detected in 2011 and 2012. All trees on the grove detected in 2011 were removed and destroyed. The last detection of chestnut blight in 2012 manifested as one small lesion on one tree on one property. The tree was immediately removed and destroyed. Fortnightly monitoring of the infected grove for the next three months did not detect any further infections, however, all trees within 10 m of the infected tree were destroyed. Samples of 1,672 nuts from 25 trees at 10, 25, 50 and 100 m from the infected tree tested negative for the presence of *C. parasitica*. A total of 5,329 chestnut and 38 oak trees were destroyed in the eradication phase of the response to June 2013. Owners of commercial chestnut groves received owner reimbursement costs under the Emergency Plant Pest Response Deed, a cost sharing arrangement between federal and state governments and industry. With the exception of the last infected grove, all other groves have been surveyed at least 15 times, without a reappearance of the disease. It is expected that given no further detections, Victoria will be able to declare eradication of chestnut blight in the Ovens Valley by spring 2013 and eradication on the last grove by mid 2014, two years after the last detection.
Diversity and classification of *Phellinus noxius* in Queensland and New South Wales

Ms Louise Shuey  
Queensland Department of Agriculture, Fisheries and Forestry  
L.Shuey@uq.edu.au

Louise Shuey (1), Alistair McTaggart (2), Geoff Pegg (1), Elizabeth Dann (2)  
(1)Queensland Department of Agriculture, Fisheries and Forestry, The EcoSciences Precinct, GPO Box 267, Brisbane Qld 4001, Australia  
(2)Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, The EcoSciences Precinct, GPO Box 267, Brisbane Qld 4001, Australia

*Phellinus noxius* (Hymenochaetaceae, Agaricomycetes) is a wood rotting fungus distributed in tropical regions including Southeast Asia, Central America, Africa and Australia. In natural settings it is saprobic, but in disturbed areas or monoculture it is often pathogenic, and causes tree deaths. It causes brown root rot of a wide range of hosts from angiosperms to gymnosperms. *Phellinus noxius* impacts productivity of avocado (*Persea americana*) and hoop pine (*Araucaria cunninghamii*) in Queensland and northern New South Wales. We studied the diversity of 90 isolates from several hosts and geographical locations around Queensland and northern New South Wales in order to determine 1) whether one pathogen was responsible for disease on such a wide host range, and 2) potential that basidiospores are involved in spread of the disease. Initial fingerprinting studies showed the population was variable and possibly more than one species existed. A phylogenetic analysis of the ITS and IGS regions recovered no clear genealogical groups that shared a common host or location. This may indicate *P. noxius* is a species complex. We conducted a separate study to determine the systematic position of *P. noxius*. Comparison of the LSU and ITS regions to other taxa of the Hymenochaetaceae showed *P. noxius* was sister to *Phellinus s. str.*, and may not be a true *Phellinus*.

Checklists, Quarantine and Trade - continuing challenges for developing countries

Prof Lester Burgess  
University of Sydney  
burgess.international@gmail.com

Lester Burgess(1)  
(1)Faculty of Agriculture and Environment, The University of Sydney, Sydney, 2006

Developing countries continue to face major challenges in respect of trade issues relating to quarantine matters. This is particularly so for countries in the early stages of development. In my Presidential Address on ‘Biosecurity, Trade and Plant Pathology’ in 2003 I argued the case for greater involvement by experienced plant pathologists in developing countries. The recognition of this need by governments and international aid agencies has led to increased support for training activities and facilities. It is commendable that many plant pathologists in APPS are involved. However the development of accurate checklists of plant pathogens for a developing country or local area remains a daunting task as is the maintenance of culture collections and herbaria of disease specimens. In this abstract I briefly discuss two of the major challenges, and propose how we might help improve capacity building activities. I will focus on fungal and fungal-like pathogens for this purpose. A key challenge especially for countries in an early stage of development is that staff designated as plant pathologists may have little or no formal training in plant pathology, and often limited University training. Limited English may also be a handicap. Attendance by such staff at short regional workshops in English is usually of little benefit. My experience is that initial training in laboratory procedures, diagnostics, pathogenicity testing and survey methods is usually best done through hands-on programs in-country over a minimum of four to five weeks accompanied by basic English tutoring as discussed elsewhere. Furthermore a volunteer plant pathologist who can consolidate the initial training and lay the groundwork for further training activities in laboratory and field is a great asset. Another major challenge is accurate identification to species level and support from an internationally recognised herbarium for deposition of cultures and/or diseased specimens. We need to expand such support from taxonomists and culture collections. We also need to help trainees develop and maintain accurate records through an electronic and hard copy database. The recent welcome changes to import conditions in Australia for nucleic acids (excluding viroid RNA) for example will facilitate identification of fungal and fungal-like pathogens on behalf of developing countries, especially as basic facilities are developed in-country to enable extractions locally. I believe that APPS can do more to help promote such programs and liaise with funding agencies. APDN already provides an excellent avenue for disease notes.
A new era for government and industry partnerships on biosecurity in New Zealand

Lois Ransom
GIA Secretariat
lois.ransom@mpi.govt.nz
Lois Ransom
25 The Terrace, Wellington, New Zealand

Biosecurity is a shared responsibility and benefits all New Zealanders. With 72% of exports derived from primary production, the effective management of biosecurity risks is essential to New Zealand’s economy. New Zealand’s natural environment and its unique native flora and fauna draw tourists from all over the world and are also vulnerable to biosecurity risks. A recently completed Government Industry Agreement (GIA) for Biosecurity Readiness and Response has laid the foundation for better biosecurity outcomes for New Zealand through partnership arrangements built on joint decision-making and cost sharing. A GIA Deed outlines the principles for the partnership between the New Zealand Ministry for Primary Industries (MPI) and primary industries that sign the Deed, and is enabled by the Biosecurity Act 1993. The Deed also sets out the commitments that each Signatory makes to engage in the wider biosecurity system and co-invest to improve collective capacity and capability of industry and government to prepare for and respond to exotic pests and diseases. It provides for the development of Operational Agreements, which are a binding contract between MPI and industry parties to each Agreement, to co-invest in and deliver actions that achieve specific biosecurity readiness and response outcomes. These outcomes may relate to specific unwanted organisms or groups of organisms, or target improvements to overall biosecurity readiness and/or response. The Deed describes minimum commitments for MPI, industry and the partnership. These capture expectations that the Signatories will maintain or improve diagnostic capacity and capability, technical and operational expertise for risk analysis and pest management, enhanced detection, analysis and management of emerging biosecurity risks, stakeholder awareness and communication, as well as capability and investment in surveillance to detect and report new organisms. Biannual biosecurity fora will be held to discuss the biosecurity system. An independent GIA Secretariat was established in 2012 and will assist a Deed Governance Group, made up of Deed Signatories, to implement the Deed. The Deed is available to all primary industries including plant, animal and aquatic sectors.

Stripe smuts of grasses: one lineage or high levels of polyphyly

Mr Kyrilo Savchenko
University of Haifa
savchenko.kyryll@gmail.com
Kyrilo G Savchenko(1), Lori M Carris(1), Lisa A Castlebury(2), Solomon P Wasser(3), Vasyl P Heluta(3), Eviatar Nevo(3)
(1) Department of Evolutionary & Environmental Biology, University of Haifa, Mt Carmel, Haifa 31905, Israel
(2) M.G. Khododny Institute of Botany of the NAS of Ukraine, 2 Tereshchenkivska St., Kyiv 01601, Ukraine
(3) Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA
(4) USDA-ARS, Systematic Mycology & Microbiology Laboratory, 10300 Baltimore Avenue, Beltsville, MD 20705, USA

Stripe smut of grasses Ustilago striiformis s.l. is caused by a complex of smut fungi widely distributed over temperate and subtropical regions. The disease results in the shredding and death of leaf tissue following the rupture of long sori in the leaves. Nearly 100 different grass species in more than 30 genera are parasitized and during the last two centuries more than 30 smut taxa have been described for members of this complex. In spite of wide application of various fungicides, the economic losses induced by these diseases worldwide are still dramatic for lawn and forage grass industries. The present study is a first attempt to clarify the taxonomy and phylogeny of the stripe smuts of grasses by analyzing both morphological and molecular data. More than 200 specimens from different continents and from all genera of the known host plants were examined and analyzed. DNA extracted from teliospores from 31 specimens from different hosts from Europe, Asia, and North America was used to amplify ITS and LSU regions used in phylogenetic analyses. The results of Maximum Parsimony and Bayesian analyses demonstrated that there are several lineages of stripe smut fungi. Hierarchical clustering analyses of morphological characters assessed with light and scanning electron microscopy (spore size and ornamentation) showed high support for the differentiation of two clades as distinct from U. striiformis s.l., i.e., Ustilago nunavutii sp. nov. and U. bromina. Two additional clades, Ustilago striiformis s.s. on Holcus and a clade containing specimens from Elymus, were identified with molecular data although morphological differences were not apparent. Further studies will likely reveal more lineages of these complex and polyphyletic fungi.
SESSION 3C – BIOSECURITY

Keeping one step ahead of invasive species: Using an integrated framework to screen and target species, for detailed biosecurity risk assessment.

Mr Sunil Singh
CSIRO Ecosystem Sciences
s11000363@yahoo.com

Sunil Singh (1), Mike Hodda (2), Gavin Ash (3)

(1)CSIRO Ecosystem Sciences, Canberra, ACT, 2601, Australia
(2)Graham Centre for Agricultural Innovation (an alliance between Charles Sturt University and the NSW Department of Primary Industries) Wagga Wagga NSW, 2678, Australia
(3)Cooperative Research Centre for National Plant Biosecurity, Bruce, ACT, 2617, Australia

Predicting which species will become invasive in any country or region before they arrive is necessary to devise and implement counter-measures to minimise the costs of biological invasions. This is literally keeping one step ahead of invasive species. A structured and systematic approach for screening large numbers of species and identifying those likely to become invasive is proposed in this paper. The Pest Screening and Targeting (PeST) framework integrates heterogeneous information and data on species biogeography, biotic and abiotic factors to first determine an overall threat index, then uses this index to identify species for a second, more detailed, threat evaluation process to provide a final ranking. Using the PeST framework, 97 species of Plant Parasitic Nematodes (PPN) were evaluated for their biosecurity threat to Australia. The species identified as greatest threats included both new and currently-recognised species. The former included Heterodera zeae, Meloidogyne graminicola, M. enterolobii, M. chitwoodi and Scutellonema bradys, while the latter included Bursaphelcnhus xylophilus, Dityelenchus destructor, Globodera pallida, Heterodera glycines and H. filipjevi. Of the ten criteria used in the PeST framework, emerging pest status, pathogenicity, host range and the SOM index (based on species biogeography) were often the most critical in assessing threat. The PeST framework also identified species where research to fill in critical knowledge gaps will be most beneficial. Where data was available, the information and associated metadata gathered for the PeST framework can be used to produce species profiles useful for management of the high-threat pests identified.

Recent changes in Colletotrichum taxonomy

Dr Bevan Weir
Landcare Research
weirb@LandcareResearch.co.nz

Bevan S Weir, Peter R Johnston
Landcare Research, Private Bag 92170, Auckland 1142, New Zealand

Colletotrichum fungi are considered to be one of the top ten important plant pathogens in the world, and have had a history of confusing taxonomy. The last major revision of the genus was done by von Arx in 1957 where many different species described on the basis of host association were synonymised to just a few names based on morphological characters. Over the past five years a major taxonomic initiative was undertaken by several research groups worldwide to clarify the taxonomy of this important pathogen. Multigene sequencing and morphological characters of voucher specimens were used to modernise the taxonomy and species concepts of the genus. This work revealed the presence of “species complexes” such as Colletotrichum gloeosporioides sensu lato that currently comprises 25 species, some of which are well established pathogens such as C. musae on bananas, while others are newly described such as the predominately endophytic C. aotearoa. Another challenge is to comply with a recent change to the ICN nomenclatural code removing dual nomenclature for fungi, this means that the Glomerella teleomorph names need to be linked and synonymised with Colletotrichum names where possible, or given new Colletotrichum names. There is the persistent problem of old names that do not have a specimen and no modern concept of what the species is. Most of these names are obscure but some such as C. crassipes are still in common use. These major changes are of particular importance for biosecurity and trade, but also for plant pathology research, some reports of variable pathogenicity of a Colletotrichum species may in fact be due to the presence of multiple cryptic species. A Colletotrichum identification website has been set up at “Q-Bank” that uses multigene data and the option of morphological characters to help quickly identify Colletotrichum species.
Dutch elm disease in New Zealand: From eradication to management

Dr Beccy Ganley
Scion
Beccy.Ganley@scionresearch.com

Ophiostoma novo-ulmi, the causal agent of Dutch elm disease (DED) is considered to be one of the 20 worst pests to have been introduced into New Zealand. The pathogen was first discovered in New Zealand in December 1989 in an inner Auckland city park. Immediately after O. novo-ulmi was discovered an eradication campaign was begun by the Ministry for Primary Industries along with surveillance programmes for Scolytus multistriatus, the only known vector of the pathogen in New Zealand. Initially the eradication campaign looked promising as there was a steady decline in the number of infected trees and locations. However, an evaluation of the program concluded that the disease was actually only being effectively managed and contained, and funding of the DED programme was discontinued with responsibility handed over to local authorities. Although limited surveys and sanitation felling are still being completed, there has been a rise in the detection and spread of both O. novo-ulmi and S. multistriatus in New Zealand. We review the eradication campaign and lessons learnt for future eradications, the current status and spread of O. novo-ulmi and S. multistriatus in New Zealand, and the control or management options for DED. This includes the feasibility of a regional-based eradication of DED and the use of viral biological control against O. novo-ulmi.

Mango malformation in the Northern Territory of Australia

Lucy Tran-Nguyen
Department of Primary Industry and Fisheries
jose.liberato@nt.gov.au

Mango malformation (MMD) is an important disease of mango (Mangifera indica) in many production areas around the world. It is caused by Fusarium mangiferae, F. sterilhyposphum, F. mexicanum and F. tupiense. MMD symptoms have been associated with several other Fusarium species. In November 2007, MMD was detected at DPIF’s research station in the Northern Territory (NT). F. mangiferae was identified and subsequently gazetted as declared and notifiable pathogen. The emergency plant pest response included back/forward tracing which identified that prior to the detection of MMD at the research station, plant material, from the exact same source had been distributed across the entire Australian mango breeding programs to both Government and private breeders, and then propagated and distributed nationally to the Australian Industry as planting material. Since 2007, F. mangiferae has been detected in nine mango trees and a new species of Fusarium was associated with MMD-like symptoms in 24 mango trees and three seedlings. Attempts to prove the pathogenicity of this new species have been unsuccessful. Several other Fusarium species have been associated with 21 mango trees with atypical symptoms of deformed inflorescences and distorted shoots. From these, F. proliferatum was found to be associated with 14 trees. The identification of the Fusarium species from MMD and associated MMD-like plant symptoms was based upon multigene analyses of single-spore derived cultures. Since October 2008, no MMD suspect samples have been received from mango growers and all detections resulted from DPIF’s MMD surveys. Up to 2012, all F. mangiferae infected trees were eradicated. Mango trees associated with the new species of Fusarium and F. proliferatum were eradicated from two DPIF’s research stations but not from private properties as these Fusarium species were not recognised as emergency plant pests. In 2012, an MMD survey was carried out during flowering and F. mangiferae was detected on six trees with atypical MMD symptoms. It is likely that these atypical symptoms could easily be overlooked in a survey and there are doubts about the efficacy of visual detection of infected inflorescences and shoots. To add to this difficulty, a high incidence of deformed or compact inflorescences was observed in two surveyed orchards where plant growth regulators were applied. These flowers senesced and fructified as normal and most attempts to isolate Fusarium from them were unsuccessful. At present MMD and MMD-like symptoms do not seem to be an economic problem in the NT.
SESSION 4A – DISEASE MANAGEMENT

Big achievement from a handful of high performing varieties: a concept in the context of crop health for wheat in Western Australia

Dr Moin Salam
Department of Agriculture and Food Western Australia
moin.salam@agric.wa.gov.au

Moin U. Salam,, Kawar P Salam,, Geoff J. Thomas,, Ciara Beard,, William J. MacLeod,, Arthur J. Diggle, and, David G. Bowran

Department of Agriculture and Food Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia

Australia and New Zealand can potentially become the food bowl of Asia by 2050. According to ANZ insight report ‘Greener Pastures: The Global Soft Commodity Opportunity for Australia and New Zealand’ (ANZ 2012), this can be achieved by meeting seven challenges, one of which is improved focus of research and development (ANZ 2012). Export of Western Australian (WA) wheat, currently worth A$1881 million per annum, can play a significant role in this endeavour. This study aimed to develop a practical crop health system to increase wheat production in WA. To achieve this aim, we identified the main driver of wheat production, and developed a system that respects the primacy of this driver and addresses management of the major foliar diseases of wheat within that constraint. Results, as supported by correlation and mean squared variation analysis, show that ‘area’ of wheat planted was the driver of wheat production from the 1950s through the 1970s; whereas, ‘yield’ has become the driver, replacing ‘area’ from the 1980s onward. The ‘yield’ is driven by ‘constraints free yield potential’ of varieties. During the last 20 years, growers have been using, on average, 45 varieties each season; however, the top variety each season occupied about 25% and the top 8 varieties about 80% of total area. These results clearly show, as the Pareto principle of ‘the law of the vital few’ describes, that targeting a handful high impact varieties can be instrumental in achieving big gains in WA's wheat production. We have developed a conceptual wheat health system that retains the growers’ variety adoption practice, and addresses crop health factors. Most of the yield loss from wheat diseases in WA results from septoria nodorum blotch (Stagonospora nodorum), teleomorph: (Phaeosphaeria nodorum) (SNB) and yellow leaf spot (Pyrenophora tritici-repentis) (YLS) (Murray & Brennan, 2008). We applied the wheat health system to address these two diseases. Based on growers’ current variety choices and a meta-analysis using 1980-2011 field trial data we have calculated the yield response, stratified according to the disease resistance level of the varieties, of one application of fungicide to control these two diseases. Given the response likely to be achieved in high and medium rainfall regions of WA, a 252,823 tonne increase in production, valued A$63 million, is possible using this system to target fungicide application. This system can be applied similarly to other health components to further elevate wheat production in Western Australia.

Control of crown canker of passion fruit (Passiflora edulis Sims.) – an acute disease problem for New Zealand passion fruit growers

Dr Pia Rheinländer
The New Zealand Institute for Plant & Food Research Ltd
pia.rheinlander@plantandfood.co.nz

Pia Rheinländer(1), Michael Spiers (2), Mark Andersen(1), Robert Fullerton(1)

(1) Plant & Food Research, Private Bag 92 169, Auckland 1142, New Zealand
(2) Plant & Food Research, Private Bag 3230, Hamilton 3240, New Zealand

Crown canker is a serious disease of the purple passion fruit (Passiflora edulis Sims.) in New Zealand often killing more than 80% of new plantings. Outbreaks only occur in winter under cold and wet conditions (May-October), and younger vines (< 18 months) appear the most susceptible to the disease. Characteristic symptoms first develop as purplish spots on the bark in the root crown area and within 50 cm of ground level. As the disease progresses, the spots develop into cankers, which extend resulting in girdling of the trunk and death of the plant. The cankers typically become covered by conspicuous pink/orange coloured masses of fungal spores. Isolations made from ten affected orchards in Northland (2), Auckland (2) and the Bay of Plenty (6) suggest Fusarium sambucinum Fückel. is the causative pathogen. The fungus was isolated from discoloured phloem and xylem in the trunk and from masses of spores from cankers. It was not recovered from roots nor was any other pathogen (e.g. Phytophthora). A pot trial provided no conclusive answer to the site of infection (entry point into vine). Vines were inoculated by wounding and applying spores of F. sambucinum to the (a) roots, (b) root crown area and (c) trunk (10 vines per treatment plus 10 untreated control vines). Infection was initiated in the vines inoculated in the trunk and crown area but was contained by the plants and did not progress into crown canker. A series of fungicidal and non-chemical trials were undertaken to find control remedies. These included (1) application of prothiocanazole and carbandazim to the trunk and larger branches using a spray lance at 3-weekly intervals, (2) raising the temperature of the root crown area and lower trunk by insulating with wood chip mulch and insulation foil, and (3) planting the vines in planter bags in a bark-coir mix to allow increased water drainage. Treatments were replicated in three orchards with 10-20 vines per treatment and untreated vines as controls. No control of the disease was achieved by either fungicide. Although F. sambucinum has optimal infection conditions at low temperatures, an increase in temperature by up to 4.7°C recorded in the root crown area of the insulated vines, did not suppress the disease. Likewise, planting the vines in planter bags did not reduce the incidence of crown canker. Vines resistant to the disease may be the best solution. However, such cultivars need to be developed.
### Enhancing natural disease resistance in *Pinus radiata*

**Dr Tony Reglinski**  
The New Zealand Institute for Plant and Food Research Ltd  
tony.reglinski@plantandfood.co.nz

Tony Reglinski (1), Robert Hill (2), Joe Taylor (3), Mike Spiers (4), Annette Ah Chee(5), Nicholas Cummings (6)

(1) The New Zealand Institute for Plant and Food Research Ltd, Ruakura Research Centre, Hamilton, New Zealand.  
(2) Bio-Protection Research Centre, Lincoln University, Christchurch, New Zealand.

New Zealand forest nurseries annually produce approximately 44 million *Pinus radiata* seedlings, cuttings or plantlets for re-establishment and new areas of forest plantation. Chemical fungicides are routinely applied to manage diseases. However, concerns about their detrimental ecological and environmental effects have led to the withdrawal of some products. The New Zealand forestry industry is supporting research to investigate the potential of biologically based control methods (inducing agents and antagonists) as more sustainable options for pest and disease management. A common criticism of biological control is that it can be highly efficacious in the laboratory or the glasshouse but extremely variable in the field environment. One possible approach to overcome this problem is to combine treatments with complementary modes of action such as the use of microbial antagonists with plant defence activators. We have investigated the use of the plant defence activator methyl jasmonate (MeJA) and *Trichoderma* spp. for their potential to protect *P. radiata* seedlings against diplodia dieback caused by *Diplodia pinae*. Foliar application of MeJA induces a dose-dependent resistance to diplodia which is greatest (c. 60% reduction in dieback, ~0.05) 1-2 weeks after treatment and persists for approximately one month. The induced resistance response is concomitant with an elevation of defence mechanisms and an inhibition of seedling growth. Root application of *Trichoderma* has been shown to promote seedling growth and/or reduce seedling mortality in commercial forest nursery trials. In glasshouse studies, *Trichoderma* isolates have been identified which induce systemic resistance to diplodia, resulting in a 20% (~0.05) reduction of dieback compared with the untreated control. Combining a foliar spray of MeJA with *Trichoderma* root treatment did not have an added effect on dieback control and did not alleviate MeJA-induced growth inhibition. However, there was evidence that the addition of *Trichoderma* primed the seedling response to MeJA-induced disease suppression, and 38 were screened for plant growth promotion. Isolates of *T. virens*, *T. atroviride* and *T. rossicum* demonstrated the greatest suppression of *R. solani* on potato plants; the percentage of diseased stolons was reduced by 41-46% (~0.05), compared with the *R. solani*-inoculated control. Two isolates, a *T. virens* and a *T. atroviride*, also increased (~0.05) average tuber weight, by 210 and 146% respectively, compared with the inoculated control. In plant growth promotion pot trials, three isolates (two isolates of *T. harzianum* and one *Trichoderma* sp.) increased (~0.05) number of tubers, total tuber weight and average tuber weight respectively, compared with the untreated control. Six isolates were selected from the disease suppression and growth promotion experiments, and were evaluated in all combinations in a 26 factorial greenhouse experiment. The multi factorial analysis demonstrated that one isolate of *T. atroviride* showed promise as a biological control agent of *Rhizoctonia* diseases of potato. Four of the isolate combinations were subsequently tested in a field trial during the 2011/12 season. This demonstrated that two *Trichoderma* combinations increased (~0.05) potato tuber yield. This research has shown potential for use of New Zealand isolates of *Trichoderma* to suppress *Rhizoctonia* diseases of potato.

### Evaluation of *Trichoderma* isolates to suppress *Rhizoctonia* diseases on potato

**Ms Emily Hicks**  
Bio-Protection Research Centre  
emily.hicks@lincoln.ac.nz

Hicks, E., Bienkowski, D., Braithwaite, M., Falloon, R.E., McLean, K.L., Stewart, A  
Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, Canterbury, New Zealand

*Rhizoctonia solani* Kühn, is a soil-borne fungal plant pathogen which causes economic losses in potato production worldwide. Symptoms include; lesions (cankers) on the below-ground shoots, stems and stolons, malformed tubers, and formation of sclerotia on the daughter tubers. *Rhizoctonia* diseases of potato are commonly managed using a combination of cultural and chemical disease control strategies to reduce soil-borne and tuber-borne inoculum. Biological control could have an important role as an additional strategy for *Rhizoctonia* disease management. Biological control agents, such as formulations of *Trichoderma* spp., are marketed for many plant pathogens worldwide, however no *Trichoderma* products are available to manage *R. solani* in New Zealand. *Trichoderma* spp. are also reported to be associated with increased crop productivity in numerous crops. In the present research, *Trichoderma* spp. from New Zealand soils were screened using potato plants, in several greenhouse experiments and one field trial. Forty-seven *Trichoderma* isolates were screened for *Rhizoctonia* disease suppression, and 38 were screened for plant growth promotion. Isolates of *T. virens*, *T. atroviride* and *T. rossicum* demonstrated the greatest suppression of *R. solani* on potato plants; the percentage of diseased stolons was reduced by 41-46% (~0.05), compared with the *R. solani*-inoculated control. Two isolates, a *T. virens* and a *T. atroviride*, also increased (~0.05) average tuber weight, by 210 and 146% respectively, compared with the inoculated control. In plant growth promotion pot trials, three isolates (two isolates of *T. harzianum* and one *Trichoderma* sp.) increased (~0.05) number of tubers, total tuber weight and average tuber weight respectively, compared with the untreated control. Six isolates were selected from the disease suppression and growth promotion experiments, and were evaluated in all combinations in a 26 factorial greenhouse experiment. The multi factorial analysis demonstrated that one isolate of *T. atroviride* showed promise as a biological control agent of *Rhizoctonia* diseases of potato. Four of the isolate combinations were subsequently tested in a field trial during the 2011/12 season. This demonstrated that two *Trichoderma* combinations increased (~0.05) potato tuber yield. This research has shown potential for use of New Zealand isolates of *Trichoderma* to suppress *Rhizoctonia* diseases of potato.
**Aweto: initial cultural studies in New Zealand**

Dr Seona Casonato  
Plant and Food Research  
seona.casonato@plantandfood.co.nz

Seona Casonato (1), Nicola Mauchline (1), Kate Stannard (1), Garry Hill (1)  
(1) The New Zealand Institute for Plant & Food Research Ltd, 412 No 1 Road, Te Puke 3182, New Zealand.

*Ophiocordyceps robertsi* (Hook.) G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora is an entomopathogen present in some forested areas in New Zealand. It is predominantly found on Lepidopteran larva and specifically associated with the family Hepialidae. In New Zealand the organism is most commonly referred to by the Maori name aweto. *Ophiocordyceps* is used medicinally in China and Japan and has an extremely high commodity value. Little is known about *O. robertsi* and its growth patterns. Initial trials have commenced to address these questions. *O. robertsi* was grown on media optimised for cordyceps growth and contained 1.95% PDA, 1.5% agar and 0.1% yeast extract. Initial temperature and light trials determined that, in culture, *O. robertsi* grows at its optimum rate in natural daylight hours at a temperature between 17-20°C. The media used for the growth of *O. robertsi* (as described above) was further amended with ground hinu leaves (*Elaeocarpus dentatus*), soil surrounding the aweto, soil not near the aweto, and ground aweto. Initial measurements indicated that *O. robertsi* grew best on the cordyceps media and the ground aweto media. Least growth was observed on the media containing ground hinu leaves.

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**Introgression breeding– towards the development of nematode resistant sugarcane variety in Australia**

Dr Shamsul Bhuiyan  
BSES Limited  
sbhuayan@bses.com.au

Shamsul A Bhuiyan(1), Barry J Croft(1), Eunice Wong (1), Phil Jackson(2), Graham R Stirling(3), Mike Cox (4)  
(1) Biosecurity, BSES Limited, Woodford, Qld, 4514, Australia  
(2) CSIRO Plant Industry, Townsville, Qld, Australia  
(3) Biological Crop Protection, Brisbane, Qld, Australia  
(4) Variety Improvement, BSES Limited, Bundaberg, Qld, Australia.

Root knot (*Meloidogyne javanica*) and root lesion (*Pratylenchus zeae*) nematodes are the most important nematode pests of sugarcane in Australia, causing in excess of A$82 million losses to the Australian sugar industry annually. Currently no commercial sugarcane varieties are resistant to these nematodes. A collaborative introgression program with Chinese institutes has used new sources of germplasm, *Erianthus arundinaceus* and *Saccharum spontaneum* clones to generate over 100 new families. In 2012, approximately 150 clones from different introgression families have been screened in a glasshouse for resistance to *M. javanica* and *P. zeae*. The initial nematode population used for inoculation of test clones (Pi) and final population recovered after 12 weeks (Pf), were used to determine the multiplication factor (MF) =Pf/Pi, which is a measure of the resistance levels of test clones. For both nematodes, the lowest multiplication factors were observed on basic *E. arundinaceus* (MF = 3 - 7) and *S. spontaneum* (MF =1.8 - 6) clones, indicating moderate to high levels of resistance. Average levels of resistance tended to decrease with successive backcrosses between the wild species and commercial sugarcane. However, approximately 30% of backcross-three (BC3) populations of *E. arundinaceus* showed moderate resistance (MF≤10) to root knot and lesion nematodes compared to commercial varieties Q208 (MF 14 - 42), Q240 (MF 20 - 24) and Q135 (MF 24 - 44). For backcross-two (BC2) *S. spontaneum* populations, 5% and 30% of clones had moderate levels of resistance (MF≤10) to lesion and root knot nematodes, respectively. Individual nematode-resistant clones will be further tested and may prove to be a useful source of resistance to nematodes for commercial production or as parents for further breeding. New introgression clones will also be screened in coming years.
Managing Ganoderma basal stem rot of oil palm: Innovative approach through endophytic microorganism application

Dr Shamala Sundram
Malaysian Palm Oil Board
shamala@mpob.gov.my

Shamala Sundram(1), Sariah Meon(2), Idris Abu Seman(1), Radziah Othman(1)

(1) Malaysian Palm Oil Board, P. O. Box 10620, 50720 Kuala Lumpur, Malaysia
(2) Agriculture Faculty, Universiti Putra Malaysia, 43400 Serdang, Selangor, Malaysia

Basal stem rot of oil palm (Elaeis guineensis Jacq.) caused by Ganoderma spp is the most devastating disease of oil palm in South East Asia. Endophytic microorganisms such as arbuscular mycorrhizal fungi (AMF) and endophytic bacteria (EB) has been previously described as potential biocontrol agents. The potential use of these endophytic microorganisms was investigated through antagonistic assessment against Ganoderma followed by in vitro compatibility between both endophytes, determination of biochemical responses and gene expression profile in pre-inoculated seedlings challenged with G. boninense, and finally field trial via seedling baiting technique. AMF (Glomus intraradices and G. clarum) and EB (Pseudomonas aeruginosa and Burkholderia cepacia) represent the endophytic microorganisms. Symbiotic interaction was observed between AMF species and EB with significant increase of germination and hyphal length of AMF spores. An interesting finding as these EB strains was never reported as potential mycorrhizal helper bacteria (MHB). Antagonistic effect of EB strains was also recorded through radial inhibition while scanning electron micrographs revealed severe morphological deformities such as shrivelling, flattening and shrinking of G. boninense hyphae in the presence EB strains. Production of POX, PPO, chitinase and β-1, 3-glucanase during pre and post infection were enhanced in pre-inoculated seedlings and confirmed by the gene expression analysis. Field evaluation via seedling bait technique recorded reduced disease development. This is the first report of field seedling baiting technique to be successfully implemented in testing microbial pre-inoculation for disease suppression. Pre-inoculation with AMF and P. aeruginosa was most effective in reducing disease severity in oil palm.

Optimising pruning wound protection for management of eutypa dieback in grapevine

Mr Matthew Ayres
South Australian Research and Development Institute
matthew.ayres@sa.gov.au

Matthew Ayres(1), Trevor Wicks(1), Eileen Scott(2), Mark Sosnowski(2)

(1) South Australian Research and Development Institute, GPO Box 397, Adelaide, South Australia, 5001
(2) School of Agriculture, Food and Wine, The University of Adelaide, Waite Campus, Glen Osmond, South Australia, 5064

Eutypa dieback is a major fungal disease of grapevines worldwide, causing decline and eventual death of vines. Pruning wounds are infected by spores of the fungus Eutypa lata, and, once infected, the only method of control is via drastic remedial surgery. In Australia, only two products are registered as pruning wound protectants, and these must be applied by hand, which is not economically viable in most commercial vineyards. In order to optimise control of eutypa dieback, appropriate rates of fungicides need to be determined and efficient methods of spray application developed. Field trials were conducted in vineyards for two seasons to evaluate a range of fungicides and alternative products for efficacy in protecting pruning wounds from infection by E. lata. Vines were treated and inoculated with 1000 ascospores/wound following pruning in winter and then canes were removed the following winter for isolation in the laboratory. Recovery of E. lata from inoculated controls in the two seasons was 92 and 55%, respectively, and natural infection was detected in 8 and 13% of non-inoculated wounds. The fungicides tebuconazole, pyrimethanil, pyraclostrobin and fluazinam, representing four chemical activity groups, provided up to 88, 77, 71 and 58% disease control, respectively. Detached cane assays were also established in the greenhouse to evaluate the fungicides at decreasing inoculum doses from 1000 to 200 spores/wound, confirming the efficacy of the above fungicides. Of the alternative treatments evaluated in the field, garlic and lactoferrin provided 52 and 65% disease control, respectively. To develop efficient methods of applying pruning wound treatments, a range of different types of commercial sprayers was evaluated in three vineyards for two seasons. Spray coverage was assessed using water-sensitive papers placed throughout the vines. There was a positive correlation (R2=0.5) between spray coverage and disease control. The most effective sprayers were those that best targeted the vine canes. Recycle and purpose-built sprayers achieved up to 93% disease control, equivalent to that achieved by hand-painting of wounds. Most commercial sprayers are designed to spray foliage of vines and therefore require nozzle adjustment to target the pruning wound zone and high water volumes (>600 L/ha) to achieve maximum wound coverage. The outcome of this research provides new options for grape-growers to manage eutypa dieback and contributes to the long-term sustainability of the Australian wine industry.
Containment and eradication of *Phytophthora cinnamomi* in natural ecosystems

Prof Giles Hardy  
Murdock University  
w.dunstan@murdoch.edu.au

William Dunstan(1), Trudy Paap(1), Michael Crone(1), Christopher Dunne(2),  
Treena Burgess(3), Colin Crane(2), Renee Hartley(2), Giles Hardy(2)

(1)Centre for Phytophthora Science and Management, School of  
Veterinary and Life Sciences, Murdoch University, Murdoch, Western  
Australia, 6150  
(2)Science Division, Department of Parks and Wildlife, Locked Bag 104,  
Bentley Delivery Centre, Western Australia 6983

The exotic soil-borne plant pathogen *Phytophthora cinnamomi* is recognized as one of 15 ‘Key Threatening Processes’ to Australia’s biodiversity. In the south-west of Western Australia an estimated 41% of the 5710 native described plant species are susceptible and over one million hectares of native vegetation is infested. Therefore, robust methods that can effectively contain and eradicate the pathogen are paramount for the protection of the remaining uninformed areas. Since *P. cinnamomi* is a poor saprotroph and that it can survive indefinitely in asymptomatic annual and herbaceous perennial species, we describe two methods that can effectively be used to eradicate and contain *P. cinnamomi* from spot infestations.

Firstly, we applied herbicides to kill plants followed by the application of the fumigants Metham and Dazomet to depth to kill the pathogen. Secondly, we used herbicides to kill all plants and ensured that no recruitment from soil seedbanks occurred over a period of two years, with no other treatments. With regular baiting of the soils we were able to show no recoveries of the pathogen up to 36 months after treatments. The methods can be applied to spot infestations in a wide range of environments to ensure large areas do not become infested through autonomous or anthropogenic spread. We are now using the herbicide approach to ensure no living hosts occur at any time to provide the pathogen with a living substrate in restored mires on rehabilitated haul roads, and topsoil and overburden stockpiles. This method will potentially allow us to return within 24–36 months of treatment large areas of jarrah forest that were infested by the pathogen prior to mining to a pathogen-free status post mining. A detailed description of the approaches together with the recommended containment, monitoring, sampling and hygiene procedures will be discussed. There is a need to incorporate this containment and eradication methodology into comprehensive management plans for high priority landscapes.

Impact of fungicide resistance in *Venturia inaequalis* on control of apple scab in New Zealand

Dr Robert Beresford  
Plant & Food Research  
robert.beresford@plantandfood.co.nz

Rob Beresford(1), Peter Wright(1), Suvi Viljanen-Rollinson(2), Peter Wood(3), Ngaire Larsen(1)

(1)The New Zealand Institute for Plant & Food Research Ltd, Private Bag  
92169, Auckland 1142, New Zealand  
(2)The New Zealand Institute for Plant & Food Research Ltd Cronin Road,  
RD1 Pukekohe, New Zealand  
(3)The New Zealand Institute for Plant & Food Research Ltd Private Bag  
4704, Christchurch, New Zealand  
(4)The New Zealand Institute for Plant & Food Research Ltd, Private Bag  
1401, Hastings 4157, New Zealand

Apple production in New Zealand, as elsewhere, relies on fungicides to control scab (black spot). Some fungicides are at risk from resistance, including the groups: demethylation inhibitor (DMI), guanidine derivative (dodine), quinone outside inhibitor (QoI or strobilurin) and anilinopyrimidine (AP). Fungicide resistance reduces disease control, which decreases revenue, increases orchard and post-harvest handling costs and threatens market access by increasing risks of chemical residues and phytosanitary failures. Of available fungicides not at risk from resistance, diithiocarbamates interfere with integrated mite control, and others increase risk of fruit russet. In spring 2009, widespread scab control failure in Nelson was initially attributed to high disease carry-over, unexpectedly early bud break and difficult spraying conditions. In conjunction with Pipfruit New Zealand Inc, the national resistance status of *V. inaequalis* to dodine, DMIs, QoIs and APs has been investigated since 2010. Fifty orchards were surveyed in Hawke’s Bay (27), Nelson (12), Otago (6) and Waikato (5), providing about 1000 *V. inaequalis* isolates. Sensitivity to two DMIs (mcylobutanil and penconazole) and to dodine was tested using agar-based mycelial growth assays. The degree of resistance associated with loss of disease control was determined for each fungicide group by a plant bioassay, using inoculated potted apple trees. QoIs were tested by DNA-based detection of the G143A mutation in the cytochrome b gene. Isolates carrying the mutation were resistant to trifloxystrobin in both agar and plant assays. An agar-based assay for AP fungicides (pyrithianil and cyproflox) was also developed and validated using plant bioassays. The national survey showed resistance to myclobutanil, sufficient to compromise disease control, occurred in all regions. Sensitivity to myclobutanil and penconazole was about 10 times lower than overseas baseline sensitivities. Plant bioassays showed the DMIs flusilazole and difenoconazole were less affected by resistance than myclobutanil, penconazole and fenbuconazole. Sensitivity to dodine had increased since the 1990s, apparently the result of more rigorous dodine resistance management guidelines since 2004. For QoIs, the G143A gene mutation frequency was high enough to compromise disease control in 59% of orchards, nationally. AP sensitivity testing is incomplete, but initial results suggest resistance is widespread in Nelson. It is now considered that the 2009 scab outbreak arose because of resistance to at least two fungicide groups, combined with a challenging season for scab control. Information from this study is being used to develop new fungicide resistance management guidelines for the New Zealand apple industry.
Heat and chemical treatments to reduce systemic infection of tissue culture derived boysenberry plants (*Rubus* spp.) by the downy mildew pathogen *Peronospora sparsa*

Ms Anusara Herath Mudiyanselage
Ecology Department, Lincoln University
Anusara.HerathMudiyanselage@lincolnuni.ac.nz

Anusara Herath Mudiyanselage(1), Marlene Jaspers(1), Hayley Ridgway(1), Monika Walter(2), Geoff Langford(2), Eirian Jones(1),

(1)Faculty of Agriculture & Life Sciences, Lincoln University, Lincoln 7647, Christchurch, New Zealand
(2)Plant & Food Research Nelson, Old Mill RD, RD3, Motueka, 7198, New Zealand
(3)Berryworld Ltd, Tai Tapu, RD 2, Christchurch, New Zealand

Downy mildew, caused by the pathogen *Peronospora sparsa*, is a major disease of boysenberry in New Zealand, which, in recent years has resulted in yield losses of 50-100% mainly due to development of dryberries which are prematurely reddened, shrivelled, hardened fruit. Systemic infection of the plants produces characteristic purple angular leaf lesions along the veins. The use of systemically infected plants for propagation has resulted in young plants being infected. To limit infection of new boysenberry canes prior to their use in tissue culture, two treatments, heat (34°C) and heat + pesticide sprays (mancozeb and phosphorous acid), were applied. The systemically infected boysenberry plants (cv. Mapua) were grown in a greenhouse for 4 weeks, during which the plants for the pesticide treatments were sprayed after 2 and 4 weeks prior to placing at 34°C, with the heat only plants. Control plants were grown in the greenhouse for the duration. After 4 weeks growth at 34°C, cane tips were used to initiate tissue culture with 1-2 cm, single-bud stem cuttings as the explant material. Survival of the tissue culture plants from heat only, heat + pesticide and control treatments was 41, 48 and 74%, respectively after 6 weeks. The plants from the above treatments were potted up and grown in the shadehouse under conditions conducive to expression of systemic symptoms for 3 months. Characteristic *P. sparsa* symptoms were observed in 13, 17 and 100% of the heat only, heat + pesticide and control treatments, respectively. A nested PCR method was used to verify infection status of the plants. An initial test indicated that, although variable, the best detection rate was achieved using leaf tissue. Leaf samples from the 127 canes produced on the plants showed that 1.6% were infected and all of these were from the heat only treatment. Plants diagnosed as free of the pathogen will be used for propagation. Random sampling will be conducted during growth of the propagated plants to ensure that they are pathogen free as the possibility remains that systemic infection was present but below the detection threshold of the nested PCR. The results indicated that treatment with heat either alone, or in combination with mancozeb and phosphorous acid, reduced the level of systemic infection in the plant material. This method, together with PCR detection to confirm uninfected status, provides a valuable tool for the production of boysenberry planting material free of *P. sparsa* infection.

Evaluation of PCR methods for detection and identification of *Xylella fastidiosa* in *Coffeea* sp. plant

Ms Françoise Poliakoff
Anses - Plant Health Laboratory
Francoise.poliakoff@anes.fr

Bruno Legendre (1), Stelly Mississipi (2), Valérie Olivier (1), Emmanuelle Morel (2), Dominique Crouzillat (2), Marie-Agnès Jaques (1), Françoise Poliakoff (1),

(1)French Agency for Food, environmental and occupational health and safety - Anses - Plant Health Laboratory, Angers, 7 rue Jean Dioméras 49044 Angers cedex 01 - France
(2)Nestlé Research Center, 101, Av. Gustave Eiffel Notre Dame d’Oé - B.P.49716 - 37097 Tours CEDEX 2 - France
(3)INRA – EMERSYS - UMR1345 Institut de Recherches en Horticulture et Semences - Centre Angers-Nantes, 42 rue Georges Morel - BP 60057 - 49071 Beaucouzé cedex – France

*Xylella fastidiosa* (Xf) is a bacterium listed in the European Directive 2000/29/EC absent in this territory. This xylem-limited bacterium is present in the Americas and recently emerges in Taiwan. As it can infect nearly 250 hosts including some of high economic importance for France (*Vitis vinifera*, *Prunus* spp., *Citrus sinensis*, *Medicago sativa*, ornamental plants and forestry trees, …), woody fruit plant coming from areas suspected to be infected are subject to a stay in quarantine facilities. Nevertherless, in 2012, Plant Health Laboratory detected in France *Xylella fastidiosa* from symptoms on imported *Coffeea* sp. plants. This finding is considered as an interception (European Plant Protection Organization (EPPO) - RS 2012/165). Detection tools as sensitive and specific as possible are necessary for quarantine laboratories to ensure release of healthy plant material. To reach this goal, the methods of detection using regular PCR (Minsavage et al. 1994) and real-time PCR (Harper et al. 2010) were evaluated on coffee plants for their performance in terms of sensitivity, specificity, detection threshold and reproducibility. A protocol for detection of *Xylella fastidiosa* is proposed to improve the control of *Coffeea* sp. plant material.
Application of the PBcast model for timing fungicide sprays to control Phytophthora blight of pepper

Dr Eunwoo Park
Seoul National University
ewpark@snu.ac.kr
Mun Il Ahn(1), Ki Seok Do(2), Kyeong Hee Lee(1), Wee Soo Kang(1), Eun Woo Park(2)

(1) Epinet Research Institute, Epinet Co. Ltd., Anyang, 431-810, Korea
(2) Department of Agricultural Biotechnology, Seoul National University, Seoul, 151-921, Korea

Phytophthora blight of pepper which is caused by Phytophthora capsici often results in serious damage to pepper production due to failure of disease control at the early stage of disease development in the field. Therefore, it is important to determine when fungicide sprays need to be initiated after overwintering to control the disease effectively. This study was conducted to evaluate the effectiveness of fungicide sprays based on the forecast by PBcast, an infection risk model for Phytophthora blight. The PBcast uses weather (daily mean temperature, relative humidity, and rainfall) and soil texture data to estimate daily infection risk of the disease. Treatments included (1) routine sprays at 7-day intervals; (2) sprays when the infection risk estimated by PBcast reached 200 (IR=200); (3) sprays when the infection risk estimated by PBcast reached 224 (IR=224); and (4) no sprays. The field plot was arranged in the randomized complete block design with four replications. The experiment was conducted at the pepper field of the Chungcheongbukdo Agricultural Research and Extension Services, Cheonggwon, 363-883, Korea.

Protection of apple budding wounds from European canker

Dr Reiny Scheper
Plant & Food Research
reiny.scheper@plantandfood.co.nz
Reiny Scheper, Owen Stevenson
The New Zealand Institute for Plant & Food Research Limited, Private Bag 1401, Havelock North, New Zealand

European canker, caused by the fungus Neoceratinia ditissima, was shown to infect apple nursery trees in a UK study. Therefore, protection of budding wounds may be important for canker management. Approximately 1800 'ELMA 9' rootstocks were planted in Motueka, New Zealand, in October 2008 and budded with 'Royal Gala' in March 2009. Ten treatments at budding included different budding tapes and methods (Buddy tape, plastic pre-cut budding strips and Flexiband type C when chip-budded, and Flexiband A rubber budding strips and Okulete O30 when T-budded), and three fungicidal treatments that were applied to chip-budded stocks taped with Buddy tape. Treatments included slaked lime (3.2% calcium hydroxide), 0.15% Pristine® (0.0192% pyraclostrobin and 0.0378% bosalid) in 50% water-based acrylic paint, and a mixture of 1% tebuconazole and 2.5% carbendazim in 50% water-based acrylic paint (4% Folinc® WG and 5% Headland Addstem, respectively). The buds tied with Okulettes were on the same rootstock as the buds tied with Flexiband C, but 20 cm above these buds, and were removed 5 months after budding. All buds, except the controls, were inoculated with conidia of N. ditissima (2x10^6 conidial/ml) after the treatment. The positive controls were chip-budded, inoculated and then taped with Buddy tape, and the negative controls were chip-budded, taped with Buddy tape and treated with 0.005% Tween® 20. Five months after budding, significantly more buds and rootstocks among the positive controls (100%) and buds that were tied with Flexiband A rubber strips after T-budding (99%) displayed canker symptoms than in all other treatments (P <0.001). Buds tied with Okulettes after T-budding displayed significantly more canker symptoms (38%) than the chip-budded buds (0-2%). Fifteen months after budding, all T-budded trees (Flexiband A) showed severe symptoms of European canker and had died. Chip-budded trees that were inoculated after tying with either plastic strips or Flexiband C displayed significantly more symptoms of European canker (16% and 18%, respectively) than those tied with Buddy tape (5%, P <t>0.001</t>). Of the uninoculated trees, 4% displayed symptoms of European canker. Either the budding wounds were infected by natural inoculum after budding, or the infection was already present in either the scion wood or the rootstock before budding. Spray painting of the budding wounds with tebuconazole/carbendazim in 50% water-based paint reduced canker symptoms significantly (1%, P <t>0.001</t>). Calcium hydroxide also reduced canker symptoms (2%) compared with the uninoculated control. Pyraclostrobin/bosalid in 50% water-based paint did not reduce canker incidence.

Protection of apple budding wounds from European canker
Heat and dessication kills *Pseudomonas syringae pv. actinidiae* on kiwifruit pollen

Dr Kerry Everett
Plant and Food Research
Kerry.Everett@plantandfood.co.nz

Kerry Everett, Michele Vergara, Ngaire Larsen, Shamini Pushparajah, Paul Sutherland, Ian Hallett, Dan Cohen

The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Mt Albert, Auckland 1142, New Zealand

Freshly harvested anthers were contaminated with a virulent strain of *Pseudomonas syringae pv. actinidiae* (Psa), the bacterium that causes kiwifruit canker, then subjected to various combinations of heat, airflow and humidity. Pollen viability and Psa survival were tested after treatment. Although short durations at high temperatures and high humidity did kill Psa, these treatments were lethal to pollen. When humidity was reduced, the time before pollen viability was lost increased, but Psa survival was also enhanced. At 35°C and a humidity of 50% or less, pollen viability was not affected even after 1200 minutes, but Psa did not survive when applied at 10^8 and 10^9 cfu/ml. Psa at higher concentrations (10^7 and 10^8 cfu/ml) did survive this treatment, suggesting the formation of biofilms or aggregates that enhanced survival. The mechanism for Psa death at 35°C is probably by dessication because this temperature is not lethal to Psa. Increasing humidity to 60% resulted in loss of pollen viability, and decreasing the temperature to 28°C resulted in Psa survival even when applied at low concentrations. This suggests that the mechanism that enables low concentrations of Psa to survive dessication at 28°C was disabled at 35°C. Extended duration at 35°C and low humidity killed all bacterial cells, and the pollen survived, but this treatment is not likely to be commercially viable.

Preliminary experiments with nitric oxide, which is known to disrupt biofilms, were promising.

Effect of biofumigation and arbuscular mycorrhizal inoculation on specific apple replant disease (SARD)

Dr Eirian Jones
Lincoln University
Eirian.Jones@lincoln.ac.nz

Eirian Jones(1), Sandy Hammond(2), Steve Wakelin(2), Hayley Ridgway(1)

(1)Agriculture and Life Sciences Faculty, PO BOX 85084, Lincoln University, Lincoln, Canterbury, New Zealand
(2)AgResearch Ltd, Lincoln Science Centre, Private Bag 4749, Christchurch, New Zealand

Systemic apple replant disease (SARD) occurs when young apple trees are planted in sites previously cultivated with apples, reducing growth and delaying development, thus causing substantial economic losses. It has been recognised as a problem in apple nurseries and orchards in New Zealand for decades with a recent survey of orchards indicating it is widespread. To limit SARD nurseries avoid planting in soil previously used to grow apple rootstocks at considerable additional cost to their operations. SARD soil obtained from an apple nursery site in Nelson was either chloropicrin fumigated or treated with biofumigation. To biofumigate the soil mustard (Caliente) was grown in SARD soil and incorporated into the soil when it achieved 50% flowering. After 2 weeks, the soil was fully aerated to remove biofumigants and used to grow apple rootstocks. Apple rootstocks (M.26) were pre-colonised with arbuscular mycorrhizal fungal (AMF) derived from New Zealand soils (LU mix), a commercial mycorrhizal treatment (Mycormax™) or untreated. Pre-colonised and untreated control plants were planted into 4 L pots containing untreated, chloropicrin treated or biofumigant treated SARD soil. At planting 50 ml (25 spores) of the appropriate AMF spore inoculum (in sand/pumice/potting mix) was placed into the planting hole prior to planting the apple rootstock. The plants were grown in a shadehouse for 6 months. The diameter of the plants between the first and second node above the soil surface was measured using a digital calliper at the time of planting and at harvest. At harvest, feeder and main root disease were assessed on a 0–4 scale (0 = all feeder roots healthy, 1 = 25% diseased or dead, 2 = 50% dead, 3 = 75% dead, 4 = 100% dead) and the shoot/root dry weight assessed. Rhizosphere soil was sampled and microbial community structure and catabolic functionality. Biofumigation and chloropicrin significantly reduced the disease score on feeder and main roots. Apple growth (increase in girth diameter, root and shoot dry weight) was significantly increased by chloropicrin but not biofumigation. Although AMF treatments had no effect on root health, apple growth was increased by AMF treatment. There was a significant difference in catabolic function in chloropicrin treated soil compared with the SARD and biofumigant treated soils. The use of biofumigation may provide an alternative method for suppressing SARD in apple nurseries and combination with AMF inoculation of the apple rootstocks may improve establishment.
Selection and characterisation of \textit{Trichoderma} isolates for suppression of \textit{Pratylenchus} in wheat roots

Mr Mark Braithwaite  
Bio-Protection Centre  
Mark.Braithwaite@lincoln.ac.nz

Mark Braithwaite\textsuperscript{(1)}, Alan McKay\textsuperscript{(2)}, Danuta Pounsett\textsuperscript{(3)}, Jessica Yardley\textsuperscript{(1)}, Nigel Percy\textsuperscript{(2)}, John Marshall\textsuperscript{(1)}, Beverley Gogel\textsuperscript{(1)}, Gavin Ash\textsuperscript{(1)}, Michael Wilson\textsuperscript{(1)}, Alison Stewart\textsuperscript{(1)(2)}

\textsuperscript{(1)}Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7467, Canterbury, New Zealand.  
\textsuperscript{(2)}SARDI, Waite campus, Plant Research Centre, 2b Hartley Grove, Umbræa SA 5064.  
\textsuperscript{(3)}The University of Adelaide, SA 5005, Australia.  
\textsuperscript{(4)}Charles Sturt University, Boorooma Street, North Wagga, NSW.  
\textsuperscript{(5)}AgResearch, Ruakura Research Centre, Private Bag 3123, Hamilton 3240.  
\textsuperscript{(6)}Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA.

Several species of root lesion nematode (\textit{Pratylenchus}) are considered serious pests of grain crops in Australia. Two species, \textit{P. neglectus} and \textit{P. thornei}, are target species for this research as they are prevalent and of economic importance, causing up to $102$ M per year. Currently, management relies on use of resistant crops and varieties and biological control could have an important role to provide more flexible management strategies. The programme is a collaboration between organisations in New Zealand and Australia and is funded by the Grains Research and Development Corporation of Australia. \textit{Trichoderma} strains have been extensively studied for their biocontrol potential and the aim of this research is to develop a commercial biofungicide based on \textit{Trichoderma} for the control of root lesion nematode when applied as a seed treatment. Over 100 \textit{Trichoderma} strains have been evaluated for their rhizosphere competence and their ability to suppress nematode populations in wheat roots in a greenhouse screening assay, and greenhouse and outdoor pot trials in both New Zealand and Australia. Rhizosphere competence varied considerably between \textit{Trichoderma} strains and species. The most consistently rhizosphere competent species on wheat roots were \textit{T. hamatum} and \textit{T. harzianum}. Suppression of live nematode numbers in the roots was up to a 65% reduction in the New Zealand greenhouse assay which compared to 55–77% for Vydate. \textit{Trichoderma} treatments resulted in a 65% reduction in nematode numbers in the roots in a New Zealand greenhouse assay compared to 55–57% for Vydate. In pot trials in Australia, some \textit{Trichoderma} strains significantly reduced nematode levels and increased wheat root biomass. A selection of strains is currently being evaluated in field trials in Australia. Results from the greenhouse bioassay, pot and field trials will be presented.
Management of Grapevine leafroll-associated virus 3 in New Zealand

Dr Daniel Cohen
The New Zealand Institute for Plant & Food Research Limited, dan.cohen@plantandfood.co.nz

Daniel Cohen (1), Vaughn Bell (2), Arnaud Blouin (3), Kar Mun Choo (4), Manoharie Sandanayaka (5), Robin MacDiarmid (6)

(1) The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Auckland, New Zealand
(2) The New Zealand Institute for Plant & Food Research Limited, Private Bag 1401, Havelock North, New Zealand
(3) School of Biological Sciences University of Auckland, Private Bag 92019, Auckland, New Zealand
(4) The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Auckland, New Zealand
(5) The New Zealand Institute for Plant & Food Research Limited, Private Bag 1401, Havelock North, New Zealand
(6) The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Auckland, New Zealand

Grapevine leafroll disease is present in all grape growing regions worldwide, but causes major quality problems in New Zealand vineyards, particularly in red varieties. The disease is more severe in North Island vineyards where a higher number of mealybugs are often present to vector the disease. The principle causal agent of the disease in New Zealand is the phloem-limited virus Grapevine leafroll-associated virus 3 (GLRaV-3) in the genus Ampelovirus. Recent studies have shown that strain variability in New Zealand is very different to that reported in other countries (see Chooi et al, this conference). It is not known whether there are biological differences in the impact of these strains on grapevines, but the New Zealand isolates NZ1 and NZ2 are more difficult to detect by ELISA and RT-PCR using previously published protocols. One of the most divergent strain, NZ2, has only been recorded in New Zealand to date, and represents a relatively high proportion of the infected samples. The reason for the very high incidence of strain NZ2 in some vineyards is not known, but may result from interactions between the climate, mealybug vectors and the vines. This presentation will discuss current research about mealybug feeding behaviour and the acquisition of GLRaV-3 as well as the importance of remnant roots after the removal of infected vines as a source of inoculum. Finally, the impact of GLRaV-3 on New Zealand viticulture will be compared with the situation in other countries.

Effects of susceptible and resistant cultivars on populations of the potato cyst nematode (Globodera rostochiensis Ro1) and on potato yields in Victoria, Australia

Dr Rudolf de Boer
Department of Environment and Primary Industries, Victoria dolf.deboer@depi.vic.gov.au

Rudolf de Boer (1), John Wainer (1), Lila Nambiar (1), Fiona Thomson (2), Sorn Norm (2), Murray Hannah (1), William Washington (2), David Beardsell (2), Nigel Crump (2), Simone Kreidt (3), Alan Yen (4)

(1) Department of Environment and Primary Industries Victoria, AgriBio Centre for AgriBIoscience, 5 Ring Road, La Trobe University, Bundoora, VIC 3083, Australia
(2) Department of Environment and Primary Industries Victoria, Knoxfield Centre, Private Bag 15, Ferntree Gully DC, VIC 3156, Australia
(3) Department of Environment and Primary Industries, Parkville Centre, 32 Lincoln Square North, Parkville VIC 3053, Australia
(4) Department of Environment and Primary Industries Victoria, Ellinbank Centre, 1301 Hazeldean Road, Ellinbank VIC 3820, Australia
(5) Victorian Certified Seed Potato Authority, Private Mail Bag 1, Healesville, VIC 3777, Australia

The potato cyst nematode (PCN) is a quarantine pest in Victoria affecting a relatively small number of properties. In one district, farmers have grown potatoes on infested sites for over 20 years, with evidence of a greater abundance of PCN and reduced potato productivity in this area due to the frequent cropping of susceptible varieties since the nematode was first detected in the State of Victoria in 1991. The option of managing the nematode populations in this area with resistant varieties had not been explored by government agencies or by industry. In trials on an infested property in 2008/09 and 2009/10, cysts were observed to be abundant on the roots of susceptible cultivars ‘Trent’, ‘Coliban’ and ‘Sebago’ at flowering time but were not apparent on the roots of the resistant ‘Atlantic’, ‘Crop 13’ and ‘Nicola’. Average pre-planting populations over the two trial sites were 746 cysts/500 g soil and 115 viable eggs/g soil per plot, with numbers in individual plots ranging from 96 to 3453 cysts/500 g soil and 21 to 390 eggs/g soil. Viable eggs were more abundant after growing susceptible cultivars (average 176 and 244 eggs/g soil in 2008/90 and 2009/10) than after growing resistant cultivars (80 and 80 eggs/g soil) (predicted means from ReML analysis with pre-planting egg numbers as a covariate). In the 09/10 trial, viable eggs were intermediate in number after a bare fallow (139 eggs/g soil) compared with numbers after susceptible and resistant cultivars. A comparison of the change in viable egg numbers between planting and harvest showed significantly more eggs after susceptible cultivars at harvest, a trend of less eggs after the resistant cultivars and no change after a fallow period. Marketable yields of the most productive resistant cultivar ‘Crop 13’ were on average 45% higher than the yields of the popular, but susceptible, ‘Sebago’. However, yields of the susceptible ‘Coliban’ were similar to the yields of the resistant cultivars, indicating a possible higher tolerance of ‘Coliban’ to root infestation by the nematode. These trials show the potential of managing R. rostochiensis Ro1 populations with resistant cultivars and show that potato yields could be significantly improved by growing resistant cultivars.
The Effect of Postharvest Hot Fungicidal Dip and Exogenous Ethylene Gas Application on the Incidence of Dendritic Spot & Stem End Rot in Kensington Pride (KP) Mangoes

Ms Arslan Qureshi
University of Queensland, Gatton campus
arslan.qureshi@uqconnect.edu.au

Arslan Qureshi (1), Victor Galea (1), Chris Akem (2), Elizabeth Aitken (1), Ian Bally (1)

(1) School of Agriculture & Food Sciences, The University of Queensland, Qld, Australia
(2) International Institute of Tropical Agriculture, Ibadan, Nigeria

Postharvest hot fungicidal dips of mango fruits have been demonstrated to be an effective postharvest management strategy to control stem end rot (Neofusicoccum parvum, Lasiodiplodia theobromae) and dendritic spot (Neofusicoccum parvum, Colletotrichum gloeosporioides). Fruit exposure to exogenous ethylene gas for early ripening is a common practice used by many mango growers in Queensland. As postharvest diseases emerge after fruit ripening, this hastened maturity may also quicken the development these diseases. A study was designed to determine the influence of hot fungicidal dips and ethylene gas exposure on the incidence of these two diseases during the 2010 and 2012 mango seasons. Mature mango fruit (variety Kensington Pride) were collected from the DAFF Ayr Research Facility and from a commercial orchard in Ayr, north Queensland. The fungicide Fludioxonil (Scholar®) was applied at a commercial rate of 120ml per at 52°C for 5 minutes using a fruit dip. The fruit was exposed to exogenous ethylene gas at the commercial rate of 10ppm using a trickle ethylene injection system with continuous venting at the commercial pack house. These two treatments were applied on the fruit in the following combinations: hot fungicidal dip only, exogenous ethylene gassing only, hot fungicidal dip followed by exogenous ethylene gassing and untreated control fruit. Five trays of 20 fruit were subjected to each treatment. The results showed that, the fruit exposed to exogenous ethylene gas and untreated fruit developed 100% incidence of dendritic spot during the 2010 season while more than 40% incidence developed during the 2012 season. The hot fungicidal dip treatment resulted in no incidence of dendritic spot during both seasons. Dipping followed by gassing showed 1.25% incidence of dendritic spot during the 2010 and 5% incidence during the 2012 season. Fruit exposed to exogenous ethylene gas and untreated control fruit developed 45 – 50% incidence of stem end rot during 2010 and 2012 mango seasons respectively. For stem end rot, fruit treated with hot fungicidal dip developed 13% incidence during the 2010 season followed by 1% incidence during 2012 season. Fruit exposed to a hot fungicidal dip followed by exogenous ethylene gas exposure developed 26% incidence during the 2010 season and 21% incidence during the 2012 season. The study confirms the effectiveness of hot fungicidal dips followed by exogenous ethylene gas exposure to quicken fruit readiness and prolong market shelf life of saleable fruit with less disease pressure.

The incidence of Huanglongbing (HLB) on 2-3 year old tangerine trees (Citrus reticulata) grown from disease free nursery stock

Dr Angsana Akarapisan
Chiang Mai University, Chiang Mai, THAILAND
angsana.a@cmu.ac.th

Angsana Akarapisan (1,2), Wanaporn Kuenpech(3), Kanchana Srimai(3)
(1)Division of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand.
(2)Center of Excellence on Agricultural Biotechnology, AG-BIO/PERDO-CHE, Bangkok 10900, Thailand

Huanglongbing (HLB) was previously known in many countries as greening disease. HLB is a bacterial disease of citrus that until recently was considered the most serious problem of citrus worldwide. HLB affects citrus trees by blocking the phloem or the vascular system of the tree limiting its ability to uptake nutrients and it is vectored by the Asian citrus psyllid Diaphorina citri (Hemiptera: Psyllidae). Occurrence of HLB disease after infection was continually monitored between 2012 and 2013 in an experimental planting of tangerine trees (Citrus reticulata) which seedlings from disease free nursery stock in Chiang Mai, Thailand. An early symptom of HLB on tangerine is the yellowing of leaves on an individual limb or in one sector of a tree’s canopy. Field trees can be identified as suspect by their foliar but verification of HLB infection requires DNA detection methods. Polymerase chain reaction (PCR) was performed by using Las606/LSS primer to detect symptomatic leaves. Specific primers, forward primer Las606 (5’- GGA GAG GTG AGT GGA ATT CCG A-3’) and reverse primer LSS (5’- ACC CGA CAT CTA GGT AAA AAC C -3’) were used for amplification of the 16S rDNA of ‘Candidateus’ Liberibacter asiaticus (Las), producing specific bands of 500 bp. The study area showed the percentage of disease incidence ranging from 0.3% in 2012 to 2.0% in 2013. It appears that there is a high incidence of HLB-infected trees at the edges of the plantation. One of potential HLB pathways is infected Asian citrus psyllids from natural movement. It is known that the Asian citrus psyllid vector of HLB has a wide host range, can achieve high populations at citrus vegetative flush, can be spread over long distances, and its control demands both continuous inspection and regular insecticide applications.

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The incidence of Huanglongbing (HLB) on 2-3 year old tangerine trees (Citrus reticulata) grown from disease free nursery stock

Dr Angsana Akarapisan
Chiang Mai University, Chiang Mai, THAILAND
angsana.a@cmu.ac.th

Angsana Akarapisan (1,2), Wanaporn Kuenpech(3), Kanchana Srimai(3)
(1)Division of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand.
(2)Center of Excellence on Agricultural Biotechnology, AG-BIO/PERDO-CHE, Bangkok 10900, Thailand

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Seed tuber incidence and pathogenicity of *Verticillium* species infecting potatoes in Australia

Mr Prakash Vijayamma Ramakrishnan Nair
The University of Melbourne
prakasvr@gmail.com

Prakash Vijayamma Ramakrishnan Nair,1, Tonya Wiechel,2, Nigel Crump,1, Paul Taylor1

1Department of Agriculture and Food Systems, Melbourne School of Land and Environment, The University of Melbourne, Parkville, Victoria, Australia
2Biosciences Research Division, DEPI Victoria, Australia

*Verticillium* wilt, caused by the soilborne fungi *Verticillium dahliae* or *Verticillium albo-atrum*, is a serious disease of potato as well as many other crops. Seed tubers that had been produced by commercial seed growers in Victorian and Tasmanian potato production areas were obtained from 2010 to 2012. A total of 83 seed lots (20 tubers/lot) containing tubers from 20 cultivars were assessed for the presence of *Verticillium* species. *V. dahliae*, *V. albo-atrum* and *V. tricorpus* were isolated from the stem end vascular tissue of seed tubers and species identification was confirmed by multigene sequence analysis. Infection by *V. dahliae* within a seed lot varied greatly and ranged from 0-55%. More than 66% of seed lots tested were not infected by *V. dahliae*. Over 12% of seed lots tested ranged from 0-5% infection within the seed lots. Only one seed lot had more than 50% of seed tubers infected with *V. dahliae*. Overall percent infection of seed lots from Victoria and Tasmania were 27.7 (*V. dahliae*), 8.4 (*V. albo-atrum*) and 4.8 (*V. tricorpus*). This was the first report of *V. albo-atrum* from potato in Australia for 40 years. Pathogenicity of selected isolates of *V. dahliae*, *V. albo-atrum* and *V. tricorpus* were assessed by root dip inoculation with potato cv Shepody. All the inoculated plants showed typical *Verticillium* wilt symptoms however, several Tasmanian *V. dahliae* isolates were highly aggressive. Most *V. dahliae* and *V. albo-atrum* isolates showed the same level of aggressiveness; with *V. tricorpus* being substantially lower. Although *V. tricorpus* was pathogenic on potato the severity of infection was quite low. This was the first record of the pathogenicity of *V. tricorpus* on potatoes in Australia.

Seasonal variations in hull rot incidence in almonds

Dr Chin Gouk
Department of Environment and Primary Industries
chin.gouk@depi.vic.gov.au

Chin Gouk,1, Simone Kreidl1,
1Department of Environment and Primary Industries, Biosciences Research Division, AgriBio, 5 Ring Road, Bundoora, Victoria 3083, Australia.

Hull rot, caused mainly by *Rhizopus stolonifer* has become a wide spread disease problem in almond orchards in Australia in recent years. The disease tended to be more noticeable during or after hull-split, generally from January onwards. Wet conditions during hull split are considered to be favourable for development of *Rhizopus* spp. on almonds. Hull rot infection leads to proliferation of black, pin-head shaped sporangia on almond nuts, and subsequent blackening of hulls and shells. Severely infected nuts are mummified, remain attached to the rachis and not easily shaken off during harvest. Fungal populations on a range of substrates in an almond orchard in North-West Victoria were studied over two growing seasons, from December 2011 through to March 2013. Samples of green nuts, mummified nuts, soils and trash were collected from before hull split through to harvest in March for assessment of hull rot incidence and fungal populations. Hull rot incidence during pre-hull split, hull split and at harvest were determined. A large difference in hull rot incidence between the two growing seasons was detected, with over 90% infection in the first season. More frequent and heavier rainfalls occurred from the beginning of hull split in December 2011 to January 2012, whilst the hull-split stage in the following year experienced relatively drier conditions. Nuts in the 2012/2013 growing season had much lower hull rot incidence, even though a large number of over-wintering mummies were present in the orchards, due to severed hull rot infections in the previous growing season. The findings indicate rain events during the critical stage of hull-split are a key factor in on-set of hull rot. Mummies on the trees and ground harboured higher numbers of *Rhizopus* spp. than new season’s nuts, soils and trash. Although *Monilinia* spp. is listed in Australian and overseas literature to be also a causal pathogen of hull rot, this fungus has not been detected in any of the samples assayed.
Stemphylium grey leaf spot infection of lupins favoured on seedlings in wet and warm conditions

Mr William MacLeod
Department of Agriculture and Food Western Australia
william.macleod@agric.wa.gov.au

Arbab Ahmad(1)(2), William MacLeod(1)(2), Geoff Thomas(3), Susan Barker(1)(2)
(1)School of Plant Biology M084, The University of Western Australia, 35 Stirling Hwy, Crawley, WA, 6009, Australia
(2)Department of Agriculture and Food Western Australia, 3 Baron-hay ct, South Perth, WA, 6151, Australia
(3)Department of Plant Pathology, University of Agriculture, Faisalabad, 38400, Pakistan

Studies were carried out in narrowed leafed lupins (NLL) to understand the optimum environmental requirements for the establishment of infection by Stemphylium spp. leading to grey leaf spot (GLS) development. Experiments were performed on excised NLL leaves in the laboratory, subsequently optimum temperature and moisture conditions were benchmarked in the glasshouse experiments. Concentrated solutions of salts were used to maintain a range of (65% to 95%) relative humidity (RH) in airight boxes. Petioles of the excised NLL leaves were immersed in DI water in 5ml tubes to maintain turgidity. Two highly virulent isolates of Stemphylium (WAC12986 and WAC13136) were used to inoculate leaves obtained from 2 week old seedlings in controlled environment studies which revealed 25/20 °C day/night temperatures as optimum. At these temperatures, 22h and 68h were required for the pathogen to cause light and severe infection, respectively, at 95% RH. No infection was observed when RH was 85% or below. Time required for infection was markedly reduced under wet conditions. Leaf wetness resulted in light and severe infection after 10h and 26h, respectively. During the glasshouse experiments, increasing wetness periods above 8h during the infection period resulted in increased disease severity. Disease severity was higher in plants subjected to initial dry period of 6h after inoculation compared to plants receiving the same wetness period without drying, while the opposite effect occurred when plants were subjected to dry periods of more than 12h after an initial wetting period of 8h. In addition to the incubation temperatures, the post-infection temperature was also important. The lower and upper limits for infection and disease development were 10 and 30 °C, respectively. Withering of leaves occurred above 30 °C in plants incubated at 25/20 °C during the infection period and GLS was suppressed by the wilting of the plant. Disease developed more slowly in 6 week old plants than in 2 week old seedlings, but final disease severity in both groups of plants was similar for most temperatures. Regression models were developed to describe the duration of wetness period for a specified level of disease severity as a function of temperature.

The effect of elevated temperature on the titre of Barley yellow dwarf virus-PAV in wheat

Ms Narelle Nancarrow
Department of Environment and Primary Industries
narelle.nancarrow@depi.vic.gov.au

Narelle Nancarrow(1)(2), Fiona Constable(1), Kyla Finlay(1), Angela Freeman(2), Brendan Rodon(2), Piotr Trebicki(2), Simone Vassilades(3), Alan Yen(1), Jo Luck(1)
(1)AgriBio, Department of Environment and Primary Industries, 5 Ring Road, Bundoora, Victoria 3083, Australia
(2)Department of Environment and Primary Industries, Horsham Centre, 110 Natimuk Rd, Horsham, Victoria 3400, Australia
(3)Department of Botany, La Trobe University, Bundoora, Victoria 3083, Australia

Barley yellow dwarf virus-PAV (BYDV-PAV) is a phloem-limited Luteovirus that is transmitted by Rhopalosiphum padi (the oat aphid) and Sitobion avenae. BYDV-PAV is associated with yellow dwarf disease, one of the most economically important groups of diseases of cereals worldwide. In this study, the titre of BYDV-PAV in wheat under current and future predicted temperature conditions for the Wimmera wheat-growing district in Victoria, Australia was quantified. Three replicate experiments were conducted to assess the impact of elevated temperature on BYDV-titre in wheat cv. Yilpi. Ten day old wheat seedlings were inoculated with BYDV-PAV and grown at ambient (5.0-16.1°C) or elevated (10.0-21.1°C) temperature treatments, simulating the current average for the Wimmera region and predicted future daily temperature conditions during the wheat-growing season respectively. Whole above-ground plant samples were collected from each temperature treatment at 0 (day of inoculation), 3, 6, 9, 12, 15, 18, 21 and 24 days after inoculation. Nucleic acid was extracted using a KingFisher 96 magnetic extractor and an Agencourt Chloropure magnetic extraction kit and treated with DNase. Each RNA sample was analysed in triplicate using a specific one-step multiplex normalised reverse transcription quantitative PCR (RT-qPCR) assay for the detection and quantification of BYDV-PAV. Physical measurements including plant height, dry and wet weight and tiller number were also taken at each sampling point. The day of symptom onset in each plant was also recorded. In each replicate experiment, the plants grown at elevated temperature were significantly higher, had greater fresh and dry weights and had more tillers compared to those grown at ambient temperature. Symptoms associated with BYDV-PAV infection appeared earlier in plants from the elevated temperature treatment than in plants from the ambient temperature treatment. The titre of BYDV-PAV in wheat plants grown at elevated temperature peaked at days 12-15, decreased until day 21 and then stabilised. The titre of BYDV-PAV in wheat plants grown at ambient temperature peaked at days 18-21 and then stabilised. The titre of BYDV-PAV in plants grown at elevated temperature was significantly greater than the titre of the virus in wheat plants grown at ambient temperature on days 6, 9, 12 and 15. The results of this study have important implications for the epidemiology of yellow dwarf disease under future climates in Australia.
The development of an elsinoe infection risk model for apple in New Zealand

Mr Peter Wood
The New Zealand Institute for Plant & Food Research Limited
peter.wood@plantandfood.co.nz

Peter Wood (1), Rob Beresford (2), Brent Fisher (1), Reiny Scheper (1),

(1) The New Zealand Institute for Plant & Food Research Limited, Private Bag 1401, Havelock North 4157, New Zealand
(2) The New Zealand Institute for Plant & Food Research Limited, 92169, Auckland 1142, New Zealand

Elsinoe leaf and fruit spot of apple (elsinoe) is a major disease in organic apple in Hawke’s Bay, New Zealand. Elsinoe is caused by the fungus Elsinoe pyri (Woron.) Jenkins, syn. E. piri, (asexual stage Sphaceloma pyrinum (Peglion) Jenkins). Elsinoe lesions express on leaves and fruit similarly as spots 1–4 mm in diameter. Fruit spots can express on previously symptomless fruit during cool storage. Although the damage is superficial, it renders the fruit unfit for sale. Lime sulphur (LS) sprays are used for elsinoe control and are applied either as protectant treatments before wet weather, or as curative treatments after wet weather. The effectiveness of LS could be improved if weather conditions suitable for infection could be defined in an infection risk model. The wetness duration required for infection of ‘Royal Gala’ leaves by E. pyri was determined in controlled temperature experiments using constant temperatures representing typical spring and summer wet-period temperatures. The product of temperature and wetness duration (degree hours) was found to predict accurately the degree of infection. A degree hour model was used in a prototype model to predict elsinoe infection risk and this was incorporated into stand-alone software by HortPlus NZ Ltd. The model predicted four categories of infection risk, nil, light, moderate or severe, according to values of an output risk index. The model was validated using ‘Royal Gala’ trap trees that were exposed to natural infection in an elsinoe-infected orchard for 24 separate wet periods during the summer of 2012–13. After exposure, the trees were incubated for 10 weeks in a greenhouse to isolate them from further infection and then assessed for elsinoe incidence. On average, the incidence of elsinoe leaf spot for modelled nil-risk was 0.8%, light-risk 2% and moderate-risk 16.7% leaves infected. As a result of the dry summer weather no severe-risk events were recorded. The next step will be to update the prototype model based on findings of this study. It appears that it will be important to include rainfall as a requirement for elsinoe infection risk (for example ‘rainfall quantity’ and/or ‘hours since last rainfall’) in the elsinoe model. Further validation during 2013–14 is planned to define more precisely the rainfall requirements for infection and to confirm the preliminary risk category boundaries to provide an accurate tool to help growers with elsinoe management.

Temperature and moisture content stimulate the growth of fungi on healthy stored grain over time

Dr Kirsty Bayliss
Murdoch University
K.Bayliss@murdoch.edu.au

Eman Barkat, Giles Hardy, YongLin Ren, Kirsty Bayliss
School of Veterinary and Life Sciences, Murdoch University, Murdoch 6150, Western Australia

When grain is harvested and correctly stored it should remain free of infestation from most pests and diseases. Issues only arise when the storage conditions are breached, allowing the entry of pests, water or other contaminants. The hypothesis of this study was that a low level of fungal contamination is always present in healthy stored grain, and that these fungi may be stimulated to grow depending on the temperature at which the grain is stored, the moisture content of the grain, and the duration of storage. Wheat grain at varying moisture contents from 10.4 to 15.2%, was stored for one, two or six months at 15, 20, 25 or 32.5°C. Gamma-irradiated grain was included as a control. At each harvest time, for each combination of temperature/moisture/storage time treatments, 10 grains were plated on to full strength potato dextrose agar to determine changes in fungal frequency. The number of grains that exhibited fungal growth was recorded, and isolates emerging from the grain were sub-cultured for identification. After one month of storage, the highest percentage of fungal contamination occurred in grain at a moisture content of 11.4 and 13.5% that was stored at 15 and 25°C. After two months of storage, the highest percentage of fungal contamination occurred in grain at a moisture content of 13.5% stored at 25°C. The lowest contamination occurred on grain of 10.4% moisture content stored at 15, 25 and 32.5°C. The most commonly isolated genera were a putative Botryosphaeriaceae (Tiarosporella) that is a likely first report on stored wheat, and Alternaria spp. Most Alternaria spp. were found in grain of 11% moisture content stored at 20°C for one month; however the frequency of isolation of Alternaria sp declined after two months in storage. Nigrospora oryzae and Rhizopus sp. occurred at low frequency. The number of putative Botryosphaeriaceae increased after two months. It is not surprising that fungi can be stimulated to grow on stored grain, particularly when it is stored at high moisture content. What is interesting is the range of fungi that are present, as many of them are capable of producing secondary metabolites such as mycotoxins. Our work is continuing to investigate how the frequency and variation of genera change over time, with the aim of developing a rapid method for early detection of fungal contamination.
Sensitivity analysis and uncertainty in a species distribution model

Mr Hossein Narouei Khandan
Lincoln University
hakhandan@yahoo.com
Hossein Ali Narouei Khandan(1), Susan Worner(1), Eirian Jones(2), Suvi Viljanen-Rollinson(3)
(1)Bio-Protection Research Centre, PO Box 84, Lincoln University, Lincoln 7647 New Zealand
(2)Faculty of Agriculture and Life Sciences, PO Box 84, Lincoln University, Lincoln 7647 New Zealand
(3)New Zealand Institute for Plant & Food Research Limited, Private Bag 4704, Christchurch 8140, New Zealand

Species distribution models can be used to develop ecological insights about a target species by relating species occurrences and environmental data such that potential mechanisms that may determine species distribution can be investigated. In particular, such investigations may reveal species climate needs that are not known from empirical studies. For about thirty years, as a (semi) mechanistic model, CLIMEX has been used to map species climate response based on assumed distribution and relationship. Despite that many studies have used CLIMEX, it is rare that a proper sensitivity analysis has been implemented to determine the outcome of different parameter values on final model output. The sensitivity of model projections to small parameter change, often within measurement error of the parameters can be critical, especially when decision-makers base future strategies on model findings. As well as highlighting the sensitivity of different parameters in the model and their effect on the uncertainty of model projections, sensitivity analysis can reveal the contribution of different variables to the model, and in some cases can indicate specifically which areas are more sensitive to particular parameter changes thereby providing more information to decision-makers. In this research, Dwarf Bunt of wheat has been used to show how the uncertainty involved in setting parameter values in CLIMEX can change baseline model predictions. We show that performing sensitivity analysis increases information and confidence about the reliability of output and consequent recommendations. Increased information about the reliability of model output and awareness of different assumptions will enable decision-makers to provide better strategies for the management of species.

Modeling the impact of disease resistance on rice yields in the Philippines and Indonesia

Dr Adam H. Sparks
International Rice Research Institute (IRRI)
a.sparks@irri.org
Adam H. Sparks(1), Jorrel Aunario(1), Confidence Duku(2), Michael Noel(3), David Raitzer(4)
(1)International Rice Research Institute (IRRI), DAPO Box 7777, Metro Manila, Philippines
(2)Africa Rice Center (AfricaRice), 01 B.P. 2031, Cotonou, Benin

Host plant disease resistance is one of the primary recommendations made by plant pathologists to farmers for controlling plant disease. Often varietal releases are based on feedback from farmers, government and extension workers as to where disease occurs. While this information is useful, it may not be available for all areas of interest and combining this information with other stress factors may be difficult. Data on the diffusion of disease resistance released by the International Rice Research Institute (IRRI) and the dates when disease resistance began to become ineffective were gathered for the Philippines and Indonesia at a sub-national level. Two models, EPIRICE and RICEPEST, were used in a geographic information system (GIS) with ten years of satellite-gathered, daily weather data to produce maps of disease severity and yield losses due to bacterial leaf blight, causal agent Xanthomonas oryzae pv. oryzae and leaf blast, causal agent Magnaporthe grisea. Disease severity values were generated using the EPIRICE model to represent both resistant and susceptible rice varieties for each disease from 2001 to 2010 in the primary and secondary growing seasons. These disease severity data were then used to provide the RICEPEST model with the necessary data to predict the yield reduction due to disease for resistant and susceptible cultivars based on the same weather data for both countries. Resistance diffusion data were applied to the yield loss data to calculate the actual effects on yield that resistance had. In both countries, bacterial leaf blight severity was predicted to be much greater than leaf blast. Following this, when yield effects were calculated bacterial leaf blight had an effect yield in most regions, however very little or no effect from leaf blast resistance was found. These sorts of analysis are useful in helping target varietal resistance releases and evaluating impact of already released resistance.
Opium poppy mosaic virus, a new member of Umbravirus isolated from Papaver somniferum and Tropaeolum majus in New Zealand

Dr Bénédicte Lebas
Ministry for Primary Industries
benedicte.lebas@mpi.govt.nz

Joe Tang(1), Bénédicte Lebas(1), Ting Wei(1), Lisa Ward(1)

(1)Plant Health and Environment Laboratory, Ministry for Primary Industries, PO Box 2095, Auckland 1140, New Zealand
(2)Molecular Virology Laboratory, Queensland Institute of Medical Research, Locked Bag 2000, PO RBWH, QLD 4029, Australia

A new virus was isolated from Papaver somniferum (opium poppy) with severe leaf mosaic and mottling symptoms in Auckland, New Zealand in 2006. The virus can be mechanically transmitted to the herbaceous species Gomphrena globosa, Nicotiana benthamiana, N. clevelandii and N. tabacum inducing local and/or systemic symptoms. No virus particles were observed by electron microscopy from crude sap of either the diseased P. somniferum or any of the symptomatic herbaceous species. The partial genomic sequence of 3270 bp obtained from P. somniferum contains four open reading frames (ORF) and shares an overall nucleotide identity of 62.7% with Tobacco bushy top virus (TBTV), 51.1% with Pea enation mosaic virus 2 (PEMV-2), 49.0% with Carrot mottle virus (CMoVM) and 46.3% with Carrot mottle mimic virus (CMoMV). The characteristic absence of virus particles, the genomic structure of the sequence and the phylogenetic relationship with TBTV, GRV, PEMV-2, CMoV and CMoMV suggest that this new virus, tentatively named Opium poppy mosaic virus (OPMV), is a distinct species in the genus Umbravirus. OPMV was also identified in a symptomatic plant of Tropaeolum majus (nasturtium) which was collected in Auckland in 2004. The T. majus plant was also found to be co-infected with another four viruses. The relationship between the two OPMV isolates and with other umbraviruses is also discussed.

Forest trials testing phosphite for control of kauri dieback

Dr Ian Horner
The New Zealand Institute Institute for Plant and Food Research Ltd
ian.horner@plantandfood.co.nz

Ian Horner, Ellena Hough
The New Zealand Institute Institute for Plant & Food Research Ltd., Private Bag 1401, Havelock North 4157, New Zealand

Kauri dieback, a disease caused by Phytophthora taxon Agathis (PTA) is a serious threat to the health and survival of kauri trees in New Zealand. Phosphite (phosphorous acid) is a potential tool for controlling PTA. In January 2012, trials were established in Auckland (Huia and Whatipu) and Northland (Raetea and Omahuta) kauri forests, in sites severely affected by PTA. Trial trees (160 in total) were classed as kauri ‘rickers’, with girths from 40 to 120 cm. All trial trees showed symptoms of PTA infection (lower trunk lesions and/or canopy thinning/dieback) at the start of the trial, and PTA was isolated from soil throughout the trial sites. Baseline assessments of each tree were made, including canopy disease ratings, and trunk lesion dimensions and activity (recent bleeding or oozing around the margins). Photographs, to be used in future comparisons, were taken of all canopies and at cardinal points around the base of each trunk. Trees were grouped into disease severity classes, and then randomly assigned to the various treatments to ensure a balance of disease severities across treatments. Chemjet® stem injectors were used to inject trees with phosphite (Agrifos®600) at concentrations of either 7.5% or 20%. Control trees were left untreated. One 20-ml injection was applied for every 20 cm stem circumference. After one year (January 2013), half of the previously injected trees were re-injected, in all cases with 7.5% phosphite. In assessments made 17 months after the initial treatment, most trial trees had canopy health and vigour similar to or slightly worse than that at the start, with no obvious differences between treatments. However, treatment differences were obvious in trunk lesion assessments. Averaged across all sites, many more lesions remained active (expressing ooze, continued expansion) in untreated trees (53%) than in phosphite treated trees (2%). There were no obvious differences in lesion activity among the different phosphite rates or regimes. On healthy twigs excised from trial trees at Omahuta and inoculated with PTA in the laboratory, growth of PTA was slower in tissue from trees that had been injected with phosphite than in untreated trees. Forest trials are continuing and will be monitored every six months for a number of years to determine both the long-term effectiveness of phosphite treatments in kauri and the necessity of repeat treatments.
Recent emergence of Fusarium dieback of tea (Camellia sinensis) in Sri Lanka and its potential link with Tea Shot Hole Borer (Euwallacea fornicates)

Ms Pradeepa Liyanage
Tea Research Institute of Sri Lanka
pradeepa.liyanage@gmail.com

Pradeepa NH Liyanage(1)(2), OVDS Jagathpria Weerasena(2), Chaminda J Liyanaraarchchi(1), Ravi LC Wijesundera(1), Sarath B Abeyesinghe(1), Robert Reeder(3).

(1)Tea Research Institute of Sri Lanka, St Coombs, Talawakelle, Sri Lanka
(2)Institute of Biochemistry, Molecular Biology and Biotechnology, University of Colombo, Colombo 03, Sri Lanka
(3)Department of Plant Sciences, University of Colombo, Colombo 03, Sri Lanka
(4)CABI Bioscience UK Centre, Bakeham Lane, Egham, Surrey, TW20 9TY, UK

Sri Lanka is the second largest exporter of tea in the world. During 2008-2013 stem cankers with unusually high incidence of twig die back was observed in about 35,000 tea bushes from commercial tea gardens. The diseased plants also exhibited sudden wilting, defoliation and discolouration of the vascular tissues. All affected bushes showed heavy yield decline and about 5% of the affected bushes were found to be dead with stem cankers. A mild infestation of Tea shot hole borer (TSHB) beetle (Euwallacea fornicates) was also noted in most of the affected bushes. A fungus was consistently isolated from 85% of the stem canker samples. The fungus was identified as Fusarium solani complex based on colony and conidia morphology. The identification was confirmed by comparison of the TEF-1α (translation elongation factor 1α gene) sequences. The TEF 1α sequences of two isolates have been deposited at GenBank (Accession No. JX467676 and KC800803). These isolates share 98% similarity in the TEF gene sequence. The blastn search indicated that the sequences of the isolates are most related to Fusarium spp. (found to be vectored by TSHB) associated with a die-back disease of Avocado in Israel, and Southern California (Accession numbers JX891896, JX891895, JX891894, and canker caused by F. solani in Bitternut Hickory in USA (Accession numbers HQ647288, HQ647286). The pathogenicity of two isolates of F. solani was tested on two-year old potted tea plants of cv TRI 2026 and TRI 2025. All inoculated plants showed lesions after six weeks while control plants remained healthy. Koch’s postulates were confirmed by consistently re-isolating F. solani from inoculated plants. TSHB is a known vector of F. solani as it has a symbiotic relationship with fungi including Fusaria. F. solani has been commonly isolated both from dissected TSHB beetles and galleries in tea bushes (usually these fungi are not pathogenic to tea). However the results indicate that the tested F. solani strains are strongly pathogenic on tea. This is the first report of F. solani causing a disease of tea in Sri Lanka.

The disease cycle of Alternaria leaf blotch and fruit spot of apple

Ms Dalphy Harteveld
University of Queensland
dalphy.harteveld@uqconnect.edu.au

Dalphy Harteveld, Olufemi Akinsanmi, Andre Drenth
University of Queensland, Centre for Plant Science, Queensland Alliance for Agriculture and Food Innovation, Ecosciences Precinct, GPO Box 267, Brisbane, QLD 4001, Australia

Leaf blotch and fruit spot of apple caused by Alternaria spp. cause significant losses to the Australian growers. Control is erratic, mainly due to paucity of information about the causal agents and the disease cycle. The aim of our study was to get a better understanding of the pathogens and the disease cycles. We investigated the identity, distribution, pathogenic and saprophytic fitness of the Australian Alternaria species and determined the sources and seasonal dynamics of Alternaria inoculum, the timing of infection, the spatial pattern of infection in the tree canopy and climatic conditions favouring spore dynamics and infection in the Australian orchards. Results showed that four Alternaria species groups are associated with the diseases; A. arborescens-like, A. tenuissima/A. mali, A. tenuissima/A. alternata intermediate and A. longipes-like. Pathogenicity experiments showed that all four species groups are pathogenic to leaves, but only 2 of the species groups are pathogenic to fruit. A. arborescens was the most common species obtained from leaves, which could be explained by a higher fecundity of isolates of this species compared to the other species groups. Alternaria inoculum overwinters in leaf litter on the orchard floor and in twigs and buds in the trees. In spring the first leaf infections occurred 20 days after bloom and the first fruit spot infection at 90 days after bloom in susceptible apple varieties. Between 70 to 110 days after bloom the majority of leaf and fruit infections occurred. Higher number of leaf and fruit infections occurred in the lower canopy compared to the upper canopy and shoot leaves were more susceptible than spur leaves. Temperature, rainfall and relative humidity influenced inoculum dynamics and infection in the field. The above information has helped to develop improved disease management for the Australian apple industry.
Melon Necrotic Spot Virus detected on watermelons in New South Wales

Dr Len Tesoriero  
NSW Department of Primary Industries  
ten.tesoriero@dpi.nsw.gov.au  
Tesoriero Len, Seyb Alison, Chambers Grant, Terras Mary Ann, Daniel Rosalie,  
NSW Department of Primary Industries EMAI Menangle NSW 2568

Melon necrotic spot virus (MNSV) is an exotic plant pest recently detected on watermelon crops in the Sunraysia region, SW NSW, Australia. MNSV is a species of the Carmovirus genus in the Tombusviridae family having a limited host range, mostly to members of the Cucurbitaceae. It has been previously reported on melons, cucumbers and watermelons in the Americas, Africa, Asia and Europe. MNSV consists of small 30 nm isometric particles with a single-stranded positive-sense RNA genome of approximately 4.3kb. It is known to be externally seed borne and is transmitted by the chytrid fungus, Olpidium bornovanus. MNSV attaches to the outer surface of Olpidium zoospores spreading with water and infecting plant roots. Hence MNSV causes serious diseases in both hydroponic and irrigated field crops. Both Olpidium resting spores and MNSV particles are very stable and remain viable in soil for many years. MNSV is also known to be transmitted by cucumber beetles and mechanical inoculation. The recent trend towards use of grafted watermelons in Australia increases the potential for this virus to be rapidly spread during nursery propagation. In the Sunraysia, affected watermelon crops displayed symptoms including necrotic lesions on leaves and stems, particularly near the crown. Other symptoms were fruit deformation and a reduction in fruit quality with severe rind necrosis, breakdown of pulp tissue, and necrotic spots or lumps on the fruit surface. Some mature plants wilted and died although vascular wilt pathogens such as Fusarium oxysporum and Verticillium dahliae were sometimes also found associated with these plants. Attempts to confirm the virus identity have proven difficult. Various coat protein gene primers failed to amplify in RT-PCR. Sequences of the RNA-dependent RNA polymerase gene have confirmed at least one isolate to be 93% homologous to MNSV whereas other isolates were shown have around 75% homology to Genbank accessions. This suggests that there is more than one MNSV strain associated with the disease in NSW given the species demarcation in the genus Carmovirus is 52% amino acid homology between polymerases. Typical MNSV isometric virions were observed by electron microscopy in negatively-stained sap preparations from roots while ELISA tests gave positive results from symptomatic leaves, fruit pulp and roots. Light microscopy of the roots also revealed smooth-walled resting spores that were consistent with those of Olpidium bornovanus. Further work will continue to characterise the strains of MNSV and confirm the fungus in the roots is Olpidium bornovanus and virus vector.

Pseudomonas syringae pv. porri: a new pathogen of Australian onions

Ms Rebecca Roach  
Department of Agriculture, Fisheries and Forestry  
Rebecca.Roach@daff.qld.gov.au  
Roach Rebecca, Harper Stephen, Carey David, Duff John, McTaggart Alistair, Gambley Cherie

The first record of Pseudomonas syringae pv. porri on onion in Australia was confirmed in September 2012. This pathogen was previously described in Australia on leek and pathogenicity tests determined it could infect other species of Allium (Hall et al. 2007; Noble et al. 2006). Isolates were recovered from water soaked lesions on onion leaf material collected from the Lockyer Valley, QLD. The disease was observed on onion and shallot the previous year. The isolates were characterized as P. syringae by biochemical tests and confirmed as the causal pathogen by Koch’s postulates. Sequences of the cfr and 16S genes from these isolates had high identity to P. syringae pv. porri from Australian leek plants and a non-fluorescent pathovar of P. syringae on onion reported from the United States (Gitaitis et al. 2012). Surveys of the Lockyer Valley and preliminary epidemiology studies were conducted to determine the range and severity of field infections. The disease was widespread across the region and favoured cool, humid conditions. A period of heat may effectively halt disease development, though precise effects of temperature require further investigation. A distinct ‘yellow leaf’ symptom was observed in many field infections and may be a response to toxins, which are reported in several other pathovars of P. syringae. This study developed a reliable method of inoculation in brown onion, red onion and shallot. Opportunities for further study will be detailed, including seed testing methods, efficacy of control methods, pathogen survivability and toxin production. The outcomes of this project will ultimately improve the productivity of the onion industry and develop diagnostic and response protocols for endemic and exotic bacterial pathogens of Allium crops.
Understanding the role of and determining practical management solutions for Quambalaria coyrecup canker disease, the cause of Corymbia calophylla (marri) decline in the south-west of Western Australia.

Dr Trudy Paap
Murdoch University
L.paap@murdoch.edu.au

Trudy Paap (1), Treena Burgess (2), Giles Hardy (3),
(1)Centre of Excellence for Climate Change Woodland and Forest Health, School of Biological Sciences and Biotechnology, Murdoch University, Western Australia, Australia

Corymbia calophylla (marri) a keystone tree species in Western Australian woodlands and forests is suffering a major decline syndrome associated with the canker fungal pathogen Quambalaria coyrecup. This pathogen also causes canker disease on other Corymbia species including C. ficifolia, an endemic to Western Australia (WA), and two exotic species to WA C. maculata and C. ptychocarpa. The disease was first recorded on marri in 1939, and by the 1960s cankers were found to occur throughout the south-west of WA. Since then, mortality attributed to the pathogen has increased, with recommendations that immediate attention be given to determine its cause and develop options for disease control being made in the early 1990s. While the cause of the disease has been determined, the incidence and severity has continued to increase, with the resulting decline and loss of marri having major economic, social and ecological implications, due to the costs associated with lost honey and pollen production, tree removal, wildlife habitats, conservation of roadside verges, amenity values such as shade, and the control of salinity and erosion by reforestation. There is now considerable community concern and support to develop methods of managing this pathogen on marri in the landscape. We will discuss (1) our on-ground assessment methods which we are using to quantify the extent, incidence and severity of the decline, (2) how we are examining the diversity and pathogenicity of Q. coyrecup from across the marri range, (3) the possible role of additional biotic and abiotic factors in the decline syndrome, (4) our approaches to control using different fungicides and application methods, and (5) how we are using community support where appropriate to help us extend our research activities. Our research will be applicable to other susceptible Corymbia species in WA and elsewhere in Australia if or when Q. coyrecup is spread to these regions and potentially overseas where species like C. ficifolia or C. maculata are planted.

Emergence of Pestalotiopsis species as the causal agent of raceme blight and dieback of macadamia

Dr Femi Akinsanmi
QAAFI, The University of Queensland
uqoakins@uq.edu.au

Olufemi A. Akinsanmi, André Drenth
University of Queensland, Centre for Plant Science, Queensland Alliance for Agriculture and Food Innovation, Ecosciences Precinct, GPO Box 267, Brisbane, QLD 4001, Australia

Macadamia is a tree nut originating in the subtropical coastal rainforests of eastern Australia. Macadamia integrifolia, M. tetraphylla and their hybrids are now widely grown for their edible kernel in several countries in Africa, Central and South America, Asia and Oceania. Macadamia flowers are borne on long peduncle racemes of 10-20 cm long each with 100-300 flowers about 12 mm long. Cladosporium cladosporioides, Botrytis cinerea, and Phytophthora capsici have been reported to cause raceme blight of macadamia. In recent years, a new raceme dieback disease was observed in major macadamia-producing areas of Bundaberg in Queensland in Australia. Over the last two seasons, total loss of flowers that resulted in significant crop failure has been observed when unopened flowers were affected. Severe infections occur and the disease is more prevalent in wet and very humid conditions. Characteristic symptoms include necrotic or dieback of the peduncle tip, the entire inflorescence (flowers and peduncle) may be affected as necrotic or dried flowers. Depending on the stage at which infection occurs, dried unopened flowers may remain attached to the peduncle but flowers infected at mid or late bloom stage dried and absconded from the peduncle. Abscised flowers may bunch together by mycelial strands on the peduncle. Identity of the isolates obtained from diseased racemes from different orchards in the 2011-13 production seasons was confirmed using morphological characteristics and DNA sequencing of the ITS region with ITS4/5 primers. The sequences were compared with other fungi by using sequence-based BLAST analyses in Genbank. The majority of the isolates obtained showed high similarity to Pestalotiopsis sp. The genus Pestalotiopsis is complex and contains a heterogeneous group of coelomycetous fungi. There are reports of Pestalotiopsis spp. causing leaf spots, needle blight, tip blight, and gray blight on a variety of hosts, but generally Pestalotiopsis spp. are primarily thought of as opportunistic pathogens that affect stressed plants. The aim of our research is to determine the identity of the causal agents of raceme blight and understand the disease cycle in an effort to minimize losses in commercial macadamia plantations due to these diseases.
Biological and molecular characteristics and geographic spread of the different biovars of Pseudomonas syringae pv. actinidiae.

Dr Joel Vanneste
Plant & Food Research
Joel.Vanneste@plantandfood.co.nz

Joel Vanneste(1), Janet Yu(1), Robert Taylor(2), Deirdre Cornish(1), Bevan Weir(1)
(1)The New Zealand Institute for Plant & Food Research Ltd, Private Bag 3123, Hamilton 3240, New Zealand
(2)Plant Health and Environment Laboratory, Ministry for Primary Industries, PO Box 2095, Auckland 1140, New Zealand

Pseudomonas syringae pv. actinidiae (Psa), the causal agent of bacterial canker of kiwifruit, is a member of a complex species of plant pathogenic bacteria (Pseudomonas syringae). All strains of Psa share the same host range (plants of the genus Actinidia), on which they are all able to cause necrotic leaf spots. However, some strains cause other symptoms such as dieback, cankers and production of a red or white exudate. The pathovar actinidiae is not homogeneous and there are other obvious differences at the biochemical, molecular, pathological and colony morphology levels between strains of Psa. The strains isolated from the Italian outbreak of 2008 differed from the strains isolated from Asia by the DNA sequence of their cts gene, a housekeeping gene. This led to the early grouping of Psa strains as cts haplotype A or cts haplotype I. Each of these cts haplotypes was associated with a distinctive BOX PCR pattern. Some strains isolated from New Zealand were similar to the strains of cts haplotype I. Differences between those Psa strains were confirmed by multi-locus sequence typing analysis using the seven housekeeping genes: acn, rpoD, pgI, pfk, gyrB, gapA and cts. This analysis revealed four distinct groups which have now been called biovars. Strains of biovar 1 and biovar 2 share a similar BOX PCR pattern but have a different cts haplotype. Furthermore, strains of biovar 1 produce phaseolotoxin and those of biovar 2 produce coronatine. Strains of biovar 1 and 2 have been isolated mostly from Japan and Korea respectively. However not all strains from Korea are biovar 2. Strains of biovar 3 or 4 do not produce either toxin; they each have a unique cts haplotype and BOX PCR pattern. Strains of biovar 3 are responsible for the global outbreak of Psa while so far strains of biovar 4 have been found only in New Zealand and Australia. Strains of biovars 1, 2 and 3 are systemic while strains of biovar 4 have been associated only with leaf spots.

The same grouping into four biovars was found when analysing the DNA sequence of the seven effector genes: avrE1, avrD1, hopA1,hopAF1, hopAN1, hopD1, and hrpK1. The four biovars of Psa are more related to each other than to any other pathovar of P. syringae except P. syringae pv. theae (Pst). Strains of Psa biovar 4 are more closely related to Pst than to strains of the other biovars.

Phytophthora pluvialis and its relation to red needle cast disease of Pinus radiata in New Zealand

Dr Nari Williams
Scion - New Zealand Forest Research Institute
nari.williams@scionresearch.com

Nari Williams(1), Ian Hood(1), Margaret Dick(1), Martin Bader(1), Peter Scott(1), Rebecca Ganley(1), Lindsay Bulman(1)
(1)Scion - New Zealand Forest Research Institute, Private Bag 3020, Rotorua 3046, New Zealand

Phytophthora pluvialis Reeser, W.L. Sutton & E.M. Hansen is the cause of a newly described disease, red needle cast, in certain stands of Pinus radiata in New Zealand that experience periodic foliage browning. Infection appears to be limited to the needles with no recoveries of P. pluvialis having been made from the roots, stems or branches. Occasionally a second species of Phytophthora, P. kernoviae, Brasier, Beales & Kirk is also recovered from needles with the same symptoms. Occurrence of the disease has been variable in incidence and severity both regionally and in different years. The early symptoms of discrete olive coloured lesions, often with a narrow dark resinous mark or band, were first recognised in winter of 2008 in plantation forests on the eastern coast of the North Island. These lesions develop further leading to rapid needle senescence and premature defoliation. The disease has been termed red needle cast in New Zealand as affected trees have a reddish appearance prior to the casting of the needles. Symptoms are first observed in late autumn through to late winter. Newly developing spring and summer foliage is seldom affected. Studies were undertaken to test the possibility that these species may be transported on pine logs either as superficial contaminants or as colonists of bark or wood. Isolation, direct inoculation and vitality studies indicate that occurrence of P. kernoviae or P. pluvialis on export logs is negligible. In addition, the demonstration of a substantial decline in vitality with time implies that the survival of any oospores that may still be present is likely to be slight or non-existent. It is concluded that there is little if any risk of transporting these Phytophthora species on New Zealand radiata pine logs.
**Myrtle rust - symptoms, impact and spread in Queensland, Australia**

Dr Fiona Giblin  
University of the Sunshine Coast  
fgiblin@usc.edu.au  

Fiona Giblin (1), Geoff Pegg (1,2), Gordon Guymear (1), Suzy Perry (1)  
(1) Forest Industries Research Centre, University of the Sunshine Coast, Locked Bag 4, Maroochydore DC, Qld, Australia 4001  
(2) Horticulture and Forestry Science, Agri-Science Queensland, Department of Agriculture, Fisheries and Forestry, GPO Box 267, Brisbane, Qld, Australia 4001  

Puccinia psidii was long considered a significant threat to Australian plant industries and ecosystems. In 2010, *P. psidii* was detected for the first time in Australia on the NSW central coast. The fungus spread rapidly and is now widespread on the east coast of Australia. Our studies aimed to determine the host range and impact of *P. psidii* on species of environmental and commercial significance in Queensland. The effect of the disease on native Myrtaceae of Australia’s ecosystems has yet to be determined as the full host and geographic ranges of the disease, and the susceptibility and damage caused to individual species, are assessed. This will depend on a range of factors including the rate of natural and human-assisted spread, and climatic conditions in potentially suitable areas. Commercial impacts are also difficult to measure. The nursery and garden industries have been impacted with losses of stock and subsequent necessity for disease management through plant selection and fungicide programs. The lemon myrtle (*Backhousia citriodora*) and forestry (*Eucalyptus spp.*) industries are screening for myrtle rust resistance. Disease development for *Puccinia psidii* is favoured following periods of rainfall and conditions of high humidity or fog when extended periods of leaf wetness are more likely to be achieved promoting spore germination and infection of the host. It is also necessary for spores to encounter a host plant during stages of active plant growth. The host range of *P. psidii* has increased rapidly exceeding 160 species from 37 different genera in Queensland. *Puccinia psidii* has now been identified from a range of native forest ecosystems including coastal heath, coastal and river wetlands, sand island ecosystems, and littoral, montane, subtropical and tropical rainforests. The impact of *P. psidii* on individual trees and shrubs has ranged from minor leaf spots to dieback and reduced fecundity. Tree death as a result of repeated infection has also been recorded for some species, with regenerating seedlings becoming infected and killed by *P. psidii*. *Puccinia psidii* infection has been recorded on flower buds, flowers and fruits of 27 host species. The most highly susceptible species recorded to date are *Syzygium jambos*, *Eugenia reinwardtiana*, *Agonis flexuosa*, *Gossia inopolia*, *Melaleuca quinquenervia*, *Rhodamnia rubescens*, *R. maideniana*, *R. angustifolia*, *Chamelacium Uncinatum* and *Decaspermum Humile*.

**Pathogenicity of Pythium spp. isolated from ginger fields in Australia**

Mr Duy Le  
The University of Queensland  
p.le@uq.edu.au  

Duy Le(1), Mike Smith(2), Elizabeth Allker(1)  
(1) School of Agriculture and Food Sciences, The University of Queensland, 4072, Australia  
(2) Queensland Department of Agriculture, Fisheries and Forestry, Nambour, 4560, Australia  

Fifteen *Pythium* species which are responsible for *Pythium* soft rot (PSR) disease on ginger have been recorded around the world. In Australia, PSR outbreaks on ginger (*Zingiber officinale*) were observed in 2007 and *P. myriotylum* Drechs. was reported as a causal agent of PSR in 2009. The PSR can cause yield losses up to 100% in some fields. Recent research reported here proposes that there may be more than one *Pythium* species involved in the PSR in Australia. One hundred and fifty isolates of *Pythium* spp. were recovered from: PSR rhizomes, or baiting using excised carrots, ginger or sorghum seeds. Nine *Pythium* species including *P. aphanidermatum*, *P. dipleurothecium*, *P. graminicola*, *P. oligandrum*, *P. perplexum*, *P. spinosum*, *P. splendidens*, *P. ultimum* and putative *P. zingiberis* were identified based on morphological characteristics and sequences of ITS and CoxII. Pathogenicity tests were conducted both *in-vitro* on excised ginger sticks and seedlings of fourteen hosts: oats (*Avena sativa*), rye (*Secale cereale*), wheat (*Triticum* sp.), millet (*Panicum milaceum*), barley (*Hordeum vulgare*), buck wheat (*Fagopyrum esculentum*), beet root (*Beta vulgaris*), spring onion (*Allium fistulosum*), carrot (*Daucus carota*), lettuce (*Lactuca sativa*), cucumber (*Cucumis sativus*), eggplant (*Solanum melongena*), alyssum (*Lobularia maritima*), and gymnosiphia (*Gypsophila elegans*) and in pot trials on ginger plants. The results showed that all representative isolates of these species were very pathogenic in *in-vitro* tests, except for *P. oligandrum* and *P. perplexum* being non-pathogenic and only slightly pathogenic, respectively. In the pot trial, putative *P. zingiberis* isolated from diseased ginger was the only species that would induce PSR symptoms a week after inoculation and putative *P. zingiberis* isolates were reobtained directly from the PSR infected rhizomes. All other *Pythium* spp. were recovered from soil baiting with carrot pieces. The results also allow us to conclude that putative *P. zingiberis* is the main causal agent responsible for the PSR on ginger in Australia and more plant crops should be screened for putative *P. zingiberis* tolerance or resistance so that a suitable rotation crop can be found.
Determining the origin of the emerging pathogen, *Phytophthora multivora*

Dr Treena Burgess  
Murdoch University  
z.l.lutz@hotmail.com  
(1) Centre for Phytophthora Science and Management, School of Veterinary and Life Sciences and Biotechnology, Murdoch University, Perth, WA, Australia  
(2) Science Division, Department of Environment and Conservation, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

*Phytophthora multivora* is widespread in Western Australia (WA); it has a wide host range and considerably variability in the sequence of the mitochondrial gene cox1 led to the hypothesis that it may be endemic to the region. To test this hypothesis, four nuclear (ITS, enolase, HSP90 and ras) and three mitochondrial (cox1, coxIGS and nadh1) loci were sequenced for 100 isolates of *P. multivora* isolated from Australia, New Zealand, USA, South Africa (RSA) and Europe and the data were subjected to phylogenetic, coalescent-based and population genetic analyses. Isolates from RSA possess greater nucleotide diversity and a greater number of alleles at three of the nuclear loci and at all three mitochondrial loci than those from elsewhere. In addition, the RSA population had more unique multilocus genotypes than other populations. While of *P. multivora* is widely distributed in natural ecosystems in WA and RSA, it is usually isolated from nurseries or horticulture elsewhere in the world. Additionally, of *P. multivora* is consistently isolated from cankers and dead and dying plants of numerous endemic hosts in WA, but is predominantly isolated from soil associated with asymptomatic plants in RSA. Based on this evidence it is proposed that of *P. multivora* is endemic to RSA and has been introduced to Western Australia.

A new *Phytophthora* disease from nurseries in Western Australia

Ms Agnes Simamora  
Murdoch University  
A.Simamora@murdoch.edu.au  
(1) Centre for Phytophthora Science and Management, School of Veterinary and Life Sciences and Biotechnology, Murdoch University, Perth, WA, Australia  
(2) Science Division, Department of Environment and Conservation, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

*Phytophthora alticola* was first isolated and described from plantation eucalypts in South Africa, and has more recently been found in Western Australia, where it has only been isolated from dead and dying plants from nurseries and urban tree plantings, predominantly from eucalypts. *Phytophthora arenaria* has been isolated from vegetation occurring on the northern sandplains of southwest WA, predominantly from *Banksia* spp. A number of isolates with similar morphological characters to *P. arenaria* have been isolated, but with some variation in ITS region sequences, and have been referred to as *P. aff arenaria* type I (with the vast majority of isolates coming from nurseries and urban tree plantings) and type II (predominantly from the northern sandplains). A re-evaluation of these species suggests that type I isolates are *P. alticola*, while type II isolates are *P. arenaria*. A detailed overview of the nursery disease and of how this taxonomical evaluation has been undertaken will be discussed. While it is thought that *P. arenaria* is endemic, we are still to ascertain whether *P. alticola* is endemic or has been introduced to Western Australia.

Determining the origin of the emerging pathogen, *Phytophthora multivora*  

A new *Phytophthora* disease from nurseries in Western Australia

**Phytophthora multivora** is widespread in Western Australia (WA); it has a wide host range and considerably variability in the sequence of the mitochondrial gene cox1 led to the hypothesis that it may be endemic to the region. To test this hypothesis, four nuclear (ITS, enolase, HSP90 and ras) and three mitochondrial (cox1, coxIGS and nadh1) loci were sequenced for 100 isolates of *P. multivora* isolated from Australia, New Zealand, USA, South Africa (RSA) and Europe and the data were subjected to phylogenetic, coalescent-based and population genetic analyses. Isolates from RSA possess greater nucleotide diversity and a greater number of alleles at three of the nuclear loci and at all three mitochondrial loci than those from elsewhere. In addition, the RSA population had more unique multilocus genotypes than other populations. While *P. multivora* is widely distributed in natural ecosystems in WA and RSA, it is usually isolated from nurseries or horticulture elsewhere in the world. Additionally, *P. multivora* is consistently isolated from cankers and dead and dying plants of numerous endemic hosts in WA, but is predominantly isolated from soil associated with asymptomatic plants in RSA. Based on this evidence it is proposed that *P. multivora* is endemic to RSA and has been introduced to Western Australia.

**Phytophthora alticola** was first isolated and described from plantation eucalypts in South Africa, and has more recently been found in Western Australia, where it has only been isolated from dead and dying plants from nurseries and urban tree plantings, predominantly from eucalypts. *Phytophthora arenaria* has been isolated from vegetation occurring on the northern sandplains of southwest WA, predominantly from *Banksia* spp. A number of isolates with similar morphological characters to *P. arenaria* have been isolated, but with some variation in ITS region sequences, and have been referred to as *P. aff arenaria* type I (with the vast majority of isolates coming from nurseries and urban tree plantings) and type II (predominantly from the northern sandplains). A re-evaluation of these species suggests that type I isolates are *P. alticola*, while type II isolates are *P. arenaria*. A detailed overview of the nursery disease and of how this taxonomical evaluation has been undertaken will be discussed. While it is thought that *P. arenaria* is endemic, we are still to ascertain whether *P. alticola* is endemic or has been introduced to Western Australia.
SESSION 6C – NEW AND EMERGING DISEASES

Blackberry decline along the Warren and Donnelly Rivers: a major disease of *Rubus anglocandicans* in south-west Australia

Prof Giles Hardy
Murdoch University
G.Hardy@murdoch.edu.au

Sonia Aghighi(1), Treena I. Burgess(1), John K. Scott(2), Michael Calver(1), Lee Fontanini(1), Paul B. Yeoh(2), Giles E. St.J. Hardy(1),

(1)Centre for Phytophthora Science and Management, School of Veterinary and Life Sciences, Murdoch University, W.A. 6150, Australia.
(2)CSIRO Ecosystem Sciences, Biosecurity Flagship, Private Bag 5, P.O. Wembley, W.A. 6913, Australia.

*Rubus anglocandicans* is the most common species of European blackberry in Western Australia (WA) and one of the weeds of national significance in the south-west of WA. It is a major weed of conservation areas, forestry and agriculture. Exotic strains of the blackberry rust *Phragmidium violaceum* have been introduced to WA as biological control agents, but in most areas it seems that they are not effective, possibly due to climate. In 2007 while monitoring establishment of the released rust strains, unexplained dead and diseased blackberry plants were discovered at two locations; along the Warren River near Pemberton and the Donnelly River near Manjimup in the south-west of WA. The extent of the disease, with noticeable changes to vegetation structure due to the removal of dense blackberry infestations, has lead to it being called “blackberry decline”. We outlined the history of the “decline” phenomenon on blackberry in the south-west of WA and propose a conceptual model, to describe the biotic and abiotic factors that are hypothesised to be involved in the decline phenomenon of *R. anglocandicans*.

First report of ‘*Candidatus*’ Liberibacter solanacearum in carrot in France

Ms Françoise Poliakoff
Anses - Plant Health Laboratory
Françoise.poliakoff@anses.fr

Marianne Loiseau (1), Soraya Garnier (1), Violaine Boirin (1), Maryse Merleau (1), Anne Leguay (1), Isabelle Renaudin (1), Jean-Philippe Renvoise (2), Pascal Gentil (1), Françoise Poliakoff (1),

(1)French Agency for Food, environmental and occupational health and safety - Anses - Plant Health Laboratory – Angers , 7 rue jean Düméras 49044 Angers cedex 01 - France
(2)French Agency for Food, environmental and occupational health and safety - Anses - Plant Health Laboratory Plant Quarantine Unit, Site de Clermont-Ferrand, 6 rue Aimé Rudel Marmilhat, 63370 LEMPDES, France

In 2012, typical symptoms of Aster yellows phytoplasma were observed in carrot field in France. Total DNA was extracted from phloem tissue of symptomatic and asymptomatic plants with CTAB method. DNA extracts were tested by real-time PCR for phytoplasmas (Christensen *et al.*, 2004) and for “*Ca. L. solanacearum*” (Li *et al.*, 2009). Two PCR targeting a portion of 16S rDNA and rpIJ/rpIL ribosomal protein genes of the bacteria were also performed to characterize it (Munyaneza *et al.*, 2012). Phytoplasmas were not detected in any of the studied samples. All carrot plants were tested positive for “*Ca. L. solanacearum*” with real-time PCR. Those positive results were confirmed by amplification of a 1,168 bp 16S rDNA fragment and a 669 bp rpIJ/rpIL fragment using specific primers for “*Ca. L. solanacearum*”. Sequences of amplicons showed strong similarity with sequences of “*Ca. L. solanacearum*” from carrot in Europe. This is the first report of “*Ca. L. solanacearum*” in carrot in France.
Exotic pests and pathogens detected by general surveillance in Victoria- 2010 to 2013

Dr Robert Holmes
Department of Environment and Primary Industries
robert.holmes@depi.vic.gov.au

Robert Holmes(1), Jacky Edwards(1), Ramez Aldaoud(1), SriKanthi de Alwis(1), Quang Dinh(1), Soheir Salibi(1), Lila Namibr(1), John Wainer(1), Con Skytas(1), Brendan Rodoni(1), Mali Malipatil(1), Fiona Constable(1), Linda Semeeran(1), Mark Blacket(1), Joanne Mackie(1), Robyn Brett(1), Chris Bottcher(1), Dean Harapas(1), Vyrna Beilharz(1), Denise Wite(1), Mirko Milinkovic(1), James Cunningham(1)

Crop Health Services (CHS), a business of the Department of Environment and Primary Industries (DEPI) in Victoria, conducts a plant diagnostic service involving discipline specialists in entomology, mycology, nematology, virology and bacteriology. Diagnoses assist the management of productivity, biosecurity and market access for the State’s plant based industries and the protection of the environment. Isolated suspect pathogens are identified using the appropriate combination of cultural, morphological, biochemical, molecular (including sequencing) and immunological techniques. Staff are members of the National Plant Biosecurity Diagnosticians Network and participate in the national proficiency testing program. CHS has an agreement with Biosecurity Victoria, DEPI, to report suspect and confirmed exotic plant pathogens and new host records to the Chief Plant Health Officer within 24 hours of detection under the State’s General Surveillance project. In the past 3 years CHS has conducted 16,000 diagnoses on samples submitted by the public, consultants, and State and Federal biosecurity agencies. In this time over 50 pests and pathogens detected have been new Australian records, new State records or new host records. The most significant of these are Cryphonectria parasitica (chestnut blight) which is currently under an eradication program, and Cantareus apertus (green garden snail) and Puccinia psidii (myrtle rust) which are under Statewide management plans.

Species and subclade composition of Leptosphaeria spp. populations causing blackleg in brassica crops in New Zealand

Ms Suhaizan Lob
Lincoln University
Suhaizan.Lob@lincolnuni.ac.nz

Suhaizan Lob(1), Megan Outram(1), Hayley Ridgway(1), Marlene Jaspers(1), Eirian Jones(1)

(1)Department of Ecology, Faculty of Agriculture and Life Sciences, Lincoln University, Canterbury, New Zealand

Phoma black leg or stem canker, caused by Leptosphaeria maculans or L. biglobosa is one of the most important diseases of brassicas, causing serious losses of canola worldwide. In New Zealand, L. maculans has been reported to cause disease of forage brassicas such as kale and dry rot of swede, whilst L. biglobosa had not been reported. A sampling was done in 2011 and 2012 to determine the causal agent of phoma stem canker/ dry rot in New Zealand cropping areas. Of the 128 isolates obtained, 125 isolates were morphologically identified as L. maculans and three isolates as L. biglobosa. The identity of representative isolates were confirmed using species-specific primers and sequencing of the ribosomal DNA, actin, and β-tubulin gene regions. Comparison of resulting sequences with sequences in GenBank confirmed identity as L. maculans ‘brassicace’ and L. biglobosa ‘brassicae’. Leptosphaeria maculans was recovered from all regions sampled (Manawatu, Hawke’s Bay, Wairarapa, Canterbury, and Southland) and from canola, kale leaf lesions and stem cankers, and dry rot lesions on swede. Leptosphaeria biglobosa was only recovered from Canterbury and from leaf lesions and stem cankers of canola and kale. Leptosphaeria maculans is a heterothallic fungus, with sexual reproduction requiring the presence of two mating types (MAT) with two idiomorphs, MAT1-1 and MAT1-2. Amplification of the genomic DNA with three primers; MAT P9, MAT P10 and MAT P11 showed the mating type ratio for New Zealand populations of the pathogen is 5:1 MAT1-1:MAT1-2. This deviation from the expected 1:1 ratio indicated a high rate of clonal multiplication in the New Zealand population. The presence of three cloned avirulence genes (AvrLm1, AvrLm6 and AvrLm4-7) in 40 L. maculans isolates was also demonstrated by amplification of genomic DNA using paired primers for each allele (forward and reverse primers of AvrLm1, AvrLm6 and AvrLm4-7). Avr7 was amplified from the DNA of seven isolates, Avr6 was amplified from DNA of all tested isolates and Avr4-7 was amplified from DNA of 16 isolates. Four isolates were positive for all three alleles tested. This information will be valuable for selecting/breeding cultivars with resistance to the pathogen population present in New Zealand. Pathogenicity tests showed all L. maculans and L. biglobosa isolates tested were pathogenic on canola and swede, causing characteristic leaf lesions. Stem cankers developed on plants inoculated with L. maculans 40 days post inoculation, but not on plants inoculated with L. biglobosa.
‘Candidatus’ Liberibacter solanacearum: its interactions with insect and plant hosts and their impacts on potato production

Dr Andrew Pitman
The New Zealand Institute for Plant & Food Research
andrew.pitman@plantandfood.co.nz

Andrew Pitman, Shirley Thompson, Natasha Taylor, Peter Wright, Farhat Shah, Nadine Berry, Sam Read, Jessica Dohmen-Vereijssen, Melanie Walker, Samuel Beard, Nina Jorgensen, Ruth Butler,
The New Zealand Institute for Plant & Food Research Ltd, Private Bag 4704, Christchurch, New Zealand

‘Candidatus’ Liberibacter solanacearum (Lso) is a phloem-limited bacterium that is emerging globally as an economically important pathogen in a variety of crop plants. In potato, Lso is associated with zebra chip, a disease characterized by dark flecking throughout affected potato tubers that upon frying results in unpalatable chips or French fries. Potato plants infected with Lso also produce a variety of foliar symptoms, including curling of emerging leaves, purple and yellow discoloration of the new shoots, shortened internodes, and swollen auxiliary buds, which culminate in the lethal collapse of the plant. Lso is vectored by Bactericera cockerelli, commonly referred to as the tomato potato psyllid (TPP), which upon feeding on the phloem transmits Lso to the plant. TPP populations that do not have Lso, however, can also cause damage to potato. The foliar symptoms that arise from feeding by such TPP, known as psyllid yellows, are similar to those of zebra chip affected plants, although plants tend to survive and tubers do not produce zeba chip. The epidemiological importance of TPP in zebra chip and psyllid yellows has focused management strategies on control of the insect, primarily through regular applications of insecticides. Yet, the significance of tuber-borne inoculum of Lso in zebra chip and its impact on potato production remains controversial. In the United States, tubers with symptoms of zebra chip are generally unable to sprout, whereas tubers infected with Lso in New Zealand frequently fail to develop zebra chip symptoms and are often able to emerge the following season. Here, we describe the results of field and shadehouse studies that have defined the disease symptoms in potato upon exposure to both TPP-borne and tuber-borne inoculum of Lso as well as to psyllid feeding. In particular, we reveal the yield and quality consequences. For example, marketable yield showed little or no reduction due to TPP pressure whether insects were Lso-positive or negative, whereas the Lso status of the mother tuber dramatically reduced yield. We also explore how these trials have shown that cultivars differ in their responses to these treatments and that these differences can influence the epidemiological significance of tuber-borne inoculum of Lso. Finally, all the data is incorporated into our latest model of how the interactions between Lso, TPP and potato might influence production in the field and how growers might more effectively manage them.

Black Scab of Jojoba (Simmondsia chinensis) – a new emerging disease in Australia caused by a new pathotype of Elsinoë australis

Amir Sohail
asohail@csu.edu.au

Amir Sohail, Ben Stodart, John Harper, Gavin J. Ash
School of Agricultural and Wine Sciences, Charles Sturt University, Boorooma Street, Locked Bag 588, Wagga Wagga, NSW-2678, Australia and E.H Graham Centre for Agricultural Innovation (an alliance between Charles Sturt University and NSW DPI)

A new pathotype of Elsinoë australis causing Black Scab of jojoba (Simmondsia chinensis), not found previously on any Australian crop, was recently discovered by pathology research team at the Charles Sturt University. Presently, Elsinoë australis is on the watch list of Plant Health Australia as a serious threat to the Australian citrus industry. Currently, economical viable Australian Jojoba industry is under threat as over 80% of jojoba plantations are found heavily infected by Elsinoë australis. In order to uncover its origin, amplification and sequencing of the complete internal transcribed spacer ITS1, 5.8S and ITS2 region was achieved from representative jojoba isolates using primers ITS-1 & ITS-4. Results showing 97% homology confirms isolates from jojoba to be Elsinoë australis. In addition, varietal screening of 5 different varieties namely, Barindji, Waradjuri Dadi Dadi, Guyambil, and Wadi Wadi, as jojoba hosts, was conducted to identify susceptible and resistant varieties. While Waradjuri proved to be the most susceptible Waddi Waddi showed mild tolerance against this pathogen. These findings strongly supported the disease survey report recently conducted by jojoba growers from various locations of New South Wales and Southern Queensland, Australia.
ABA2 disjoints ABA pathway into an upstream part required for Bamboo mosaic virus accumulation and a downstream part required for plant resistance

Mr Mazen Alazem
Academia Sinica - IPMB
mazen@gate.sinica.edu.tw

Mazen Alazem (1), Na-Sheng Lin (1)

(1) Institute of Plant and Microbial Biology, Academia Sinica, Taipei 115, Taiwan, ROC.
Molecular and Biological Agricultural Sciences Program, Taiwan International Graduate Program, National Chung-Hsing University and Academia Sinica, Taipei 115, Taiwan, ROC.

Graduate Institute of Biotechnology, National Chung-Hsing University, Taichung, 402, Taiwan, ROC.
Biotechnology Center, National Chung-Hsing University, Taichung, 402, Taiwan.

Abscisic acid (ABA) has been reported to play multifaceted roles in plant defense depending on the timing of induction and the lifestyle of the pathogen. Plenty of works have covered ABA roles under fungal or bacterial infections. However, ABA-virus interaction has gained less attention, and only few works indicated that ABA supports plant resistance to viruses. In our study we elucidated the work on ABA-virus interaction, and discovered a unique and novel role for ABA2, which is involved in the biosynthesis of ABA, by supporting the accumulation of Bamboo mosaic virus (BaMV). The Arabidopsis thaliana mutant aba2-1 greatly reduced the accumulation (+)RNA, (-)RNA and the coat protein of BaMV. The upstream biosynthesis mutant nced3, to less extent, also reduced BaMV accumulation. In addition, spraying plants with ABA inhibitor also reduced the viral titer. It was shown that the reduced levels of BaMV were always accompanied with low levels of ABA2 in these 3 experiments, whereas downstream biosynthesis mutant aao3 or signaling mutants such as abi-1-1, abi-3 or abi-4 enhanced the accumulation of BaMV RNA although ABA was significantly induced in 2 insensitive mutants, indicating that the ABA signaling pathway is required for plant resistance against BaMV. This was proven by using a transgenic line (OsNCED3-O/E) that over produces ABA, but not ABA2, this line suppressed the accumulation of BaMV, and supported the finding that ABA signaling pathway is required for the resistance. Interestingly Cucumber mosaic virus (CMV) was also repressed in aba2-1 mutant. Additionally, knocking down ABA2 in Nicotiana benthamiana plants showed similar response to A. thaliana mutant aba2-1. Infecting N. benthamiana plants with BaMV or CMV increased the accumulation of ABA and simultaneously induced SA and ABA pathways, indicating the infection with these two RNA viruses disrupts the antagonism between ABA and SA.

Dothistromin: a fungal virulence factor encoded by a fragmented gene cluster

Dr Rosie Bradshaw
Massey University
r.e.bradshaw@massey.ac.nz

Rosie E. Bradshaw (1), M. Shahjahan Kabir (1), Pranav Chettri (1), Pierre J.G.M. de Wit (2)

(1) Bio-Protection Research Centre, Institute of Fundamental Sciences, Massey University, Palmerston North, New Zealand
(2) Laboratory of Phytopathology, Wageningen University, Wageningen, The Netherlands

Dothistroma needle blight is a foliar disease of pines caused by the fungal pathogen Dothistroma septosporum. The pathogen secretes a non-host-specific toxin, dothistromin, which is remarkably similar in structure to the aflatoxin precursor versicolorin A. Genes for dothistromin biosynthesis are unusual in being dispersed over one chromosome instead of being clustered like aflatoxin genes, but are regulated by an ortholog of the aflatoxin regulator, AfIR. The aims of this study were to determine the role of dothistromin in pine needle disease. Mutants of D. septosporum that lack the ability to make dothistromin are able to infect pine needles and complete their life cycle. However, disease lesions produced by these mutants are smaller and contain significantly fewer spores than lesions produced by wild-type strains that make dothistromin. These results suggest an important role for dothistromin in virulence. During the infection cycle, there is a latent period of several weeks during which very little fungal growth or dothistromin production occurs. Toxin production increases concomitantly with increase in fungal biomass and the first appearance of necrotic symptoms. The closely-related tomato pathogen, Cladosporium fulvum, is a biotroph and does not make dothistromin despite having relics of dothistromin biosynthetic genes in its genome. On the basis of our results we propose that dothistromin is not required for initial host cell death but may contribute to further necrosis as well as stimulating sporulation, either directly or indirectly.
Phytophthora root rot of avocado - why are some rootstocks more resistant?

Ms Merran Neilsen
Queensland Alliance for Agriculture and Food Innovation
merran.neilsen@uqconnect.edu.au

Merran Neilsen(1), André Drenth(1), Elizabeth Dann(1), Paul Campbell(1)
(1)Ecosciences Precinct, 2C West, 41 Boggo Rd, Dutton Park, QLD, Australia

A major production-limiting factor for avocado is Phytophthora root rot caused by Phytophthora cinnamomi. Current management practices include usage of tolerant rootstocks, disease-free nursery material, applications of phosphorous acid and good cultural practices. Significant losses still occur however, particularly after periods of heavy rain. Rootstocks bred for resistance are only partially resistant to the disease, and are subject to a strong genotype x environment effect. The mechanisms of resistance to Phytophthora root rot are poorly understood. Previous work has deduced that components of resistance may include root regenerative ability, differential zoospore attraction and encystment, production of internal structural barriers, and induced or constitutive biochemical defences. The purposes of our research are to identify and quantify the different resistance mechanisms of avocado rootstocks to the disease. Techniques have been developed to measure root regeneration in the presence and absence of P. cinnamomi, and to quantify zoospore encystment on roots of different varieties. Currently, the hypothesis being tested is that root regeneration is a major component of the resistance of various rootstocks. An in depth knowledge of the components of Phytophthora root rot resistance will contribute valuable information for future targeted selection and breeding programs, helping to lessen the impact of the disease.

Investigating the role of strigolactones in pea (Pisum sativum) interactions with soilborne fungal pathogens

Sara N. Blake
University of Tasmania
sara.blake@utas.edu.au

Sara N. Blake(1), Karen Barry(2), Eloise Foo(1)
(1)School of Plant Science, University of Tasmania, Private Bag 55, Hobart, 7001, Australia
(2)Tasmanian Institute of Agriculture, University of Tasmania, Private Bag 54, Hobart 7001, Australia

Strigolactones (SLs) are a recently identified group of novel plant hormones that are produced in the root and exuded into the rhizosphere. SLs from plant host roots cause seeds of plant parasitic weeds to germinate and promote spore germination and hyphal branching of arbuscular mycorrhizal fungi. Phytopathogenic soilborne fungi are also important (parasitic) partners of plants but the role of SL on these disease-causing soilborne fungi is unknown. To investigate the role of SL in plant fungal disease, a genetic approach was taken using the carotenoid cleavage dioxygenase8 mutant of Pisum sativum (pea) that contains a mutation in the SL biosynthesis gene RAMOSUS (RMS) coding for a key enzyme in the biosynthetic pathway. Root exudates and root tissue of rms1 pea plants have no detectable SL concentration. We investigated the development of disease in pea mutants compared to wild type (Torsdag cv.) grown in controlled environment growth cabinets inoculated with the pea pathogens Fusarium oxysporum f. sp. pisi (Fop) or Pythium irregulare (Pi). We are also examining the expression of hormone and disease-related genes and SL levels in this system. In vitro assays were also conducted to assess the effects of the SL synthetic analogue, GR24, on Fop and Pi growth in culture. These findings have implications for agriculture and disease management. Any attempt to harness SL as a crop application, either as germination stimulant of parasitic plants prior to crop planting, or for promotion of mycorrhiza to enhance nutrient acquisition in low fertility soils, must be carefully weighed against potential effect on disease development in interactions with phytopathogenic fungi.
**Botryosphaeriaceae fungi as a potential mycoherbicide for prickly acacia**

Mr Ahsanul Haque  
The University of Queensland  
ahsanul.haque@uqconnect.edu.au

Ahsanul Haque(1), Victor Galea(1), Ken Goulter(1), Rieks D van Klinken(2)

(1)School of Agriculture and Food Sciences, The University of Queensland, Gatton, Qld 4343, Australia  
(2)CSIRO Ecosystem Sciences, GPO Box 2583, Brisbane Qld 4001, Australia

Prickly acacia (*Acacia nilotica* ssp. *indica*) is one of the Weeds of National Significance (WONS) in Australia. Recently, dieback symptoms ranging from stem lesions, partial crown death through to widespread death of plant populations were observed in many locations across north Queensland. Fungi were isolated from stem tissues of symptomatic plants and identified by sequencing of the ITS region. This revealed the consistent presence of *Botryosphaeria mammame* from every site. Several other species of Botryosphaeriaceae and various mitosporic fungi were also recovered. All the isolates were screened for pathogenicity under laboratory conditions using a seedling bioassay. A sub-set of aggressive isolates across the range of species found were used to challenge juvenile plants by stem inoculation under glasshouse conditions to determine the potential use of these fungi as mycoherbicides. Based on preliminary glasshouse trials, three highly pathogenic isolates identified as *Botryosphaeria mammame*, *Botryosphaeria sp.* and *Lasiodiplodia pseudotheobromae* (all Botryosphaeriaceae) were selected for further testing. Of these, *Lasiodiplodia pseudotheobromae* (sourced from dieback-affected parkinsonia) was shown to be highly pathogenic to prickly acacia in preliminary trials. These three isolates were then tested singly and in all combinations in both glasshouse and field trials. Fungi were applied in field trials using a gelatine capsule delivery system. In the glasshouse trial, *Lasiodiplodia pseudotheobromae* alone and in combination with *Botryosphaeria mammame* and a *Botryosphaeria sp.* developed significant externally and internally visible stem lesions. Field trials were first assessed six months after inoculation. Stem lesions and stem bleeding (similar to that observed in the glasshouse trial) were observed at one location. Symptoms such as defoliation, stem and branch cankers and crown distortion were not observed but observations are ongoing. Findings from the glasshouse trial and preliminary field observations suggest that *Lasiodiplodia pseudotheobromae* shows promise as a mycoherbicide for prickly acacia.

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**Profiles of *Fusarium* species and mycotoxin on white corn varieties in the Philippines**

Dr Cecilia Pascual  
Philippine Phytopathological Society  
cbpascual22@yahoo.com

Cecilia Pascual, Eureka Teresa Ocampo, Ana Kristine Barcos  
Crop Science Cluster-Institute of Plant Breeding, College of Agriculture, University of the Philippines Los Baños, College, Laguna Philippines 4031

In the Philippines, the last five years has seen the rise in atmospheric temperatures and consequent increase in Fusarium ear rot incidence. *Fusarium* from corn produces a carcinogenic class of mycotoxins called Fumonisins that have been implicated in esophageal cancer in corn-eating communities and also causes detrimental animal disorders. To determine the *Fusarium* species and the isolates that produce Fumonisins, Fusarium–infected corn ear samples were collected from major corn growing areas of the country. Isolation into pure culture and identification were done following the standard protocol. Of the two hundred ten (210) *Fusarium* isolates collected, 184 were *Fusarium verticillioides* based on morphological and cultural characteristics. This was confirmed by PCR using species-specific primers. The ability to produce Fumonisins was also assessed using Fumonisin-specific primer and by ELISA. A total of 175 *Fusarium verticillioides* isolates produced Fumonisins. Isolates that were positive to Fumonisins but were not *F. verticillioides* were tested for other *Fusarium* species such as *F. proliferatum* and *F. graminearum* using species-specific primers. However, only *F. proliferatum* was detected in 10 out of 15 Fumonisin-producing isolates. Further investigation will be conducted to verify the identity of other 5 isolates. During the regional collection of Fusarium-infected ears in corn-eating communities in the province of Cebu, it was observed that some localities were still planting the traditional variety Tingigub, a very low-yielding and short cob white corn. Fusarium ear rot was seldom observed in Tingigub. Infected Tingigub showed very mild symptom of pinkish discoloration of kernels and was negative to Fumonisin although microscopic observation indicated that the isolates were *Fusarium* species based on conidial morphology. Severe symptoms of whitish pink to lavender fungal growth were observed in IPB Var 6, a newly introduced high-yielding white corn variety. *Fusarium* isolates from IPB Var 6 were Fumonisin-producing *F. verticillioides*. Further evaluation with artificial inoculation of virulent *F. verticillioides* isolate will be conducted in these two varieties to confirm resistance.

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**References**

(1) Ahsanul Haque, Victor Galea, Ken Goulter, Rieks D van Klinken

(2) School of Agriculture and Food Sciences, The University of Queensland, Gatton, Qld 4343, Australia

CSIRO Ecosystem Sciences, GPO Box 2583, Brisbane Qld 4001, Australia

**About the Authors**

Dr Cecilia Pascual

Philippine Phytopathological Society  
cbpascual22@yahoo.com

Cecilia Pascual, Eureka Teresa Ocampo, Ana Kristine Barcos  
Crop Science Cluster-Institute of Plant Breeding, College of Agriculture, University of the Philippines Los Baños, College, Laguna Philippines 4031
**Manipulating the ‘Boom and Bust’ cycle of blackleg disease of canola saves Australian farmers $20 million in 2012**

Dr Angela Van de Wouw  
School of Botany, University of Melbourne  
apvdw2@unimelb.edu.au

Angela Van de Wouw(1), Steve Mcarcroft(2), Barbara Howlett(1)

(1) School of Botany, University of Melbourne, Vic, Australia, 3010  
(2) Marcroft Grains Pathology, Grains Innovation Park, Horsham, Vic, Australia, 3400

Blackleg caused by *Leptosphaeria maculans*, is the most important disease of canola/oilseed rape worldwide. Field populations rapidly adapt to selection pressure from sowing of varieties with major gene resistance and can ‘overcome’ resistance within a few years of release of a variety. We are taking a ‘Genome to Paddock’ approach to controlling blackleg. For the last decade we have monitored virulence of blackleg populations and disease severity of canola varieties in field trials across Australia. We have also developed high throughput molecular and ‘ascospore shower’ assays to assess frequencies of avirulence genes in blackleg populations derived from stubble. Concurrently with French colleagues we have sequenced the genome of the blackleg fungus and discovered the basis of the high evolutionary potential of this fungus. Key disease-related genes known as effectors, including avirulence genes, are embedded in AT-rich, gene-poor regions of the genome with transposable elements that have been degenerated by Repeat Induced Point (RIP) mutations. Thus these key disease genes are easily gained, lost or inactivated during sexual reproduction, which occurs prolifically on stubble. Using these approaches, we have analysed blackleg isolates collected before and after resistance of sylvestris-derived isolates ‘broken down’ in 2003 after two seasons of extensive sowing on the Eyre Peninsula, South Australia. Deletions, RIP mutations and amino acid substitutions accounted for rapid evolution of four linked effectors, including the avirulence gene complementary to the resistance gene, that had been overcome. Furthermore there was an eight-fold increase in frequency of virulence alleles of effector *AvrLm1* in blackleg isolates after the resistance breakdown. Application of these monitoring techniques allowed us in early 2012 to predict that resistance of canola varieties with a different source of resistance to that described above would ‘breakdown’ if these varieties were sown in 2012 on the Eyre Peninsula. Our advice not to grow these varieties was heeded by growers and has been vindicated, as our recent field trial data showed high disease levels in this variety on Eyre Peninsula. The resistance ‘breakdown’ averted in 2012 saved canola growers $20 million AUD (based on conservative estimates of area sown, predicted yield loss and current canola prices).

**Phyllosphere microbes influence Succinate dehydrogenase activity in mitochondria of tomato**

Prof P. K. Paul  
Amity University Uttar Pradesh, Noida, India  
prab_kp@rediffmail.com

P. K. Paul, Joyeeta Mitra  
Amity Institute of Biotechnology, Amity University, Uttar Pradesh, Sector-125, Express Highway, NOIDA-201303, Uttar Pradesh, India

Phyllosphere microbes, besides being natural biocontrol agents for several pathogens, also influences host plants physiology. However, negligible studies have been done to correlate the functioning of mitochondria with activity of microbes on phyllosphere. Succinate dehydrogenase (SDH), a crucial enzyme in plant respiration, is bound to the inner mitochondrial membrane. It participates in both citric acid cycle and electron transport chain. *Lycopersicum esculentum* (variety: Pusa early dwarf) were raised and maintained under aseptic conditions in a culture room with a temperature of 25±1°C, 75% RH and 12L/12D light cycle. Eight week old plants were divided into six groups of 45 plants each. They were either treated with *Pseudomonas syringae* pv. *tomato* only, metabolite of *Fusarium oxysporum* (isolated from same variety of tomato grown in fields), premix inoculation of pathogen and fungal metabolite, fungal metabolite treatment preceding the pathogen inoculation, pathogen inoculation prior to fungal metabolite treatment and sterile distilled water (control). Activity of SDH in isolated mitochondria was analyzed using DCPIP as substrate. The initial significant enhancement in activity of the enzyme was probably due to ROS production in mitochondria leading to development of defense mechanisms in host plants. Tomato plants inoculated with pathogen had significantly low SDH activity. Fungal metabolite treated plants had significantly high SDH activity within 24-48 hours of treatment (P<0.05). Plants treated with fungal metabolite prior to pathogen inoculation had maximum SDH activity (P<0.05). The perusal of the data shows that phylloplane microfungals probably critically regulate the activity of SDH and may be that of mitochondria as an organelle.
Mechanisms by which dual NB-LRR genes confer disease resistance in Arabidopsis

Dr Kee hoon Sohn
Massey university
k.sohn@massey.ac.nz

Kee Sohn(1), Cecile Segonzac(2), Ghanasyam Rallapalli(1), Panagiotis Sarris(1), Simon Williams(1), Jooyong Woo(1), Kyunghee Paek(1), Bostjan Kobe(1), Jonathan Jones(1)

(1) Institute of Agriculture and Environment, Massey University, Palmerston north, New Zealand
(2) The Sainsbury Laboratory, Norwich Research Park, Norwich, United Kingdom

Plant innate immunity is activated upon recognition of pathogen-associated molecular patterns (PAMPs) or effector proteins secreted by pathogens. The PAMP- or effector-triggered immunity (PTI or ETI) is conferred by cell surface localized pattern recognition receptors (PRRs) or intracellular disease resistance (R) proteins, respectively. The R proteins often carry the conserved nucleotide-binding (NB) and leucine rich repeat (LRR) domains with variable N-terminal domains, coiled coil (CC) or toll interleukin 1 receptor (TIR). Understanding how R proteins are activated by corresponding effectors and initiate immune responses is one of the major questions in plant biology. Arabidopsis R proteins, RPS4 and RRS1 (resistance to Pseudomonas syringae) and RRS1 (resistance to Ralstonia solanacearum), are genetically required for recognition of AvrRps4 and PopP2 that are secreted by the bacterial pathogens Pseudomonas syringae and Ralstonia solanacearum, respectively. The mechanistic details by which RPS4 and RRS1 i) recognize two sequence-unrelated effectors and ii) activate transcription of defence genes are mysterious. In Arabidopsis genome, RPS4 and RRS1 are very closely located to each other (254 bps of intergenic region) and encode TIR-NB-LRR proteins. In addition, RRS1 atypically carries WRKY DNA-binding domain (DBD) at the C-terminus suggesting its role in the transcriptional regulation of defence associated genes. In this study, we aim to better understand how the paired R proteins, RPS4 and RRS1, function cooperatively. Together with B. Kobe (Univ. of Queensland) and P. Dodds’s (CSIRO) labs, we have discovered that TIR-TIR heterodimerization of RPS4 and RRS1 is required for AvrRps4-triggered immunity. The sensitive to low humidity (slh) 1 mutant (Arabidopsis accession No-0 background) carries single amino acid (Leu) insertion at WRKY DBD of RRS1 and causes autoimmune phenotype. By screening the EMS-mutagenized slh1 population, we isolated a number of sushi (suppressor of slh1 immunity) mutants with varying degree of phenotypes. Intriguingly, we discovered that some sushi mutants carry causal mutations in RPS4. The detailed genetic and biochemical analysis of these sushi mutants will provide better understanding of dual R protein function and immune signalling in plants.

Unraveling the cause of Black Pod Syndrome of narrow-leaved lupin: Survey data, Satisfying Koch’s postulates, and Next generation sequencing of virus isolates

Monica Kehoe
University of Western Australia
10127799@student.uwa.edu.au

Monica Kehoe (1)(2), Bevan Buirchell (1)(2), Roger Jones (1)(2)

(1) School of Plant Biology and Institute of Agriculture, The University of Western Australia, 35 Stirling Hwy, Crawley, WA 6009, Australia
(2) Department of Agriculture and Food Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia

Black pod syndrome (BPS) causes devastating losses in narrow-leaved lupin crops in south-west Australia. A number of possible causes were studied in the past, including abiotic factors such as competition between pods on the main stem or nutrient deficiencies. However, late infection by biologically distinct strains of Bean yellow mosaic virus (BYMV) that cause necrotic symptoms in narrow-leaved lupin has become generally accepted as the major cause of BPS. This project aims to establish whether BYMV is acting alone in causing this syndrome, or whether it might also have additional causes. A hypersensitive resistance gene to BYMV was identified previously in narrow leafed lupin (Nbm-1). In 2011, a survey was conducted late in the lupin growing season across seven sites (three at Esperance, two in Perth, and one each at Pingelly and Arthur River) in south-west Australia. Whole plant samples showing BPS were collected, sub-sampled and tested for virus presence by both ELISA and RT-PCR. RT-PCR proved the most reliable. Biological studies using late growth stage sap inoculations with BYMV in the glasshouse successfully reproduced BPS symptoms in narrow-leaved lupin plants. Partial virus coat protein gene sequencing confirmed BYMV presence in samples from plants with BPS, thereby satisfying Koch’s postulates and confirming late BYMV infection in the field as the primary cause of BPS. A better understanding of the complete genomes of BPS causing BYMV was sought through Next Generation Sequencing on the Illumina HiSeq 2000 of 13 BPS-BYMV isolates plus an additional eight other BYMV isolates. Previously, just nine complete BYMV genomes were available on Genbank. From a virologist’s perspective, Next Generation Sequencing analyses pose unique challenges, some of which will be discussed in addition to the BYMV genome results particularly with regards to BYMV isolates from plants with BPS.
Quantitative measurement of the impacts of virus infection in *Arabidopsis thaliana*

Dr Kieren Arthur  
The New Zealand Institute for Plant & Food Research Ltd  
kieren.arthur@plantandfood.co.nz

Kieren Arthur\(^{(1)}\), Tracey Immanuel\(^{(1)}\), Gardette Valmonte\(^{(1)}\), Kate Olliver\(^{(1)}\), Colleen Higgins\(^{(1)}\), Robin MacDiarmid\(^{(1)}\)

\(^{(1)}\)The New Zealand Institute for Plant & Food Research Limited, New Zealand  
\(^{(2)}\)School of Biological Sciences, The University of Auckland, New Zealand  
\(^{(3)}\)Institute for Applied Ecology New Zealand, School of Applied Sciences, Auckland University of Technology, New Zealand

For the model plant *Arabidopsis thaliana* there are well documented descriptions of symptoms caused by viral infection, such as leaf mosaics and a stunted growth appearance. However, the impacts of viral infection in terms of quantitative measurements of plant growth parameters have not been well determined. This research has two purposes; first to define a list of characteristics in *A. thaliana* which can be used as parameters to quantify the effects that different virus infections have on the plant, and second to use these parameters to screen for genes involved in plant-virus interactions. First, using *A. thaliana* ecotype Col-0, we collected multiple plant growth measurements including plant height, rosette diameter, and numbers of leaves, comparing healthy plants with those infected with a diverse range of viruses, including *Turnip mosaic virus* (Potyvirus), *Turnip vein clearing virus* (Tobamovirus), and *Cauliflower mosaic virus* (Caulimovirus). Measurements were taken every three to four days up to 28 days post inoculation. Where possible, virus titres were also quantified. Those growth measurements that showed a significant difference between healthy and virus-infected plants were selected to assess the impact of virus infection on mutant T-DNA lines of *A. thaliana*. Second, we used T-DNA mutant lines of the Calcium dependent protein kinase (CPK) gene family to determine if these plant growth characteristics could be used to identify genes involved in plant-virus interactions. CPKs are involved in signalling a range of stress responses in plants, including pathogen attack. Infected and healthy plants from three sets of T-DNA lines were compared: (1) mutant lines of CPKs that have been shown to respond to viruses, (2) mutant lines of CPKs with no reported function in virus infection, and (3) mutant lines of other genes known to be involved in plant-virus interactions. It is expected that T-DNA lines of genes involved in virus infection will show differences in virus progression, symptom severity and/or virus titre relative to control plants. This tool will provide a quick and quantitative method to screen mutant T-DNA lines for genes involved in plant-virus interactions, which will enable statistical analysis of changes in symptom development and definition of gene-dependent interactions between plants and viruses.

In search of resistance to grapevine trunk diseases

Dr Mark Sosnowski  
South Australian Research and Development Institute  
mark.sosnowski@sa.gov.au

Mark Sosnowski\(^{(1)}\), Matthew Ayres\(^{(1)}\), Trevor Wicks\(^{(1)}\), Michael McCarthy\(^{(1)}\)

\(^{(1)}\)South Australian Research and Development Institute, GPO Box 397, Adelaide, South Australia 5001

Trunk diseases such as eutypa and botryosphaeria dieback contribute to grapevine decline, reducing productivity and longevity, of vineyards. Causal fungi, *Eutypa lata* and species of the Botryosphaeriaceae infect vines primarily through pruning wounds causing dieback and death of wood, and in the case of eutypa dieback, stunting of shoots and leaves. As reports of resistance or tolerance of *Vitis vinifera* cultivars to trunk disease are limited, the aim of this preliminary study was to identify potential sources of resistance. A germplasm collection in the Barossa Valley, South Australia consisting of mature (31-36 years old) *V. vinifera* wine cultivars (83 red and 95 white) were assessed in spring 2012 for severity of eutypa foliar symptoms and trunk disease symptoms that developed as a result of natural infections. The later included presence of dead spurs, cordon die-back and trunk cankers. Seven red and 16 white wine cultivars had less than 10% severity of trunk disease symptoms. Disease severity was greater than 80% for 11 red and four white wine cultivars, including the cv. Shiraz and Sauvignon Blanc, most prominently grown in Australia and New Zealand. A detached cane assay was used to evaluate *V. vinifera* x *V. cinerea* and *berlandier* rootstocks that are resistant to powdery mildew. Thirty nine genotypes plus the cv. Shiraz (known to be susceptible) were inoculated with *E. lata* and colonisation assessed 4 weeks later. *E. lata* was recovered 21 mm from the point of inoculation in Shiraz canes compared with 5 to 20 mm for all other genotypes. Although further assessments will be undertaken in spring 2013, these results suggest tolerance or resistance to trunk disease in both *V. vinifera* and crosses. Further research is underway to investigate resistance of selected cultivars and rootstock genotypes to infection and colonisation by trunk infecting fungi. Improved resistance to trunk disease in vineyards in the future will contribute towards a more sustainable and profitable wine industry.
Variable disease resistance to *Sclerotinia sclerotiorum* in traditional New Zealand / Maori sweet potato cultivars

Dr Rebekah Fuller  
University of Auckland  
r.fuller@auckland.ac.nz  
Rebekah JM Fuller, Mike N Pearson  
School of Biological Sciences, The University of Auckland, Private Bag 92019, Auckland Mail Centre, Auckland 1142, New Zealand

Sweet potato (*Ipomea batatas* (L.) Lam.) or kumara, is a crop of cultural significance brought to New Zealand by Maori nearly 1000 years ago. Current commercial production in New Zealand is based on three cultivars ‘Beauregard’, ‘Owairaka red’ and ‘Tokatoka Gold’, which are affected by the field and storage diseases *Sclerotinia sclerotiorum* (pink rot) and *Rhizopus stolonifer*. Access to export markets in the US and EU is compromised by use of fungicides to control these diseases. Appealing alternatives to chemical control of fungal pathogens are genetic resistance and biological control. A possible source of disease resistance is the traditional cultivars which have been selected for survival and sustainable yield over many centuries rather than high yields in intensive cultivation. Therefore we compared 8 traditional cultivars traditional and three commercial cultivars to determine whether there was any significant difference resistance to *S. sclerotiorum*. Stem cuttings were inoculated with *S. sclerotiorum*, incubated in moist chambers at 20°C and the lesion length measured daily. The experiment was repeated twice with the 8 traditional cultivars, then three traditional cultivars were chosen and compared with three commercial cultivars. The cultivars showed a range of susceptibilities to *S. sclerotiorum*, the most resistant being the commercial cultivar ‘Beauregard’ and the traditional cultivar ‘Taputini’, while the most susceptible was the commercial cultivar ‘Tokatoka Gold’. Given that ‘Taputini’ is at least as resistant as the most resistant commercial cultivar it could potentially be used in breeding more resistant and uniquely New Zealand cultivars, and also offers a good option for organic growers and those growing traditional cultivars wanting to replace susceptible sweet potato crops.

Characterisation of toxins from *Pyrenophora teres f. teres* in net form net blotch disease of barley

Dr Amanda Able  
The University of Adelaide  
amanda.able@adelaide.edu.au  
Ismail Ismail (1), Hugh Wallwork (1), Celeste Linde (2), Dale Godfrey (3), Amanda Able (1)

(1) School of Agriculture, Food & Wine, University of Adelaide, Glen Osmond, SA 5064, Australia  
(2) SARDI, GPO Box 397, Adelaide, SA 5001, Australia  
(3) RSBS, Australian National University, Acton, ACT 0200, Australia

The fungus that causes net form net blotch disease (NFNB) of barley, *Pyrenophora teres f. teres* (*Ptt*), uses proteinaceous toxins to cause leaf necrosis but little is known about the relationship between toxin production and virulence in NFNB. Proteinaceous phytoxins have therefore been isolated from culture filtrates of *Ptt* and characterised further. Thirty-six isolates were chosen for phytoxin production based on: the barley variety from which isolates were collected, when isolates were collected, how virulent they were and their genetic sub-group. Subsets of isolates sharing genetic similarity were determined by genotypic analysis (microsatellite markers) of over 300 isolates. Virulence/aggressiveness of isolates was tested against 12 key varieties (Barque, Buloke, Clipper, Commander, Fleet, Franklin, Keel, Maritime, Schooner, Skiff, SloopSA, Navigator) and compared with symptoms caused by culture filtrates. The types and extent of symptoms induced by culture filtrates and individual toxins varied significantly between isolates and on different varieties. Where an isolate infected a large number of varieties, its proteinaceous phytoxin mixture (from culture filtrates) also caused damage across a large number of varieties suggesting they may be useful in screening for resistant germplasm. Over 70 individual proteins that may act as virulence factors have also been identified from culture filtrates using a proteomics approach. Seven of these virulence-related candidate proteins have now been characterised in some detail: a ceratoplatin (PttCP1), a cupin-like protein (PttNF1), a bifunctional glucose/aldose epimerase (PttGALM), an isochorismatase (PttCHFP1), an endo-1,4-β-xylanase A (PttXyn11A), a glycosphatidylinositol (GPI)-anchored common in fungal extracellular membrane (CFEM) domain-containing protein (PttGPI-CFEM) and an unknown proteinaceous secreted (but conserved) hypothetical protein (PttSP1). Roles attributed to these proteins in other plant-pathogen interactions include plant defence; cell wall degradation and necrosis induction; hyphal attachment and growth; and fungal networking. PttNF1 and PttSP1 contain an effector motif (allowing host specificity) but their actual function is yet to be determined. Of most interest is PttXyn11A which was expressed more abundantly by the more virulent isolates during the plant-pathogen interaction while the heterologously expressed PttXyn11A protein caused necrosis suggesting that endo-1,4-β-xylanase A plays a role in the virulence of *Ptt* on barley.
Internal movement of *Pseudomonas syringae* pv. *actinidiae* through symptomless kiwifruit tissues.

**Ms Joy Tyson**
The New Zealand Institute for Plant and Food Research Ltd
Joy.Tyson@plantandfood.co.nz

Joy Tyson(1), Carol Curtis(1), Mike Manning(1), Bill Snelgar(2), Peter Blattman(1)

(1) Plant and Food Research Limited, Mt Albert, Auckland, New Zealand
(2) Plant and Food Research Limited, Te Puke, New Zealand

Bacterial canker of kiwifruit caused by *Pseudomonas syringae* pv. *actinidiae* (Psa) is a relatively new disease to New Zealand and was first detected in Te Puke in 2010. The disease is characterised by leaf spots, cane dieback, cankers and the production of orange-red or milky-white exudates. In this study, systemic movement of the bacterium was examined using potted kiwifruit vines kept in a polythene greenhouse. Trunks of fifteen two-year old potted *Actinidia chinensis* ‘Hort16A’ on the rootstock *A. delicosa* ‘Bruno’ were wound-inoculated with Psa at a concentration of $4 \times 10^9$ cfu/ml. Vines inoculated with bacteriological saline served as controls. At three times after inoculation, five vines were destructively sampled by excising stem segments at intervals between the shoot tip and the soil line. Segments were macerated in bacteriological saline and assayed for the presence of Psa by plating onto semi-selective medium, followed by a quantitative polymerase chain reaction (qPCR)-based detection method. Thirty-eight days after inoculation, Psa was detected 2 cm above and below the inoculation site. After 80 days Psa was detected 30 cm above and below the inoculation site and by 151 days Psa was found up to 95 cm from the point of inoculation. Psa was never recovered from the control plants. No external symptoms typical of kiwifruit canker were observed on the plants in the timeframe of the experiment. On dissection, some of the inoculated vines had red staining in the tissues above the inoculation site. No staining was observed below the inoculation sites, however, Psa was found to be present in the symptomless tissues as far below the inoculation site as above the inoculation site. This experiment showed that Psa moved up and down the trunks at a similar rate, and that movement through the scion (‘Hort16A’) and the rootstock tissues (‘Bruno’) were also similar. Psa was not inhibited by the graft and was able to move through the graft into the rootstock and down to the level of the soil (roots were not sampled).

Crop growth enhancement and disease control using nursery-inoculated *Trichoderma* root endophytes isolated from local healthy plants

**Dr Robert Hill**
Bio-Protection Research Centre, Lincoln University
robert.hill@lincoln.ac.nz

Robert Hill, Nicholas Cummings,
Bio-Protection Research Centre, P O Box 85084, Lincoln University, Lincoln 7647, Christchurch, New Zealand

A novel approach to the challenge of selecting the most effective growth-promoting and disease suppressive *Trichoderma* isolates has been used successfully in a range of forestry and agricultural crops both in New Zealand and Southeast Asia. The approach targets roots from exceptionally healthy representatives of a wide variety of wild and cultivated plant species growing in the locality of the crop. Root fragments from selected host plants are washed, surface sterilised, and *Trichoderma* root endophytes growing from within roots are isolated in pure culture. Isolates are then tested on the crop plant of interest to select the most effective for growth promotion or disease suppression. Inoculation of seed or growing medium before seed-sowing or setting of cuttings ensures very early colonisation of crop roots by *Trichoderma* and has proved to be a practical and cost effective strategy. Nursery trials to select the best *Trichoderma* isolates have been based on seed germination, seedling establishment, growth rate, general health and the proportion of seedlings meeting specification for sale (by 50% or more) in New Zealand and SE Asia. Nursery inoculated stock has also been monitored following field plantation. Benefits include increased growth (up to 15%) and reduced mortality from diseases (often by greater than 30%).
Role of OASTL-A1 in plant immunity and interaction with NBS-LRR immune receptor

Dr Jibran Tahir
Massey University
j.tahir@massey.ac.nz

Jibran Tahir(1), Mutsumi Watanabe(2), Hai-Chun Jing(2), Donald A. Hunter(2), Takayuki Tohge(2), Adriano Nunes-Nesi(2), Yaniv Brotman(2), Alisdair R. Fernie(2), Rainer Hoefgen(2), Paul P. Dijkwel(3)

(1)Institute of Fundamental Sciences, Massey University, Palmerston North, New Zealand
(2)Max-Planck-Institut fuer Molekulare Pflanzenphysiologie, Wissenschaftspark Golm, Potsdam-Golm, Germany
(3)Centre for Bioenergy Plants Research and Development, Institute of Botany, Chinese Academy of Sciences, Beijing, China, and
(4)The New Zealand Institute for Plant & Food Research Limited, Palmerston North, New Zealand

Various receptor proteins have been identified in plants, which develops a layer of immune system, as they detect divergent activities of pathogenic/foreign molecular patterns. Resistance (R) proteins are intriguing receptors which activate hypersensitive response against pathogen effector-induced virulence. This mode of immunity is termed as specific/monogenic immunity and provides strong resistance against specific pathogens in respective habitats. In most cases R-mediated innate immunity has been shown to be dependent upon modifications in specific plant proteins that are being targeted by effectors. In the light of such evidences, Guard hypothesis has been proposed which suggests that R protein(s) guard against modifications in the host/guardee proteins when targeted by the pathogen effectors to promote effector triggered susceptibility. Absence or modification of the guardee plant proteins via mutations has been shown to auto activate R-mediated immune response indicating R proteins detects modified-self. In this study we identified a novel interaction between R protein encoding gene(s) and an O-acetyl serine (thiol) lyase (OASTL-A1) encoding gene. OASTL-A1 is involved in cysteine biosynthesis and sulfur assimilation. A mutation in the cytosolic OASTL-A1 enzymatic protein resulted in auto-activation of immunity in specific Arabidopsis accessions. The autoimmunity was found to depend on Recognition of Peronospora Parasitica 1 (RPP1)-like disease resistance R gene(s) indicating reception of modified-self to OASTL-A1 by the RPP1-protein(s). RPP1 genes have been previously identified to provide resistance against the downy mildew pathogen of Arabidopsis Hyaloperonospora arabidopsidis by detecting the virulence activity of its effector molecules. OASTL-A1 may therefore be guarded directly or indirectly by the RPP1-like R protein(s) against an unknown pathogen virulence activity. As cysteine and its derived metabolites are also required in the synthesis of immune-associated metabolites we also identified that OASTL-A1 enzyme is involved in basal defense in Pseudomonas syringae DC3000 pathogen interaction. These findings highlight the role of cysteine metabolism and OASTL in basal immunity and provide the evidence for the molecular components that may be involved in sulphur-induced resistance in plants. Finally this study shed new light on the metabolic basis of autoimmunity in plants, a view previously unknown. In conclusion, the work present novel and new insights into the role of OASTL protein in cysteine metabolism, biotic stress defense and R-mediated innate immunity. (Tahir, et al.,(2013), The Plant Journal, 73: 118–130. doi: 10.1111/tpj.12021)

Secretome analysis identifies conserved putative effectors of the fungal pathogen Ciborinia camelliae

Mr Matt Denton-Giles
Massey University
m.denton-giles@massey.ac.nz

Matt Denton-Giles, Murray Cox, Rosie Bradshaw, Paul Dijkwel

(1)Centre for Bioenergy Plants Research and Development, Institute of Botany, Chinese Academy of Sciences, Beijing, China, and
(2)The New Zealand Institute for Plant & Food Research Limited, Palmerston North, New Zealand

Many Camellia species and cultivars are susceptible to infection by the host-specific fungal phytopathogen Ciborinia camelliae L. M. Kohn (Sclerotiniaceae). This pathogen specifically infects floral tissue resulting in the development of brown petal lesions and premature flower fall. Economically, C. camelliae has impacted detrimentally on both the Camellia floriculture and Camellia oil seed industries. This study aimed to identify potential fungal virulence factors of C. camelliae using a transcriptomic approach. Total RNA was independently isolated from infected and mock infected petal tissue, converted to cDNA and sequenced using the Illumina Hi-Seq platform. The resulting sequence reads were de novo assembled into a combined plant-pathogen transcriptome, consisting of ~138,000 non-redundant expressed sequence tags (ESTs). To select fungal ESTs from the mixed EST library, a draft reference genome of C. camelliae was sequenced using Illumina’s Miseq sequencing platform. Genome assembly resulted in 2,583 sequence scaffolds and a combined genome length of 40MB, which is comparable with close relatives Botrytis cinerea (38 MB) and Sclerotinia sclerotiorum (39 MB). Fungal ESTs were identified based on their BLASTN alignment e-value with the draft C. camelliae genome, their absence in the mock control EST database and their presence in the infected EST database. To identify the fungal secretome, fungal ESTs were initially translated and subjected to open reading frame (ORF) prediction. Following ORF prediction 384 putative secreted proteins were identified based on the presence of predicted signal sequences and the absence of any transmembrane domains. Sequence annotation indicated that many of the 384 putative secreted proteins were involved in fungal or plant cell wall modification (14%), protein modification (12%) and redox homeostasis (6%). Interestingly, 8% of the putative secreted proteins were small, cysteine rich, poorly annotated proteins. Half of these proteins shared 10 structurally conserved cysteine residues. Alignment of these conserved ESTs back to the C. camelliae draft genome showed that members of this group were often clustered at the same genomic locus. Effector motif analysis indicated that the majority of these proteins shared the Y/F/WxC motif which is common to a conserved family of effectors in Blumeria graminis. Future research will aim to characterize the temporal expression patterns of these conserved putative effectors and determine their localization during infection.
Towards a molecular tool for identifying virus infected plants

Ms Sonia Lilly
Plant and Food Research
sonia.lilly@plantandfood.co.nz

Importation of plant germplasm can result in unintentional co-import of stowaway infectious agents. Most, if not all, plants are susceptible to viruses, which can cause reductions in yield or quality and a subsequent reduction in market value. A tool to monitor the health status of a plant, any deviations from which might suggest virus presence, would be of great assistance to biosecurity. Current methods, such as ELISA, PCR, microarray, microscopy, dsRNA sequencing and identification of coat proteins, detect aspects of the viruses themselves rather than the impact of the virus on the plant. Plants respond to virus infection through an antiviral mechanism, RNA interference (RNAi), and through stress-related pathways that include increased expression of salicylic acid, defence genes and heat shock proteins. Changes in these response pathways provide a basis for searching for molecular indicators to identify virus-infected plants. Such tools will be of importance to the Post-Entry Quarantine Biosecurity section of the Ministry of Primary Industries, which is responsible for keeping new plant virus infections from crossing the border. I will discuss how these aims are being addressed by investigating whether a range of viruses infecting Arabidopsis elicit the same responses in this host and whether the identified responses are solely indicative of virus infection. In particular, two tools have been developed to monitor known responses to virus infection. The first tool involves quantifying the accumulation of small RNAs (sRNAs) that accumulate during RNAi in response to viral infection. The second tool involves qPCR amplification of cDNA derived from transcripts of components of the RNAi pathway and of transcripts from other genes that have shown significant changes in response to a number of plant viruses, as identified from microarray data.

Analysis of the accessory genome of the kiwifruit pathogen Pseudomonas syringae pv. actinidiae

Dr Matthew Templeton
The New Zealand Institute for Plant & Food Research Limited
matt.templeton@plantandfood.co.nz

Most crops were domesticated centuries - even millennia - ago, thus limiting opportunity to understand the emergence of disease. Kiwifruit is an exception: domestication began in the 1930s with outbreaks of canker disease caused by P. syringae pv. actinidiae (Psa) first recorded in the 1980s. Based on SNP analyses of two circularized and 30 draft genomes, Psa is comprised of distinct clades exhibiting negligible within-clade diversity, consistent with disease arising by independent samplings from a source population. Three clades correspond to their geographical source of isolation; a fourth, encompassing the Psa-V lineage responsible for the 2008 outbreak, is now globally distributed. Psa-V has an overall clonal population structure, however, genomes carry a marked signature of within-pathovar recombination. Most SNP polymorphisms reside within PPHGI-1-like conjugative elements whose evolution is unlinked to the core genome. Removal of SNPs due to recombination yields an uninformative (star-like) phylogeny consistent with diversification of Psa-V from a single clone within the last ten years. These analyses capture a pathogen in the early stages of emergence from a predicted source population associated with wild Actinidia species. Genomic comparisons show a dynamic genome with evidence of positive selection on type III effectors and other candidate virulence genes. Each clade has highly varied complements of accessory genes encoding effectors and toxins with evidence of gain and loss via multiple genetic routes. Genes with homologs in vascular pathogens were found exclusively within Psa-V.
Population structures of *Neofusicoccum* species from nurseries and vineyards indicate movement and origins of infection

Dr Regina Billones-Baaijens  
Lincoln University, New Zealand  
Regina.Billones@lincoln.ac.nz  
Regina Billones-Baaijens, Jeyaseelan Baskarathevan, Eirian Jones, Marlene Jaspers, Hayley Ridgway, . ,  
Faculty of Agriculture and Life Sciences, PO Box 85084, Lincoln University, Lincoln, Canterbury 7647, New Zealand  

Surveys in 2007-08 showed that Botryosphaeriaceae species were prevalent in New Zealand grapevine nurseries and vineyards. From the seven species identified from nurseries, six of these were also commonly found in vineyards. However, the prevalence of the different species differed with *Neofusicoccum parvum* dominating in the vineyards and *N. luteum* in the nurseries. Pathogenicity studies showed that although both species were pathogenic to grapevines, symptoms differed; *N. parvum* caused severe cankers while *N. luteum* caused less distinct browning of trunk tissues. To investigate reasons why the two species dominated different environments, this study investigated the genetic structures of their populations from nurseries and vineyards using universally-primed polymerase chain reaction (UP-PCR). For *N. parvum*, 46 vineyard and 33 nursery isolates were analysed by UP-PCR using five primers which amplified 51 loci (66% polymorphism). For *N. luteum*, 25 vineyard and 39 nursery isolates were also analysed by UP-PCR using five primers which amplified 54 loci (44% polymorphism). PAUP analysis showed high genetic diversity among *N. parvum* and *N. luteum* populations, with 92% and 78% of the isolates, respectively, being of unique genotypes. The neighbour joining trees generated identified four (N. parvum) and three clades (N. luteum), however, vineyard and nursery populations were found in different positions within the trees. For *N. parvum* populations, seven vineyard genotypes clustered in Clade I while 14 nursery genotypes clustered in Clade II. In Clades III and IV, two groups of nursery genotypes clustered with several vineyard genotypes but were separated from them in one sub-branch within each clade. In contrast, the two *N. luteum* populations showed high similarities with nursery and vineyard genotypes being randomly distributed in different branches of the neighbour-joining tree, which indicated nursery-vineyard relationship. Overall results indicated that the *N. parvum* vineyard population were genetically distinct from the nursery population, suggesting that nursery infections by this canker-producing species were interrupted during the nursery grading process and fewer of these infections were carried over into new vineyards. Its high prevalence in vineyards is probably due to naturally dispersed spores infecting pruning wounds, thus, early detection and control of this aggressive species in vineyards is very important. The genetic similarity between *N. luteum* nursery and vineyard populations indicated that the vineyard population may have originated from infected nursery plants with indistinct symptoms that were less likely recognised and were unwittingly sold to vineyards. Therefore, management of this species should start at the nursery level.

Myrtle rust in *Eucalyptus grandis*: identification and expression of host defence genes

Prof David Guest  
University of Sydney  
peri.tobias@gmail.com  
Peri Tobias(1), David Guest(1), Sham Nair(2)  
(1)Faculty of Agriculture and Environment, University of Sydney, Biomedical Building C81, 1 Central Ave, Australian Technology Park, Eveleigh, NSW 2015, Australia  
(2)Department of Biological Sciences, Faculty of Science, Macquarie University, North Ryde, NSW 2109, Australia  

*Eucalyptus grandis* is an Australian myrtaceaeous tree grown for timber in many parts of the world. *E. grandis* is susceptible to *Puccinia psidii* sensu lato, causal agent of myrtle rust, which was first identified in Australia in 2010. A draft annotated genome sequence of *E. grandis* was released in 2011, making it a useful host species on which to study interactions with *P. psidii*. Chitinases are present in plants and cleave glycosidic bonds of chitin, the major structural component of fungal cell walls. They are encoded by an important class of genes known to be up-regulated in response to pathogen invasion. The up-regulation of chitinases is also an indicator of systemic acquired resistance (SAR). The current study identified 40 chitinase gene models within the *E. grandis* sequence data set. Sequences were aligned and analysed as conforming to the currently recognised chitinase classes (I–IV). Primers were designed for six of these genes and for two house-keeping genes, all of which successfully amplified their targets in inoculated plants. Inoculated plants varied for six of these genes and for two house-keeping genes, all of which successfully amplified their targets in inoculated plants. Inoculated plants varied in response to *P. psidii*, with 40% displaying resistance. On subsequent inoculation using the same pathogen isolate none of the plants were susceptible, indicating the likely triggering of SAR. Determining the different classes of chitinases, and the development of specific primers, will provide the basis for a quantitative expression assay to be conducted on infected plants of *E. grandis*, both under controlled conditions and in native vegetation.
SESSION 8A – POPULATION GENETICS

Development of a multiplexed microsatellite library for a population genetics study of *Stagonosporopsis tanaceti* the cause of ray blight disease of pyrethrum in Australia

Ms Niloofar Vaghefi
The University of Melbourne
n.vaghefi@student.unimelb.edu.au

Niloofar Vaghefi(1), Frank Hay(2), Peter K. Ades(1), Sarah J. Pethybridge(3), Rebecca Ford(1), Marc E. Nicolas(4), Paul W.J. Taylor(1)

(1) Melbourne School of Land and Environment, the University of Melbourne, Melbourne, VIC 3010, Australia
(2) Tasmanian Institute of Agriculture, University of Tasmania, Burnie, TAS 7320, Australia
(3) The New Zealand Institute for Plant and Food Research, Christchurch, 8140, New Zealand

A multiplexed microsatellite library was developed and validated for population genetic studies of *Stagonosporopsis tanaceti*; the causal agent of ray blight disease of pyrethrum (*Tanacetum cinerariifolium*) in Australia. Hundreds of microsatellite loci were identified through de novo genome assembly of Illumina paired-end reads, forty-three of which were selected for marker development based on the number of repeat motifs. A set of four multiplex panels containing 20 polymorphic markers was used for temporal and geographical genetic structure analyses of the pathogen populations in Australia. Bayesian population analyses detected two distinct clonal lineages, each characterised by a complex of closely-related genotypes. The observed structure could not be attributed to the geographical origins or host genotypes from which the individuals had been isolated. Instead, it may be due to the introduction of two distinct clones which may have evolved and diversified independently in the apparent absence of a sexual stage in the field, thus the lack of genetic exchange between the two groups. High gene flow and no geographic structure of the pathogen, combined with the absence of airborne ascospores in the field, are indicative of the important role of human-mediated movement of the inoculum as the major cause of dispersal. In addition, nine and 11 of the developed markers were transferable to the closely-related species *S. chrysanthemi* and *S. inoxydabilis*, respectively, and will be informative in the future study of these species populations.

Simple sequence repeat markers (SSRs) for understanding population structure of *Colletotrichum coccodes* infecting potato in Australia

Mr Jiang Chang
The University of Melbourne
jichang@student.unimelb.edu.au

Jiang Chang(1), Paul Taylor(1), Dolf de Boer(2), Pedro Crous(3)

(1) Department of Agriculture and Food System, Melbourne School of Land and Environment, The University of Melbourne, Victoria 3010, Australia
(2) Department of Environment and Primary Industries, Agribio Center, Bundooora, Victoria 3083, Australia
(3) CBS Fungal Biodiversity Center, Uppsalalaan 8, 3584 CT Utrecht, Netherlands

*Colletotrichum coccodes* infects more than 58 plant species, and is an important pathogen of potato (*Solanum tuberosum*), causing black dot disease. Knowledge of the population genetic diversity of *C. coccodes* is important for understanding population structure and adaptive potential. Multi-gene phylogenetic analysis of the internal transcribed spacer, partial actin, glyceraldehyde-3-phosphate dehydrogenase, beta-tublin, histone and chitin synthase1 gene regions, confirmed the taxonomy of isolates collected from potato petiole and tuber tissue from South-Eastern Australia as *C. coccodes*. To study population genetics, a library of simple sequence repeat (SSR) primer pairs was developed. The *C. coccodes* genome was sequenced through 454 GS-FLX sequencing technique, and microsatellite loci identified through de novo genome assembly of Illumina paired-end reads. Primers were then designed to the flanking regions of 40 SSR loci. After screening 20 *C. coccodes* isolates, 19 microsatellite loci were found to be polymorphic, and 10 haplotypes were identified. In order to rapidly detect alleles of different loci, the primers were optimized into four multiplex panel sets. The developed SSR markers will be used to study the genetic structure of 200 *C. coccodes* isolates collected from different regions in Australia and overseas.
Phylogeny and Secreted In Xylem (SIX) gene characterisation of Fusarium oxysporum f.sp. canariensis in Australia.

Dr Matthew Laurence
The Royal Botanic Gardens and Domain Trust
matthew.laurence@rbgsyd.nsw.gov.au

Matthew Laurence(1), Brett Summerell(1), Edward Liew(1)
(1)The Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney, NSW 2000, Australia

Fusarium Wilt of Phoenix canariensis, caused by Fusarium oxysporum f.sp. canariensis, is a lethal disease which has been reported in Argentina, Australia, the Canary Islands, France, Greece, Italy, Japan and the USA. The Australian F. oxysporum f.sp. canariensis strains have previously been shown to be highly diverse and did not cluster with international strains on the basis of enterobacterial repetitive intergenic consensus (ERIC) fingerprinting and vegetative compatibility groupings (VCG). These results indicated that the Australian strains may have evolved from indigenous F. oxysporum population, as was the case with two VCGs of the cotton wilt pathogen F. oxysporum f.sp. vasinfectum. The primary aim of the current study was to elucidate the phylogenetic relationship between Australian and international F. oxysporum f.sp. canariensis. The secondary objective was to characterise and compare the pathogenicity genes, Secreted In Xylem (SIX), between Australian and international strains. Implications for the origin of F. oxysporum f.sp. canariensis in Australia are discussed.

Next Generation Sequencing reveals unexplored Phytophthora diversity in Australian soils.

Dr Treena Burgess
Murdoch University
tburgess@murdoch.edu.au

Treena Burgess(1), Santi Català(1)(2), Diane White(1), Bill Dunstan(1), Michael Crone(1), Giles Hardy(1)
(1)Centre for Phytophthora Science and Management, School of Veterinary and Life Sciences and Biotechnology, Murdoch University, Perth, WA, Australia
(2)Institute Agroforestal Mediterráneo, Universitat Politècnica de València, Spain

The Vegetation Health Survey (VHS) at the Department of the Environment, Western Australia has a Phytophthora collection extending back to 1979. Isolates in this collection have been recovered during routine monitoring on natural ecosystems in Western Australia for the presence of Phytophthora cinnamomi. Through molecular re-evaluation of this collection we have subsequently described 11 new Phytophthora species and the diseases associated with them and additional descriptions are underway. Elsewhere in Australia, however, there is extremely limited information on Phytophthora diversity within natural ecosystems. However using modern molecular techniques such as Next Generation Sequencing, it is possible to determine Phytophthora species diversity from environmental soil samples. In this study, DNA was extracted from soils obtained from 400 locations around Australia. ITS1 amplicons were generated using Phytophthora specific primers and pyrosequenced on a Roche Junior GS platform. For the first 50 samples roots and rhizosphere soil were extracted separately. Results to date reveal an astonishing diversity, several new species and very different species profiles when comparing roots and rhizosphere soil from the same location. Species described and known only from Western Australia have an Australia-wide distribution raising intriguing questions in regards to origin and movement of species.
An expanded \textit{AvrLm6}-like gene family in scab fungi

Mr Jason Shiller  
La Trobe University  
jshiller@students.latrobe.edu.au

Jason Shiller\(^{(1)}\), Angela van de Wouw\(^{(2)}\), Dan Jones\(^{(1)}\), Joanna K. Bowen\(^{(3)}\), Matthew Templeton\(^{(4)}\), Kim Plummer\(^{(4)}\)

\(^{(1)}\)La Trobe University, Melbourne, Australia  
\(^{(2)}\)University of Melbourne, Australia  
\(^{(3)}\)Plant and Food Research, Auckland, New Zealand

\textit{Venturia inaequalis} and \textit{Venturia pirina} are hemi-biotrophic fungi that cause apple scab and pear scab disease respectively. These diseases result in significant losses to growers worldwide and control is generally reliant on heavy fungicide use. There is race specific resistance in this system which follows the gene-for-gene model, whereby a gene coding for a resistance protein in the host will have a cognate gene coding for avirulence protein (or effector) in the fungus, recognition of the effector by the resistance protein leads to a resistance response. These effectors are yet to be characterised, but whole genome sequencing of \textit{V. inaequalis} and \textit{V. pirina} isolates has revealed predicted proteins with sequence similarity to \textit{AvrLm6}, a \textit{Leptosphaeria maculans} effector that triggers a resistance response in \textit{Rlm6} canola. \textit{AvrLm6}-like genes from sequenced \textit{Venturia spp} form large families, which vary among races but in some cases consist of more than 30 members, while only one \textit{AvrLm6} paralogue has been identified in \textit{L. maculans}. We have shown that the \textit{AvrLm6}-like gene from \textit{V. inaequalis} with the highest amino acid sequence identity to \textit{AvrLm6} was unable to trigger a resistance response in \textit{Rlm6} canola. However, these proteins are still strong effector candidates. RNA-seq and qRT-PCR gene expression analysis of \textit{in planta} and \textit{in vitro} grown \textit{V. inaequalis} has revealed that many of the \textit{AvrLm6}-like genes are up-regulated during infection. Fluorescent labelling of the most highly up-regulated \textit{AvrLm6} orthologue from \textit{V. inaequalis} has been used to study its localisation during infection, which is predominantly in the subcuticular stroma. Further experiments are underway, including gene silencing and additional fluorescent protein tagging to understand the function of these genes.

Dynamics of \textit{Dasheen mosaic virus} population structure in evolutionary space and time.

Mr Wee-Leong Chang  
Auckland University of Technology  
wchang@aut.ac.nz

Wee-Leong Chang\(^{(1)}\), Mary Cong\(^{(1)}\), Annie Yuan\(^{(1)}\), Michael N. Pearson\(^{(1)}\), Colleen M. Higgins\(^{(1)}\)

\(^{(1)}\)Institute for Applied Ecology New Zealand, School of Applied Sciences, Auckland University of Technology, New Zealand  
\(^{(2)}\)School of Biological Sciences, The University of Auckland, New Zealand

Understanding the genetic diversity along with the evolutionary mechanisms of plant viruses is critical to understanding their ecology and epidemiology. \textit{Dasheen mosaic virus} (DsMV) is an important and conspicuous viral disease of ornamental and edible aroids throughout the South Pacific and worldwide. However, little is known about the spread of DsMV in \textit{Colocasia} (taro) and \textit{Xanthosoma} (tannia) sp., and the patterns of biodiversity have only been studied in limited geographical space. To further investigate this virus, phylogenetic and population genetics based methods were used to investigate the temporal and spatial dynamics of the evolutionary mechanism and genetic variability among the DsMV isolates. A selected region of the coat protein (CP) gene was amplified and sequenced to infer genetic relationships between viral isolates at the temporal and spatial scales. From this, we demonstrated that (i) genetic variation occurs between the DsMV isolates and (ii) the population structure of DsMV in individual plants consisted of a consensus sequence and a pool of similar but not identical sequences, consistent with the quasispecies concept described for many RNA viruses. The quasispecies-like nature of the DsMV population suggested that the virus is capable of rapid evolution and adaptation in response to changing ecological factors and agricultural practices. Analysis of DsMV isolates on a temporal scale suggested the role of stochastic or selection-fitness levels are the key determinants in the dynamics of plant virus population genetics and evolution. On the other hand, special emphasis was given to understand the spatial dynamics and the divergence time of the virus utilizing time stamped data analysis. With the major ecological transitions facilitating their emergence, time stamp data analysis suggested that the genetic diversity in currently circulating viral populations has a far more recent ancestry, indicative of continual lineage turnover. Results also suggested that diversification and spread of DsMV have been concomitant with an extension of human migration and taro/tannia cultivation in the South Pacific islands. The combined actions of genetic drift or selection pressure have continually remodelled this diversity, creating a geographic mosaic in the degrees of diversity found within and between geographic regions.
**Dasheen mosaic virus and Vanilla mosaic virus: using deep sequencing to compare virus strains and identify functionally important genome regions**

Dr Colleen Higgins  
Auckland University of Technology  
colloen.higgins@aut.ac.nz

Colleen M. Higgins(1), Subuhi Khan(1), Gardette Valmonte(1,2), Wee-Leong Chang(1)

(1) Institute for Applied Ecology New Zealand, School of Applied Sciences, Auckland University of Technology, New Zealand  
(2) The New Zealand Institute for Plant & Food Research Limited, New Zealand

The genus *Potyvirus* is one of the largest of plant viruses with around 180 definitive and possible members i.e. 30% of all known plant viruses. Like other RNA viruses, potyviruses exist as sequence populations within a host plant that allow them to adapt rapidly to changing replicative environments by selecting pre-existing variants with better fitness, or possibly altered host range. Therefore, several important virus properties cannot be explained by a single consensus sequence, but require knowledge about the microvariants present in viral populations within and between host plants. These sequence variants may be critically relevant to viral diagnostics, evolution, spread and virulence. With the advent of deep sequencing technologies, it is now possible to determine the full extent of genetic diversity of a virus within a host, and potentially identify regions of functional importance. The potyviruses *Vanilla mosaic virus* (VanMV) and *Dasheen mosaic virus* (DsMV) are strains of the same virus, yet have non-overlapping host ranges. VanMV infects only Orchidaceae (*Vanilla* sp) while DsMV only infects plants of the Araceae family (e.g. taro). Understanding the molecular relationship between these viruses may provide insights into *Potyvirus* variability and evolution as well as general functional mechanisms of this genus. The aims of this work are four-fold: firstly, to determine the genome sequence of VanMV; secondly, to determine if strains of DsMV show the same degree and pattern of diversity, thirdly, to identify conserved genome regions that may have functional importance, and fourthly, to identify genome regions likely to determine host range. Illumina sequencing technology was used to determine the full length genomes of VanMV and different strains of DsMV (NZ and B). Variation within each genome assembly was similar to other assemblies, indicating that the degree of sequence plasticity was common between strains and isolates, and finite. DsMV-B was more variable than –NZ; sequence diversity varied along the length of the genomes, with short stretches of conserved nucleotides, which may have significant roles in translation and/or replication. Identification of such conserved regions is ongoing, as is the identification of candidate host range determinants.

**Molecular characterisation of Grapevine leafroll-associated virus 3 variants in New Zealand**

Dr Kar Mun Chooi  
The New Zealand Institute for Plant & Food Research Limited  
karmun.chooi@plantandfood.co.nz

Kar Mun Chooi(1), Arnaud G. Blouin(1), Michael N. Pearson(2), Daniel Cohen(1), Robin M. MacDiarmid(1,2)

(1) The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Auckland, New Zealand  
(2) School of Biological Sciences, University of Auckland, Private Bag 92019, Auckland, New Zealand

Grapevine leafroll-associated virus 3 (GLRaV-3) is an economically important virus that is found in all grapevine growing regions worldwide. Its accurate detection in nursery and field samples is of high importance for certification schemes and disease management programmes. Genetic variability within a pathogen population can compromise the accuracy and sensitivity of detection. Currently studies have shown GLRaV-3 variants can be classified into six different phylogenetic groups. Based on a genetic diversity study, variants representative of at least five of the six phylogenetic groups (all but group IV) and a tentative seventh phylogenetic group have been identified in New Zealand. Further molecular characterisation of the complete genomes for five variants from groups I, II, V, VI, and VII was conducted. At the nucleotide level, NZ-1B (group VI) and NZ2 (group VII) are more than 20% different from the previously published GLRaV-3 sequences, from phylogenetic groups I to V. Phylogenetic analysis indicated NZ-1B is a variant of the previously identified divergent NZ-1 (group VI), while NZ2 is a novel sequence with only 76% nucleotide identity to group VI GLRaV-3 variants NZ-1, GH11, and GH30. As a result of the significant sequence differences, previously designed GLRaV-3 specific molecular assays did not detect GLRaV-3 variants from groups VI and VII. Therefore to improve diagnostic testing for GLRaV-3, based on the new sequence data, generic and group specific molecular assays have been developed. Amino acid analysis of the NZ1-B and NZ2 proteins indicate significant substitutions that are likely to modify protein structure and/or functionality. For instance, when compared with group I variants, NZ1-B and NZ2 have five non-conservative substitutions between amino acid positions 70 to 84 within the coat protein that are predicted to alter the secondary structure. Based on DAS-ELISA testing using monoclonal and polyclonal antibodies, both divergent GLRaV-3 variants are observed to have reduced immunological reactivity to the monoclonal antibody developed against a group I variant, indicative of changes to the protein structure. Future studies are required to investigate the link between genetic diversity and biological aspects including vector transmission efficiency, virus virulence, and symptom severity.
Identity, genetic diversity and relative virulence of botryosphaeraceous species causing blueberry decline in New Zealand.

Dr Hayley Ridgway
Lincoln University
Hayley.Ridgway@lincoln.ac.nz

Hayley Ridgway, Sarena Che Omar, Dalin Brown, Jackie Sammonds, Marlene Jaspers

Faculty of Agriculture & Life Sciences, Lincoln University, Lincoln 7647, Christchurch, New Zealand

New Zealand blueberry production occupies >520 ha of land and has an estimated total value of $40M with $14.5M from the export market. Farmers in the North Island have identified increasing incidence of stem dieback and crown rot. A 2008 survey of six North Island blueberry farms recovered 93 isolates of botryosphaeraceous species. Isolates were recovered from all farms. The isolates, derived from single spores, were identified using a PCR-RFLP method and DNA sequencing of taxonomic genes. Results showed that four species, *N. luteum*, *N. australe*, *N. parvum*, and *D. seriata*, were present. *Neofusicoccum austral* (n=18) was the most prevalent followed by *N. parvum* and *N. luteum* (both n=12). Genetic diversity analysis of all isolates of *N. parvum*, *N. luteum*, *N. austral*, and *N. ribis* was done using UP-PCR with 11 primers. The results showed that the populations were diverse both within and between farms. Recovery of multiple isolates from a single plant showed that infection by three species (*N. luteum*, *N. parvum* and *D. seriata*) was present. Three isolates from each of the four main species were inoculated as mycelium colonized agar plugs onto wounded succulent green shoots of cultivars Maru and Centurion. After 7 d there was no difference in lesion size between cultivars (P=0.257), but there was a difference between fungal species (<0.001). On green shoots *N. ribis* and *N. parvum* created the longest lesions and *N. luteum* the shortest. When the inoculation was repeated on whole plants there was no difference between cultivars (P=0.134) after 3 weeks but a significant difference between fungal species. *Neofusicoccum ribis* was the most virulent with an average lesion size twice as long (68 mm) as *N. parvum* (33 mm). These results demonstrate that blueberries are infected by a range of botryosphaeraceous species that cause symptoms of dieback and crown rot.

Genetic Diversity and Genetic Structure of *Fusarium oxysporum f. sp. sesami*, the Causal Agent of Yellows and Wilt of Sesame in Fars Province in Iran by Using IGS-RFLP

Dr Seddiqe Mohammadi
Shiraz Islamic Azad University
Mohammadi.pp@gmail.com

Seddiqe Mohammadi(1), Mohammad Razavi(2), Saeid Rezaee(3), Rasul Zare(4), Hamid Reza zamani Zade(1)

(1) Department of Plant Pathology, College of Agricultural Sciences, Shiraz Islamic Azad University, Shiraz, Iran
(2) Department of Plant Pathology, Iranian Research Institute of Plant Protection, Tehran, Iran
(3) Department of Plant Pathology, College of Agriculture and Natural resources, Science and Research Branch, Islamic Azad University, Tehran, Iran
(4) Department of Botany, Iranian Research Institute of Plant Protection, Tehran, Iran

To determine population genetic diversity and genetic structure of *Fusarium oxysporum f. sp. sesami* in Fars province in Iran, 65 isolates were sampled from sesame plants during 2010 and 2011 growing seasons. Ribosomal DNA- IGS regions were amplified using CNS1 and CNL12 primers and fragments with 2600 bp were amplified. PCR products were digested with restriction enzymes EcoRI, Avall, Hinfl, Heall, Mspl, Hhal and HindII and totally 38 fragments were produced. 18 fragments (47.37%) were polymorphic. Among the enzymes used, four enzymes produced polymorphic bands. Maximum polymorphic bands were produced by Avall with 6 bands (33.33%). Cluster analysis of IGS-RFLP was conducted using UPGMA method and Simple Matching coefficient and 5 groups were detected at 89% similarity level. There was correlation between groupings of the isolates based on IGS-RFLP with their geographic origin. This study showed that there was a gene flow among different locations of Fars province and maximum gene flow, was observed between Estahban and Nourabad and minimum gene flow was observed between Darab and Estahban. Maximum genetic diversity was observed among Nourabad isolates.
Evaluation of nutrient media to quantify thaxtomin expression in pathogenic Streptomyces spp. the cause of common scab on potatoes

Dr Arati Agarwal
Department of Environment and Primary Industries
arati.agarwal@depi.vic.gov.au

Arati Agarwal, Tonya J Wiechel, Mark Wardzynski, Fran Richardson, Rudolf de Boer
Department of Environment and Primary Industries, AgriBio, Centre for AgriBioscience, La Trobe University, 5 Ring Road, Bundoora, Victoria 3083, Australia.

Common scab, caused by the filamentous pathogenic bacteria Streptomyces including Streptomyces scabies, is a significant soilborne disease of potatoes. Pathogenic Streptomyces strains produce a phytotoxin called thaxtomin A, a cellulose synthesis inhibitor that is essential for disease development. When the pathogen infects the host, the host responds to thaxtomin toxin secretion by producing suberised tissue on the potato tubers. Our research focuses on the management of common scab using nutrient amendments. To better understand the effect of specific nutrients on pathogen virulence there is a need to identify an appropriate minimal media for culturing Streptomyces to investigate the effect of individual nutrients on thaxtomin gene expression. A pathogenic and non-pathogenic Streptomyces strain were grown in replicates in full, half, quarter and one eighth strength each of Yeast Malt Extract (YME) and Goyer & Loria (G&L) media. RNA was extracted from the biomass, all samples processed for real-time two-step reverse transcription PCR (RT-qPCR) and the thaxtomin expression quantified. Overall G&L produced two and a half times more biomass than YME. PCR amplification in all the samples of the pathogenic strain confirmed the expression of thaxtomin whereas thaxtomin was not detected in the non-pathogenic strain. More thaxtomin was expressed in one eighth dilution G&L and quarter strength YME than in the other dilution even though less biomass was produced at these lower dilutions. Half strength G&L media will be used in future experiments for the growth of Streptomyces to quantify thaxtomin expression.

Optimising stem inoculations for prickly acacia (Acacia nilotica) bioherbicides

Ms Celeste Cook
The University of Queensland
celeste.cook@uqconnect.edu.au

Celeste Cook, Victor Galea, Ken Goulter
School of Agriculture and Food Sciences, The University of Queensland, Gatton, QLD 4343 Australia

Prickly acacia (Acacia nilotica subsp. indica (Benth.) Brenan) is a declared class 2 pest plant and a weed of national significance (WONS) in Australia. An exotic plant, it readily grows along bore drains and wetlands posing a risk to both the grazing industry and environment. In recent times, it has become more widespread changing naturally treeless savanna systems such as the Mitchell Grasslands into woodland. In Queensland alone, landholders spend up to $5M annually in weed control measures which are largely achieved via mechanical or chemical means with biological agents thus far being unsuccessful. A survey of prickly acacia across northern Queensland in 2010 yielded a large collection of fungal isolates associated with dieback and canker affected trees. This isolate bank has previously been evaluated for its potential to yield bioherbicides for this woody weed through laboratory and glasshouse screening methods. Initial field evaluation of a selection of these isolates is reported elsewhere. The objective of this research is to optimise the stem inoculation process for introducing a bioherbicide to A. nilotica. It will examine the infection success of the bioherbicide agent and that of the inoculation methods employed. The bioherbicide candidate chosen for this research is an isolate of Lasiodiplodia pseudotheobromae (NT039). Five inoculation methods were chosen for assessment in a field experiment established at a site near Rockhampton (Qld) called “Pink Lily Lagoon” in April 2013. The first three involved a mechanically drilled 10mm diameter (30mm deep) hole with a gelatine capsule containing NT039 inserted into the tree, and sealed with one of three methods; a domestic silicone roof and gutter sealant or a solid plastic plug (either 10 or 20mm long). The final inoculation methods used bullet casings (0.22 calibre) containing ground NT039 inoculum either hammered directly through the bark or inserted into a 6 mm diameter (2-5 mm deep) pilot hole to remove surface bark. Untreated control trees were identified and marked for comparison. Three trial assessments would be conducted at 3 monthly intervals to determine overall health status of the trees. Destructive samples taken of some stems will allow assessment for internal and external signs of infection and the success of inoculation techniques. In mid-July 2013 the first of three assessments was performed. Indications thus far are of successful infection by NT039 for all inoculation treatments, and detailed sample analysis is currently underway.
Detection of Phytophthora in Gondwana Rainforests

Dr Rosalie Daniel
Department of Primary Industries
rosalie.daniel@dpi.nsw.gov.au

Rosalie Daniel(1), David Guest(2), Thomas Bishop(2)
(1)Department of Primary Industries, Menangle 2567, New South Wales
(2)The University of Sydney, Sydney 2006, New South Wales, Australia

_Physopthora cinnamomi_ (Phytophthora) occurs throughout Australia and has become infamous as a cause of large-scale disruption of native ecosystems. Sampling for Phytophthora, particularly in remote areas, can involve large inputs of time, labour and money. A new approach, using a spatial prediction model, was developed and tested for its efficacy in detecting sites affected by Phytophthora, so that sampling could be targeted to areas where Phytophthora was more likely to occur. The Gondwana Rainforests World Heritage Area in eastern Australia was sampled for Phytophthora and the sample data used in combination with previous surveys to create a map of the probability of Phytophthora being present at a given site. A spatial prediction model was created using GIS data layers relating to environmental factors that are known to favour Phytophthora and dieback disease, or pathogen spread. The most important predictors were found to be vegetation type, eastings, annual rainfall, northing, slope and a solar irradiation index. Overall the model quality was good with an overall AUC statistic of 0.78, ranging from 0.59-0.80 in different regions of the Gondwana rainforests. Sampling confirmed the presence of Phytophthora in all but three of the reserves and parks in the GRWHA. A database of more than 950 sites from which samples have been taken and the presence or absence of Phytophthora confirmed has been established. Sequence analysis revealed that more than one _Phytophthora_ species occurs in the GRWHA, including _P. cinnamomi_ and _P. cryptogea_. The impact of _Phytophthora_ species on the plants that occur in the Gondwana rainforests is unknown. Soil sampling surveys and mapping of the distribution of Phytophthora lay the groundwork for the development of management strategies for Phytophthora dieback.

QPCR analysis of leaves to predict the incidence of postharvest fruit rots of avocado

Dr Kerry Everett
Plant and Food Research
Kerry.Everett@plantandfood.co.nz

Kerry Everett(1), Jonathan Rees-George(1), Shamini Pushparajah(1), Michele Vergera(1), Henry Pak(2), Roger Barber(2)
(1)The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Mt Albert, Auckland 1142, New Zealand
(2)New Zealand Avocado Industry Council, Level 5 Harrington House, Harrington Street, PO Box 13267, Tauranga

DNA was extracted from leaf tissue collected from the three major avocado growing regions in New Zealand, the Far North, Whangarei and the Bay of Plenty during spring 2012. The amount of leaf infection by postharvest rot fungi was quantified using real-time PCR to generate a Ct value. Avocado fruit were harvested from each of these orchards 1-2 months later, coolstored for 28 days, then evaluated for rots when fruit reached eating ripeness at 20°C. The Ct values produced following qPCR analysis of avocado leaves predicted the incidence of postharvest rots in fruit from the Whangarei region to a level of accuracy of 80% after an outlier value was removed from the analysis. When the number of copper fungicides applied during the season was included in the analysis, the incidence of postharvest rots in fruit from the Bay of Plenty region was predicted by Ct values to a level of accuracy of 65% after an outlier value was removed from the analysis. When a second outlier value was removed from the analysis, the Ct values and number of copper fungicides applied during the season predicted the incidence of postharvest rots in the Bay of Plenty region to a level of accuracy of 82%. No significant relationship was found between Ct values and fruit rots for the fruit harvested from the Far North region. These results suggest that there was another factor with a strong influence on fruit rots in the Far North that was not accounted for. The Ct value from leaves appeared to be a good predictor of postharvest rot for fruit from the Whangarei region, and when applied in combination with fungicide use, a good predictor of rots in the Bay of Plenty. Further work is required to identify the factors that make an orchard an outlier.
Validating changes to DAS ELISA (Double-antibody sandwich enzyme linked immunosorbent assay) with five potato viruses

Ms Sue Pederick
South Australian Research and Development Institute
sue.pederick@sa.gov.au

Sue Pederick, Barbara Hall
South Australian Research and Development Institute, GPO Box 397, Adelaide, South Australia 5001

DAS ELISA testing is a relatively low cost diagnostic tool used for potato virus detection. This paper reports on validation of changes to the ELISA NATA protocol used for Potato Leaf Roll Virus (PLRV), Tomato Spotted Wilt Virus (TSWV), Potato Virus X (PVX), Potato Virus Y (PVY) and Potato Virus S (PVS). Positive controls can be stored as frozen extracted sap or infected leaf material, however the longevity of the virus is variable. Sap was extracted in buffer from leaf tissue previously tested positive by ELISA for one or all of the five viruses, decanted into aliquots of approximately 300µL in 1.5mL Eppendorf tubes and stored at -25°C. Positive leaf material was placed in a plastic bag without buffer before also freezing at -25°C. The aliquots and leaves were tested regularly to confirm positive titre. The results of these tests indicate that sap of PLRV, TSWV, PVY, PVS and leaf tissue of PVX and PVS can survive in frozen storage for at least 30, 5, 12, 10, 110, 108 months, respectively. The PVY conjugate buffer recipe provided with the agdia® test kit has recently changed, using serum albumin and polyvinylpyrrolidone. As this new buffer is less toxic and quicker to make and to avoid using separate buffers for each of the five virus tests, the buffer was tested to determine whether it was equally effective with the other four viruses. Results showed that for PVY and PVS the buffer improved detection, with reduced background colour. There were no changes with results of the other three viruses. Most buffers are required to be made daily on use, however would improve costs and reduce labour. Carbonate coating buffer, extraction buffer and substrate buffer were stored at 5-7°C. These buffers were considered viable as long as the positive and negative controls in the test remained consistent. Buffers have remained viable for at least 4 weeks and testing is continuing. By confirming the longevity of buffers and positive controls and the compatibility of a safer and more effective conjugate buffer, the NATA requirements for integrity of all processes has been maintained, and the changes in procedure will increase the productivity of the tests.
Volatiles organic compounds produced by fire blight infected apple flowers reduce honeybees visits

Dr Francesco Spinelli
Department of Agricultural Sciences, University of Bologna
Francesco.spinelli3@unibo.it

Volatiles organic compounds produced by fire blight infected apple flowers reduce honeybees visits. Honeybees have been demonstrated to vector Erwinia amylovora, the causal agent of fire blight, which is the most destructive disease of pome fruits. Since bees choose the flowers they visit based on by flower colour and shape, nectar composition, pollen production and volatile compounds (VOCs) emission, the present study we characterized all these parameter in healthy and infected apple flowers. VOCs were collected by closed-loop-stripping-analysis (CLSA) and by solid phase microextraction (SPME) and analysed by gas chromatography-mass spectrometry (GC-MS). To determine whether honeybees show a preference for healthy or infected flowers, an experiment was performed in controlled conditions on flowering scions. To monitor bees visits on flowers direct counting, and other methods, developed in this study, were used. In details, a pollen insert, placed at the exit of the hive, was loaded with a lyophilized preparation of an epiphytic bacterium (Pantoea agglomerans strain P10c). Exiting the hives, bees carried P10c to the flowers they visited. Presence of this bacterium on flowers was determined by q-PCR and direct isolation. A complementary method for estimating bees preference was based on the quantification of E. amylovora cells on the pollen collected by bees. The population of E. amylovora on collected pollen is thought to be correlated to the percentage of infected flowers visited. The three complementary methods used to estimate bees preference provided similar results showing that bees visited more often healthy flowers. This behaviour was independent of whether bees had been previously exclusively either healthy or infected flowers. No difference in pollen production, nectar composition and flowers colours was observed. Therefore, our results suggest that VOCs may play a critical role in determining which flower bees prefer to visit. This is the first evidence of a VOCs-based ecological interaction occurring between host plant, pathogen and pollinator. In addition, the results show that the role of bees in diffusing E. amylovora might need further studies to be fully clarified.
TRFLP profiling of potato field soils with low and high common scab symptoms

Dr Tonya Wiechel
Department of Environment and Primary Industries Victoria
Tonya.Wiechel@depi.vic.gov.au

Common scab is an important disease in potato worldwide. Pathogenic Streptomyces produce thaxtomin which elicits a host response that suberizes tissue around the infection. The disease affects the quality of the potato by producing superficial, raised and deep pitted lesions on the tuber surface. There are no effective control methods for common scab as they are inconsistent and often fail. To better understand why some potato fields get common scab and others do not, we sought to validate a DNA based microbial community typing method (TRFLP) on 28 soils. Soils in this experiment came from potato fields showing no disease (healthy) or a high incidence of disease (unhealthy). These were further divided into groups based on the presence or absence of pathogen DNA. These soils were used to generate fresh rhizosphere samples from tissue culture plantlets of cv Kennebec. TRFLP analysis was done on DNA extracted from these laboratory grown rhizospheres. Principle component analysis (PCA) was used to differentiate between common scab unhealthy and healthy soils. Soils that produced disease symptoms fell into the unhealthy group and soils that were symptomless fell into the healthy group. No peaks for the pathogen were detected in the unhealthy soils suggesting the pathogen is either a minor component of the bacterial rhizosphere community or is not being sufficiently amplified in comparison to other bacterial species when soil inoculum is present. TRFLP profiles of soil bacterial communities appear to group based on common scab disease potential. TRFLP profiling is a technique suited to measuring microbial diversity. In the case of common scab we have been able to distinguish soils into unhealthy and healthy groups using TRFLP profiling. The fact that other non-pathogen DNA signals were able to distinguish between unhealthy and healthy soils suggests that microbial diversity in general might serve as a useful and even more accurate bioindicator of disease than pathogen DNA itself. Efforts are underway to identify key players or factors that may be responsible for the reduced disease seen in the healthy sites.

Bioinformatics analysis of G protein signalling in the grass mutualist Epichloë festucae

Mr Alexander Bisson
Massey University
a.bisson@massey.ac.nz

The fungal endophyte Epichloë festucae forms a mutualistic association with perennial ryegrass, in which the hyphae display synchronised growth. To maintain this regulated pattern of growth in planta, signalling between the symbiont and its host grass is required. To sense the extracellular environment and respond to changes, filamentous fungi rely on G protein-coupled receptors (GPCRs), which transmit signals predominantly via heterotrimeric G proteins, which then transduce these signals to downstream pathways such as the cAMP/Protein kinase A (PKA) and MAPK signalling pathways. In phytopathogenic fungi, G protein signalling and the associated cAMP/PKA and MAPK signalling pathways are often essential for normal host interaction. In a first step towards understanding what role G protein and cAMP/PKA signalling may play in establishment and maintenance of the beneficial E. festucae–perennial ryegrass association we performed a comprehensive bioinformatics analysis of the E. festucae genome to identify the genes involved in these signalling pathways. A number of GPCRs homologous to the well-characterised GPCRs of Neurospora crassa were identified in E. festucae, including the pheromone receptors Pre1 and Pre2, carbon sensor Gpr4, nitrogen sensor Gpr5 and the opsin Orp1. The E. festucae genome was also found to encode a homologue of the N. crassa cAMP-receptor-like GPCR, Gpr2, but no homologue of Gpr3. Interestingly, two homologues of another N. crassa cAMP-receptor-like GPCR, Gpr1, were identified in the E. festucae genome (gpr1a and gpr1b), possibly due to gene duplication. Hypothetically, duplication of Gpr1 may allow for diversification of one of the copies into a sensor for host-derived molecules. While Gpr1b shows typical GPCR protein structure, Gpr1a is predicted to comprise just five transmembrane domains instead of the canonical seven. Results of the bioinformatics analyses of the GPCRs, and components of the cAMP signalling pathway will be presented. RNA sequencing analysis of the expression of the different E. festucae GPCRs in planta will also be presented.
Development of a *Trichoderma atroviride* LU132 variant active at lower temperatures for control of *Botrytis cinerea* on grapes using protoplast technology

Mr Mark Braithwaite  
Bio-Protection Research Centre, PO Box 84, Lincoln University  
Mark.Braithwaite@lincoln.ac.nz

Mark Braithwaite(1), Janaki Kandula(1), Johanna Steyaert(1), Amanda Hay(2), Alison Stewart(1,2)

(1) Bio-Protection Research Centre, PO Box 84, Lincoln University, Lincoln 7647, New Zealand.  
(2) Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA.

*Botryotinia fuckeliana* (de Bary) Whetzel, anamorph *Botrytis cinerea* Pers., causes grey mould or bunch rot of grapes and is an economically important disease worldwide. The commercial product Sentinel® (a.i. *Trichoderma atroviride* isolate LU132) provides an alternative to fungicides for grey mould control. To improve the performance range of this product, protoplasts were generated and selected under cold conditions (6°C) to produce a new strain of *T. atroviride* LU132 biologically active at cooler temperatures (6°C) compared with the parent strain. In detached necrotic strawberry leaf assays, LU806 significantly suppressed *B. cinerea* growth and sporulation statistically equivalent to the parent strain. In two shade-house experiments, variant LU806 significantly suppressed *B. cinerea* symptoms on grape flowers and fruit, to levels statistically equivalent or better than the parent strain. In an additional cool temperature controlled growth room experiment, only LU806 provided significant control of latent *B. cinerea* infection of grape berries. However, LU1132 and LU806 both significantly reduced *B. cinerea* berry infections compared with the infected control. Incorporation of this variant strain into the Sentinel® product may facilitate use of this product in cool temperature viticulture.

Incorporation of trehalose into *Trichoderma atroviride* conidia and its effect on viability of conidia during storage

Mr Mark Braithwaite  
Bio-Protection Research Centre  
Mark.Braithwaite@lincoln.ac.nz

Janaki Kandula(1), Mark Braithwaite(1), Johanna Steyaert(1), Amanda Hay(2), Alison Stewart(1,2)

(1) Bio-Protection Research Centre, PO Box 84, Lincoln University, Lincoln 7647, New Zealand.  
(2) Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA.

Biocontrol agents are living organisms that require stabilisation, usually through product formulation, to attain an acceptable shelf life of 1-2 years. Trehalose (a storage carbohydrate in a wide variety of organisms) is an osmo-protectant that is stable under hot and acidic conditions and is able to protect fungal spores against freezing or excess heat. Trehalose has also been shown to increase spore viability in fungi. In the current research, the ability of trehalose to prevent loss of *Trichoderma atroviride* conidial viability during storage under conditions of accelerated aging to simulate long-term storage was evaluated. *T. atroviride* conidia were produced by solid substrate fermentation, with the initial broth amended with varying amounts of trehalose (ranging from 0-24.4 mM). Conidia were harvested in sterile water and allowed to air-dry before storage at either 4 or 30°C with uniform water activity. Conidial viability was assessed at monthly intervals by counting percentage germination. At harvest, trehalose amendment of the growth media resulted in a significant increase in trehalose content of *T. atroviride* conidia of between 18 and 42%, when compared with the untreated controls. The 0.8 mM trehalose significantly increased viability of conidia, as measured by the area under the conidia viability progress curve, in both the 4 and 30°C storage treatments by 5 and 12%, respectively. However, at this concentration, trehalose did not significantly extend shelf-life of *T. atroviride*. The addition of higher concentrations of trehalose significantly reduced spore viability.
BIOLOGICAL INTERACTION AND PLANT DISEASE
POSTER BOARD 13

The effect of plant disease on soil microbes in a natural vegetation community

Dr Rosalie Daniel
Department of Primary Industries
rosalie.daniel@dpi.nsw.gov.au

Rosalie Daniel(1), Carolyn Blomley(2), Floriane Bardeau(2), Peter Beard(3), Peter McGee(2), David Guest(2)

(1)Department of Primary Industries, Menangle 2567, New South Wales, Australia
(2)The University of Sydney, Sydney 2006, New South Wales, Australia
(3)National Parks and Wildlife Service, Gloucester 2422, New South Wales, Australia

The breakdown of organic material by soil bacteria and fungi results in the release of minerals into the soil. The process contributes fundamentally to soil stability, plant growth and ecosystem function, however little is known about the effect of plant pathogens on soil biology. Dieback associated with the soilborne Oomycete Phytophthora cinnamomi in Australian woodland communities results in the decline and death of susceptible plant species. The death of susceptible plants not only deprives the pathogen of host plants, but adds significant amounts of organic matter to the soil, potentially stimulating the activity of antagonistic and competitive soil microbes. Our hypothesis is that these consequences of dieback may facilitate ecosystem maintenance or recovery. Transects were established across the dieback disease margin on dry sclerophyll vegetation in Barrington Tops National Park, NSW (Australia). Soil biological activity and fungal biomass were highest close to the infested side of the disease margin, corresponding with the massive organic matter inputs to the soil resulting from the death of susceptible plants. Microbial diversity (t-RFLP) changed depending on the distance from the disease margin, suggesting that microbial populations respond and adjust to the availability of nutrients as plant residues are broken down. Understanding the effect of disturbances, such as disease, on plant communities, improves our understanding of ecosystem structure, function and sustainability.
**CoBub2-CoBfa1 complex, a component of mitotic exit network regulator in Saccharomyces cerevisiae, is required for interphase cell cycle progression and pathogenesis in Colletotrichum orbiculare**

Ms Fumi Fukada  
Kyoto Prefectural University  
ddswb383@yahoo.co.jp

Fumi Fukada, Ayumu Sakaguchi, Yasuyuki Kubo  
Graduate School of Kyoto Prefectural University, Life and Environmental Sciences, Shimogamo, Kyoto, Japan

Morphogenesis in filamentous fungi depends on accurate cell cycle progression. In *Saccharomyces cerevisiae*, **BUB2** is a component of spindle position checkpoint (SPOC) which prolongs mitosis by inhibiting mitotic exit network when the spindle fails to align along the mother-daughter axis. Here, we analyzed functional roles of **BUB2** homolog in cucumber anthracnose fungus, *Colletotrichum orbiculare* by generating gene disruption mutants. Morphogenesis analysis of the **cobub2** mutants showed that conidia developed appressoria with abnormal hyphae, creeping on the surface of cellulose membranes used as a model substrate. The **cobub2** mutants had defects in penetrating into host plant cells and failed to cause full disease lesions on cucumber leaves. Importantly, time course observations of histone H1-GFP introduced strains and by DAPI staining confirmed that Co**BUB2** is involved in the timing of mitosis and proper assignment of nuclei during appressorium development. Furthermore, the experiments of interphase specific inhibitors revealed that the transition from G1 phase to S phase of the **cobub2** mutants accelerated about 2h than that of the wild type. In *S. cerevisiae*, Bub2 forms GTPase activating protein (GAP) complex with Bfa1, and Bub2-Bfa1 GAP complex constitutes SPOC. Then we generated **bfa1** homolog mutants in *C. orbiculare*. The **cobub2** mutants showed similar mitotic behavior and pathogenesis to the **cobub2** mutants. Functional complementation experiments of **cobub2/cobfa1** mutants with **BUB2/BFA1** of *S. cerevisiae* are in progress. Our results suggest that the CoBub2-CoBfa1 complex plays critical roles in G1 phase to S phase progression and pathogenesis in *C. orbiculare* although the Bub2-Bfa1 complex of *S. cerevisiae* functions as a regulator of mitotic exit network.
Characterization of Bangladeshi native isolates of *Trichoderma* sp. and assessment of their bio-control efficiency against plant pathogens

Mr MD Monirul Islam  
Niigata University, Japan  
mmislambau@gmail.com  
M M Islam\(^1\), M D Hossain\(^1\), N Harada\(^2\),  
\(^1\)Bangladesh Agricultural University, Bangladesh  
\(^2\)Graduate School of Science and Technology, Niigata University, Japan

Monoconidial cultures of 20 isolates of *Trichoderma* from different districts, Bangladesh were characterized on the basis of morphological, physiological, biochemical and molecular features. All of them were screened for proteinase, endochitinase and β-1,3 glucanase activities and internal transcribed spacer 1 and 2 regions (ITS1 and ITS2) of rDNA were sequenced. TR5 and TR8 isolates showed strong proteinase, endochitinase and β-1,3 glucanase activities. They were identified as *Trichoderma virids* based on the sequences of internal transcribed spacer 1 and 2 regions (ITS1 and ITS2). The ability of the *Trichoderma* isolates to antagonize soil-borne fungal plant pathogens was examined using a dual culture assay against seven fungal species such as *Penicillium* sp., *Fusarium oxysporum*, *Sclerotium rolfsii*, *Rhizoctonia solani*, *Aspergillus flavus*, *Colletotrichum* sp. and *Phomopsis vexans*. The highest inhibition values (L) were obtained against *Aspergillus flavus* and *Fusarium oxysporum*. The highest inhibition values (L) were obtained against *Aspergillus flavus* and *Fusarium oxysporum*

Indigenous *Trichoderma* population size and diversity in the rhizosphere of onion and potato under different crop rotations in a five year field trial

Dr Eirian Jones  
Lincoln University  
Eirian.Jones@lincoln.ac.nz  
Emmanuel Bourguignon\(^1\), Leo Condon\(^2\), Kirstin McLean\(^3\), Alison Stewart\(^2\), Rhys Minchin\(^2\), Eirian Jones\(^4\)  
\(^1\)Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln, Canterbury, New Zealand  
\(^2\)Agriculture and Life Sciences Faculty, PO Box 85084, Lincoln University, Lincoln, Canterbury, New Zealand  
\(^3\)Marrone Bio Innovations, Davis, California, 95618 USA

*Trichoderma* species are ubiquitous soil fungi commonly found in agricultural soils and have been shown to suppress soil-borne plant pathogens. The effect of management strategies such as crop rotation and green manure amendments on the indigenous *Trichoderma* population structure is not well understood. Changes in the *Trichoderma* population size and species diversity in the rhizosphere were investigated in a 5 year field experiment which included six different crop rotations, namely continuous onion, continuous potato, onion/potato rotation, potato/onion rotation, –onion-potato-oats-brassica-onion, and potato-onion-oats-brassica-potato. The oat crops were short-term green manures. For each crop, rhizosphere *Trichoderma* colony forming units (CFU) was determined by soil dilution plating onto selective medium and identification of colonies to species level based on colony morphology and confirmed by PCR-RFLP and sequencing. There was no significant differences observed for *Trichoderma* populations in the rhizosphere of onion and potato (1.35 and 1.5 x 10^3 CFU/g soil, respectively) throughout the experiment. However, *Trichoderma* populations were significantly higher in the rhizosphere of the oat green manure crop compared with onion and potato in the other treatments. This increase in *Trichoderma* populations was maintained into the subsequent crops planted in the sustainable rotation treatments indicating a significant effect of green manure application rather than a rhizosphere effect of the different crops on *Trichoderma* populations. Five *Trichoderma* species *T. asperellum*, *T. atroviride*, *T. hamatum*, *T. harzianum* and *T. koningii* were recovered from the rhizosphere of both onion and potato. The crop rotation treatments did not have any significant effect on the diversity, with *T. hamatum* (33%), *T. koningii* (23%) and *T. harzianum* (21%) being the most frequent. However, lower species diversity was identified in the bulk soil at the beginning of the experiment, with only *T. atroviride* (80%), *T. hamatum* (13%) and *T. harzianum* (7%) being recovered. Since the *Trichoderma* diversity in the rhizosphere is selected from this population it indicates that there is higher diversity in the bulk soil than can be detected by this method.
**Molecular characterization of a novel Sclerotinia sclerotiorum mycovirus representing a new genus of Hypoviridae**

Mahmoud Khalifa  
School of Biological Sciences, The University of Auckland  
mkha201@aucklanduni.ac.nz  

A 15 kb dsRNA (dsRNA-L) element was detected in *Sclerotinia sclerotiorum* ICMP#5472. Sequence analysis revealed that it is 14581 nts long excluding the poly (A) tail at the 3' terminal region of its coding strand. The coding strand contains a single long open reading frame (ORF) (nt positions 314-14222) flanked with two untranslated regions (UTRs) at the 5' and 3' termini and codes for a polyprotein of 4635 amino acids (aa) with an expected molecular weight of 522,450 kDa (P522). Two papain-like cysteine protease, a RdRp and a helicase domains with typical aa conserved motifs of each domain were detected in P522 and shared low aa sequence identities with its closely related members of the mycovirus family Hypoviridae. Phylogenetic analysis based on multiple alignments of papain-like cysteine proteases, RdRp, helicase domains as well as the full-length sequence of P522 clustered dsRNA-L with members representing Alphahypovirus and Betahypovirus; the two genera of Hypoviridae. The distances between dsRNA-L aa sequence and those of the members of Hypoviridae genera were less than the distances between members of the Alphahypovirus and Betahypovirus. This suggests that dsRNA-L represents a novel mycovirus of a proposed new genus Gamahypovirus and consequently it was tentatively assigned the acronym Sclerotinia sclerotiorum gamahypovirus 1 (SsGHV1). To our knowledge, SsGHV1 has the longest genome among members of Hypoviridae, with previously recorded genome sizes of ~9 to 13 kb. Possible phenotypic and virulence alterations by SsGHV1 remain to be addressed.
**Free-air CO$_2$ enrichment (FACE) affects the susceptibility of Brassica juncea to foliar pathogens**

Mr Piyush Mathur  
University of Delhi  
piyushmathur110@gmail.com

Piyush Mathur(1), Shiv Dhar Singh(2), Ved Pal Singh(1), Rupam Kapoor(1)

(1)Department of Botany, University of Delhi, Delhi- 110 007, India  
(2)Centre for Environment Sciences and Climate Resilient Agriculture, Indian Agricultural Research Institute, Delhi- 110 007, India

The atmospheric concentration of carbon dioxide CO$_2$ has increased by at least 35%, since the start of industrial revolution. With increasing concern about the effects of global climate change on food production, it is important to devote greater effort towards studying the impact of various aspects of elevated CO$_2$ on the development of plant disease epidemics and the specific plant-pathogen interactions under field conditions. Brassica juncea (L.) Czern. & Coss. (Indian mustard) is an important oilseed crop grown both in tropical and sub tropical regions of the world, yielding essential edible oil. The mustard crop suffers severely from major foliar diseases like alternaria blight (Alternaria brassicae (Berk.) Sacc.), downy mildew (Hyaloperonospora brassicae (Gäum.)), and white rust (Albugo candida (Pers.) Kuntze). The mustard plant’s susceptibility to pathogens depends on both structural and biochemical characteristics of leaves. Elevated CO$_2$ had a substantial effect on the stomatal density and stomatal pore size of leaves. There was an increase in the concentration of total sugars leading to increase in C/N ratio under elevated CO$_2$. The excess of carbon led to change in the production of plant defensive secondary chemicals such as phenolics and glucosinolates (GSs) and enzymes like phenylalanine ammonia lyase. These all changes in turn notably affected natural incidence and severity of alternaria blight, downy mildew and white rust. The study provides evidence suggesting that elevated atmospheric CO$_2$ can have an impact on mustard crop pathosystems and will consequently provide understanding in disease surveillance protocols and management strategies of these pathogens under high CO$_2$ environment.

**Study on the Morphological Characteristics and Virulence of Macrophomina phaseolina isolates from Sesame Plants in Different Areas of Iran**

Ms Mohsen Naderpour  
Tarbiat Modares University  
naderpour.mohsen@yahoo.com

Mohsen Naderpour(1), Naser Safaie(1)

(1)Department of Plant Pathology, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran  
Phone: +982148292346  
FAX: +982148292200

Morphological characteristics (chlorate phenotype, relative growth rate at 30, 37, and 40°C, colony color and shape, density of aerial mycelia, the time and frequency of microsclerotia formation at 30, and 37°C on potato dextrose agar medium under dark conditions of incubations) of the isolates were studied. Also, the virulence of the isolates was investigated following stem inoculation with a plug of fungal culture under green house conditions. The frequency of feathery growth phenotype (48.8%) was the highest, while that of limited and dense growth on chlorate medium were 28.8% and 22.2%, respectively. The optimal temperature for growth was found 30°C (1.62 mm/h) and the most unfavorable temperature was 40°C (0.24 mm/h). The average growth rate at 37°C was 1.06 mm/h. Temperature had a significant impact on the changes in the phenotypic frequency of the isolates. Based on the sum of the all calculated indices applied in virulence test of isolates, the frequency of weakly, averagely, and highly virulent isolates was respectively determined as 44.44%, 26.66%, and 28.88%. The highly virulent isolates indicated high tendency to form microsclerotia early and more abundantly. No relationship was found between virulence and morphological characteristics in one side and geographical origin of the isolates in another side. Most of the isolates of sensitive phenotype were highly virulent. A high diversity in morphology and virulence of Iranian population of the pathogen was observed similar to that in other countries. Quantitative traits are more meritorious than qualitative traits for the classification of the isolates. The research indicated the high difficulty or impossibility of the morphology or pathology-based identification and description of the pathogen subgroups because of the high intraspecific diversity under environmental and in vitro conditions, as well as problems with the quantification of these traits.
Biological races of *Fusarium oxysporum* f. sp. *niveum* Australian watermelon production regions

Mr Victor Puno
The University of Sydney / Royal Botanic Garden Sydney
victor.puno@rbg syd . nsw . gov . au

Victor I. Puno1,2, Len A. Tesoriero3,4, Lucy T.T. Tran- Nguyen6,7, Barry Conde8, David I. Guest9, Edward C.Y. Liew10,
1 Faculty of Agriculture and Environment, The University of Sydney, C81 - Biomedical Building, Australian Technology Park, NSW 2006, Australia.
2 The Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney NSW 2000, Australia.
3 NSW Department of Primary Industries, Private Bag 4008 Narellan NSW 2567, Australia.
4 Plant Industries Group, Department of Primary Industry and Fisheries, GPO Box 3000 Darwin, NT 0801, Australia

Fusarium wilt of watermelon is an ongoing problem which causes significant economic losses and limits industry growth worldwide. The causal agent, *Fusarium oxysporum* f. sp. *niveum* (Fon), is a soil borne pathogen and has been sporadically reported in Australian production regions since the late 1960s. There are, at present, four races of Fon (Race 0, 1, 2, and 3) reported worldwide; however, it is currently unknown which races of Fon are present in the country. The current study aims to determine the presence of Fon and its races in Australia. A field survey comprising of six sites from south Queensland and five sites from central New South Wales was conducted. Each site was visually assessed for the presence of wilt disease, with samples of diseased plants and soil collected for laboratory analysis, diseased plants and soil samples were received from Western Australia. Stem, crown, and root tissue of diseased plants were plated onto selective and general medium. Soil isolates were obtained by live baiting with universally susceptible watermelon cultivar, ‘Sugar Baby’. Fifteen isolates (7 from Queensland, 3 from Western Australia and 5 from New South Wales) were selected for race determination using differential cultivars ‘Sugar Baby’ (susceptible to all races), ‘Crimson Sweet’ (susceptible to Race 1 and 2), ‘Allsweet’ (susceptible to Race 2 and 3), and ‘SP-f’ (susceptible to Race 3). This paper presents and discusses results obtained from the field survey, pathogen isolation and race determination study.

Phylogenetic analysis of *Burkholderia andropogonis* based on gyrB, rpoD and 16S rRNA gene sequences

Ms Lucilene Lopes Santos
Universidade Estadual de Campinas (UNICAMP)
lulopes.bio@gmail . com

Lucilene Lopes dos Santos1,2, Mariana Ferreira Tonin3, Daniele Bussioli Alves Corrêa1,4, Renata Comparoni1,5, Lucila Gonçalves Andrade4, Renata Geminari4, Marcio José da Silva4, Suzele Aparecida Lanza Destefani1

1 Instituto Biológico, Campinas/SP-Brazil
2 FPPG-Genética e Biologia Molecular/Universidade Estadual de Campinas (UNICAMP), Campinas/SP-Brazil
3 CBMEG-Centro de Biologia Molecular e Engenharia Genética/Universidade Estadual de Campinas (UNICAMP), Campinas/SP-Brazil
4 Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), São Paulo/SP-Brazil

*Burkholderia andropogonis*, initially described by Smith (1911) as the causal agent of disease in sorghum (*Sorghum bicolor*), affects a wide range of host plants economically important with an extensive geographical distribution. It is the cause of leaf spots, streaks and stripes. *B. andropogonis* strains are highly similar both in morphological and in physiological characteristics, however genetic and pathogenicity variabilities were observed. In order to study the phylogenetic relationship among *B. andropogonis* and other *Burkholderia* species, a phylogenetic tree was built using the combined nucleotide sequences of *gyrB* and *rpoD*; and also 16S rRNA gene sequences which were determined by the sequencing of PCR-amplified fragments. On the basis of *gyrB* and *rpoD* sequences, the strains were divided into two main clusters: one including the eight *B. andropogonis* strains isolated from different hosts among which was observed a high similarity (from 99% to 99.8%); and the other cluster included *B. cepacia*, *B. glumae*, *B. gladioli*, *B. plantarii* and *B. caryophylii* strains with similarity ranging from 80.9% to 95.5% among them. Although the strains analyzed belong to the same genus, the similarity observed between the two main clusters was below 67%. On the phylogenetic tree reconstructed from the 16S rRNA sequences including variable regions, the same clusters were obtained, in which the similarity values among *B. andropogonis* strains ranged from 99% to 99.7%, while among *Burkholderia* species and *B. andropogonis* the similarity was from 93.2% to 96.3%. The analysis of *gyrB*, *rpoD* and 16S rRNA gene sequences showed that *B. andropogonis* is phylogenetically distant from the other *Burkholderia* species. In order to thoroughly investigate the data obtained herein, other housekeeping genes will be included in this study to confirm if the *B. andropogonis* strains belong to this genus.
Pathogenicity of species implicated in Eutypa dieback disease of grapevines

Dr Mark Sosnowski
South Australian Research and Development Institute
Mark.Sosnowski@sa.gov.au
Wayne M Pitt(1), Florent P Trouillas(2), Walter D Gubler(3), Sandra Savocchia(4), Mark R Sosnowski(5)
(1)National Wine and Grape Industry Centre, School of Agricultural and Wine Sciences, Charles Sturt University, Wagga Wagga, NSW 2678, Australia
(2)Department of Plant Pathology, University of California, Davis 95616, USA
(3)South Australian Research and Development Institute, Adelaide, SA 5001, Australia

In addition to Eutypa lata, which causes Eutypa dieback, numerous other fungi in the Diatrypaceae family have been isolated from diseased grapevines (Vitis vinifera) and other woody hosts. Pathogenicity trials comprising 70 strains of diatrypaceous fungi representing nine species in six genera were conducted to determine whether these fungi, collected in Australia, were pathogenic to grapevines. When inoculated into wounded trunks of ‘Cabernet Sauvignon’, eight species, including E. lata, E. leptoplaca, Cryptosphaeria ampelina, C. rabenhorstii, Eutypella citricola, E. microtheca, Diatrypella vulgaris, and a Diatrype sp. produced necrotic lesions significantly longer than on controls. In addition, all nine species (including a Cryptosphaeria sp.) were reisolated from the margins of developing lesions and at varying distances above and below the point of inoculation. Diatrypaceous fungi were frequently isolated from asymptomatic or otherwise healthy tissue several centimeters ahead of the disease margin. Methods to control diseases associated with diatrypaceous fungi must take into account their propensity to colonize woody tissues ahead of, or in the absence of visible symptoms. Current recommendations for the management of Eutypa dieback using remedial surgery and pruning wound protection appear sufficient for the control of the other diatrypaceous fungi included in this study.

The volatile compounds emitted by Erwinia amylovora infected apple plants induce host defences on neighbouring plants

Dr Francesco Spinelli
Department of Agricultural Sciences, University of Bologna
Francesco.spinelli3@unibo.it
Francesco Spinelli(1), Antonio Ceflini(2), Giampaolo Buriani(3), Irene Donati(1), Valentino Giammuzi(1), Maria Teresa Rodriguez-Estrada(4), Stefano Savoletti(5), Brian Fametti(6), Franco Biasioli(7), Simona Cristescu(8), Joel Vannevel(9), Guglielmo Costa(10)
(1) Department of Agricultural Sciences, Alma Mater Studiorum -University of Bologna, viale Fanin 46, 40127 Bologna - Italy
(2) Faculty of Science and Technology, Free University of Bolzano, piazza Università 5, 39100 Bolzano - Italy
(3) Department of Food Science and Technology, Alma Mater Studiorum -University of Bologna, viale Fanin 40, 40127 Bologna - Italy
(4) Food Quality and Nutrition Department, Research and Innovation Centre - Fondazione Edmund Mach, Via E. Mach 1, 38010 S. Michele all'Adige (TN)- Italy
(5) Radboud University, Institute of Molecules and Materials, Heyendaalseweg 135, 6525AJ Nijmegen - The Netherlands
(6) Plant & Food Research, Ruakura, Private Bag 3123, Waikato Mail Centre, Hamilton, 3240 - New Zealand
(7) Plant & Food Research, Auckland, New Zealand
(8) Plant & Food Research, Ruakura, Private Bag 3123, Waikato Mail Centre, Hamilton, 3240 - New Zealand
(9) Plant & Food Research, Ruakura, Private Bag 3123, Waikato Mail Centre, Hamilton, 3240 - New Zealand

Fire blight, caused by Erwinia amylovora, is a destructive disease of pome fruits. Several analytical techniques, namely gas chromatography-mass spectrometry (GC-MS), proton transfer reaction-time of flight mass spectrometry (PTR-TOF-MS), laser photoacoustic detection (LPD) were used for characterizing the volatile emission by apple plants (Malus domestica cv. Golden) infected by E. amylovora. These techniques demonstrated that different volatiles are emitted by healthy and infected plants. In addition, the possible biological role of these volatiles was investigated. For this purpose, the headspace of infected plants was used to treat healthy plants which were successively inoculated with E. amylovora. Healthy plants, exposed to VOCs from infected ones, showed reduced CO2 fixation capacity, and increased total leaf area. Bacterial population and migration inside plant tissues were significantly lower than in control plants. A qPCR assay was developed to monitor the expression of key genes involved in the activation of plant defences, namely: (1) the jasmonic acid-precursor enzyme, LOX (two isoforms); (2) one of the salicylic acid precursor enzyme, PAL; (3) three SA-induced genes, PR1, PR5 and PR8; (4) two products involved in SA reception and signal transduction, SABP2 and NPR1. All the SA-related genes, except PAL, were found to be induced in healthy plants exposed to VOCs from infected ones, whereas the subsequent infection of the pre-exposed plants greatly reduced their expression. On the other hand, the LOX genes were stimulated by infection in pre-exposed plants. Those results suggest a biological, hormone-like activity of VOCs emitted by E. amylovora infected plants, on modulating the plant defence system in neighbouring plants.
Supplements and the bacterial biocontrol agent HR42 reduce infection of detached avocado fruit by Colletotrichum acutatum.

Ten compounds were evaluated for their effects on the efficacy of the bacterial biological control agent (BCA) HR42 against the avocado postharvest rot fungus, Colletotrichum acutatum. The effects of the 10 compounds (chitin, D-glucose, glycol chitosan, L-serine, L-aspartic acid, calcium chloride, calcium carbonate, potassium chloride, ammonium molybdate and sodium carbonate) at four different concentrations (1, 10, 100 and 1000 mM) were tested separately on bacterial and fungal growth. L-serine, L-aspartic acid and calcium chloride all stimulated growth of HR42 and suppressed mycelial growth of C. acutatum in vitro. The BCA and these compounds were then tested in combination on detached avocado fruit for their ability to inhibit lesion development following wound-inoculation. A high concentration of a 10 μl aliquot of HR42 (107 cfu/ml) dried onto a wound made with a needle on a detached avocado fruit significantly inhibited the development of lesions caused by 10³ and 10⁷ conidia/ml of C. acutatum applied subsequently. There was no improvement of inhibition by the addition of any of the three compounds. L-serine and calcium chloride applied alone at high concentrations completely inhibited lesion development by C. acutatum. These results show that HR42 has biocontrol activity against C. acutatum in a detached fruit test, but there was no enhancement of control by the addition of supplements. HR42, calcium chloride and L-serine show potential for controlling the disease in their own right and should be tested in the field.

Characterisation of durable stripe rust resistance in the wheat cultivar ‘Monad’

Stripe rust, caused by Puccinia striiformis f. sp. tritici, is considered one of the most damaging diseases of wheat. While the use of stripe rust resistant wheat cultivars can effectively control the disease, P. striiformis is highly adaptable and new pathotypes regularly overcome the major resistance genes in many wheat cultivars. Breeding strategies are now heavily focused on developing wheat cultivars with durable resistance controlled by multiple gene loci to stripe rust. The wheat cultivar ‘Monad’ has been identified as a source of durable stripe rust resistance, remaining highly resistant to stripe rust in New Zealand for over 20 years. This cultivar is postulated to carry the Yr6 gene and a combination of unknown genes that contribute to its durable adult plant resistance (APR). This project aimed to characterize the durability of resistance to stripe rust in ‘Monad’ leading to better strategies of developing durable stripe rust resistant wheat cultivars. Three hundred and ninety double haploid (DH) lines generated from a ‘Monad’ × ‘Tiritea’ population were assessed for their APR to stripe rust in the 2010–11 and 2011–12 field seasons. A glasshouse phenotype study was undertaken on 44 of the DH lines covering a range from most resistant to most susceptible infection response in the field studies) on their seedling resistance against two stripe rust cultures collected in 1993 from wheat cultivars ‘Monad’ and ‘Delphier’. Symptoms of seedling infection were assessed on a 0–9 infection type (IT) scale. Two groups of DH lines which showed either seedling resistance or APR were identified. Five DH lines carrying potential seedling resistance maintained low infection types in both seedling and adult plant stages in the glasshouse and field studies. Three DH lines (entries 414, 242 and 338) had high seedling infection in the glasshouse but demonstrated APR in the field. The DH lines from these two groups will be used as bases for characterising the Yr genes carried by ‘Monad’ against characterised older and recent stripe rust pathotypes. In order to better understand the genetic basis of durable resistance of ‘Monad’ wheat, future work will also characterise the quantitative trait loci to explain the phenotypic variance of the DH lines.
Inner Plant Space - bacterial endophytes of mānuka (*Leptospermum scoparium*)

Mr Wisnu Wicaksono  
Lincoln University  
Wisnu.Wicaksono@lincolnuni.ac.nz

Wisnu Adi Wicaksono(1), Eirian Jones(1), Amanda Black(1), Jana Monk(1), Hayley Ridgway(1)

(1)Department of Ecology, Faculty of Agriculture and Life Sciences, PO Box 85084, Lincoln University Lincoln, Canterbury, New Zealand  
(2)BioProtection Research Centre, PO Box 85084, Lincoln University, Lincoln, Canterbury, New Zealand  
(3)AgResearch, Lincoln Research Centre Cnr Springs Road and Gerald Street Private Bag 4749Christchurch 8140, New Zealand

In the discipline of plant-microbial interactions considerable attention has recently been directed at exploring the “inner plant space” which is populated by highly specialised micro-organisms termed endophytes. Endophytes are metabolically innovative as the result of sustained and prolonged reactions against host-defense mechanisms. Biologically and economically they are interesting because of their ability to improve plant growth, alter plant metabolites and create healthier plants. They can also generate and/or direct the formation of unique bioactive compounds including novel antibiotics, antmycotics, immune-suppressants, and anticancer compounds. Mānuka (*Leptospermum scoparium*) is a culturally important rongoā plant to Māori and here preliminary investigations have indicated a unique and biologically interesting endophyte community within mānuka plants. The aim of this research is to characterize the seed, leaf, stem and root bacterial endomicrobiome of mānuka using molecular techniques and standard microbial culturing. Results have yielded 110 bacterial endophytes recovered from leaves, roots and stems collected from two South Island sites (Island Hill Station and Paringa) and one North island site (Makirikiri Trust, Wairarapa). PCR-RFLP of the 16S ribosomal RNA will be done using restriction enzymes. To date these enzymes have identified 11 unique genotypes from 41 bacteria. Representatives of the genotypes were sequenced and 500-700 bp fragments of the 16S ribosomal RNA were used to identify the 11 bacterial isolates. Six genera were identified, namely; *Burkholderia*, *Pseudomonas*, Enterobacteriaceae, *Bacillus*, *Paenibacillus* and *Janthibacterium*. Key bacteria will be characterized *in vitro* for their bioactivity and *in vivo* for their ability to improve the growth of mānuka. This research will contribute to our understanding of the relationship between endophytes and their plant hosts.

Development of a wheat/root lesion nematode bioassay to screen beneficial *Trichoderma* strains

Ms Jessica Yardley  
Bio-Protection Centre  
Jessica.Yardley@lincoln.ac.nz

Jessica Yardley(1), Mark Braithwaite(1), John Marshall(1), Michael Wilson(2)  
(1)Bio-Protection Research Centre, PO Box 84, Lincoln University, Lincoln 7647, New Zealand  
(2)AgResearch, Ruakura Research Centre, Private Bag 3123, Hamilton 3240.

Root lesion nematode (RLN) are a major pest of grain crops, with the most common species *Pratylenchus neglectus* and *P. thornei* costing the grain industry in Australia alone more that AU$102M a year in yield loss. A high throughput greenhouse bioassay was needed to screen potential biocontrol agents for activity against RLN for a bionematicide development programme. A nematode screening method designed for RLN resistance screening in developed by the South Australian Research and Development Institute (SARDI) was modified for this assay. The bioassay was designed to screen *Trichoderma* strains for their ability to suppress nematode levels in the roots of young wheat seedlings. Wheat seeds were coated with spores of individual *Trichoderma* strains or a commercial product (VOTIVO (Bayer)), and planted in tubes containing sand 5 days prior to inoculation with RLN. Un-inoculated wheat seed and Vydate® (DuPont™) were used as controls. The microbes were applied at 106 spores per seed and the RLN inoculated at approximately 1500 nematodes/lube. This RLN rate resulted in significant reduction in the plant biomass after 21 days growth compared to un-inoculated plants. After this time, the nematodes were extracted from the roots by mist extraction and counted using a Doncaster dish. This bioassay was useful as it provided a rapid processing of samples and had the capacity to screen increased numbers of microbes, enabling greater numbers of microbe strains to be evaluated for the programme. Using this screening method, *Trichoderma* strains have been identified that can reduce nematode numbers in plant roots and significantly increasing total plant biomass. This relatively cheap and quick greenhouse screening assay enables high throughput screening of different potential biocontrol agents that prior to further evaluation in pot or field trials.
Exotic pest and pathogen incursions: case studies of economic impact and changes in management practices

Mandy Christopher
Department of Agriculture, Fisheries and Forestry

WITHDRAWN

BIOSECURITY

POSTER BOARD 32

Viroid testing of tomato and capsicum seed shipments to Australia

Mr Grant Chambers
NSW Department of Primary Industries
grant.chambers@industry.nsw.gov.au

Grant Chambers(1), Alison Seyb(1), Susan Austin(1), David Letham(2), Kevin Davis(2), Mark Gibbs(2), Fiona Constable(2), Joanne Mackie(2), Brendan Rodini(2)

(1) NSW Department of Primary Industries, PMB 4008, Narellan, NSW, 2567 Australia
(2) Australian Government Department of Agriculture, Fisheries and Forestry (DAFF), Biosecurity Plant Division, 7 London Circuit, Canberra City, ACT, 2601, Australia
(3) AgriBio, Department of Environment and Primary Industries, 5 Ring Road, Bundoora, Victoria, 3083, Australia

In 2008 DAFF introduced new measures requiring freedom based on active testing of tomato (Lycopersicon esculentum) seed for Potato spindle tuber viroid (PSTVd), and Pepino mosaic virus (PepMV). This has since been extended to testing for 6 pospiviroids including Columnea latent viroid (CLVd), Pepper chat fruit viroid (PCFVd), Tomato apical stunt viroid (TASVd), Tomato chlorotic dwarf viroid (TCDVd), Tomato planta macho viroid (TPMvd) in addition to PSTVd and PepMV. Testing of capsicum (Capsicum annuum) seeds for PCFVd, CLVd and PSTVd begun in early 2013. If imported tomato and capsicum seed is not accompanied by an acceptable phytosanitary certificate it must be tested for viroids and PepMV on arrival into Australian ports. Samples of up to 20000 seed per consignment are forwarded to the Victorian Department of Environment and Primary Industries or, NSW Department of Primary Industries Laboratories for testing. The seedlots are divided into sub-samples containing a maximum of 400 seed. Total RNA is extracted directly from the sub-sample after crushing the seeds with a hammer. Pospiviroids are detected with a conventional one-step RT-PCR assay using generic primers. CLVd is not detectable with the pospiviroid primers therefore CLVd and PepMV are detected using separate RT-PCR assays. Consignments that are found to carry pathogens are destroyed or re-exported. Since 2008, pathogen testing of approximately 500 tomato and capsicum seedlots has been completed. Approximately 10% of seedlots have been found to contain viroids. The level of contaminated seed in a single seedlot can be as low as 1 infected sub-sample in 50 sub-samples. PSTVd is the most common pospiviroid detected in the seedlots entering Australia. PCFVd, CLVd and TCDVd have also been detected in seedlots. Detection of multiple viroids within the single seed lot occur. Citrus exocortis viroid (CEVd) has been detected in several seedlots. This pospiviroid is widespread in Australia and these consignments were allowed entry if CEV was the only pathogen present. No PepMV has been detected to date.
BIOSECURITY

POSTER BOARD 33

A Game of Molecular ‘Guess Who’: Developing a Molecular Diagnostic for Fusarium Wilt

Ms Elizabeth Czislowski
The University of Queensland, Australia
elizabeth.czislowski@uqconnect.edu.au

Elizabeth Czislowski(1), Sam Fraser-Smith(1), Emanuel Zander(1), Elizabeth Aitken(1)
(1) School of Agriculture and Food Science, The University of Queensland, St. Lucia, Australia

Banana is Australia’s second largest horticultural industry with an annual farmgate value of $450 million. However, the banana industry is currently threatened by a novel strain of the devastating disease, Fusarium wilt caused by the fungus Fusarium oxysporum f.sp. cubense. This novel strain of the Fusarium wilt fungus is pathogenic on the commercial banana cultivars, Cavendish and Lady Finger. Preventing the spread of diseased material and soil through quarantine strategies is the most effective approach to control the disease due to the lack of chemical controls. Current diagnostic procedures to identify F. oxysporum f.sp. cubense from field samples are expensive and labourious. Therefore, we are working towards developing a rapid molecular diagnostic capable of diagnosing the new strain of F. oxysporum f.sp. cubense. The traditional genes used in molecular diagnostics to identify fungal pathogens cannot be successfully used in F. oxysporum f.sp. cubense. Thus, the use of high-throughput, next generation sequencing has allowed us to evaluate the use of genes involved in pathogenicity for the development of the diagnostic.

BIOSECURITY

POSTER BOARD 34

Re-assessment of Colletotrichum species present in New Zealand

Stephanie Fitzgerald
Ministry for Primary Industries
inga.meadows@mpi.govt.nz

Inga Meadows(1), Heather Pearson(2), Stephanie FitzGerald(1), Brett Alexander(1)
(1) Plant Health and Environment Laboratory, Ministry for Primary Industries, PO Box 2095, Auckland 1140, New Zealand
(2) Surveillance and Incursion Investigation, Ministry for Primary Industries, PO Box 14018, Christchurch 8544, New Zealand

A number of species within the genus Colletotrichum are important plant pathogens worldwide on a variety of plants including fruit and vegetable crops, grains, herbaceous landscape plants, and woody trees and shrubs. As many species can be difficult to distinguish based on morphology alone, the separation of species has not been clear. However, as sequence data of multiple gene regions from multiple isolates has become readily available, species designations can be more clearly identified. As a result, the genus is undergoing major revision and new species are being described at a rapid rate. For example, in 2012, an extensive revision of three major complexes was published that includes many species which occur only in New Zealand (NZ). As new names are applied, it becomes important for biosecurity and trade to determine the species which occur in NZ. To apply the most recent names and to identify any novel species present in NZ or intercepted at the border, the Plant Health and Environment Laboratory (PHEL) is re-assessing isolates of Colletotrichum species from samples received from 2009 to the present, many of which had been identified as “Colletotrichum sp.” or as one of the species complexes recently revised. Identities are based on sequence data and confirmed by examination of morphology. To date, PHEL’s isolates corroborate those reported in 2012. Additionally, several species of Colletotrichum have been intercepted at the border and some of which are not known to occur in NZ. Details on species and their occurrences are discussed.
The national plant biosecurity diagnostic network – towards a national diagnostic system

Barbara Hall  
Chair, Subcommittee on Plant Health Diagnostic Standards  
barbara.hall@sa.gov.au  
The Subcommittee on Plant Health Diagnostic Standards  
Department of Agriculture, Fisheries and Forestry, GPO Box 858, Canberra ACT 2601

The National Plant Biosecurity Diagnostic Network (NPBDN) was formed in 2011 as an initiative of the Subcommittee on Plant Health Diagnostic Standards (SPHDS) (1) and as a step towards a nationally coordinated diagnostic system (2). The NPBDN seeks to enhance communication and information sharing amongst Australasian plant health diagnosticians to support decision making for plant biosecurity. The NPBDN is open to Australasian plant diagnosticians from government, academic, commercial and institutional sectors, and includes entomologists, plant pathologists, virologists, mycologists, nematologists, botanists and weed scientists. The NPBDN is formalised through the role of SPHDS as the executive of the network and is supported by the Australian Government, State and Territory Governments, CSIRO, Plant Health Australia (PHA) and the Plant Biosecurity Cooperative Research Centre. Both the National Plant Biosecurity Strategy 2010 and the National Plant Biosecurity Diagnostic Strategy 2012 (available on PHA and NPBDN websites) had identified the need for a nationally integrated diagnostic network. In 2011 SPHDS facilitated a workshop of key stakeholders, and following positive feedback, formally formed the NPBDN in December 2011. Since then, the NPBDN has held two Annual Diagnosticians’ Workshops and in 2013 launched the NPBDN website to support its activities. NPBDN members benefit from advice and assistance from other members, professional development activities and sharing insights on a range of diagnostic tools and resources. The NPBDN delivers numerous biosecurity benefits, including: removal of impediments that currently restrict open multi-jurisdictional interactions through the development of standard operating procedures and agreements; identification and development of responses to emerging risks and gaps to diagnostic services that may be recognised across the biosecurity continuum; provision to deliver seamless surge capacity during pest incursions; increased information flow through the use of contemporary IT and secure social network services; identification and reduction of unnecessary duplication of effort; and promotion of delivery of education and training for plant diagnosticians.

Has *Papaya ringspot virus* spread in Queensland in the last 20 years?

Ms Christine Horlock  
Queensland Department of Agriculture, Fisheries and Forestry  
Christine.Horlock@daff.qld.gov.au

Christine Horlock(1), Ceri Pearce(2), Rebecca Breaden(3),  
(1) Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, Biosecurity Queensland Control Centre, 53 Seventeen Mile Rocks Road, Oxley Qld 4075, Australia  
(2) Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, Centre for Wet Tropics Agriculture, South Johnstone Road, South Johnstone Qld 4859, Australia

**Papaya ringspot virus** (PRSV) is a devastating disease of papaya worldwide (Persley and Ploetz 2003). PRSV is a species in the genus *Potyvirus* in the family *Potyviridae* (Fauguet et al. 2005). Based on host range, PRSV is classified into two types, type-P isolates that infect papaya and cucurbits, and type-W isolates that only infect cucurbits. In Australia, PRSV-P was first detected in south east Queensland in 1991 (Thomas and Dodman 1993). To protect Queensland’s papaya industry, a Papaya Ringspot Pest Quarantine Area (PQA) was declared under Queensland’s *Plant Protection Act* (1989) and *Plant Protection Regulation* (2002), to prevent the further spread of PRSV-P to Australia’s main papaya production area in north Queensland. Prior to the survey reported here, PRSV-P was only recorded from locations within the PQA (Persley 1998; Thomas and Dodman 1993). This distribution is supported by 12 years (1998–2010) of surveillance data from Biosecurity Queensland (unpublished). Biosecurity Queensland undertook a state-wide surveillance blitz for PRSV-P between January and June 2012. A total of 373 sites were surveyed by Biosecurity Queensland staff: 370 with papaya and three with cucurbit plants only. In total, 19,288 papaya plants and 225,190 cucurbit plants were inspected. From these inspections, 72 samples were collected and assessed. An extensive awareness campaign was also undertaken to encourage growers, commercial nurseries, relevant government personnel and the wider community to report suspected papaya ringspot disease symptoms, and to gain their assistance in identifying sites for surveillance. Media releases resulted in 63 PRSV-related media activities (newspaper articles, radio and television interviews). The Biosecurity Queensland Papaya Ringspot Disease homepage recorded 702 hits over a four month period. Eighty public reports were received and investigated across Queensland, including 56 from within the PQA. PRSV-P was not detected outside the Papaya Ringspot PQA. It was detected at nine sites in areas where it was previously known to occur such as suburban Brisbane and Bundaberg. All nine positive detections were from within the PQA. It should be noted that the data provided by this survey represents a snapshot in time. The low incidence of disease detected may be the result of seasonal factors such as temperature, humidity and plant growth, as well as factors influencing PRSV-P vectors e.g. prevailing winds, insecticide use and proximity of host plants to one another.

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**Fusarium species associated with mango malformation in Australia.**

Dr Edward Liew  
The Royal Botanic Gardens and Domain Trust  
edward.liew@rbgsyd.nsw.gov.au  
Edward C Y Liew(1), Lucy T Tran-Nguyen(2), Jose Liberato(2), Matthew H Laurencier(3), Ceri Pearce(1), Suzy Perry(4), Greg I Johnson(5), Yu Pei Tan(6), Tony Cooke(7),  
(1) The Royal Botanic Gardens and Domain Trust, Mrs Macquaries Rd, Sydney NSW 2000, Australia  
(2) Plant Industries Group, Department of Primary Industry and Fisheries, GPO Box 3000 Darwin, NT 0801, Australia  
(3) Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, PO Box 20, South Johnstone, QLD 4859, Australia  
(4) Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, GPO Box 1241, Oxley, Qld 4075, Australia  
(5) Horticulture 4 Development, PO Box 412, Jamison, ACT 2614, Australia  
(6) Biosecurity Queensland, Department of Agriculture, Fisheries and Forestry, GPO Box 267, Brisbane QLD 4001, Australia  
(7) Agri-Science Queensland, Department of Agriculture, Fisheries and Forestry, GPO Box 267, Brisbane QLD 4001, Australia

Mango malformation (MMD) is an economically significant disease of mango (*Mangifera indica* L.) that results in devastating crop losses in many production areas in tropical and subtropical regions. After much uncertainty surrounding the aetiology of the disease, Koch’s postulates were completed initially for *Fusarium mangiferae*, followed by *F. sterilihyphosum*, *F. mexicanum* and *F. tupidens* from various parts of the world. Several other species have also been implicated as the causal agent, including *F. proliferatum* and *F. pseudocircinatum*. In Australia MMD is a notifiable disease and recognised as a high priority exotic pest threat to the mango industry but only *F. mangiferae* and *F. sterilihyphosum* have been gazetted. In 2007 malformation symptoms on mango were first observed in the Northern Territory (NT) and *F. mangiferae* was isolated. The emergency pest response activities that ensued, including eradication, back/forward tracing and follow-up surveillance, led to further detections of malformation symptoms in various parts of the NT and Queensland from 2008 to 2011. Numerous *Fusarium* species were recovered including established and implicated pathogens, as well as new undescribed species. This paper outlines these *Fusarium* species and discusses implications on quarantine and research priorities and the need for pathogenicity tests.
**The systematics of *Puccinia lagenophorae* in Australia**

Dr Alistair McTaggart  
Queensland Alliance for Agriculture and Food Innovation  
alistair.mctaggart@daff.qld.gov.au  
Alistair R McTaggart(1,2), Andrew DW Geering(1), Roger G Shivas(2),  
(1)Queensland Alliance for Agriculture and Food Innovation, The  
University of Queensland, Ecosciences Precinct, GPO Box 267,  
Brisbane, Queensland 4001, Australia.  
(2)Department of Agriculture, Fisheries and Forestry, Ecosciences  
Precinct, GPO Box 267, Brisbane, Queensland 4001, Australia.  

*Puccinia lagenophorae* is an Australasian rust species established in Africa, Europe and America, where it is a pathogen and biological control agent of ornamental and weedy Asteraceae. The current host range of *P. lagenophorae* includes about 110 species of Asteraceae. The host range is expanding and hybridization with closely related species of *Puccinia* has occurred. Rusts that infect plants in the Goodeniaceae are considered conspecific with *P. lagenophorae*. This study investigated the systematics of *P. lagenophorae* and closely related species on endemic Australian hosts with a combined morphological and molecular approach. Phylogenetic analyses were conducted on combined datasets of the ITS and LSU regions of rDNA from over 50 specimens. Our systematic study determined that (i) some Australian rusts on Haemodoraceae, Stylidiaceae, Apiaceae, Goodeniaceae and Asteraceae are monophyletic, (ii) *P. lagenophorae* is distinguished from closely related taxa by life cycle, molecular barcode loci, and restriction to members of the Asteraceae, and (iii) a genealogical concordance approach to systematics is not necessarily straightforward with recently diverged taxa.

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**A look inside the human body: An analogy to improve understanding how the plant biosecurity system works**

Dr Abu-Baker Siddique  
Department of Agriculture, Fisheries and Forestry, Qld  
siddique.abu-baker@daff.qld.gov.au  
(1)Abu-Baker M Siddique, (2) Isabel Arevalo-Vigne  
(1)Plant Biosecurity and Product Integrity, Biosecurity Queensland,  
Department of Agriculture Fisheries and Forestry, Brisbane Qld 4001  
Australia  
(2)School of Agricultural & Resource Economics, Faculty of Natural & Agricultural Sciences, University of Western Australia, Perth WA 6009 Australia  

Biosecurity protects the economy, environment, food security and people's health from potential biological risks. The sustainability of agriculture depends on effective management practices, including plant biosecurity. Through a wide range of actions, plant biosecurity develops a multilayered defence system against exotic pests at different stages of risk exposure. The functions of an individual defence layer depend on various factors associated with the risk. One difficulty is to transmit these concepts to lay people, so they can understand and comply with the necessary biosecurity requirements to avert risks at different stages: from production through to markets. This challenge can be overcome using an appropriate analogy to facilitate the understanding of complex issues or theoretical information such as the biosecurity system. Here we propose comparing the plant biosecurity system (regulated by human management) with the human immune system (regulated by inbuilt body response) for a better understanding of a defence system against invasive organisms that alter or damage normal functions to plant systems. Both systems consist of several non-specific and specific components and each of these components act at different levels of the defence system to stop the invader(s) proceeding further and causing damage. The non-specific components are natural, and act either as barriers or destroyers of a wide variety of invaders without specificity, whereas the specific components are adaptive and evolve in response to any new invaders encountered. An effective biosecurity system plays vital role in addressing biological risks. Implementation, underpinned by robust policy and operational frameworks, safeguards the food supply chain from biosecurity threats. Building a sustainable biosecurity system demands a clear understanding about the function of its individual components and the associated factors that control the system. A deepening of this understanding can be assisted with the use of appropriate analogies.
More new *Phytophthora* species from natural ecosystems in Western Australia

Ms Agnes Simamora
Murdoch University
A.Simamora@murdoch.edu.au

Agnes Simamora(i), Giles Hardy(ii), Mike Stukely(ii), Treena Burgess(ii)

(i)Centre for Phytophthora Science and Management, School of Veterinary and Life Sciences and Biotechnology, Murdoch University, Perth, WA, Australia
(ii)Science Division, Department of Environment and Conservation, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

In 2009 (Plant Dis. 93:215-223) we reported 11 apparently new *Phytophthora* species, designated P.sp.1-11, from natural ecosystems in Western Australia WA). Since then many of these species have been described: *P. arenaria* (P.sp.1), *P. elongata* (P.sp.2), *P. thermophila* (P.sp.3), *P. multivora* (P.sp.4), *P. gregata* (P.sp.7), *P. fluvalis* (P.sp.8), *P. constricta* (P.sp.9), *P. litoralis* (P.sp.11). P.sp.5 falls in the *P. cryptogea* species complex and P.sp.6 has been identified as *P. taxon personii*. Additionally, we have described *P. gibbosa* and *P. amnicola*. Further sampling and continued molecular re-evaluation of the culture collection at the Department of Environment and Conservation’s Vegetation Health Service (VHS) has uncovered more new species tentatively named *P. aff. humicola*, *P. aff. rosacearum*, *P. aff. elongata*, *P. aff. arenaria*, *P. aff. captiosa*, *P. taxon. kwongan* (=P.sp.10), *P. taxon. casuarina*. These new species are from ITS clade 6, sub-clade I and they have been isolated from dead and dying plants across a range of species in remote natural vegetation. To date, all known species and taxa in sub-clade I, with the exception of *P. humicola*, have been isolated in WA, perhaps indicating a WA origin for this clade. Studies are currently underway to formally describe the new species in conjunction with large scale pathogenicity trials of these and the other newly described species.

Circular leaf spot of persimmon (*Diospyros kaki*) caused by *Mycosphaerella nawae* in New Zealand

Mr Raja Thangavel
Ministry of Primary Industries
thangavel.raja@mpi.govt.nz

Raja Thangavel(i), Wellcome Ho(i), Ian Harvey(ii), Travis Ashcroft(ii), Dave McLellan(ii), Brett Alexander(ii)

(i)Plant Health and Environmental Laboratory, Ministry for Primary Industries, PO Box 2095, Auckland 1140, New Zealand
(ii)PLANTwise Services Ltd, PO Box 69181, Lincoln 7640

Multiple persimmon growers from the Gisborne area observed circular leaf spot symptoms on persimmons which lead to premature defoliation of trees during the 2011-12 growing season. Multiple samples were sent initially to Plantwise Services Ltd and then to the Ministry for Primary Industries (MPI), Plant Health and Environment Laboratory for diagnosis of the cause. Early samples had no fungal sporulation. Spermata were soon detected and eventually weathered leaf samples yielded ascogenous fruiting bodies and the cause was suspected to be *Mycosphaerella nawae*. DNA sequencing of colonies produced from ejected ascospores confirmed this diagnosis. This fungus is known to cause circular leaf spot of persimmons which can lead to early defoliation. This pathogen is also associated with early fruit maturation and premature fruit drop results in significant decreases in productivity and quality overseas, e.g. in Korea. *Mycosphaerella nawae* has also been reported in Japan and Spain, and possibly in Australia (as *Mycosphaerella* sp.). In New Zealand, similar leaf spot samples were reported in previous years, but since no specimens were submitted for identification (only to a laboratory for analysis as a possible nutritional deficiency) it is not known if these previously reported symptoms were caused by *M. nawae*. High rainfall and humidity during the 2011-12 growing season appears to have resulted in high disease incidence in some orchards, promoting ascospore release and subsequent rapid development of the characteristic symptoms. It is unknown how and exactly when this disease arrived in New Zealand. Other fungi were also isolated from some of the samples taken from the Gisborne area. *A. Discosia* species (also reported as new to New Zealand) was isolated from several leaf spots. This was identified as *D. aquatica* by DNA sequencing, however it is unclear how this fungus contributed to the disease symptoms. A black spot on Japanese persimmon caused by *Adisciso kaki* is genetically close to *D. aquatica* but morphologically distinct.
Fusarium wilt of watermelon in the Northern Territory, Australia

Dr Lucy Tran-Nguyen
NT Department of Primary Industry and Fisheries, AU
lucy.tran-nguyen@nt.gov.au

Fusarium wilt is one of the most severe diseases of watermelon (Citrullus lanatus (Thun) Matsum & Nakai) and is caused by the soil borne pathogen, Fusarium oxysporum f. sp. niveum (Fon). This forma specialis is only pathogenic on watermelons and is divided into four races (0, 1, 2 and 3), where race 3 is the most virulent race. Worldwide Fusarium wilt of watermelon is a major yield-limiting factor in production and occurs on every continent bar Antarctica. Symptoms include damping-off, seedling wilt or general wilting during any plant developmental stage. Watermelon production in the semi-arid tropical north of the Northern Territory (NT) occurs between March and October, and in the arid southern NT region, from September to November and March to May. The NT production for 2011-2012 was estimated to be $47.8 million from ca. 900 ha. Fusarium wilt of watermelon was first detected in the NT in May 2011 in three triploid seedless watermelon varieties. These plants expressed symptoms such as leaf necrosis, necrotic blotching, seedling deaths, wilt and vine collapse. Previous to this, two of the Fon races were detected in Australian eastern states. Koch’s postulates was completed and confirmed the NT isolates were pathogenic. This was the first time that Fon was detected in triploid seedless watermelons with symptoms similar to bacterial blotch and typical wilt in Australia. Current work is underway to determine the NT Fon race(s) using several race differential lines. This paper will outline the initial detection of Fusarium wilt of watermelon in the NT and the consequent research to determine the Fon race(s).

The potential of Karnal bunt to establish in New Zealand as indicated by two meteorological models

Dr Suvi Viljanen-Rollinson
The New Zealand Institute for Plant & Food Research Limited
suvi.viljanen@plantandfood.co.nz

Karnal or partial bunt caused by the smut fungus Tilletia indica Mitra is a disease of wheat (Triticum aestivum and T. durum) and triticale (x Triticosecale). Tilletia indica was first reported in 1930 in Karnal, northern India, and has since spread to some areas of United States, Brazil and South Africa. It is listed as a quarantine pest in a large number of countries. It is not present in New Zealand, but establishment of T. indica on wheat may have a significant impact on grain quality and restrict trade of grain or grain products. The objective of this work was to assess the risk of T. indica establishment in wheat growing regions of New Zealand using two different models. The Climate Match Index (CMI) was generated using the regional, climate-based risk-modelling software CLIMEX (CSIRO, Brisbane, Australia and Hearne Scientific Software Pty Ltd, Melbourne, Australia) to compare climate data from Bloemfontein in South Africa (where T. indica occurs on wheat) with climate data from New Zealand. The Humid Thermal Index (HTI, defined as the monthly average 3 pm relative humidity divided by the average monthly maximum temperature) for the month preceding anthesis in wheat crops, was used to determine the suitability of the climate for the spread and establishment of T. indica on three wheat cultivars (early, intermediate and late maturing) in Lincoln, Canterbury, New Zealand. A CMI higher than 0.7, which indicates an overall good climate match, occurred in three locations, Christchurch, Timaru and Blenheim in the South Island of New Zealand. A HTI model was used in the future to calculate the likelihood of establishment and spread of T. indica in other wheat growing regions in New Zealand.
**DISEASE MANAGEMENT**

**POSTER BOARD 46**

**Laboratory Studies of Some Control Measures against Sclerotinia spp. the Causal of Foliage Blight Disease of Cucumber and Pepper Plants in Egypt**

Prof Mokhtar Abdel-Kader
National Research Centre
mokh_nrc@yahoo.com

Mokhtar M. Abdel-Kader, Nehal S. El-Mougy, Sirag M. Lashin
Plant Pathology Dept., National Research Centre, Egypt

Surveyed plastic houses at different Protected Cultivation Stations throughout Egypt revealed that the Sclerotinia blight disease incidence was observed cucumber and pepper plants, respectively. The isolated causal pathogens for cucumber and pepper foliage blights were identified as Sclerotinia sclerotiorum (Lib.) de Bary and S. minor Jagger, respectively. This is thought to be the first report of these fungi to cause foliage blights on cucumber and pepper in Egypt. As control measures antagonistic agents and fungicides against the growth both pathogenic fungi under in vitro conditions were evaluated. Recently, interest has been shown in combining microbial bio-control agents with other chemical components to increase their activity against plant pathogens. To reach the proposed aim, determination of the efficacy of some plant-derived essential oils, plant resistance inducers and plant extracts in combination with bio-control agents against the growth of Sclerotinia foliage blight pathogens S. sclerotiorum and S. minor was carried out under in vitro conditions. The obtained results in the present study has shown the potential of tested materials as effective inhibitors against pathogenic fungi when combined factors with antagonistic bio-agents. Acknowledgement This work was supported financially by the Science and Technology Development Fund (STDF), Egypt, Grant No. 1059.

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**BIOSECURITY**

**POSTER BOARD 45**

**On-site detection and diagnosis of exotic plant pathogens using loop-mediated isothermal amplification**

Dr Linda Zheng
Department of Environment and Primary Industries
linda.zheng@depi.vic.gov.au
Linda Zheng(1), Rachel Mann(1), Brendan Rodoni(1)
(1)Centre for AgriBioscience, Department of Environment and Primary Industries, 5 Ring Road, Bundoora, Victoria 3083, Australia

Plant pathogens pose a significant economic risk to Australia's agriculture industries and the accidental or intentional importation of exotic pathogens present a serious biosecurity threat. To assist plant pathology labs and quarantine agents, portable and robust molecular tools are required for the on-site rapid identification of exotic pathogens at our borders. Loop-mediated isothermal amplification (LAMP) is a novel approach to nucleic acid amplification, which uses a single temperature incubation coupled with photometry for detection. Due to its simplicity and robustness, LAMP has the potential to be used under field conditions, which is particular useful for surveillance, plant quarantine and infectious disease diagnosis. In this project, we report the first use of LAMP assays in Australia for the detection of *Erwinia amylovora* (causal pathogen of fireblight) and *Potato spindle tuber viroid*, both of which are high priority emergency plant pests. The LAMP assays were easy to use and results were obtained in less than 30 minutes. It is envisaged that the LAMP tests validated in this study will be used by quarantine and surveillance officers for on-site detection of these pathogens at our docks and airports.
DISEASE MANAGEMENT

POSTER BOARD 47

Rhizoctonia in onion: Pathogenicity, cultivar susceptibility and fungicide evaluation

Dr Simon Anstis
South Australian Research and Development Institute
simon.anstis@sa.gov.au

Onions grown on sandy soils are frequently affected by patches of stunted growth resulting in bulbs of an unmarketable size. To confirm the role of Rhizoctonia solani AG8 in stunting, soil and roots from stunted onion patches were analysed for the presence of pathogenic Rhizoctonia solani. Cultivar susceptibility and fungicide applications were evaluated as potential management strategies. Of 43 R. solani isolates taken from stunted patches, 13% were R. solani AG2.1, 13% AG5, 32% AG8 and 32% unassigned AG. While AG8 isolates were virulent pathogens, unassigned and AG5 isolates were avirulent. Isolates of AG2.1 ranged from moderate to no pathogenicity in pot assays. 45 bulb, 5 bunching and 1 spring onion cultivars were evaluated in seedling bioassays against R. solani AG8. While leaf weight varied in pots with no pathogen, all Allium species and cultivars were susceptible. There was a 59% reduction in pots with 1 agar plug and 96% growth reduction with 3 agar plugs. Growth of seedlings in pots inoculated with R. solani AG8 could not be correlated with either pre-planting seed weight or rate of germination. In pot experiments using soil inoculated with R. solani AG8, seedling growth was increased (mean 1364%) and AG8 in soil reduced (mean 14%) with seed treatments of fludioxonil (100g/L), thiram (200g/L) or flutolanil (500g/L) at 2mL/kg, or penflufen (500g/L) or fluxapyroxad (250g/L) at 2mL/kg, or penflufen (42mL/L), penthiopyrad (500g/L) and a combined application of boscalid (179g/L) with pyraclostrobin (90g/L) at 2mL/L increased seedling growth (mean 3656%) and reduced AG8 in soil (mean 44%). In field trials, treatment of soil with azoxystrobin (250g/L) at 1.2L/ha 2 or 3 days prior to barley cover crop sowing increased total bulb yield by a mean 9% across two sites, R. solani AG8 present in these two trials was low (6 pg R. solani AG8 DNA/g soil) and increased yields may have been due to protection from other root diseases. A range of onion bulb cultivars and Allium species are susceptible to R. solani AG8 infection although use of seed and soil fungicides can reduce disease and may form part of a management strategy. Evaluation of onion cultivars under field conditions is needed as plant agronomic factors such as rooting vigour may impact yield in paddocks with R. solani AG8.

DISEASE MANAGEMENT

POSTER BOARD 48

Potential disease suppression of common scab (Streptomyces scabies) of potato in a natural field soil

Mr Desmond Auer
Department of Environment and Primary Industries, Victoria
Desmond.Auer@depi.vic.gov.au

Common scab is a major disease of potatoes worldwide. Disease symptoms include superficial, raised and deep pitted lesions on the tuber surface that can significantly reduce tuber quality and hence marketability. Apart from growing disease-resistant cultivars, there are no reliable control measures. Common scab occurs in the central highlands region of Victoria, Australia, a major processing potato production area. However, on one farm in this region used for disease management trials, the incidence of common scab has been negligible over many decades. In soil tests conducted over several years, DNA of the pathogen has not been detectable and soil nutrient concentrations are not at levels that may suppress this disease. To investigate the possibility of biological suppression on this farm, soil taken from potato fields was either heat treated to 80°C for 48 hours, γ-irradiated (25 kGrays) or left untreated. These soils were inoculated with 10% vermiculite infested with S. scabies or left uninoculated, planted with two-week old tissue-cultured potato plants (cv Shepody) and maintained in a glasshouse. An inoculated potting media was used as a pathogen control. At harvest, common scab was not found on progeny tubers grown in the inoculated natural field soil. However, 72% of tubers grown in the inoculated potting media developed common scab, significantly more than in the inoculated heat-treated and the γ-irradiated soil (18% and 30%, respectively). Pre-planting TRFLP profiling of soils showed differences in the bacterial and fungal populations between treatments. Post-harvest TRFLP profiling of bacterial populations showed differences between γ-irradiation and other treatments. While post-harvest TRFLP profiling of fungal populations showed differences between natural and other treatments. Thus, we have been able to distinguish between soil treatments using TRFLP profiling. Our results indicate the possibility of biological suppression of common scab. We hypothesize that, in this soil, suppression is via spore-forming bacteria since disease is reduced by γ-irradiation, but not heat treatment. Further research is required to determine if this suppression can be transferred to a common scab conducive soil.
Mud on footwear: a pathway for the translocation of Phytophthora species

Dr Stanley Bellgard
Landcare Research
BellgardS@landcareresearch.co.nz

Phytophthora "taxon Agathis" (PTA), has been identified as the causal agent of the “kauri dieback” disease of New Zealand kauri Agathis australis. In the Waitakere Ranges Regional Park phytosanitary hygiene protocols have been implemented by the Auckland Council. These include the installation of boot wash stations at the start and end of the Auckland City Walk. The role that humans play in the local- and long-distance dispersal of Phytophthora has been demonstrated for the sudden oak death pathogen P. ramorum. The results of the study presented here address two questions: 1) what Phytophthora species are collected in the soil from the foot-wash stations, and is it still capable of initiating disease, and 2) is PTA able to be transferred via footwear moving mud along a bush-track in wet-soil conditions? Soil samples were collected from the boot-wash station at the Kitekite track in February 2011 by Auckland Council staff, and another sample was collected in June 2011 from the Auckland City Walk boot wash station. Two, two hundred gram sub-samples of soil were bioassayed using lupin cotyledons and cedar needles floated on flooded soil samples. A total of six oomycetes were recovered including; P. gonapodyides, P. citrophthora, P. multivora, P. "taxon Pgclamydo" and two unknown, hymexazol-resistant, species of Pythium. Soil was also collected from the bottom of five pairs of boots / shoes used to walk the Lower Kauri Track in wet soil conditions. The soil collected was also bioassayed; with five Phytophthora species being recovered, including P. cinnamomi. Three species; P. cinnamomi, P. gonapodyides and P. multivora were recovered from the soles of one pair of boots from a total of six grams of mud.

Efficacy of flutriafol fungicide Sinker® for the control of sugarcane smut in Australia

Dr Shamsul Bhuiyan
BSES Limited
sbhuiyan@bses.com.au

Currently, two triazole fungicides, triadimefon and propiconazole, are used to control sugarcane smut (Sporisorium scitamineum) in seedcane as a dip treatment. The dip treatment can only be applied to mother stock planting material because of the logistics of dipping large quantities of seedcane and it is difficult to dispose of the large volumes of waste fungicide solution in an environmentally safe manner. Earlier research in small plots demonstrated that flutriafol is effective in controlling sugarcane smut (S. scitamineum) and pineapple sett rot (Ceratocystis paradoxa) when applied as a spray over the cuttings (setts) in the furrow at planting. The aim of this research was to determine the efficacy of flutriafol fungicide(Sinker®) against sugarcane smut when applied through the existing pineapple sett rot control equipment on a commercial whole-stalk planter. Two experiments were established at Mackay and Bundaberg in August and September 2010 to assess the efficacy of flutriafol fungicide(Sinker®) against sugarcane smut-susceptible cultivar Q205. The stalks of Q205 were inoculated with smut spores by dipping the stalks in a spore suspension and incubating the stalks for 24 (Bundaberg) or 48 (Mackay) hours. The fungicide was applied during planting by a whole-stalk planter fitted with pineapple sett rot spray equipment. Sinker® was applied at rates of 0, 250, 375, 500, 625 and 750 mL/ha. Sinker® reduced smut infection by 61 and 88% 5 months after planting at rates of 250 and 750 mL/ha, respectively, in Bundaberg and by 74 and 93% in Mackay compared to the untreated control. The Sinker® treatments had significantly higher tonnes sugar/ha (TSH) and tonnes cane/ha (TCH) than the inoculated control plots at both Bundaberg and Mackay. The 500 mL/ha rate of Sinker® increased tonnes sugar/ha by 51.7% compared to the inoculated control at Bundaberg (17.6 versus 11.6 TSH) and 203.6% at Mackay (8.5 versus 2.8 TSH). The yield in the Sinker® treated plots was significantly higher than the uninoculated control at Bundaberg suggesting that there were additional benefits from the application of the fungicide, probably due to control of other diseases such as pineapple sett rot. The experiments demonstrated that the fungicide Sinker® will be an important management tool for sugarcane smut.
**DISEASE MANAGEMENT**

**POSTER BOARD 51**

**Mycroflora associated with seeds of Canola and Sarson**

Mr Moaz Bin Riaz  
UAF, Pakistan  
moazrandhawa@gmail.com

Moaz Bin Riaz, Amer Habib, Safdar Ali  
Department of Plant Pathology, University of Agriculture Faisalabad, Pakistan

Oilseed crops have prodigious importance as food ingredient all over the world. To combat domestic oil demands, Sarson (Brassica campestris) and Canola (Brassica napus) are locally been grown in all parts of the Pakistan. Though advancements in production technologies have attributed to the higher yields of oilseeds crops, a significant part of the produce is lost due to numerous seed borne diseases. Different diseases are associated with seeds of oilseed crops including Canola and Sarson. In vitro experiment was conducted to identify the mycoflora associated with 5 cultivars of Sarson and 4 cultivars of Canola. Efficacy of different fungicides and plant extracts in different concentrations was checked in the lab conditions against seed borne fungal pathogens. Experiments were conducted in CRD layout and will be repeated at least three times. Aspergillus flavus showed the higher percentage than the other species on the seeds of canola and sarson. Mancozeb showed the best effect on germination (89.26%) of canola and sarson seeds. Raydar also showed the approximately same result as of Mancozeb while the seeds sown without treatment of any fungicide suspension and infested only with fungal isolates showed the lowest germination (65.25%).

**Oats and Sorghum Put Breaks on Root Knot**

Dr Sarah Collins  
Department of Agriculture and Food, Western Australia  
sarah.collins@agric.wa.gov.au

Carla Wilkinson, Sean Kelly, Xiaohui Zhang, Jodie Teasdale, Lucy DeBrincat, Vivien Vanstone, Helen Hunter, Sarah Collins  
Department of Agriculture and Food, Western Australia, South Perth, Australia

Root knot nematodes (RKN, Meloidogyne spp) are a major cause of income loss to the Australian vegetable industry. A survey of vegetable growing paddocks in the south west of Western Australia (WA) in 2011 detected RKN in 70% of the paddocks sampled. Many growers plant consecutive vegetable crops with no rotation and rely on soil fumigants for control of RKN. These chemicals are expensive, non-specific and can biodegrade in high use areas. Some vegetable growers use break crops between cash crops to increase nitrogen levels, protect the soil from erosion and for pasture. They commonly use field peas, oats, sub clover and millet as break crops. Plant varieties vary in their susceptibility to RKN and crop rotation can be utilised to decrease nematode numbers in the soil and reduce damage to the subsequent vegetable crop.

We screened eight potential break crops in a field trial for their resistance to three RKN species found in WA. From glasshouse trials on 22 plant cultivars, eight were chosen to test in a field situation in Spearwood sands, Medina, WA. Crops were tested over summer and cultivars used were, field pea (Dunwa), millet (Shirorie, Nutrifeed), mustard (Yellow), oat (Swan), Rhodes grass (Katambora), sorghum (Jumbo) and sub clover (Trikkala), which was used as a known susceptible crop. Plots were either left un-inoculated or inoculated with M. hapla, M. incognita and M. javanica using approximately 600 eggs/L of soil one day prior to seeding break crops. Fifteen weeks after sowing (Feb 2012) plants, soil was collected from each plot and the number of eggs/g of dry roots and nematodes/g soil was calculated. Swan oats and Jumbo sorghum were resistant to the RKN species tested and may be effective summer break crops to reduce nematode numbers. Unfortunately the amount of organic matter produced by Jumbo sorghum may exclude it as a practical alternative for WA potato growers. Rhodes Grass (var. Katambora) may also be an effective break crop, but was not as resistant as oats or sorghum. Field peas and sub clover are susceptible and may increase nematode numbers.
Endophytes and their potential use for biocontrol of Phytophthora cinnamomi in natural ecosystems

Ms Sian Contarino
Murdock University
sian.contarino@optusnet.com.au

Sian Contarino, Giles E. St. J. Hardy, Philip A. O’Brien
School of Veterinary & Life Sciences, Murdoch University, Murdoch, WA 6150 Australia

Plant diseases caused by Phytophthora cinnamomi are causing massive devastation of native ecosystems across the southern parts of Australia, particularly in the botanical province of the southwest of Western Australia and in the Grampian Ranges in Victoria. However damage caused by the pathogen is not limited to these two regions, but is also reported from South Australia, Tasmania and new South Wales. One option for managing the pathogen is the use of phosphite a more reduced analogue of phosphate. Phosphite specifically inhibits growth and colonisation of plants by oomycete plant pathogens such as Phytophthora. An alternative to phosphite is biological control by endophytic bacteria and fungi. Endophytes live within the tissues of plants and often confer advantages on plants such as increased resistance to abiotic stresses, increased growth, and protection against infection and colonisation by pathogens. In recent years there have been many reports on biocontrol of Phytophthora diseases in horticultural crops by endophytic bacteria and fungi. In many cases the level of protection that can be achieved is as great as achieved by the application of fungicides. Biological control in native ecosystems involves a different set of challenges. Unlike horticultural ecosystems there is a tremendous diversity of host species and protection is required over a longer time frame than with crops. In our search for an effective biocontrol agent we are comparing endophytes from host species in P. cinnamomi infested and adjacent non-infested sites. We are looking for endophytes that are found in host species from non-infested sites and that are present in a number of different host species. The rational is that we are looking for an organism that is present in non-infested sites only, and that does not show strict species or site specificity. Isolates will be evaluated both in vitro and in planta for antagonism of P. cinnamomi and other Phytophthora species.

New strategies and techniques for reducing the impact of Phytophthora cinnamomi within native plant communities across south-west Australia

Prof Giles Hardy
Department of Parks and Wildlife
Colin.Crane@dpaw.wa.gov.au

Chris Dunne(1), Colin Crane(1), Bryan Shearer(2), Renee-Claire Hartley(2), Peter Scott(2), Ryan Hooper(2), Joel Camkin(3), William Dunstan(6), Trudy Paap(6), Yong Lin Ren(6), Giles Hardy(6)

(1) Science Division, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia
(2) Astron Environmental Services, 129 Royal St East Perth, WA 6004, Australia
(3) New Zealand Forest Research Institute Ltd. Scion 49, Sala St, Private Bag 3020, Rotorua 3046, New Zealand
(4) Soil Water Group, 45 Gladstone St
(5) Soil Water Group, 45 Gladstone St
(6) Science Division, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

Phytophthora cinnamomi is one of the most destructive invasive species worldwide and a key threatening process to Australia’s biodiversity. The plant pathogen infects the roots of susceptible plant species resulting in necrosis that eventually girdle and kill the host. When the pathogen is introduced into a vulnerable plant community it causes a disease commonly referred to as Phytophthora Dieback. The introduction of P. cinnamomi into the highly vulnerable native plant communities within south-west Australia has already infested over 1 million ha of remnant vegetation leading to a permanent loss in biodiversity, plant community structure/composition and downstream impacts of other ecosystem components such as dependant fauna. Recent management projects have prioritised the remaining healthy but highly vulnerable vegetation areas across the south-west region. Intensive collaborative management by research scientists, government and community aims to prevent the spread, reduce the impact, contain and eradicate P. cinnamomi within these top priority protection areas including the International Biosphere Reserve encompassing the Fitzgerald River National Park. These ambitious management projects have required the development of novel control techniques that have broad applicability in the management of Phytophthora and other soil-borne pathogens. These include in-situ and ex-situ soil fumigation, hydrological catchment engineering, animal vectoring prevention, in-situ baiting traps for early detection of pathogen spread, host destruction at different scales, high intensity phosphite application and remote sensing technologies. To support the deployment of these control techniques a strategic, multi-disciplinary and adaptive management framework was implemented that aimed to build the capacity of the project team, utilised quantitative risk assessment approaches, conducted detailed hydrological catchment modelling, tailored hygiene procedures for each site and/or specific activity, targeted broad scale surveillance and optimised pathogen detection.
Cross protection with Tamarillo mosaic virus?

Ms Samantha Edwards
The New Zealand Institute for Plant & Food Research Limited
samantha.edwards@plantandfood.co.nz

Samantha Edwards(1), Arnaud Blouin(1), Kar Mun Chooi(1), Daniel Cohen(1), Robin MacDiarmid(1)
(1)The New Zealand Institute for Plant & Food Research Limited, Auckland, New Zealand
(2)School of Biological Sciences, The University of Auckland, Auckland, New Zealand

The tamarillo (Cyphomandra betacea), is a solanaceous plant which bears small egg-shaped fruit. Fruit are harvested over a 6-month period and available in several varieties; ranging from mild to tart flavoured. The tamarillo fruit is nutritionally beneficial, as it contains high levels of potassium and anthocyanins. New Zealand is the largest tamarillo producer in the world, averaging $2M in revenue per annum. While the market is relatively small in comparison to other fresh fruit exports, the ability of the market to grow is severely hampered by the incidence of Tamarillo mosaic virus (TamMV, Potyvirus). TamMV is the name given to isolates of Potato virus A that infect tamarillos causing leaf mosaic symptoms, lowered plant vigor and fruit yield and, importantly, discoloration of the fruit’s exocarp. While discoloration of the exocarp does not impact the taste or quality of the flesh, the blemishes cause the fruit to be less visually appealing and therefore downgraded. Recently, a naturally occurring, mild strain of TamMV was discovered. This strain, LL6, displays mild or no symptoms on three genotypes of tamarillo. In addition to the mild symptomatology, LL6 is able to systemically infect tamarillo and has an overall sequence identity of 98% with the sequenced, symptom bearing, TamMV strain reported by Cohen et al. (2011). The discovery of a mild strain raises the question as to whether or not this strain may be used as a source for cross protection. Cross protection by LL6 TamMV mild strain virus will be determined by challenging LL6-pre-inoculated tamarillo plants, with a TamMV severe strain inoculum, by three different methods. First, challenging of LL6 pre-inoculated tamarillo seedlings with a range of viral titres of severe challenge inoculum will be undertaken. Second, the ability of pre-inoculated LL6 tamarillo seedlings to protect against a severe TamMV virus strain, when delivered via the aphid vector, Myzus persicae, will be investigated. Third, to reflect the viral pressure experienced in the orchard, LL6 inoculated tamarillo plants will be placed amongst established virus-infected tamarillo trees in a commercial orchard. The ability of the tamarillo industry within New Zealand to thrive is directly linked to the impacts of TamMV within the orchard. The ability of the LL6 TamMV mild strain to successfully induce cross protection may provide growers with a control method and increase profitability within the industry.
Age – a factor in induction of defense responses in tomato

Mr Navodit Goel
Amity Institute of Biotechnology, Amity University, Noida
navoditgoel1985@gmail.com
Navodit Goel, P K Paul
Amity Institute of Biotechnology, J-3 Block, Amity University, Sector 125, Noida, Uttar Pradesh, India - 201303

Plant age is important in its resistance to pathogens. A number of PR proteins are also involved in induction of SAR in plants. In the present study, the activity and isoforms of Peroxidase (POX) at various ages of tomato plants were analysed. The plants at each age were treated with neem fruit extract either singly or in combination with the pathogen. Activity of peroxidase, number of expressed isoenzymes and disease intensity (after 2 weeks of neem treatment) were analysed for all treatments. Age was found to significantly affect the enzyme activity and isoenzyme patterns. The 10 weeks old neem treated plants had highest POX activity and maximum number of isozymes. In general, neem could elicit POX activity. The neem alone treated plants had significant increase in POX activity. Treatment with neem prior to pathogen inoculation could significantly enhance POX activity as compared to post or concomitant treatment. Neem extract enhanced POX isofoms expression, both qualitatively and quantitatively. The results depict that prior treatment with neem extract primes the plants to establish an extensive defense response whereas if the pathogen establishes before neem treatment then it probably interferes with elicitation effect of neem. The disease intensity varied with plant age but was lowest in 10 weeks old plants. From the results, it appears that at 10 weeks of age (among all the ages considered) the plant’s genome is most responsive to induction by neem treatment. This is evident from the rapid expression of varied isoenzymes at this age. The observations are further supported by low disease incidence in 10 week old plants which can only be possible if the biochemical resistance of host plants is at or more than threshold level which are generally a result of expression of specific defence genes. Results demonstrate that plant age is a crucial factor in induction of host defense. Neem fruit extract can be effectively used as an elicitor for induction of defense responses which also varies with age.

Use of nutritional supplements against root knot nematode (*Meloidogyne incognita*) infection in potato

Mr Amjad Shahzad Gondal
PMAS Arid Agriculture University, Rawalpindi
amjadshahzad@live.com
Amjad Shahzad Gindal(1), Nazir Javed(2), Sajid Alem Khan(2)
(1) Department of Plant Pathology, PMAS Arid Agriculture University Rawalpindi Pakistan
(2) Department of Plant Pathology, University of Agriculture Faisalabad, Pakistan

The effect of foliar application of micro-power, humic acid and plant protector containing benzoic acid was examined for the management of root knot nematode (*Meloidogyne incognita*) in a susceptible potato cultivar FD-8-1. Application of plant protector significantly reduced the number of galls and egg masses and promotes overall plant growth followed by micro-power and humic acid as compare to control. Foliar application of plant protector 4% endorsed the number of leaves, shoots development, tuber weight and decreased the root weight followed by micro-power 4%, micro-power 2% and humic acid 4%. Minimum number of root galls and egg masses was recorded in case of plant protector 4% followed by micro-power 4%, micro-power 2% and plant protector 2%. Nematode fecundity rate was observed to be maximum in case of control with poor plant growth and maximum number of galls and egg masses. The significantly lower number of galls and egg masses and enhanced plant growth in case of plant protector containing benzoic acid @ 4% concentration indicated to be best one.
Tests of pruning or cauterising to reduce spread of cankers caused by *Pseudomonas syringae pv. actinidiae* in kiwifruit

Dr Ian Horner
The New Zealand Institute of Plant & Food Research Ltd.
ian.horner@plantandfood.co.nz

The New Zealand Institute for Plant and Food Research Ltd, 412 No.1 Road, RD2, Te Puke, New Zealand

*Pseudomonas syringae pv. actinidiae* (Ps) causes a serious disease of kiwifruit vines, with symptoms ranging from leaf spotting, to cane and leader cankers, or vine death. Growers attempting to manage canopies showing shoot, cane or leader symptoms need management strategies to restrict the spread of canker symptoms and dieback, whilst minimising canopy loss. The current project investigated whether pruning beyond the visible canker, or cauterising cankers, had any long-term effect in containing symptom development, compared with no treatment. The study, commenced in October 2012 in the Te Puke district, New Zealand, included 87 ‘Hayward’ (*Actinidia delicosa*) vines on two orchards and 72 ‘Zesy002’ (A. *chinensis*) vines on one orchard. From one to 30 canes or leaders with Psa-canekers were monitored on each vine. Cankers were either untreated, cauterised using a gas blowtorch, or pruned 40 cm below the lowest observed symptom. Cankers were marked at the outset and canker advance was measured after 1, 3 and 7 months. A final assessment is planned after 12 months. In ‘Hayward’, pruning has proven to be effective with only 13% and 2% of pruned canes showing any signs of canker advance after 7 months on the two orchards respectively. Most pruning wounds had callused and appeared to have healed very well. The New Zealand Institute for Plant and Food Research Ltd, Private Bag 1401, Havelock North 4157, New Zealand

Pruning beyond the visible canker, or cauterising cankers, respectively. In the cauterised and untreated vines, more than 80% of cankers expanded beyond the original boundary marked in October 2012. Pruning beyond the visible canker appears to reduce the continued spread of *Psa* canker symptoms, compared with cauterising cankers or leaving them untreated. Discrimination between treatments is likely to increase over time as unpruned cankers continue to expand.

Influence of fungicides on species spectrum associated with *Fusarium* head blight of wheat

Dr Kamil Hudec
Slovak University of Agriculture in Nitra
kamil.hudec@uniag.sk

Department of Plant Protection, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic

*Fusarium* head blight (FHB) is a serious disease causing yield losses and mycotoxin contamination in wheat and other cereals. The study is focused on relationship between fungicide efficacy and developed species spectrum on treated ears and kernels of winter wheat. Seven fungicides were applied to the wheat ears at beginning of blossom. The FHB symptoms, fungicide efficacy and *Fusarium* species spectrum were analyzed on treated heads and kernels from harvested yield. Average fungicide efficacy against FHB (FE-FHB) varied between 39.7 – 89.6 %. The most effective was prothioconazole + tebuconazole, followed by tebuconazole, prothioconazole + fluoxastrobin, prochloraz + tebuconazole, metconazole, propiconazole + cyproconazole, epoxiconazole + kresoxim-methyl, and azoxyarin + cyproconazole. The FE against *Fusarium* kernels infestation was much variable and lower than FE-FHB, varied between 0 - 72.7 %. *F. graminearum* was the most frequent causal agent of FHB, followed by *M. nivale, F. avenaceum, F. culmorum* and *F. poae*. Fungicide treatment by prothioconazole + tebuconazole, metconazole, prothioconazole + fluoxastrobin, tebuconazole significantly eliminated *F. graminearum* from infected heads. Occurrence of *M. nivale* in heads was significantly increased by all fungicides in comparison with check, excepting azoxystrobin + cyproconazole. In Gold3, the extent of canker expansion was greater than that noted in ‘Hayward’. Pruning 40 cm below the visible canker margin did not remove the infection from the cane and symptoms continued to expand in 18.4% of cases. This compares with the 27.6 and 27.8% of cankers that have expanded beyond the 40-cm mark in the untreated and cauterised vines, respectively. In the cauterised and untreated vines, only 8% of cankers expanded beyond the original boundary marked in October 2012. Pruning beyond the visible canker appears to reduce the continued spread of *Psa* canker symptoms, compared with cauterising cankers or leaving them untreated. Discrimination between treatments is likely to increase over time as unpruned cankers continue to expand.

Dr Ian Horner
The New Zealand Institute of Plant & Food Research Ltd.
ian.horner@plantandfood.co.nz

The New Zealand Institute for Plant and Food Research Ltd, Private Bag 1401, Havelock North 4157, New Zealand

The New Zealand Institute for Plant and Food Research Ltd, Private Bag 92169, Auckland 1142, New Zealand

The New Zealand Institute for Plant and Food Research Ltd, 412 No.1 Road, RD2, Te Puke, New Zealand
In vitro and in vivo evaluation of homeopathic products and plant extracts against *Xanthomonas campestris* pv. *malvacearum* causing bacterial blight of cotton

Mr Muhammad Talha Javed
Plant Pathology Department, University of Agriculture, Pak
talhauaf@yahoo.com

Muhammad Talha Javed, Dr. Muhammad Aslam Khan, Muhammad Ehetisham-ul-haq
Department of Plant Pathology, University of Agriculture Faisalabad, Pakistan.

In vitro Homeopathic products (Aviaria, Influenzium and Hepatitis) and plant extracts (*Moringa oleifera*, *Datura metal*, *Azadirachta indica* and *Syzygium cumini*) were evaluated at 5, 10 and 15% concentration keeping the streptomycine sulphate as control. At 15% concentration from homeopathic products and plant extracts the Influenzium and *Datura metal* respectively inhibited the growth of *Xanthomonas campestris* pv. *malvacearum* by making the inhibition zone in diameter of 1.78 and 2.1 cm as compare to streptomycine sulphate of 2.2 cm zone. *Moringa oleifera* was at least with less than 0.5 cm zone at 15% concentration. The trial was also conducted in green house and field condition. The Influenzium and *Datura metal* significantly managed the disease incidence in greenhouse and field condition respectively. The purpose for evaluation of these different treatments was that they are eco-friendly and not leave residues in environment.

Towards the understanding of *Puccinia hordei* in management perspective

Dr Kithsiri Jayasena
DAFWA
kithsiri.jayasena@agric.wa.gov.au

Kithsiri Jayasena(1,), Yehoshua Anikster(2) and Kazue Tanaka(1)

(1)Department of Agriculture and Food, 444 Albany Hwy, Albany, WA, 6330, Australia
(2)The Institute for Cereal Crops Improvement, Tel Aviv University, Ramat Aviv, 69978, Israel

Leaf rust cause by *Puccinia hordei* Oth, causes considerable yield losses and grain quality on barley (*Hordeum vulgare* L. subsp. vulgare) in Australia. If the disease control is not in place then potential loss estimated to be A$ 96 million in Australia. At present estimated average annual losses is A$ 21 million (Murray and Brennan 2009). It is important to understand pathogen life cycle to successfully manage the disease. From 1978 many virulence pathotypes of *P. hordei*, have been mainly detected in South Australia, Victoria, Tasmania and New South Wales and to a lesser extent Western Australia (WA). The detection of new virulence can be due point mutation, exotic introductions, somatic hybridisation or sexual recombination in the presence of alternate host such as *Ornithogalum* spp. No research has been done to understand the pathogen in alternate host environment in Australia. The cross done within WA isolates and between WA isolates and also with Israel isolates revels that the resultant F1 isolates carries homozygote recessive gene or heterozygote gene. For example the gene for virulence on *Berge, Reka 1, Ricardo, Estate, Magnif 104, Prior and Cutter* (differential lines) is a heterozygote state and in PI 531849 and PI 584760 appears to be homozygote. The present study clearly demonstrates that the leaf rust pathogen can change from non-virulence to virulence form after sexual recombination in the presence of alternate host *Ornithogalum* spp. Since the pathogen can overcome resistance to deployed single gene with time in where the alternate hosts are present, gene pyramiding is worth considering in the barley breeding to maintain durable resistance.
How Pinteresting, I’m All-A-Twitter: Social Media and Plant Disease Diagnosis and Control

Dr Greg I Johnson
Horticulture 4 Development
greg.johnson@velocitynet.com.au

G.I. Johnson
Horticulture 4 Development, PO Box 412, Jamison, ACT 2614, Australia

As plant pathologists seeking to identify the cause of plant diseases and recommend or develop control measures, we make use of a variety of diagnostic tools and information sources. The last decade has seen the emergence of several social media tools that are proving useful for plant pathologists seeking to enhance networks and access to information - Facebook in February 2004; Twitter in March 2006; Pinterest in March 2010; Scoop.it in November 2011 and Instagram in March 2012. They complement other internet based services including Yahoo Groups such as PestNet, access to Journals-on-Line, and email alerts such as ProMed, to provide the modern plant pathologist with access to a wealth of facts, ideas and information. This poster will display some of the sites that relevant to Plant-Pathology.

Cotyledon inoculation: A rapid technique for the evaluation of bacterial antagonists against *Sclerotinia sclerotiorum* in canola under control conditions

Mohd. Mostofa Kamal
Charles Sturt University
mkamal@csu.edu.au

M.M. Kamal, K. Lindbeck, S. Savocchia, G.J. Ash
Graham Centre for Agricultural Innovation (an alliance between Charles Sturt University and NSW DPI) School of Agricultural and Wine Sciences, Charles Sturt University, Boorooma Street, Locked Bag 588, Wagga Wagga, NSW 2678, Australia

Sclerotinia stem rot (SSR), caused by *Sclerotinia sclerotiorum* (Ss), is a devastating disease of canola in Australia. Prior to field testing, a rapid antagonistic bacterial evaluation involving a cotyledon screening technique was adapted against SSR in canola. Isolates of *Bacillus* (W-67, W-7-R, Sc-S, P-1 and E-2-1), previously shown to be antagonistic to Ss invitro, were used for further evaluation. Ten days old canola cotyledons were detached, surface sterilized and inoculated with 10 µL of a suspension of the *Bacillus* strains (1x10⁸ CFU mL⁻¹) on moist blotting paper in sterile Petri dishes for colonization. After 24 hours macerated mycelium (1x10⁴ mycelial fragments mL⁻¹) of three day old potato dextrose broth grown Ss was similarly drop inoculated onto canola cotyledons under controlled glass house conditions (19±10°C). Concurrently, intact seedlings (ten days old) were inoculated with using the same methods in a glasshouse. Both experiments were repeated thrice with five replications. Five days after inoculation no necrotic lesions were observed on seedlings inoculated with W-67, Sc-S, P-1; a few lesions (≤10%) were formed on seedlings inoculated with W-7-R and E-2-1 strains while severe necrotic lesions covered more than 90% area in control cotyledons both invitro and in the glass house. Further field investigation and correlation between field data and cotyledon inoculation assay may establish a relatively rapid technique to evaluate the performance of antagonistic bacteria against SSR of canola.
Determining the susceptibility of immature and mature stonefruit to *Monilinia fructicola* to improve disease forecasting in Australia

Ms Simone Kreidl  
Department of Environment and Primary Industries  
simone.kreidl@depi.vic.gov.au

Simone Kreidl(1), Oscar Villalta(1)

(1) Biosciences Research Division, Department of Environment and Primary Industries, AgriBio, Centre for AgriBiosciences, 5 Ring Road, LaTrobe University, Bundoora, VIC 3083, Australia

Brown rot, caused by *Monilinia fructicola* and *Monilinia laxa*, is a major disease problem of stone fruit in Australia both pre and postharvest. Management of brown rot relies on the application of fungicides, although crop losses still occur, especially during wet seasons. This is partly due to inadequate timing of sprays, which are often applied at irregular intervals without consideration/or knowledge of the key factors influencing infection risk. In addition, several important components of brown rot epidemiology are poorly understood, such as *Monilinia* survival mechanisms, pathogenicity and the importance of blossom blight in rot development. Work over the last few years has shown that *M. fructicola* is the dominant species found in stone fruit growing areas while the less aggressive *M. laxa* has mainly been sampled from suburban areas. The ability to predict infection risk using weather and crop susceptibility based tools is vital for managing brown rot infection and improving fungicide use in Australian stonefruit production. Weather based disease prediction tools, centred on temperature and hours of leaf wetness, have been developed overseas but have not been validated for use under Australian conditions. This research is investigating key aspects of *Monilinia* biology and host susceptibility, including susceptibility of both mature and immature fruit to infection, to better define *M. fructicola*’s infection requirements. Preliminary results from detached fruit inoculation experiments showed that: Under optimum infection conditions (20°C for 24 hours), peaches, nectarines, apricots and plums were all susceptible to *M. fructicola* at pre and post pit-hardening and ripe fruit stages. Fruit post pit-hardening was less susceptible and wounding increased susceptibility at all stages; In cross inoculation experiments, *M. fructicola* isolates from all four crops were more pathogenic than *M. laxa* on each of the four host crops. In each case, plums had the lowest level of infection indicating that plums have fruit characteristics which reduce susceptibility to *M. fructicola*; Mature fruit from all four crops were able to be infected by *M. fructicola* after relatively short wetness durations (3, 5 and 7 hours at 15 or 20°C), with the level of infection increasing as the wetness duration increased. Information collected on fruit susceptibility and *Monilinia* spp. infection requirements will be used to develop a weather and crop based model to identify wetness events (infection periods) conducive to infection with the aim of improving fungicide use. Further work will determine the infection requirements of immature fruit and flowers.

Developing a method for determining sensitivity of *Venturia inaequalis* to anilinopyrimidine fungicides in New Zealand apple orchards

Ms Ngaire Larsen  
The New Zealand Institute for Plant & Food Research Ltd  
ngaire.larsen@plantandfood.co.nz

Ngaire Larsen(1), Rob Beresford(1), Peter Wood(2), Peter Wright(2), Brent Fisher(2)

(1) The New Zealand Institute for Plant & Food Research Limited  
(2) Mt Albert Research Centre, Private Bag 92169, Auckland 1142  
(3) Hawke’s Bay Research Centre, Private Bag 1401, Havelock North 4157

Few studies have investigated methods for testing resistance of *Venturia inaequalis* (apple black spot) to anilinopyrimidine (AP) fungicides. Monitoring disease control on inoculated host plants is a reliable method for testing fungicide efficacy but this approach is resource consuming and requires sophisticated plant growth facilities. In order to reduce the reliance on using host plants for testing resistance of *V. inaequalis* to AP fungicides, the development of an agar-based method is desirable because it would be compatible with concurrent testing of other fungicide groups. Conventional mycelial growth assays performed on nutrient agar are unsuitable, however, as the presence of exogenous growth factors negates the mode of action of this fungicide group. Any medium used, therefore, must not interfere with, or mask, the effects of the fungicide on the pathogen. A synthetic agar mycelial growth assay, adapted from a method used for *Botrytis cinerea*, was used to determine the sensitivity of isolates of *V. inaequalis* to two AP fungicides, cyprodinil and pyrimethanil. Nineteen single-conidium isolates of *V. inaequalis* suspected to be either AP resistant or sensitive were tested using this method. Isolates were classified as sensitive (S) or resistant (R) to cyprodinil and pyrimethanil after 21 days growth, according to fungicide concentrations that inhibited growth by 50% ($E_{50}$). In vitro sensitivity was compared with disease control by AP fungicides on potted apple trees inoculated with one of three S or one of three R isolates. The three S isolates were inhibited by AP fungicides on plants. The three R isolates caused disease on fungicide-treated leaves, although one isolate, classified as R for both fungicides on agar, was inhibited by cyprodinil on plants. *V. inaequalis* isolates from organic orchards were sensitive to both fungicides in all tests. $E_{50}$ sensitivity thresholds were determined for cyprodinil and pyrimethanil with S isolates inhibited by 0.05 mg/L (cyprodinil) and 0.5 mg/L (pyrimethanil) while R isolates were not inhibited by 0.5 mg/L (cyprodinil) and 2.5 mg/L (pyrimethanil). This synthetic agar method will be used for screening isolates collected in New Zealand orchard surveys in order to determine the sensitivity of *V. inaequalis* populations to AP fungicides. To complement this, plant tests of selected isolates will be included as references to determine implications for orchard disease control.
In vitro activity of two synthetic antimicrobial peptides (AMPs) against plant pathogenic bacteria

Ms Virginia Marroni
The New Zealand Institute for Plant & Food Research Limited
virginia.marroni@plantandfood.co.nz

Virginia Marroni, Kirsty Boyd-Wilson, Andrew Catanach, Ruth Butler, Grant Smith,
The New Zealand Institute for Plant & Food Research Limited, Private Bag 4704, Christchurch, New Zealand.

The efficacies of two synthetic antimicrobial peptides, AMP143 and AMP100, obtained from Anti Microbial Biotechnologies S.L (AMP Biotech), were tested in vitro against three strains each of the economically important pathovars of Pseudomonas syringae: P. syringae pv. actinidiae (Psa), causing bacterial canker of kiwifruit; Pseudomonas syringae pv. syringae van Hall (Pss); and Pseudomonas syringae pv. morsprunorum, (Psm), causing bacterial canker of sweet cherry. The Minimum Inhibitory Concentration (MIC), defined as the concentration at which there is no bacterial growth after 48 h, was determined for each peptide. Both were active against all three strains of each pathovar tested, with MICs ranging from 1.56 to 6.25 µM, but differences were found in the activity of both peptides to the different strains within each of the pathovars. AMP143 expressed higher activity against strains Psa1LB and Psa3v (both with MIC of 3.12 µM) than against strain Psa2v (MIC of 6.25 µM), while it showed a similar activity against the three strains of both Pss and Psm (MIC of 1.56 µM). AMP100 was more active against Psa1LB (MIC of 3.12 µM) than against Psa2v and Psa3v (both with MIC of 6.25 µM), while it showed higher activity against Pss2v, and against Psm2 and Psm3 (MIC of 1.56 µM) than against Psa1 and 3 and Psm1 (MIC of 3.12 µM). Overall, strains of Psa, Pss and Psm were more sensitive to AMP143 than to AMP 100. MIC values obtained in this test were similar to those observed by other researchers for major groups of plant pathogenic bacteria, including P. syringae pv. syringae, Erwinia amylovora and Xanthomonas axonopodis pv. vesicatoria for the same or similar synthetic peptides, and compared well with standard antibiotics. AMPs appear to be very promising products against plant pathogenic bacteria. Future work to assess activity of selected peptides could include detached plant organ experiments and whole plant systems.

In vitro control of Mycosphaerella arachidis deighton the early leaf spot disease pathogen of groundnut by the extracts from six medicinal plants.

Adebola Matthew
Ibrahim Badamasi Babangida University
adebolamo@gmail.com
Adebola, Matthew O(1), Amadi, Jude E(2), Dadi-Mamud, N. J. (3), Baba John,(3)

1Ibrahim Badamasi Babangida University, Department of Biology, Lapai, Nigeria.
2Department of Botany, NnamdiAzikiwe University, Awka, PMB 5025, Awka, Nigeria.
3Ibrahim Badamasi Babangida University, Department of Microbiology, Lapai, Nigeria.

Ground nut (Arachis hypogaea) is one of the most popular commercial crops in Nigeria. Its successful production has been drastically affected by early leaf spot disease caused by Mycosphaerella arachidis Deighton. In vitro control of the pathogen by six medicinal plants (Entada africana, Vitex doniana, Lawsonia inermis, Azadirachta indica, Alcypha hispida and Nuaclea latifolia) was assessed in this study. The extracts of the plants were prepared using cold and hot water and alcohol. The pathogen was isolated from ground nut infected with early leaf spot disease. The results revealed a great significant difference (P<0.05) in yield of extracts between cold water, hot water and alcohol extracts. A significant difference (P<0.05) was observed in percentage concentrations of the various phytochemical constituents present in the extracts. Flavonoids percentage concentration was the highest (0.68 - 1.95%) followed by saponinnin(0.09 - 1.53%) in N. latifolia extracts. Steroids had the least percentage concentrations (0.00- 0.09%) followed by terpenoids(0.00 – 0.95%). N. latifolia extracts produced the highest percentage concentrations (0.07 – 1.95%) of all the phytochemicals followed by A. indica(0.05 – 1.64%)and least concentrations were obtained in A. hispida(0.09 – 0.87%)and V. doniana (0.00 – 0.88%). The extracts inhibited spore germination and growth of M. arachidis. The inhibition by alcohol extracts was high and significantly different (P>0.05) from cold and hot water extracts. Alcohol extract of L. inermis gave 100% spore germination inhibition followed by N. latifolia and A.indica with 97.75% and 85.60% inhibition respectively. Therefore, field trials of these six medicinal plants on the control of early leaf spot disease of ground nut are recommended. Key words: Ground nut; Phytochemicals; Medicinal plants; Extracts; Inhibition
Bioefficacy of Plant Extracts to Control *Nattrassia mangiferae* on Date palm

Dr Muntasir Mohamed Elamien
Dongola University-Sudan
muntasiradam@yahoo.com

Muntasir Adam. M.
Dongola University Faculty of Agric. Science. Dept. of Plant Protection
TELL 00249912805451

Sooty canker disease is an important disease of date palm in the Northern State of the Sudan causing severe damage of off-shoots, date palm trees and reduction in yield. In present study, the pathogenic fungus was isolated from infected plant parts and identified based on morphological and cultural characters as *Nattrassia mangiferae*. The *in vitro* efficacy of different plant extracts Neem (*Azadirachta indica*), Mint (*Mentha spicata*), Ryhan (*Ocimum basilicum*), and Maharab (*Cymbopogon schoenanthus* Poixmus) were tested to control sooty canker pathogen. Different concentrations 5, 10, 15 and 20% of plant extracts were tested for their effect on the inhibition of mycelial germination. All the plant extracts showed significant inhibition of fungal mycelial growth. Among the different extracts, complete inhibition of fungal mycelial growth was exhibited at 20% of *Ocimum basilicum* was found most effective followed by *Mentha spicata* with only retardation of mycelial growth while, Neem (*Azadirachta indica*), and Maharab (*Cymbopogon schoenanthus* Poixmus) was the least effective. Application of plant extract which are easily available for controlling plant diseases are non-pollutative, cost effective nonhazardous and do not disturb ecological balance. Investigations are in progress to test the bioefficacy of these extracts in field applications. Four chemical fungicides namely Tilt, Benlate, Bayfidan, and Baylon at different conc. (10 ppm, 20ppm,30ppm, 40ppm,50ppm) were also used for their effect on the mycelial germination, all of them inhibited the germination the most effective one was Tilt at 30-50 ppm, followed by Benlate while Baylon and Bayfidan at high concentration 50 ppm inhibited the growth of the fungus. The effect of plant extract are more effective for controlling the fungus as compare to the fungicides. Key words: date palm sooty canker fungicides *Nattrassia mangiferae*, Plant extract

Study on the Partial Resistance of Sesame Genotypes to Charcoal Rot Disease under Greenhouse Conditions

Ms Mohsen Naderpour
Tarbiat Modares University
naderpour.mohsen@yahoo.com

Mohsen Naderpour(1), Naser Safaie(1),
Department of Plant Pathology, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran
Phone: +982148292346
FAX: +982148292200

Charcoal or stem rot induced by *Macrophomina phaseolina* (Tassi) Goid is one of the most important diseases of sesame throughout the world and the use of resistant cultivars provides an effective, economical, and ecodriendly approach toward disease control. With this study, The partial resistance of 37 sesame genotypes against *M. phaseolina* was studied using an inoculum of 10 highly virulent isolates in greenhouse as a 5% (w/w). The experiment was carried out using completely random design with 3 replicates for each treatment (genotype). Each replicate included 3 pots each of 10 seeds. Control for each genotype included a replicate of 3 pots each of 10 seeds. Significant variations were found among genotypic reactions to *M. phaseolina*. Based on the percentage of infected plants ninety days after sowing, Six genotypes Darab 14, Jiroft 13, TN-238, Varamin 2822, Hajiabad, and TN-240, respectively of 6.17, 6.35, 7.42, 8.26, 9.47, and 10% infected plants were grouped as highly resistant against charcoal rot. Other genotypes were discerned as 4 resistant, 7 moderately resistant, 7 moderately susceptible, 4 susceptible, and 9 highly susceptible genotypes. No genotype was found immune. Compared to controls, the highly resistant and resistant genotypes indicated the least percentage of shoot fresh and dry weight, root dry weight, as well as plant height. Also, they displayed the lowest disease severity based on stem lesion length, number of infected internodes, and root disease severity. Based on the measured indices, cluster analysis using UPGMA method and Euclidean distance grouped the genotypes according to their level of resistance and susceptibility to *M. phaseolina*. The resistant genotypes can be applied in sesame breeding programs. Additionally, some of the resistant genotypes of agronomically favourable traits can be grown in vast scale.
Analysis of the natural genetic variation of phosphate sensitivity in *Arabidopsis thaliana*.

Dr Philip O’Brien
Murdoch University
P.Obrien@murdoch.edu.au

Daniel Koehn, Giles E, St,J, Hardy, Philip A. O’Brien, Oliver Berkowitz

School of Veterinary & Life Sciences, Murdoch University, Western Australia,
ARC CoE Plant Energy Biology, University of Western Australia

Many horticultural crops are susceptible to infection by the oomycete pathogens *Phytophthora* and *Pythium*. The necessity to implement management strategies to reduce the effects of infection poses considerable constraints on production. These pathogens also cause considerable damage in native ecosystems in many parts of the world, most notably in Australia. One option for management of diseases caused by these pathogens is the application of phosphate, a reduced analogue of phosphate to plants. Interference of phosphate in the phosphate homeostasis, in host and pathogen, are believed to be connected reduced mycelial growth and pathogenicity, as well as boosted plant defence responses, thus reducing colonization of the host. Application of phosphate delays colonization of the plants by the pathogen. It is not yet known how phosphate protects the plant against infection, or why some plant species are protected by low concentrations of phosphate whilst others require comparatively high concentrations. To gain a better understanding of the effects of phosphate on plant growth and defence we have been studying variation in the sensitivity to phosphate in ecotypes of the model plant *Arabidopsis thaliana*. Accessions with contrasting sensitivities to phosphate were identified and corresponding Recombinant Inbred Lines (RIL) screened to identify Quantitative Trait Loci linked to phosphate sensitivity. In another approach EMS-mutagenized plants are being screened for increased tolerance to phosphate. A number of potential mutants have been identified.

Development of an inoculation method suitable for evaluating *Fusarium* wilt resistance in strawberry

Ms Michelle Paynter
DAFF

WITHDRAWN
DISEASE MANAGEMENT
POSTER BOARD 73

Control, regulation, and phytosanitary issues on banana propagative material for French overseas departments: the stakes for the French National Laboratory of Reference network

Ms Françoise Poliakoff
Anses, Plant Health Laboratory
Françoise.poliakoff@anses.fr
Delphine Massé, Aude Chaibird, Nathalie Cassam, Gilles Cellier, Aurélie Moreau, Bruno Hostachy
Anses, Plant Health Laboratory, Tropical Pests and Diseases Unit, Pole de Protection des Plantes, 7, Chemin de l'IRAT, 97410 SAINT PIERRE - Reunion Island

Started at the beginning of the 20th century, but drastically increased from the 60's, the banana industry production in the French overseas departments (Guadeloupe and Martinique) is mostly dedicated to the European market. Throughout this period, banana industry has been impacted by deep technical and phytosanitary modifications and revolutions. In-vitro plants took over the majority of banana plantations in the 90’s by providing better growth homogeneity and sanitation toward viruses, bacteria, and nematodes, associated with banana production; resulting into a significant reduction of chemical applications. Legislation also had to adapt in order to create a framework allowing a safer importation of in-vitro plants. Hence, specifications have been adopted in 1995, based on an agreement delivered by the French Ministry of Agriculture to both sides: companies that produce in-vitro plants from basic material; and to nurseries that grow certified plants until ready for plantation. At different stages of the production scheme, banana material undergoes several phytosanitary tests targeting viruses and bacteria, previously identified by an extensive Pest Risk Assessment (PRA). This PRA targets four viruses: CMV, BBTV, BSV, and BBMV; and a bacterium: Ralstonia solanacearum (Moko disease). The Tropical Pests and Diseases Unit (LSV-RAPT) of Anses Plant Health laboratory, located in Reunion Island (SW Indian Ocean) represents the French reference laboratory in charge of (i) evaluating and publishing detection methods in France and Europe; (ii) supervising and coordinating the activity conducted by officially approved French laboratories, certified by French Ministry of Agriculture. To ensure that these laboratories are delivering robust and reliable analytical results, interlaboratory proficiency tests are then organized in accordance with the requirements of the ISO 17043 standard. Detection scheme of in-vitro transmissible diseases of banana was shown to be in adequation with safety requirements, relatively to: Sensitivity, Specificity, Detection threshold, and Repeatability. To date, official methods for the detection of CMV, BBMV, and BBTV by ELISA, IC PCR, PCR, and real time PCR have been evaluated and validated by LSV-RAPT and officially published by the French ministry of agriculture. LSV-RAPT is heading towards validating methods for BSV, Moko disease and Xanthomas vasicola pv. musacearum. Three years proficiency results on CMV and BBTV have been collected on laboratory network and showed their ability to perform official methods. Future proficiency tests will associate the detection of several viruses on the same sample in conditions closer to the routine analysis.

DISEASE MANAGEMENT
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Heat treatments for killing Pseudomonas syringae pv. actinidiae in dormant kiwifruit canes

Ms Shamini Pushparajah
Plant and Food Research
shamini.pushparajah@plantandfood.co.nz
Shamini Pushparajah(1), Mike Currie(1), Jonathan Rees-George(1), Kevin Patterson(2), Alison Duffy(3), Michele Vergara(4), Kerry Everett(5)
(1) The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Mt Albert, Auckland 1142, New Zealand

All cells of a virulent strain of Pseudomonas syringae pv. actinidiae (Psa-V) in an aqueous suspension were killed by heat treatment at 50°C for 5 minutes or longer. In contrast, a 5 minute hot water treatment (HWT) at 50°C was not sufficient to kill Psa-V in inoculated budwood of Actinidia chinensis ‘Hort16A’. However, the lag time for the internal tissues of the budwood to reach 50°C would be expected to reduce the efficacy of this treatment. When ‘Hort16A’ budwood inoculated with a rifampicin resistant strain of Psa-V was hot water treated at 50°C for 15 minutes, no bacterial cells were recovered indicating that the time of treatment was adequate to bring the tissues to a temperature lethal to the pathogen. Hot water treatment of Actinidia delicosa ‘Hayward’ budsticks at 50°C for more than 15 minutes resulted in some loss of bud viability when held in water after treatment. In contrast, ‘Hort16A’ buds remained viable after up to 30 minutes of hot water treatment at 50°C. However, a longer duration at 50°C tended to result in termination of the ‘Hort16A’ shoots developing from buds and could indicate that longer term viability would have been compromised. When treated bud wood was grafted onto five year old stumps in Te Puke, there was no evidence that either a 10 or 15 minute HWT at 50°C had a negative impact on graft success for ‘Hayward’, but there was some reduction in number of growing shoots for ‘Hort16A’ after 15 minute HWT but not after 10 minute HWT. Hot water treatment of ‘Hort16A’ cuttings rooted in a greenhouse resulted in over 50% lower survival, than control (unheated) cuttings. This was not affected by the length of treatment (10 or 15 minutes). Rooting of Hayward cuttings was not affected by HWT. HWT is a viable treatment, for eliminating Psa from propagation material.
Antifungal activity of some natural products against Alternaria blight of tomato

Dr Hesamedin Ramezani
Department of Agriculture, Payame Noor University, P.O. Box. 19395-3697, Tehran, Iran
hramezani18@yahoo.com
Hesamedin Ramezani
Department of Agriculture, Payame Noor University, Tehran, Iran

Among all the extracts tested, Eucalyptus leaf extract showed significant reduction in radial growth, sporulation and spore germination. Under Laboratory conditions, leaf extracts of Eucalyptus, Ocimum and Anagallis showed maximum reduction (92.5, 91.6 and 91.4 % decrease over check, respectively) in radial growth whereas Ocimum, Eucalyptus and Urtica showed minimum sporulation intensity (0.26, 0.28, and 0.81 × 10^5 respectively). Significantly lowest reduction of spore germination was observed with Urtica followed with Ocimum and Eucalyptus (86.6, 79.4 and 78.9 %, respectively). Studies carried out under glasshouse conditions revealed that Eucalyptus spray gave significantly lesser number of spores / leaf (2.05), minimum size of spores (1.28 mm), minimum sporulation intensity (1.22 × 10^5) and minimum disease index (13.96) followed by Calotropis, Ocimum and Polyanthai extracts spray. Key words: Alternaria solani, Botanicals, Lycopersicon esculatum, Management.
**DISEASE MANAGEMENT**

**POSTER BOARD 77**

*Colletotrichum* species, causing mango anthracnose in Thailand and pre-harvest management to reduce this disease

Dr Somsiri Sangchote  
Kasetsart University  
agrsrs@ku.ac.th

Somsiri Sangchote\(^{(1)}\), Rattipats Chiangsiri\(^{(1)}\), Kawit Warichkul\(^{(2)}\), David Guest\(^{(2)}\)

- **(1)** Department of Plant Pathology, Faculty of Agriculture, Kasetsart University, Ngam Wong Wan Rd, Bangkok 10900, Thailand
- **(2)** Department of Horticulture, Faculty of Agriculture, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom 73140, Thailand

Casual pathogens of anthracnose disease of mango cv. Nam Dok Mai See Thong caused by *Colletotrichum* was investigated in three main areas of mango production in the Northern, Central and Northeastern of Thailand. Morphological and molecular characteristic of 53 isolates was determined. Morphological characteristic of these isolates were classed as *C. gloeosporioides*. Species-specific primers, including *CgInt* for *C. gloeosporioides* and *Caln2* for *C. acutatum*, were used to analyzed grouping of these isolates through their sequences. The results showed that 12 isolates from Northern, 5 isolates from Northeastern, and 10 isolates from Central were identified as *C. gloeosporioides* whereas 18 isolates from Northeastern, and 8 isolates from Central were *C. acutatum*. Reduction of *C. gloeosporioides* latent infection on young mango fruit cv. Nam Dok Mai See Thong before bagging was conducted. Young mango fruits (31-45 days after fruit set) were treated with propineb, azoxystrobin, difenoconazole, prochloraz, and carbendazim concentration at 1050, 125, 750 and 500 ppm (recommended dose) respectively and then, bagged the fruits. Prochloraz treated fruits showed the lowest disease incidence at 18.75 % at ripening stage. Artificial inoculation of young mango fruits with conidia suspension of *C. gloeosporioides* concentration 2 x 10⁶ conidia/ml and then, sprayed with prochloraz concentration at 750 ppm compared with non sprayed followed by bagging the fruits. Prochloraz was also reduced anthracnose disease severity from 18.20% to 9.78 %, although was not reduced disease incidence. Protection of mango fruits from an infection of *C. gloeosporioides* by bagging with new-and used-carbon bag (1 season usage) compared with unbagged fruits. Disease incidence and disease severity on the fruits which were bagged with new-carbon bag was 69.46 % and 3.6 % and used-carbon bag was 64.66 % and 5.5 % which were not significant but significant difference from unbagged fruits (91.19 % and 17.4 %). Infection of *C. gloeosporioides* through new- and used-carbon bag was further investigated. Fruits which were bagged with these carbon bags showed no symptom of anthracnose at ripening stage.

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**DISEASE MANAGEMENT**

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Study on biocontrol potential of the mites *Caloglyphus mycophagus* and *Tyrophagus putrescentiae* against bean, canola, corn, lettuce and wheat damping off caused by *Rhizoctonia solani* under laboratory conditions

Dr Abbas Sharzei  
University of Tehran  
asharze@ut.ac.ir

Evaz Ghorbani\(^{(1)}\), Abbas Sharzei\(^{(2)}\), Hadi Ostovan\(^{(2)}\)

- **(1)** Department of Plant Pathology, Marvdasht Branch, Islamic Azad University, Marvdasht, Iran
- **(2)** Department of Entomology and Plant Pathology, Aburaihan Campus, University of Tehran
- **(3)** Department of Entomology, Science and Research Branch, Islamic Azad University, Fars, Iran

*Caloglyphus mycophagus* and *Tyrophagus putrescentiae* are mycophagous mites that can be found in fungal cultures. Their potential to control the damping off disease of bean, canola, corn, lettuce and wheat, caused by *Rhizoctonia solani*, was studied. A female and fertile mite from each species was selected and transferred into a glass jar containing sawdust and fresh onion chips, which produced a high mite population. Inoculated negative controls (free of mites) showed damping off and crown necrosis after two weeks. However, in mite treated pots, 70- 80% of plants survived and showed a normal growth during the 45 days of observation under greenhouse conditions. The results showed that these mites can be successful biocontrol candidates.
Cereal cultivars can be uniformly characterised for resistance to root-lesion nematodes (*Pratylenchus thornei* & *P. neglectus*) using diverse procedures.

Mr Jason Sheedy  
Department of Agriculture, Fisheries and Forestry Queensland  
jason.sheedy@daf.qld.gov.au

Jason Sheedy(1), Alan McKay(2), Vivien Vanstone(3), Susan Fletcher(3), Alison Kelly(5), John Thompson(5)

(1)Department of Agriculture, Fisheries and Forestry Queensland  
(2)Plant and Soil Health, South Australian Research and Development Institute [SARDI], Waite Campus, Unrthane, South Australia, Australia 5064  
(3)formerly Department of Food & Agriculture Western Australia [DAFWA], 3 Baron-Hay Court, South Perth, Western Australia, Australia 6151

The root-lesion nematodes (RLN) *Pratylenchus thornei* and *P. neglectus* are widely distributed in Australian grain producing regions and can reduce the yield of intolerant wheat cultivars by up to 65%, costing the industry ~$123 M/yr. Consequently, the Northern, Southern and Western regions have independently developed procedures to evaluate the resistance of cereal cultivars to RLN but have not routinely compared resultant cultivar classifications for consistency. To evaluate the consistency of cultivar classification between procedures, each region conducted resistance experiments using a standardised set of 26 and 36 cereal cultivars replicated six times for *P. thornei* and *P. neglectus* respectively. The Northern and Southern regions also investigated the effect of planting date and experiment duration on RLN reproduction and cultivar classification. Results show the genetic correlation between cultivars tested using the Northern and Southern procedures evaluating *P. thornei* resistance was 0.93. Genetic correlations between experiments using the same procedure but with different planting times were 0.99 for both Northern and Southern procedures. The genetic correlation between cultivars tested using the Northern, Southern and Western procedures evaluating *P. neglectus* resistance ranged from 0.71 to 0.95. Genetic correlations between experiments using the same procedure but with different planting times ranged from 0.91 to 0.99. This study shows that, even though experiments were conducted in different geographic locations with different trial management practices, the diverse nematode resistance screening procedures classify cultivars uniformly. Subsequently, the RLN resistance data can be pooled across regions to provide consistent national classifications of cultivars.

Powdery mildew resistance in cucumber transplants grown under different light and atmospheric conditions

Dr Toshio Shibuya  
Osaka Prefecture University  
shibuya@envi.osakafu-u.ac.jp

Toshio Shibuya(1), Kaori Itagaki(2), Motoaki Tojo(2), Ryosuke Endo(3)

(1)Graduate School of Life and Environmental Sciences, Osaka Prefecture University, Sakai, Osaka, Japan

The closed-type transplant production systems have been developed and commercialized in Japan as a way to produce high-quality transplants. In these systems, light and atmospheric conditions are optimized in closed chambers regardless of the weather conditions. The use of pesticides can be omitted in these systems, because the systems are perfectly closed to pathogens and their vectors. In addition, the growing of transplants in the closed system may further reduce the use of pesticides after transplantation through the enhancement of physiological and morphological properties of host plant. Here, we examined the powdery mildew resistance in cucumber (*Cucumis sativus*) transplants grown under different light and atmospheric conditions. The cucumber ‘Hokushin’ seedlings were grown under different light sources (fluorescent lamps or artificial solar lamps), relative humidities (10% or 90%), or CO2 concentrations (360 or 960 µmol mol−1) until cotyledons were expanded, and were then inoculated with spores of powdery mildew fungus (*Podosphaera xanthii*). The inoculated seedlings were placed in the same conditions, and then the powdery mildew colonies on the leaves were counted 7 days after inoculation. The colony densities on the seedlings grown under fluorescent lamps, low relative humidity or high CO2 concentration was less than those on the seedlings grown under artificial solar lamps, high relative humidity or low CO2 concentration, respectively. This indicates that colony development of powdery mildew was inhibited through the enhancement of host plant resistance responded to the light and atmospheric treatments. The seedlings which had greater resistance to powdery mildew (i.e. seedlings grown under fluorescent illumination, low relative humidity or high CO2 concentration) had thicker epidermal tissues and greater leaf mass per area, but did not show significant changes in physiological properties. Thus, the enhanced powdery mildew resistances were probably due primarily to the changes in leaf morphological properties.
Substrate pH during conidial morphogenesis influences long-term cold storage of *Trichoderma atroviride* and *Trichoderma hamatum* conidia

Dr Johanna Steyaert  
Bio-Protection Research Centre, Lincoln University  
johanna.steyaert@lincoln.ac.nz  
Johanna Steyaert (1), Amanda Hay (2), Alison Stewart (2)  
(1) Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand  
(2) Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA

To preserve genetic integrity it is desirable to place potential biocontrol agents (BCAs) into long-term storage as soon as possible after isolation. One recommended method is storage at extremely low temperatures, such as -80°C which has the effect of suspending metabolic activity. Extreme low-temperature storage is not a viable option for many commercial biocontrol producers and -20 or 4°C is more commonly used. In this study we examined the influence of substrate pH on conidial yield and long-term viability at 4°C, -20°C and -80°C for two biocontrol agents from our collection (*T. atroviride* LU132 and *T. hamatum* LU593). *Trichoderma* isolates are typically stored in conidial form at -80°C; it is somewhat surprising therefore, that within a short space of time over 50% of conidia stored at -80°C had lost the ability to germinate. More dramatic losses were observed at -20°C and 4°C and, for all temperatures evaluated, the reduction in germination potential varied depending on the substrate pH for conidiogenesis and the isolate being tested. Together these studies suggest the ability to tolerate low temperature storage is not universal in fungi, and is instead dependent on a variety of factors such as species, isolate and cultivation conditions. Further, cultures inoculated with low germinability spore stocks do not produce conidia with high tolerance to -80°C storage suggesting this trait is not able to be selected for and therefore not heritable.

Management of Late blight of potato caused by *Phytophthora infestans* (Mont.) de Bary through botanicals

Mr Muhammad Nasir Subhani  
University of the Punjab, Lahore, Pakistan  
nasirsuhbani@hotmail.com  
(1) Muhammad Nasir Subhani, (2) Shahbaz Talib Sahi, (3) Safdar Hussain  
(1) Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan  
(2) Department of Plant Pathology, University of Agriculture, Faisalabad, Pakistan  
(3) College of Agriculture, D.G. Khan Sub Campus University of Agriculture, Faisalabad, Pakistan

Chemical control remains the most important control measure against late blight. Growing potatoes without using fungicides has become unthinkable in most parts of the world. Severity of the disease was fluctuating between cropping seasons depending on the prevalent weather conditions. The majority of them, in fear of losing their crop apply abundant fungicides as a preventive measure at calendar based spraying intervals. The use of chemical fungicides has resulted in an increased degree of pathogen resistance, force farmers to follow different strategies or some alternative ways of disease control. In this regard we tested bio-fungicide and plant extracts. In protective disease management Neem (*Azadirachta indica*) leaf extract was the most effective followed by Garlic (*Allium sativum*) extract but Neem (*Azadirachta indica*) oil was least effective on all the five varieties (Cardinal, Karoda, Rodio, Shanan and Siply Red). Most effective dose of Neem (*Azadirachta indica*) leaf extract and all other plant extracts was 3% followed by 2% and 1% being least effective while 7 days spray interval was most effective as compared to 14, 21 and 28 days. In curative disease management program Neem (*Azadirachta indica*) leaf extract @3% was most effective followed by Garlic (*Allium sativum*) extract @3% while eucalyptus (*Eucalyptus globulus*) leaf extract @3% being least effective on all the five varieties (Cardinal, Karoda, Rodio, Shanan and Siply Red). Three consecutive sprays after disease appearance were most effective among all the tested plant extracts followed by 2 and 1 sprays. Control efficiency of Neem (*Azadirachta indica*) leaf extract, as protective and curative was more pronounced on moderately resistant cultivar (Shanan) as compared to highly susceptible (Karoda). This clearly indicates the involvement of resistance in combined effort to control late blight of potato. By sowing moderately resistant cultivars and spraying Neem (*Azadirachta indica*) leaf extract or Garlic (*Allium sativum*) extract @3% or moderately resistant varieties/lines combined with half the recommended dose of fungicides can protect the crop efficiently.
**Antagonistic Mechanisms of Trichoderma spp. Against Fusarium solani, the Causal Agent of Potato Dry Rot**

Ms Zahra Taghizadeh  
Shiraz Islamic Azad University, Iran  
Taghizadeh_1642@yahoo.com

Zahra taghizadeh(1), Sedighe Mohammadi(2), Hosein Alaie(3),
(1) Student of M.S. of Department of Plant Pathology, Shiraz, Branch Islamic Azad University, Shiraz, Iran.  
(2) Assistant Professor of Department of Plant Pathology, Shiraz, Branch Islamic Azad University, Shiraz, Iran.  
(3) Assistant Professor of Department of Plant Pathology, Branch Vali asr University, Rafsanjan, Iran.

Regarding to high capability of Trichoderma in biological control of a lot of pathogens and this point which Fusarium solani, causal agent of Fusarium dry rot of the potato’s causes a lot of important economic loss in agricultural products; for biological control of this pathogen four isolates of Trichoderma harzianum (1, 2, 3, 4) and one isolate of Trichoderma longibrachiatum, Trichoderma virens, Trichoderma koningii, against F. solani, are studied under laboratory conditions. In dual culture, isolates of T. harzianum 3, T. longibrachiatum, T. virens and T. koningii were able inhibit the mycelial growth of F. solani. T. longibrachiatum had the highest percent of growth inhibition (41/18, 62/5& 82/35%) at three times interval. In microscopic investigation of dual region of Trichoderma isolates and F. solani observed hyphal contact and hyphal coiling of Trichoderma spp. and lysis of hyphal of pathogen and T. harzianum (1, 2 & 4) and T. koningii penetrated in hyphal pathogen and hyphal fragmentation of F. solani observed by these antagonists. The effect of Volatile Metabolites (VM) of all Trichoderma isolates inhibited mycelial growth, and T. longibrachiatum had the highest percent of growth inhibition 72/88%. In of investigation of effect of Non Volatile Metabolites (NVM) of Trichoderma isolates on mycelial growth of F. solani indicated that using of 5 and 10 ml of NVM of 2 isolates (2 & 4) with 9/76 and 14/28 % had the highest effect on mycelial growth of pathogen.

**Bioefficacy of plant extracts to control Rhizoctonia solani causing stem rot of french bean**

Dr Phatik Tamuli  
Darrang College, Tezpur - 784 001, Assam, India  
tamulip@yahoo.com

Phatik Tamuli(1), Jayashree Das(2)
(1) Microbiology and Pathology Laboratory, Department of Botany, Darrang College, Tezpur – 784 001, Assam, India  
(2) Biotechnology Division, Defence Research Laboratory, Tezpur – 784 001, Assam, India

Some plant extracts play significant role in the inhibition of seed-borne pathogens and in the improvement of seed quality and field emergence of seeds. An investigation was carried out to ascertain the efficacy of certain plant extracts in controlling stem rot of french bean (Phaseolus vulgaris) caused by Rhizoctonia solani. In-vitro evaluation of plant extracts was done followed by pot trials using seed treatment. Results showed that all the plant extracts, viz., Polygonum hydropiper, Solanum melongena, Piper beetle and Alamanda cathartica at 2 mg/ml concentration were efficacious in enhancing seed germination rate and shoot length as compared to control. Disease infection and mortality rate were comparatively less in treated seeds. Seed germination was highest (94.44%) in A. cathartica treated seeds whereas in inoculated control it was 33.33%. However, further studies, such as, mass field trials are going on to confirm their efficacy under different agro-climatic conditions.
**Elicitors for control of Neonectria ditissima**

Dr Monika Walter  
Plant & Food Research  
monika.walter@plantandfood.co.nz

Monika Walter(1), Owen Stevenson(1), Peter Alspach(1), Reiny Scheper(2), Tony Reglinski(3)

(1) The New Zealand Institute for Plant & Food Research Limited (Plant & Food Research), Old Mill Road, Motueka, NZ  
(2) Plant & Food Research, Cnr Crosses St and Georges Road, Hawke’s Bay, NZ  
(3) Plant & Food Research, East Street, Ruakura Research Centre, Hamilton, NZ

*Neonectria ditissima* (syn. *Neonectria galligena, Nectria galligena*) is the causal organism of European canker. The fungus infects leaf scars in autumn causing cankers on branches and potentially tree trunks of apple. The potential use of elicitors to reduce susceptibility of leaf scars to European canker infections was studied. Two elicitors, acibenzolar-S-methyl, a synthetic analogue of salicylic acid (Actigard® 50WG) and 2-hydroxy benzoic acid or salicylic acid (Treet™), were applied post harvest (11, 18, 25 May 2012) to ‘Braeburn’ trees at the Plant & Food Research orchard in Riwaka. At approximately 48% natural leaf fall, on 1 June 2012, 0-, 1-, 2- and 3-day-old leaf scars were artificially inoculated with a *N. ditissima* conidial suspension ($1 \times 10^{5}$ conida/mL). Control treatments consisted of a captan application prior to artificial pathogen inoculation and a nil control (unsprayed). Leaf scar infections decreased with increasing leaf scar age for all treatments. Irrespective of leaf scar age, captan-protected leaf scars had the least amount of disease, followed by acibenzolar-S-methyl, salicylic acid and nil control treatments. Compared with the nil control, all treatments had significantly lower European canker lesion counts. In conclusion, captan, applied prior to an infection event, provided good control of leaf scar infections by *N. ditissima* and trees sprayed three times postharvest with salicylic acid or with acibenzolar-S-methyl had less disease than untreated ‘Braeburn’ trees. These results should be validated and application method, timing of applications and elicitor concentrations should be determined. Salicylic acid-mediated defences play a critical role in plant disease resistance and this approach may hold great promise to assist with the control of European canker in apples.
Identification of Diaporthe (anamorph Phomopsis) pathogen caused sunflower stem canker diseases and diseases epidemiology in Slovakia (Central Europe)

Dr Peter Bokor
Slovak University of Agriculture in Nitra
peter.bokor@uniag.sk

Peter Bokor(1), Juraj Medo(2), Kamil Hudec(1), Monika Tóthová(1)

(1)Department of Plant Protection, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic
(2) Department of Microbiology, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic

The aim of the research was to evaluate the occurrence and epidemiology of stem canker diseases on sunflower (Helianthus annuus) in Slovakia and to identification of Diaporthe (anamorph Phomopsis) species caused stem canker of sunflower in Slovakia using DNA sequences analysis. Stem canker diseases epidemiology was studied in sunflower fields at more localities during five years. There were evaluated the plants after flowering during July and August at each locality. During five years the number of plants infected by D. helianthi varied depending on weather factors. The occurrence of pathogen Diaporthe helianthi was higher in the Southeast Slovakia compare with Southwest Slovakia, especially in 2008 and 2010. In these years level of infection exceeded 70% was recorded at three localities. The higher sum of precipitation was recorded during the early stages of sunflower growth period and during flowering in these years. It was found that the number of infected plants by pathogens D. helianthi significantly depended on locality and year. The identification of 12 Diaporthe, anamorph Phomopsis isolates associated with stem canker of sunflower obtained from various localities in Slovakia was studied using morphology and ITS rDNA sequences analysis. Phylogenetic analysis determined isolates as Diaporthe helianthi species. This is the first confirmation on the base of DNA that stem canker on sunflower is caused by pathogen Diaporthe helianthi in Central Europe.

Tunisia: the impact of farming systems and culture on Fusarium diseases of cereals

Prof Lester Burgess
University of Sydney
burgess.international@gmail.com

Samia Gargouri(1), Mohamad Gharbi(2), Eya Khemir(1), Samira Chekili(3), Moez Fakhfakh(1), Samira Berries(2), Lester Burgess(1)

(1) National Institute of Agricultural Research, Ariana, Tunisia
(2) National Institute of Field Crops, BouSalem, Tunisia
(3) Faculty of Agriculture, The University of Sydney, Sydney 2006 Australia

A knowledge of local farming systems and culture is critical to an understanding of the epidemiology of diseases caused by soil-borne fungal pathogens and the development of management practices. Fusarium diseases are no exception. Studies by the senior authors have shown that Fusarium foot and root rot (FFRR) caused by F. culmorum is the dominant Fusarium disease of wheat and barley in Tunisia where durum wheat is the major cereal. Crown rot caused by F. pseudograminearum is a minor problem. This contrasts to Australia where crown rot is the dominant Fusarium disease of wheat and barley in most areas. Tunisia has a typical Mediterranean climate — AAR varies from 700 mm in the north to 300 mm on the southern margin of the main grain belt. The rainfall is reasonably reliable in the north and less reliable in the central and southern areas where late stress is common leading to whitehead formation in plants affected by FFRR. The practice of small-holder sheep herders having the traditional right to heavily graze stubbles is a key factor contributing to the dominance of FFRR. This unique feature of the farming system is deeply embedded in the culture of the region where wheat has been grown for over 2000 years. Furthermore the demand for baled straw for drought feeding in the arid grazing areas of the south-central region is such that there is little scope for adopting stubble retention practices without significant social upheaval in rural areas. Tunisia is a small country with the central and southern areas where late stress is common leading to whitehead formation in plants affected by FFRR. The paucity of cereal rangelands on the fringe of the Sahara. The paucity of cereal residues means there is minimal carryover of the crown rot pathogen as it persists mainly as hyphae in residues. However F. culmorum can also persist in soil as chlamydospores that presumably form abundantly in infected root systems. Consequently this pathogen has an effective mode of persistence in the absence of residues. While the adoption of direct seeding per se is unlikely to affect inoculum levels, the retention of stubble residues would significantly increase inoculum levels and yield loss. The authors are investigating the impact of various rotations on inoculum levels through temporal studies at permanent reference sites in commercial fields and field trials.
EPIDEMIOLOGY

POSTER BOARD 90

Endogenous *Banana streak virus* species in the Philippines

Dr Fe Dela Cueva
Institute of Plant Breeding
fmducueva@yahoo.com

Fe Dela Cueva(1), Eric Dinglasan(1), Mark Angelo Balendres(2)

A study was conducted to detect, identify and determine the frequency of endogenous *Banana streak virus* (BSV) species in *Musa* germplasm in the Philippines using DNA-based technique, Polymerase Chain Reaction (PCR). Their distribution and occurrence were also investigated in both *in situ* (field genebank) and *in vitro* (tissue-cultured plantlets) germplasm collections. PCR analysis revealed the presence of three known endogenous BSV species (*Mysore*, *Goldfinger* and *Imove*) in some accessions and cultivars. These endogenous BSV species were closely associated with accessions/cultivars containing at least one B allele in the genome. This study showed the presence of endogenous BSV species that can potentially turn into an activated, pathogenic state that causes the devastating Banana Streak disease. Moreover, the study also provided information for breeders and researchers the options on what accessions/cultivars can be used for future disease-resistant banana breeding programs.

POSTER BOARD 89

Capture of *Pseudomonas syringae* pv. *actinidiae* in rainsplash in a New Zealand kiwifruit orchard

Ms Carol Curtis
Plant and Food Research Limited
carol.curtis@plantandfood.co.nz

Carol Curtis(1), Joy Tyson(1), Shirley Dobson(2), Mike Manning(3),
(1)Plant and Food Research Limited, Mt Albert, Auckland, New Zealand
(2)Plant and Food Research Limited, Te Puke, New Zealand

Many *Pseudomonas* species are frequently said to be splash and wind dispersed, and general field observations suggest that splash dispersal is important. Although there is little information on how far *Pseudomonas* species can move in splash droplets, it appears that splash is most important in short-distance dispersal and potentially as a ‘take-off’ mechanism for dispersal by aerosols. When kiwifruit bacterial canker, caused by *Pseudomonas syringae* pv. *actinidiae* (Psa), was first discovered in New Zealand in 2010 there was little knowledge of how it would move within and between vines, orchards and regions within New Zealand. It was considered that splash dispersal (rain-splash or wind-blown rain) might be a primary means of movement of this pathogen. The aim of this study was to attempt to capture viable Psa from the air so that “inoculum activity” could be monitored over time. Passive weathervane-type traps that present an exposed semi-selective agar plate to the wind in the orchard to capture airborne Psa were used over 24 hour periods. From 5 March to 14 June 2012, traps were placed under kiwifruit in a heavily infected old *Actinidia chinensis* ‘Hort16A’ block on the Te Puke Research Orchard (TPRO). From 18 June to 30 August 2012 traps were placed in an adjacent block of newly grafted cultivars that had little to no canopy. Plates from each 24 hour sampling period were incubated at 20°C for three days. Psa-like colonies were subsequently counted and DNA extractions made on the mixed-colony plates, followed by a quantitative polymerase chain reaction (qPCR)-based detection method. Results showed that Psa was captured by the weathervane-type traps under the heavily infected ‘Hort16A’ canopy during rain periods. Psa was only captured during a “dry” period during pruning, at which time a large amount of debris was present on the agar plates. Within the block of newly grafted cultivars, Psa was only detected twice, both of which coincided with rain periods. This suggested that the inoculum may have originated from outside the block due to the lack of canopy at the trap site. It is apparent that rainfall is crucial to the capture of Psa in kiwifruit orchards.
Soilborne diseases identified as potential yield constraints in New Zealand potato crops

Prof Richard Falloon
New Zealand Institute for Plant & Food Research Ltd
richard.falloon@plantandfood.co.nz

Richard Falloon(1), Sarah Sinton(1), Farhat Shah(1), Hamish Brown(1),
(1) The New Zealand Institute for Plant & Food Research Limited, PB 4704, Christchurch 8140, New Zealand
(2) Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand

A survey of processing potato crops was carried out in Canterbury during the 2012/13 growing season. The study was instigated by Potatoes NZ Inc., McCain Growers Unincorporated Society, and Ravensdown Ltd, because crop yields have been less than optimum, in spite of high input crop management. Eleven commercial crops were selected. Soil samples from the fields were assayed for DNA of important soilborne pathogens. The crops were planted with the cultivars ‘Russet Burbank’ or ‘Innovator’, and were in fields classified as “new” (no potatoes in the previous ten growing seasons) or “old” (more recent potato crops). The crops were monitored every 10-14 days during the growing season (ten visits per crop). Plant samples were assessed for incidence of diseases, and other potential yield-limiting factors. Individual plants affected by particular factors were identified, and tuber yields were assessed at crop maturity and converted to yield/ha using plant population data. Commercial yields were also measured for each crop. Soil assays identified pathogen DNA in ten of the fields, and large amounts of DNA of potentially important pathogens (Rhizoctonia solani AG2-1, Spongospora subteranea, Colletotrichum coccodes) were detected in some of the fields. During crop growth, Rhizoctonia stem canker was observed in all of the crops, with some crops more severely affected than others. Spongospora root galls were found in six of the crops, and in five of these, soil compaction was also identified as likely to be yield-limiting. FolIage diseases were well controlled with frequent fungicide applications until late in the season. Commercial yields from the crops varied from 49 to 66 t/ha. These were always 20 to 42 t/ha less than “potential” yields, calculated using a model which predicts yield from local radiation and temperature data. Individual plant yields from “healthy” plants were equivalent to 91 t/ha, while yields from “diseased” plants in compacted soil were equivalent to 26 t/ha. Other yield-limiting factors in specific crops included uneven emergence related to poor seed tuber quality (one crop), inefficient irrigation (two crops), and weed infestation (two crops). This survey has identified soilborne diseases (particularly those caused by Rhizoctonia solani and Spongospora subteranea) as factors likely to be adversely affecting yields from crops of intensively managed processing potatoes.
Analysis of weather variables to develop a disease forecast model for *Marssonina* blotch of apple in Korea

Ms Jeonghee Jo
Seoul National University
jeongheejo@senu.ac.kr

Jeonghee Jo(1), Yunsu Do(2), Ki Seok Do(1), Wee Soo Kang(1), Eun Woo Park(1)
(1) Department of Agricultural Biotechnology, Seoul National University, Seoul, Korea
(2) Apple Research Station, National Institute of Horticultural and Herbal Science, Gunwi, Korea

Marssonina blotch of apple which is caused by *Marssonina coronaria* is a recently emerging disease on apple in Korea. Disease forecast models for Marssonina blotch of apple were evaluated for their accuracy in predicting disease development using weather and disease data obtained from apple orchards at 13 locations in Korea. Six models obtained from the literature were empirical models including three infection period models based on hourly and daily temperature and relative humidity; one disease incidence model based on 10-day moving averages of daily temperature and relative humidity; one disease initiation model predicting the date of first disease occurrence based on daily temperature and rainfall; and one air-borne spore model based on daily temperature and rainfall. The daily weather data (mean, maximum and minimum temperatures, relative humidity, rainfall, and wetness duration) for each locations were estimated based on observed data from automated weather stations installed at 86 locations using the inverse distance weight method with calibration for elevation. The classification and regression tree (CART) model was applied to estimate daily wetness duration. Marssonina blotch data were obtained from 9 field plots at the Apple Research Station (ARS) of the National Institute of Horticultural and Herbal Science, and 5 commercial apple orchards during 2006-2012. Incidence of diseased leaves was assessed one to seven times during the growing seasons depending on orchards and years. Also, the number of air-borne spores collected at field plots of ARS using rotor-type spore samplers was included in the analyses. The spore samplers were operated twice a day at 04:00-06:00 and 16:00-18:00 during the growing seasons. The disease development for individual orchards and years varied greatly in terms of the initiation date, disease intensity and shapes of disease progress curves as well. In this study it is expected to determine critical weather variables significantly affecting development of the disease and consequently develop a disease forecast model that can be applied to control Marssonina blotch in the integrated pest management system for apple orchards in Korea.

Risk Analyses of Leaf Blast and Sheath Blight of Rice in Korea According to the Climate Change Scenarios Projected by the Representative Concentration Pathways

Dr Wee Soo Kang
EPINET Co., Ltd.
kangws@epinet.kr

Wee Soo Kang(1), Sung Chul Yun(2), Mul Il Ahn(1), Eun Woo Park(2)
(1) R&D Center, EPINET Co., Ltd., Anyang 431-062, Korea
(2) Department of Applied Biological Sciences, Sun Moon University, Asan 336-708, Korea

Leaf blast (caused by *Magnaporthe oryzae*) and sheath blight (caused by *Rhizoctonia solani*) are important diseases of rice in Korea. The BLAST model estimates daily infection risks of leaf blast based on air temperature, relative humidity, and rainfall. The SHBLIGHT model estimates daily increments of lesion height of sheath blight based on air temperature and relative humidity. Both models have been dominantly used to forecast the diseases in Korea since 1993. Using the models, change patterns of the estimated daily risks of the diseases were projected for the period from 2011 to 2100 at the 32 major rice growing areas according to the climate change scenario. The climate change scenarios of Korea projected by the Representative Concentration Pathways (RCPs) were released by the Korea Meteorological Administration in 2012. The RCP 8.5, which introduces the highest CO2 emission scenario in the four RCPs, was used in the analyses. For rice blast, number of days with the highest grade of blast risk (DHBR) was calculated for each year. Slopes and amount of decrease in DHBR during the 90 years were determined for each region using linear regression analyses. The rice growing areas were classified into 8 categories by considering pattern of the estimated DHBRs, slopes, and the amount of decrease in DHBR. The estimated DHBRs were decreased 10-40 days during the period. It implies that the occurrence of leaf blast is expected to become less severe in the future. For sheath blight, total increment of lesion height (LH) for each year was calculated. Slopes of the changes in LH were determined over the 90 years until 2100. The rice growing areas were classified into 7 categories by the slopes. LHs for all areas were increased during the 90 years. It implies that the occurrence of sheath blight will be more severe until 2100. It was found that the areas with high risk of leaf blast will have low risk of sheath blight and vice versa. Increasing air temperature and frequent rain appear to be the major factors affecting the change in possible occurrence of the diseases.
Survival of *Phoma koolunga* on field pea stubble on or below the soil surface

Mr Mohsen Khani  
University of Adelaide  
mohsen.khani@adelaide.edu.au

Mohsen Khani(1)(2), Jenny A Davidson(2), Mark R Sosnowski(2), Eileen S Scott(2)

(1)School of Agriculture, Food and Wine, the University of Adelaide, Australia  
(2)South Australian Research and Development Institute, Adelaide, Australia  
(3)College of Agriculture and Natural Resources, Shiraz University, Darab, Iran

*Phoma koolunga* is a causal agent of blackspot (Ascochyta blight) of field pea (*Pisum sativum*). Unlike the other three blackspot pathogens (*Mycosphaerella pinodes*, *Phoma medicaginis* var. *pinodella* and *Ascochyta pisi*), survival of *P. koolunga* is poorly understood. We examined survival of this fungus on field pea stubble on the surface of, and buried in, field soil. Stubble was harvested from severely diseased, artificially inoculated plants. Stem pieces (10 cm) were placed in 104 plastic mesh bags (15 cm², mesh pore size 1 mm²). 15 pieces per bag. Each bag was placed on, or buried 5-10 cm below, the soil surface in 20 litre pots outdoors at Urrbrae, SA, in February 2012. Four bags from each treatment were retrieved monthly for 12 months and a final set was removed in month 15. Stems were rinsed and then dried for 48 h at room temperature. Four 0.5 cm sections, one from each end and two from the middle of each of five randomly selected pieces of stubble were plated onto semi-selective agar medium developed for this fungus and incubated at 22° C under fluorescent and near ultraviolet light (12 h/12 h dark/light). The isolation frequency of *P. koolunga* was recorded as the percentage of small stem sections that yielded *P. koolunga*. The pathogenicity of retrieved stubble over time was tested in a bioassay. Plants of cv. Kaspa with four fully-expanded leaflets were sprinkled with 0.25 g milled stubble, kept in a humidity chamber for 48 h, and blackspot lesions were counted over 10 days. In the first month, *P. koolunga* was recovered from 93% of stubble sections retrieved from the soil surface and 36% of buried stubble samples. Frequency decreased over time, such that recovery from the soil surface was 5% at 12 months and 0% at 15 months, whereas *P. koolunga* was not recovered from stubble buried in soil after 11 months. Most blackspot lesions developed on plants inoculated with stubble retrieved from the soil surface after one month. Pathogenicity of the fungus decreased over time; stubble that had been buried or left on the soil surface for 7 and 11 months, respectively, did not cause blackspot. Pea stubble may play a role in survival of *P. koolunga*, especially if it remains on the soil surface.

**Rhizoctonia solani** (AG8): Surviving the summer after various winter crops

Mr Bill MacLeod  
Department of Agriculture and Food, Western Australia  
william.macleod@agric.wa.gov.au

Daniel Hüberli, Miriam Connor, Shahajahan Miyan, and, Bill MacLeod  
Department of Agriculture and Food, Western Australia, 3 Baron-Hay Court, South Perth, WA, 6151, Australia

The effect of crop rotation and management practices on *Rhizoctonia solani* root disease and inoculum survival over two summers was examined in a 2-year paddock trial. In the first year (2011), there were treatments of barley, wheat, canola and chemical fallow, and in the second year (2012), barley plots of untreated, seed dressing (Dividend), in-furrow application of an unregistered fungicide or tilling to a depth of 10 cm below the seeding depth. Inoculum survival in five paddocks (two canola, two wheat and one barley) was monitored over summer (February–June) 2013. In the 2-year trial, inoculum levels increased for cereals in the 2011 growing season, while for canola and fallow, they declined. *Rhizoctonia* root disease on barley roots in 2012 were highest following barley. Inoculum levels in cereals were significantly higher over summer 2012 compared with those for the canola and fallow plots. Inoculum in the latter two plots had declined to below detection levels at sowing in June 2012, while barley plots were still significantly higher compared to the other plots. For the five paddocks, inoculum levels over summer is postulated to be affected by the previous crop and significant summer rainfall events. A break crop of canola or a chemical fallow in paddocks with severe *Rhizoctonia* bare-patch, may reduce inoculum levels and reduce disease in the following cereal crop. Barney exacerbates disease substantially compared to the other crops, so in paddocks with high levels of *R. solani* inoculum it is recommended that another crop is sown.
Quantification of Phytophthora Dieback in the Greater Blue Mountains World Heritage Area

Ms Zoe-Joy Newby
Royal Botanic Gardens and Domain Trust
zoejoy.newby@rbgsyd.nsw.gov.au

As a Key Threatening Process, land managers need to take a proactive stance against disease caused by Phytophthora cinnamomi in natural ecosystems in Australia (herein referred to as Phytophthora Dieback). Effective disease management requires an understanding of the pathogen’s distribution, host susceptibility, and the environment in which disease is most likely to occur. The disease triangle of Phytophthora Dieback was modelled in the Greater Blue Mountains World Heritage Area (GBMWHA) within the context of a geographical information system. The distribution of P. cinnamomi was modelled using the maximum entropy algorithm (Maxent) and the results of a field survey conducted across the GBMWHA between 2010-2012. Of the twelve climatic, topographic and anthropogenic variables included in the initial model, three were selected following a jack-knife procedure: topsoil clay percentage, annual rainfall and the minimum temperature of the coldest quarter. The final AUC of the training data was determined by Maxent was 0.93 and identified the higher altitude areas were most suitable for P. cinnamomi establishment. The model was also re-run with variable temperature (incrementally increased by 5°C) and rainfall inputs (incrementally increased and decreased by 10%) to assess the changing distribution of P. cinnamomi in a changing environment. The area inhabited by P. cinnamomi was positively correlated with rainfall but negatively correlated with temperature. In addition, the distribution of 124 hosts known to be susceptible to P. cinnamomi and occurring in the GBMWHA was modelled using Maxent, using species records compiled in the Atlas of Living Australia Database. The combined species models with an average AUC of 0.88, identified that hosts were most abundantly distributed in a north-south band along the western perimeter and the most eastern region of the GBMWHA. Individual species models were then multiplied by a susceptibility score then all were combine together generating a map of the distribution of host susceptibility and abundance across the GBMWHA. Finally the pathogen distribution was combined with the host distribution to map the areas most at risk of Phytophthora Dieback. The region most at risk was the central west of the GBMWHA. This region coincides with much of the tourism activity of the GBMWHA which has significant implication for disease management.
**POSTER BOARD 99**

**The effect of bagging on the incidence of dendritic spot and stem end rot in Kensington Pride and R2E2 varieties of mango**

Ms Arslan Qureshi  
The University of Queensland  
arlsan.qureshi@uqconnect.edu.au

Arslan Qureshi(1), Victor Galea(1), Chrys Akem(2), Elizabeth Aitken(1), Ian Bally(3)

(1) School of Agriculture & Food Sciences, The University of Queensland, Qld, Australia  
(2) International Institute of Tropical Agriculture, Ibadan, Nigeria  
(3) Queensland Department of Agriculture, Fisheries & Forestry, Mareeba, Qld, Australia

Postharvest diseases are a major concern to the Australian mango industry as well as for other mango growing countries. Stem end rot (Neofusicoccum parvum, Lasiodiplodia theobromae) and dendritic spot (Neofusicoccum parvum, Colletotrichum gloeosporioides) emerge as a serious postharvest threat to mango fruit when anthracnose is well managed by adopting suitable control measures. Preharvest foliar sprays are not sufficient to control postharvest losses without opting effective postharvest fruit treatments. A study was designed to determine the effect of bagging at different fruit growth stages on the incidence of stem end rot and dendritic spot. Mango of varieties Kensington Pride (KP) and R2E2 were used in this study. The experiment was carried out during the 2010, 2011 and 2012 seasons in Ayr, north Queensland. The first bagging was carried out when the fruit was around golf ball size. A total of four baggings were done each year with two weeks interval between each bagging. After harvest, the fruit was stored at 21°C to ripen and assessed for the incidence of stem end rot and dendritic spot. The results showed that, early bagging resulted in lower incidence of stem end rot and dendritic spot as compared to fruit which was bagged at later stages. During the 2010 mango season, fruit bagged 60 days before harvest showed 54% incidence of dendritic spot and 8.4% incidence of stem end rot while fruit bagged 11 days before harvest and the unbagged control fruit developed 100% incidence of dendritic spot and 35 to 48% incidence of stem end rot. Similar results were observed when the experiment was repeated during the 2011 - 2012 mango season where early bagging reduced the incidence of dendritic spot (0%) and stem end rot (19%) as compared to the fourth bagging (10 days before harvest) and control fruit, which had (30% incidence of dendritic spot and 46% incidence of stem end rot) followed by similar results during 2012 - 2013 mango season. The study determined that, the use of recommended cultural practices during early fruit growth stages other than fungicidal sprays can reduce the postharvest disease incidence under storage. Keywords: Mango, Stem end rot, dendritic spot, fruit bagging

**POSTER BOARD 100**

**One well received, the other not - a tale of two epidemiological models for crop disease management**

Dr Moin Salam  
Department of Agriculture and Food Western Australia (DAFWA)  
moin.salam@agric.wa.gov.au

Moin U. Salam, Kawsar P. Salam, and, Arthur J. Diggle  
Department of Agriculture and Food Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia

Embracing advances of science and technology, plant pathology has adopted the ‘discipline of modelling’. Models that forecast risks are termed attractively as ‘disease predictor’, ‘disease forecaster’, decision support system’, and ‘expert system’. They are intended to play decision aiding role in crop disease management. However, as reviewed in the recent issue of Annual Review of Phytopathology 2013, ‘with few exceptions, these systems typically do not have direct sustained use by growers’. To understand why, we analyse two models: ‘Blackleg Sporacle’ (Salam et al. 2003, Phytopathology 93: 1073-1081) that forecasts the risk of ascospore shower the emerging canola seedlings may expect in relation to blackleg disease, and ‘G2 Blackspot Manager’ (Salam et al. 2011 Australasian Plant Pathology 40: 632-639) that provides field pea ascochyta sowing guide by overlaying ascochyta blight risk over the risk related to abiotic factors. The two models were developed by the same developer, used similar scientific rigour, adopted similar objectives and intended to be used by the same group of growers. However, one had been extremely successful from growers’ reception and adoption points of view, while the other was not. This paper investigates the reasons and recommends the keys to success growers’ adoption for a system in crop disease management.
EPIDEMIOLOGY

POSTER BOARD 101

Koch’s postulates of *Elsinoe pyri* on apple

Dr Reiny Scheper
The New Zealand Institute for Plant & Food Research Limited
reiny.scheper@plantandfood.co.nz

Reiny Scheper, Peter Wood, Brent Fisher,
The New Zealand Institute for Plant & Food Research Limited, Private Bag 1401, Havelock North, New Zealand

Elsinoe leaf and fruit spot is a minor disease of apple and pear. The disease is economically important in some organic orchards in New Zealand. Very little is known of the biology and life cycle of the causal agent *Elsinoe pyri* (Woron.) Jenkins, syn. *E. piri*, (asexual stage *Sphaceloma pyrinum* (Peglion) Jenkins). Spots on leaves and fruit are whitish-grey to pale yellow brown with a brown or dark red margin, 1–4 mm in diameter, and may occasionally coalesce. In the centre of the spots, dark brown fruiting structures (acervuli) may be visible. The fungus was isolated from spots on apple fruit. Cultures were slow-growing, convoluted, pulvinate, rust brown to dark red or purple in colour, with a diameter of approximately 10 mm after 1 month’s growth on potato dextrose agar at 20°C. The conditions needed for spore production were examined using different culture media, plating techniques and culture ages. When small (1–2 mm²) pieces of a 2- to 6-week-old culture from PDA were sub-cultured onto corn meal agar (approximately 30 pieces per plate) for 2 days, large numbers of viable conidia were produced. Conidial germination occurred between 10°C and 26°C, with the highest germination percentage at 20°C and 26°C, and greatest germination tube elongation at 20°C. To fulfil Koch’s postulates, potted ‘Royal Gala’ trees in a glasshouse were inoculated with conidia of *E. pyri* grown on a culture that had been isolated from a typical elsinoe spot on apple fruit. At least 200 conidia per leaf were required to infect the leaves. Typical elsinoe spots were visible 6 weeks after inoculation. Four months after inoculation, acervuli were visible in many of the elsinoe spots. Conidia from the acervuli resembled typical *E. pyri* conidia (5–6 × 2.5 µm) and grew into typical brick-red cultures of *E. pyri* on PDA.

EPIDEMIOLOGY

POSTER BOARD 102

Cryptodiaporthe salicella – a destructive disease of some Swedish biomass willow varieties grown in Slovakia (Central Europe)

Dr Monika Tóthová
Slovak University of Agriculture in Nitra
monika.tothova@uniag.sk

Monika Tóthová(1), Katarína Adamčíková(2), Kamil Hudec(1), Peter Bokor(1),
(1)Department of Plant Protection, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovakia
(2)Institute of Forest Ecology, Slovak Academy of Sciences, Branch for Woody Plants Biology - Nitra, Akademická 2, 949 01 Nitra, Slovakia

The present study was conducted to assess a susceptibility of different Swedish biomass willow varieties to the stem cancer – *Cryptodiaporthe salicella* (Fr.) Petr. 1921 (Ascomycetes, Sphaeriales, Valscaceae) under natural conditions. Short rotation coppice willow (*Salix* spp.) experimental plantation at the Slovak University of Agriculture in Nitra is situated in Kolíňany (48° 22′ 0″ N, 18° 12′ 0″ E). This region belongs to temperate-warm and temperate-humid climatic region with the mean temperature 9.9°C per year and mean annual precipitations of 550 mm. Plantation lies at an altitude of 180 meters. Disease was studied on 5 Swedish biomass willow varieties (Tora, Gudrun, Tordis, Inger and Sven) and two Hungarian varieties (Express, Csala) in two consecutive years (2009 and 2010). Stem cancer was observed for the first time in spring 2009 – two years after plantation establishment, and a year after the cutback of one year old plantation. The focal spot was localized at the centre of variety Inger, seriatelly the 3rd of five planted Swedish variety. Simultaneously, this variety was the most severely attacked. The share of infected trees increased from 37 to 86 % after a year, however the share of heavily damaged trees accounted to only 9 % and up to 6.5 % of fully grown plants died out. The killed stems and whole trees were about 4 m in height. Infection gradually invaded also to the other varieties. The most resistant to the stem cancer seems to be a variety Gudrun and adjacent Sven, with up to 5 and 23 % of infected plants, respectivelly. Both Hungarian willow varieties were symptomless. The first symptoms of stem cancer in 2008 were overlooked due to severe occupation of stems by the stem feeding aphids – *Tuberolachnus salignus*. According to our observations, infections caused by *C. salicella* was localized just around the focal point of *T. salignus* outbreak.
**Pseudomonas fuscovaginae affects the germination and early growth of rice and other cereals grown in Australia**

Ms Nirodha Weeraratne  
Charles Sturt University  
nweeraratne@csu.edu.au

Nirodha Weeraratne(1), Chris Steel(2), Gavin Ash(1), Ben Stodart(1), Sandra Savocchia(2).

(1)Graham Centre for Agricultural Innovation School of Agricultural and Wine Sciences, Charles Sturt University, Locked Bag 588, Wagga Wagga 2678, NSW, Australia  
(2)National Wine and Grape Industry Centre, School of Agricultural and Wine Sciences, Charles Sturt University, Locked Bag 588, Wagga Wagga 2678, NSW, Australia

_Pseudomonas fuscovaginae_, the cause of sheath brown rot of rice, was first reported from Japan in 1976 and subsequently recorded in the rice growing region of Australia in 2005. The pathogen causes lesions on the flag leaf sheath, grain discolouration, poor spike emergence and panicle sterility of rice and can damage the plant at all stages of growth. _Pseudomonas fuscovaginae_ is globally distributed and it has been reported to cause significant yield loss. The bacterium has also been reported as a pathogen on cereal crops such as wheat, maize, and sorghum, as well as the broadleaf Quinoa, however, the host range of strains isolated from Australia is not known. This study was conducted to assess the effect of strains of _P. fuscovaginae_ isolated from Australian rice on the germination and early growth of several cereal crops which are economically important to Australia. The early detection of disease resistance by seed soaking with a 10^7 cfu/mL inoculum concentration and measuring the reduction in seedling height after 10 days has been used to evaluate resistance in rice genotypes. Strains of _P. fuscovaginae_ from Japan, Madagascar and Australia were used to inoculate seeds of rice, wheat, durum, barley, triticale, canola and millet. Seeds were surface sterilised, before soaking in 10^7 cfu/mL of _P. fuscovaginae_. Controls consisted of seeds soaked in sterile distilled water. Petri dishes containing 20 seeds each on moistened filter paper were maintained at 25°C for 10 days, in a completely randomised trial consisting of four replicates. From each replicate, the percentage of germinated seeds were calculated, while the length of shoot, and both number and length of roots were assessed from 10 seedlings. Inoculation of seeds with _P. fuscovaginae_ was found to significantly reduce the germination rate, root number, root length and shoot length of ten bread wheat varieties. A similar result was observed for the two durum, two triticale and two barley varieties. For rice, a significant reduction in shoot length, root number and root length was observed for one variety and two breeding lines tested. One rice breeding line showed significant tolerance (to a strain of the pathogen from Japan), in terms of unaffected germination, shoot length, number of roots and root length.

**NEW & EMERGING DISEASES**

**Ambrosia and bark beetle-associated tree death in macadamia**

Dr Femi Akinsanmi  
QAAFI, The University of Queensland  
uqoakins@uq.edu.au

Olufemi A. Akinsanmi(1), Craig Maddox(2), André Drenth(3)

(1)University of Queensland, Centre for Plant Science, Queensland Alliance for Agriculture and Food Innovation, Ecosciences Precinct, GPO Box 267, Brisbane, QLD 4001, Australia.  
(2)NSW Department of Primary Industries, 1243 Bruxner Highway, Wollongbar NSW 2477, Australia.

The emergence and prevalence of tree death associated with ambrosia and bark beetles is increasing in macadamia worldwide. The recent increase in the occurrence of the beetle-associated disease on different macadamia cultivars in the main production areas in Australia and Guatemala is becoming a significant concern to the macadamia industry. The underlying factors that result in the development of the beetle–associated problems in macadamia are still obscure, their attack and severity appear to be favoured by tree stress. The beetles occupy a niche within the forest or orchard system that generally seeks out the sick and dying trees. The problem magnifies when the attack of a scolytid beetle is combined with a serious tree pathogen. It is unclear how these host-vector-pathogen systems developed. The choice of tree by the beetle is a fascinating aspect. Could it be that anything that reduces the sap flow makes it easier for the beetles to penetrate the tree defences and establish galleries? Field observations have linked the occurrence of tree death to water stress, oversize of ethephon or root stresses due to _Phytophthora cinnamomi_ attack or flooding in Australian macadamia orchards. Once the ambrosia beetles have established themselves in these stressed trees they emerge on mass to find new hosts, and there is some evidence to suggest they will randomly attack all neighbouring trees and can establish into previously healthy trees. Single and multiple holes on branches and main trunks have been observed in affected macadamia trees. In some cases, both ambrosia and bark beetle have been detected on the same macadamia tree. These beetles belong to the _Scolytinae_ subfamily: _Cryphalus_ and _Xyleborinus_ including _Hypothenemus_ spp., _Cryptalus_ sp., _Xyleborus_ spp. _Cnestes_ sp. and _Euwallacea_ sp. and platypodinae subfamily: _Megaplatypus_ spp. Different fungi have been isolated from beetle-infested trees, mostly the _Botryosphaeriaceae_ in Australia. Pathogenicity tests on grafted macadamia trees in the glasshouse showed that these fungi are able to cause tree death within three months above the point of inoculation. The main goal of our research is to gain a better understanding of the identity of the beetles, their associated pathogens and their interaction with macadamia causing tree death.
NEW & EMERGING DISEASES
POSTER BOARD 106

First Report of Brenneria goodwinii from Iran

Mr Meysam Bakhshi Ganjeh
Tarbiat Modares University (TMU)
meysambakhshi24@yahoo.com
Meysam Bakhshi Ganjeh(1), Heshmat Rahimian(2), Masoud Shams-Bakhsh(3)
(1)Department of Plant Pathology, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran
(2)Department of Plant Pathology, Sari Agricultural Sciences and Natural Resources University, Sari, Iran
(3)Department of Plant Pathology, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran

Forest tree decline is a complex disease not attributable to a single causal factor. Current sampling has an instances to accessions a new epidemic in oak trees forest at northern Iran. Therefore strains that isolated from trees showing canker's symptoms, were examined by biochemical, morphological, molecular and protein electrophoresis to identification and affirm pathogenicity. Strains were facultative anaerobic, negative for oxidase, nitrate reduction, indole, urease, arginine dehydrolase, licitinase, protease, and positive for catalase. Their ability to use nitrogen and carbon resources such as; fructose, mannose, galactose, trehalose, L-arabinose, sodium-D-gluconate, sucrose, sorbitol, glycerol, galactose, esculin, H2S were positive, while their ability to use meso-erythritol, D-arabinose, L-rhamnose, L-tartarate are negative and for raffinose, melibiose, D-xylene, α-D-methyl glycoside this ability showed variability. Protein electrophoresis demonstrated that there were a few differences between selected strains and this data enabled to ranking mentioned strains. Results from amplification and sequencing of 16S rRNA showed that selected strain with 99% identity are Brenneria goodwinii.

Therefore, these findings showed that B. goodwinii with pale cream, round, convex, smooth entire margin colonies on NAS medium is probably one of causal agents of oak canker in oak trees forest at northern Iran. This is the first report of B. goodwinii from Iran.

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NEW & EMERGING DISEASES
POSTER BOARD 105

Fungi associated with diseases of Pinus in Victoria, Australia

Dr Ramez Aldaoud
Department of Environment and Primary Industries

Jacky Edwards(1), Robert Holmes(1), Ramez Aldaoud(1), SriKanthi de Alwis(1), Quang Dinh(1), Soheir Salib(1), Con Skyllas(1), David Smith(2), Stephen Elms(3)
(1)Biosciences Research Division, Department of Environment and Primary Industries Victoria(DEPI), AgriBio, Centre for AgriBioscience, 5 King Road, La Trobe University, Bundoora VIC 3083, Australia.
(2)Plant Biosecurity and Product Integrity, DEPI, 650 Burwood Hwy, Knoxfield VIC 3180, Australia.
(3)HVP Plantations, 50 Northways Rd, Churchill VIC 3842, Australia

The Crop Health Services (CHS) at the Department of Environment and Primary Industries (DEPI), Victoria, Australia provides fee-based diagnostic services of pests and diseases affecting plants mainly in the State of Victoria. In the past six months, there have been more than 20 samples of Pinus species from around the State submitted to CHS for diagnosis. In most cases, these were Pinus radiata and the symptom was blue-staining of the wood. CHS consistently identified Ophiostoma ips, Sphaeropsis sapinea, Sydowia polyspora (syn. Sclerophoma pythiophila) and undetermined Botryosphaeria species from these blue stained wood samples. Identification was based on a combination of fungal morphology and ITS sequence analysis. Sphaeropsis sapinea and/or Botryosphaeria sp. were recovered from 96% of the blue-stained wood logs and branches. The Botryosphaeria species did not undergo ITS sequencing, so may in fact also be S. sapinea. Ophiostoma ips was recovered from 16%. In the cases where O. ips was detected, the bark-infesting beetles Ips grandicollis were also present. Of particular interest, samples were sent in from the Lone Pine (Pinus brutia) growing at the Melbourne Shrine of Remembrance. This tree was grown from a pine cone brought back by a soldier returning from Gallipoli. Sphaeropsis sapinea was recovered from the wood of the Lone Pine and was considered to be the cause of dieback and death of this significant tree. Although S. sapinea is common in Australia and has a very wide host range among conifers, to our knowledge this is the first record of it from Pinus brutia worldwide.
Barcoding Myrtaceae for rapid identification of plant species in preparation for myrtle rust incursion

Ms Anna R Caird
SCION
anna.caird@scionresearch.com
Anna R Caird, Matt H Buys, Heather J Flint, Rebecca J Ganley
SCION, 49 Sala Street, Rotorua, New Zealand

Puccinia psidii is a rust fungus that infects many species of Myrtaceae. The myrtle rust fungus is present in Australia and it is highly likely that this pathogen will cross the Tasman Sea to New Zealand as poplar, asparagus and wheat rust diseases have in the past. DNA barcoding of plant species that are hosts to myrtle rust would enable rapid identification of plant species in the event of an incursion. This would assist with accurate surveillance of the spread of the disease in nature reserves, state forests and urban areas. It will also allow better decision making for the implementation of biosecurity measures to protect threatened plant species and communities and reduce the risk of spread to new areas. A list of 102 Myrtaceae species was compiled based on species that are known to be susceptible to myrtle rust and present in New Zealand, prioritising those with high economic and cultural significance. The internal transcribed spacer (ITS) and maturase K (matK) gene regions were selected for barcoding and sequence data were mined from existing databases or DNA extracted and sequenced from herbarium samples. The sequences obtained have been used to generate a barcode library for the high priority Myrtaceae species.

Rotylenchulus reniformis – an emerging pest in Queensland?

Ms Jennifer Cobon
Department of Agriculture, Fisheries & Forestry, Queensland
jennifer.cobon@daff.qld.gov.au
Jennifer Cobon(1), Wayne O’Neill(1), Tony Pattison(2), Tegan Kukulies(2),
(1) Department of Agriculture, Fisheries and Forestry, Queensland, Ecosciences Precinct, 41 Boggo Road, Dutton Park, QLD 4102
(2) Department of Agriculture, Fisheries and Forestry, Queensland, Centre for Wet Tropics Agriculture, Experimental Station Rd., South Johnstone QLD 4859

In Queensland, Rotylenchulus reniformis has been regarded as a minor nematode pathogen rarely found south of Yeppoon (23.13° S) and causing little economic damage. However, recent surveys have found heavy infestations of this nematode in cotton crops as far south as Theodore (24.95° S) and in sweet potato crops in Bundaberg (24.85° S). After recently identifying R. reniformis on the roots of stunted cotton plants, extensive soil sampling post-harvest has been undertaken in the cotton growing areas of Theodore (QLD). Of the 335 samples counted representing 3,350 ha, 56% have been identified with R. reniformis with numbers as high as 8,000/200 mL of soil. Reniform nematode numbers as high as 18,000/200 mL soil have been extracted from soils in the Bundaberg area used in sweet potato production. Soil naturally infested with R. reniformis from a zucchini production system in north Queensland was inoculated with an increasing number of Reniform nematodes, with up to 1,000 nematodes added to 100 g of soil. After four weeks, the nematodes were extracted from the soil and plant growth measured. Increasing the numbers of nematodes reduced the growth of cucumber seedlings in the non-suppressive soil. High numbers of R. reniformis found in “old” banana production soils, were primarily responsible for a lengthening of the vegetative crop phase and a delay in bunch development in the ratoon crops of bananas. The nematode also affected the uniformity of the banana crop, which adds additional expenses to harvest costs. So far the losses to Queensland agriculture have been determined by ad-hoc surveys and limited project work. However, with the increasing development of agriculture in tropical and subtropical regions, the extent of the problem, seriousness of crop losses and necessary nematode management strategies need to be determined. Pre-plant soil sampling will be undertaken to help determine economic threshold figures for Reniform nematode on cotton in Australian soils. In terms of horticultural losses, further research is required to determine the best ways to crop minimise losses.
Meloidogyne fallax in Western Australia

Dr Sarah Collins
Department of Agriculture and Food, Western Australia
sarah.collins@agr.wa.gov.au

Sarah Collins, Carla Wilkinson, Xiaohui Zhang, Vivien Vanstone
Department of Agriculture and Food, Western Australia, South Perth, Australia

Meloidogyne fallax was first identified in Western Australia (WA) in 2006 in a potato crop which was rendered unmarketable. It causes stunting and yellowing of plants, small galls on roots, pimple like swellings as well as internal discoloration of potato tubers which cannot be peeled or polished. Very little is known about this root knot nematode (RKN) species and the impact it may have on agricultural crops in WA. Vegetables are produced commercially on 456 properties in the south west of WA covering almost 11,000 ha with potatoes and carrots grown on more than 3,000 ha. Most growers in WA rely on soil fumigants for control of all RKN species. Chemicals are expensive, non-specific and some may soon become unavailable in Australia. Biodegradation can be an issue in high use areas. Resistant break crops can be used prior to cash crops to reduce nematode levels. To gain a better understanding of the distribution of M. fallax in WA a survey of 26 paddocks for RKN and root lesion nematodes was conducted, targeting potato and carrot growers. Only the results for M. fallax are presented. To investigate potential break crops for paddocks infested with M. fallax, a glasshouse trial was conducted testing nine plant species and a known susceptible control (Tiny Tim Tomato). Other potential break crops tested were millet (Japanese and Nutrifeed), oat (Swan), Rhodes grass (Katambora, Nemkat), rye grass (Concord, Dargo) and sorghum (Jumbo). Field Survey: Meloidogyne fallax was detected in five of 26 paddocks surveyed and four of these, were in the Pemberton area, close to where M. fallax was first found. The Pemberton paddocks had loamy soil, while the fifth infested paddock was in a sandy soil at Myalup. Levels of M. fallax were very low in all paddocks and may not have been high enough to cause crop damage. This is the first time M. fallax has been detected on commercial farms in WA since it was first identified in 2006. Glasshouse Trial: Millet (Nutrifeed) was the only cover crop resistant to M. fallax in the glasshouse. Rhodes grass (Nemkat and Katambora) and Jumbo sorghum were slightly susceptible while all other crops were moderately to highly susceptible to this RKN species. Swan oats, which is resistant to other RKN species, was moderately susceptible to M. fallax. More crops need to be tested to find more resistant cultivars and field trials are needed to confirm glasshouse results.

Southern sting nematode – a new challenge for Western Australia

Dr Sarah Collins
Department of Agriculture and Food, Western Australia
sarah.collins@agr.wa.gov.au

Sarah Collins
Department of Agriculture and Food Western Australia, South Perth, WA, 6151, Australia

Turf grasses are commonly infested with plant-parasitic nematodes. However, the Western Australian (WA) turf industry and amenities managers have been challenged by the gradual, unrelenting spread of the Southern Sting Nematode Ibipora loli (previously known as Morulaimus giga). This nematode is not native to WA and was probably introduced on turf from New South Wales in the 1970’s. It has continued to spread on infested turf and in soil attached to machinery and equipment. A survey of metropolitan Local Governments conducted by the Western Australian Local Government Association (WALGA) showed that Southern Sting Nematode is now significantly impacting sports fields, local government reserves, parks and recreational areas. The survey identified that in 3 Local Governments had sting nematodes in at least one of their reserves. Industry experts found this pest in at least 50% of Perth’s amenity turf areas. Costs of up to $10,000/ha are estimated for additional management required for infested areas. Once an area is infested, it is not possible to eradicate Ibipora loli. Major concerns are held that it may move into horticultural production areas via passive movement on shoes and equipment and as land previously utilised for turf production becomes available to the horticulture industry. A similar Sting Nematode (Belonolaimus longicaudatus), found in other parts of the world, is a damaging pest of numerous vegetable crops including potato, tomato, cauliflower, onion, carrot, cantaloupe and strawberry. This is of particular concern in WA, as Belonolaimus is found primarily in irrigated coastal sandy soils similar to WA’s horticultural area on the swan coastal plain. Sting nematodes are large ectoparasitic nematodes 2-3mm in length, which feed primarily on root tips and result in abbreviated or stubby roots which are unable to function efficiently. Crops damaged by sting nematodes often wilt, are stunted and show symptoms of nutrient deficiency. Seedlings may germinate and then cease growing. Yield losses can be severe, approaching 100 percent in localised areas. Similarly in turf, typical symptoms are patches of yellowed and thinning turf, particularly under drought, mowing or wear stress. While similar morphologically to Belonolaimus little is known of the biology or lifecycle of the Southern Sting Nematode Ibipora loli. Further study of the Australian species is required to develop management options to reduce impacts to turf and other horticultural industries.
**NEW & EMERGING DISEASES**

**POSTER BOARD 111**

**Chestnut blight – to be or not to be? Cryphonectria parasitica vs Holographia eucalypti**

Dr Quang Dinh  
Department of Environment and Primary Industries

Jacky Edwards(1), James Cunnington(2), Quang Dinh(1), Ramez Aldaoud(1), SriKanthi de Alwis(1), Stephen Dougherty(1), Bob Emmett (1), Robert Holmes(1), David Riches(2), Soheir Salib(1), Con Skylas(1), Oscar Villalta (1)

(1) Biosciences Research Division, Department of Environment and Primary Industries Victoria(DEPI), AgriBio, Centre for AgriBioscience, 5 Ring Road, La Trobe University, Bundoora VIC 3083, Australia.  
(2) DAFF, 620 Burwood Hwy, Knoxfield, VIC 3180 Australia.

In September 2010 Chestnut Blight, caused by the fungus *Cryphonectria parasitica*, was detected for the first time in Australia. The initial sample was identified by Crop Health Services at DEPI, and originated from a property in the Ovens Valley in the north east of Victoria. This is in the middle of the largest chestnut growing area in Australia. During the delimiting phase of the incursion response, more than 300 samples were collected for testing. Many of these samples contained the orange stroma typical of *Cryphonectria parasitica* and other members of the Cryphonectriaceae. Of particular concern was the eucalypt canker fungus, *Holocryphia eucalypti*, which has been recorded on chestnut in Victoria and which superficially looks identical to *C. parasitica*. Identification was verified using DNA sequence data from the ribosomal DNA internal transcribed spacer region and an intron rich region of the ß-tubulin gene. *Cryphonectria parasitica* and *H. eucalypti* were easily distinguishable using either of these regions, and could readily be matched to reference sequences on GenBank. Of the 300 samples tested, only a few were determined to be *C. parasitica* and these were all restricted to properties within the Ovens Valley. *Holocryphia eucalypti* was found on over 20 properties from a range of locations in the north east and south of Victoria. This important distinction provided evidence for the potential feasibility of successful eradication and consequently an eradication program is currently in progress.

**NEW & EMERGING DISEASES**

**POSTER BOARD 112**

**The characterisation and development of diagnostic tools for ilarviruses infecting Prunus species in Australia**

Mr Wycliff Kinoti  
La Trobe University  
wkinoti@students.latrobe.edu.au

Wycliff Kinoti(1,2), Fiona Constable(2), Brendan Rodoni(2)  
(1) La Trobe University, 5 Ring Road, Bundoora, Victoria, 3083, Australia.  
(2) AgriBio, Centre for AgriBiosciences, Department of Environment and Primary Industries, 5 Ring Road, Bundoora, VIC, 3083, Australia

*Prunus* species are susceptible to a number of pests and pathogens, including ilarviruses, which affect fruit quality and yield and have subsequent economic impacts on nurseries, growers and processors of summer fruit species and almonds. The three most common and economically important *ilarivirus* species of summer fruit species and almonds are *Apple mosaic virus* (*ApMV*), *Prunus necrotic ringspot virus* (*PNRSV*) and *Prune dwarf virus* (*PDV*) and each virus is transmitted by grafting, pollen and seed. These three viruses can occur as single infections or as mixed infections which further increases their damage to the infected trees. Ilarviruses can be detected by biological indexing using sensitive indicator plants which express indicative symptoms of virus infection. They can also be detected using specific PCR for individual virus species or generic PCR tests that can detect multiple species in the *ilarivirus* genus. Using these tests a putative distant strain or species other than PNRSV, PDV and ApMV was detected in diseased *Prunus* trees in south-east Australia. It was also observed that strain variation exists within different *ilarivirus* species and multiple *ilarivirus* infections occur within *Prunus* trees. This project will use advanced molecular technologies, including next generation sequencing (NGS) strategies, to characterise isolates of PNRSV, PDV and ApMV and related ilarviruses from diseased trees, alternate hosts and different regions of Australia. This information will be used to design and develop molecular diagnostic tools for specific detection of *ilarivirus* species and generic detection of the *ilarivirus* genus that infect summer fruit and almonds in Australia. Surveys will be conducted across Australia to validate the diagnostic tools and to provide accurate surveillance data on the distribution of ilarviruses in Australian summer fruit and almonds.
Leaf scorch of African mahogany caused by *Rhizoctonia solani* AG-1-IA in Australia

Lucy Tran Nguyen  
Department of Primary Industry and Fisheries  
jose.liberato@nt.gov.au  
Jose R Liberato, Lucy TT Tran Nguyen  
Department of Primary Industry and Fisheries, Plant Industries Group,  
GPO Box 3000, Darwin, NT 0801, Australia

African mahogany (*Khaya senegalensis*) is a hardwood timber species with estimated 16,000 ha of industrial plantations in the Northern Territory (NT). In December 2008 symptoms of leaf scorch were observed on seedlings growing in the Darwin region. Lesions were present on both sides of the leaves, no bacterial streaming was found and except for *Rhizoctonia*-like mycelium, no other plant pathogen was observed, even after the leaves were placed in a moist chamber for 48 h. *Rhizoctonia* (isolate DNAP 4675) was isolated from these lesions. Most sclerotia on the surface of 7-day-old cultures on PDA plates (n ≥ 70/plate) were brown, up to 5 mm in diameter. Fluorescent microscopy on a 3-day-old culture in water-agar, stained with DAPI, revealed DNAP 4675 had 3-15 nuclei/cell. Two pathogenicity tests were conducted using seedlings 20–30 cm tall. One test used a 5-day old mycelium suspension which was sprayed onto the seedling leaves. The second test used 4-day old PDA mycelial plugs placed on the upper leaf surface. In the first test, leaf scorch symptoms were observed five days after inoculation on four out of five inoculated seedlings but not on the control. In the second test, leaf scorch symptoms were observed three days after inoculation on four out of five inoculated seedlings. DNA was extracted from the DNAP 4675 culture and the IGS region was amplified using universal ITS PCR primers and sequenced. Bioinformatic analyses indicated that DNAP 4675 clustered with the *R. solani* anastomosis A-1-IA group. Consequently, DNAP 4675 analyses indicated that DNAP 4675 clustered with the *R. solani* AG-1-IA group. The PCR product was stained with DAPI, revealed DNAP 4675 had 3-15 nuclei/cell. The DNA sequences of the cultures re-isolated from deposited into GenBank and assigned the Accession Number JQ311915. The DNA sequences of the cultures re-isolated from both pathogenicity tests matched the original DNAP 4675. The disease was never observed in adult plants in the field and has never been seen on seedlings again.

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Does *Melampsoridium hiratsukanum* occur in New Zealand?

Dr Eric McKenzie  
Landcare Research  
mckenziee@landcareresearch.co.nz  
Eric McKenzie, Mahajabeen Padamsee  
Landcare Research, Private Bag 92170, Auckland Mail Centre, Auckland  
1142, New Zealand

East Asian alder rust, *Melampsoridium hiratsukanum*, is one of three *Melampsoridium* species known to attack *Alnus* species (*Betulaceae*). This rust was found in Estonia and Finland in mid 1990s and later confirmed as the cause of an epidemic outbreak on *Alnus* spp. in other European countries. The rust is continuing to spread throughout Europe, and most recently was reported from Wales, and also British Columbia, western Canada. A heavy rust infection noted on *Alnus cordata* in Auckland in winter 2012 was suspected to be caused by *M. hiratsukanum*. Investigations revealed that rust had been previously found in May 1980 on young *Alnus* plants in a forestry nursery in New Zealand, and that since the 1990s rust has been prevalent on both *Alnus* and *Betula* plants in a Nelson tree nursery. In neither case had the rust(s) been identified. A second rust, *M. betulinum*, occurs on *Alnus* and *Betula* spp. in Scotland, and was reported in New Zealand on *B. pendula* in 1919. Measurements of urediniospores, taken from both *Alnus* and *Betula* leaves in New Zealand, were found to lie between those reported for *M. hiratsukanum* and *M. betulinum*. However, the presence of long tapering ostiolar cells in the uredinia and the formation of urediniospores in chains were two features that matched recent descriptions of *M. hiratsukanum* from Europe. Both uredinia and telia have been found on leaves of *Alnus* and *Betula* in New Zealand. The fungi were also examined by molecular methods. The nuclear ribosomal large subunit (LSU) locus and the nuclear ribosomal internal transcribed spacer region (ITS) locus of both New Zealand and European samples were amplified. Molecular analyses indicated that the rust on both *Alnus* spp. and *Betula* spp. in New Zealand is *M. betulinum* and not *M. hiratsukanum*. The presence of distinctive ostiolar cells and chains of spores is a character of both *M. hiratsukanum* and *M. betulinum*. However, there is considerable genetic variation between isolates determined as *M. betulinum* (both from New Zealand and overseas) and a broader multigene sequencing is needed. Interestingly, there was no rust infection on *Alnus* trees in Auckland in 2013, although infection was severe in the Nelson nursery. Observations in the tree nursery suggest variation in susceptibility to rust with some species remaining rust-free, including several Asiatic *Betula* spp. and a 35-year-old *A. nepalensis* tree.
**NEW & EMERGING DISEASES**

**POSTER BOARD 115**

*Fusarium* species causing foot rot and bakanae disease of rice in Fars province, Iran

**Dr Abbas Sharzei**
University of Tehran
asharze@ut.ac.ir
Bijan Naderpour(1), Seddiqeh Mohammadi(1), Abbass Sharzei(2)
(1)Department of Plant Protection, Shiraz Branch, Islamic Azad University
(2)Department of Entomology and Plant Pathology, Aburaihan Campus, University of Tehran

Rice bakanae and foot rot is one of the most important diseases in paddy-culturing areas. Infected plants may become short and chlorotic with foot and root rot. In summer 2011, suspected rice plants were collected in seedling, tillering, stem elongation and booting stages from the paddy nurseries and fields of Fars province, Iran. Samples were surface sterilized by 0.5% sodium hypochlorite and cultured on PDA. A total of 74 isolates of *Fusarium* spp. were obtained and identified using authentic keys. Pathogenicity tests were performed on rice seedlings using both root-dip technique and injection of conidial suspension into the crown of seedlings. Inoculated seedlings were incubated at 25-30°C for one month. Isolates of *F. moniliforme*, *F. proliferatum*, *F. oxysporum*, *F. avenaceum* and *F. sportichioidei* caused foot rot in both inoculation methods; however, isolates of *F. solani* and *F. subglutinans* produced symptoms only in injected plants. The fungi were reisolated from the seedlings. This is the first report of *F. subglutinans* and *F. culmorum* from rice in Iran and in the world, respectively. To our knowledge, *F. oxysporum*, *F. solani*, *F. avenaceum*, *F. sportichioidei* and *F. subglutinans* have not been previously reported as the causal agents of rice foot rot from Iran and possibly from other countries.

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**NEW & EMERGING DISEASES**

**POSTER BOARD 116**

New plant virus records in New Zealand: update 2010-2013

**Ms Stella Veerakone**
Ministry for Primary Industries
stella.veerakone@mpi.govt.nz

The Plant Health & Environment Laboratory is responsible for the surveillance of pests and diseases and the maintenance of the Plant Pest Information Network data base (PPIN) in New Zealand. Between 2010 and 2013, 21 viruses were recorded in New Zealand for the first time. Five viruses were recorded in *Actinidia* sp. (kiwifruit), three viruses in *Rosa* sp. (rose), three cryptic viruses in *Capsicum annuum* (pepper) and three viruses in *Vitis* sp. (grapevine). Other new virus records include *Bougainvillea chlorotic vein-banding virus* in *Bougainvillea* sp., *Fragaria chiloensis latent virus – Y* in *Smallanthus sonchifolius* (yacon), *Hosta virus x* in *Hosta* sp., *Radish yellow edge virus* in *Griselinia lucida* (puka) and an ilarvirus in *Raphanus rapanistrum*. The significance of these findings is discussed.
Multilocus Sequence Typing of *Pseudomonas* spp. from kiwifruit plants and orchards discerns pathogenic from non-pathogenic strains

Ms Sandra Visnovsky
The New Zealand Institute for Plant & Food Research Ltd
sandra.visnovsky@plantandfood.co.nz

Sandra Visnovsky(1), Ashley Lu(1), Kerry Everett(1), Shamini Pushparajah(2), Robert Taylor(3), Andrew Pitman(3),

(1) The New Zealand Institute for Plant & Food Research Ltd, Private Bag 4704, Christchurch 8140, New Zealand
(2) The New Zealand Institute for Plant & Food Research Ltd, Private Bag 92169, Auckland 1142, New Zealand
(3) Plant Health and Environment Laboratory, Ministry for Primary Industries, P.O.Box 2095, Auckland 1140, New Zealand

*Pseudomonas* spp. can cause disease on kiwifruit; one (blossom blight) that only affects buds and flowers, and another (kiwifruit canker) that can kill vines. However, non-pathogenic pseudomonads also exist in orchards. The diversity of these bacteria in kiwifruit orchards has been explored using biochemical and plant tests, but diagnostics to differentiate them are limited. In this study, the range of pseudomonads on kiwifruit was examined by Multilocus Sequence Typing (MLST) of 30 *Pseudomonas* strains collected from orchards in New Zealand and overseas. MLST was conducted by DNA sequencing of four housekeeping genes (gapa, gltA, gyrB and rpoD). The concatenated sequences were compared with those obtained from the Plant Associated and Environmental Microbes database (PAMDB). Sequences from the newly classified *P. syringae pv. actinidiae* (Psa) V and LV strains and representatives from eight of the nine genomospecies of *P. syringae* described previously by Gardan, were included. MLST divided the pseudomonads into two groups. Group 1 contained type strains plus other well characterised isolates of *P. syringae*. Twenty-one isolates from kiwifruit plants were also assigned to Group 1, and distributed amongst six of the nine genomospecies and all four MLST groups of *P. syringae* described by Sarkar and Guttman (2004). One of the uncharacterised isolates was a Psa LV strain. Four isolates from buds or necrotic flowers, considered to be associated with blossom blight, were distributed within three of the genomospecies. Inoculation of leaves of all Group 1 isolates collected from kiwifruit orchards of 3-month old plantlets of ‘Hayward’ and ‘Hort16A’ confirmed their pathogenicity; leaves of both cultivars showed disease lesions within 72 hpi. Group 2 included nine isolates from kiwifruit orchards and well characterised non-pathogenic pseudomonads including *P. fluorescens* and *P. putida*. As expected, pathogenicity tests confirmed that isolates belonging to Group 2 were unable to generate disease lesions on inoculated leaves of ‘Hort16A’ and ‘Hayward’ plantlets. Lack of symptoms in plants suggests that isolates in this group do not pose a risk to kiwifruit production. An isolate of *P. marginalis*, considered to be a saprotroph, was also assigned to this group. Interestingly, pathogenicity assays using this isolate resulted in a minor lesion on the leaf of one out of six plantlets of ‘Hayward’, and no lesions on ‘Hort16A’. In conclusion, MLST can be used to differentiate pathogenic and non-pathogenic pseudomonads in kiwifruit orchards. Differentiation of these groups suggests that diagnostics could be developed for their detection.

Effect of the inoculation time with *Meloidogyne javanica* and *Macrophomina phaseolina* on development and severity of the disease complex on green bean

Saleh Al-Nadhari
King Saud University
nadary44@gmail.com

Saleh Al-Nadhari(1), Ahmed Al-Hazmi(1), Fahad Al-Yahya(1), Younes Molan (1), Ahmed Dawaba(1), Mahmoud El_komy(1), Hamzeh Lafi(1)

(1) Department of Plant Protection, College of Food and Agricultural Sciences, King Saud University, PO. Box 2455, Riyadh 11451, Saudi Arabia

The effect of inoculation time with *M. javanica* and *M. phaseolina* on development and severity of the disease complex on green bean (*Phaseolus vulgaris cv. Contender*) was investigated in a greenhouse (25 ± 2°C) pot experiment. Treatments included; nematode inoculation (N) @ 8 eggs/g soil, fungus inoculation (F) with 8 sclerotia/g soil, nematode + fungus inoculation (N+F), fungus inoculation, two weeks prior to nematode inoculation (F before N), nematode inoculation, two weeks prior to fungus inoculation (N before F) and non-inoculated check. Pots were arranged in a randomized complete block design (RCBD) with five replicates for each treatment. Results showed that both N+F and N before F treatments inhibited the growth of the green beans, compared to the other treatments. N+F treatment resulted in the highest nematode and fungus infection (root-knot and root-rot indices). N+F and F before N treatments adversely affected the nematode reproduction, but enhanced the fungus reproduction. On the other hand, N and N before F treatments resulted in the highest nematode reproduction factors, respectively. As well, F before N treatment resulted in the highest colonization of the green bean roots with *M. phaseolina*. This study clearly obviated that the development and severity of the *M. javanica* and *M. phaseolina* disease complex on green beans is greatly affected by the inoculation time with each pathogen.
Utilization of carbon and nitrogen by *Pseudomonas syringae* pv. *actinidiae*

Ms Kirsty Boyd-Wilson  
The New Zealand Institute for Plant & Food Research Limited  
kirsty.boyd-wilson@plantandfood.co.nz

KSH Boyd-Wilson(1), S Nardozza(2), M Walter(1)

1) The New Zealand Institute for Plant & Food Research Limited, Gerald Street, Lincoln 7608, New Zealand
2) Plant & Food Research, Private Bag 92 169, Auckland 1142, New Zealand

In plant pathology, knowledge of the growth characteristics (growth phenotypes) of cells in elemental compounds has a number of applications, for example to define and distinguish bacterial species and to investigate pathogenicity differences between strains. This information may also allow the nutrient status of a leaf surface to be manipulated to provide a competitive advantage for a biological control agent (BCA) over a pathogen such as *Pseudomonas syringae* pv. *actinidiae* (Psa). The aim of this research was to gather this basic information for Psa for use in further studies. The utilization of 190 carbon and 95 nitrogen compounds was assayed using Biolog™ proprietary phenotype microarrays (PM) for four isolates of the virulent (V) haplotype of Psa and two isolates of the low virulent (LV) haplotype. A cell suspension of a known concentration was prepared in a solution that contained salts to maintain cell viability, and a tetrazolium redox dye. This solution was pipetted into the wells of the PM plates, which were incubated at 23°C in the dark. After 48 h, the redox dye reaction was manually scored from 0 (no utilization) to 4 (high utilization) as a measure of cell respiration. Descriptive analysis showed that the results were reasonably consistent within a haplotype. There were differences in utilization between the two haplotypes. LV utilized 141 compounds and V utilized 124 (positive result for all isolates of a haplotype). Compounds that were highly utilized by V (≥3) were also highly utilized by LV. Compounds that were highly utilized by LV were not always highly utilized by V (≥2). There were compounds that were utilized by only LV and compounds that were utilized by only V. Based on these findings and phenotypic growth studies on a selected BCA (results not presented), eighteen compounds were identified that were utilized by the BCA but not by either haplotype of Psa. Further studies on these compounds at a range of concentrations are in progress.

Pathogenicity genes of *Leptosphaeria maculans*, the fungus that causes blackleg disease of canola (*Brassica napus*).

Ms Kylie Chambers  
The University of Melbourne  
k.chambers3@student.unimelb.edu.au

Kylie Chambers, Angela Van de Wouw, Rohan Lowe, Barbara Howlett  
School of Botany, The University of Melbourne, Victoria, Australia, 3010.

*Leptosphaeria maculans* causes blackleg, the most serious disease of canola (*Brassica napus*) worldwide. Current approaches to control blackleg are through the use of agronomic practices such as crop rotations and sowing disease-resistant canola varieties; however, *L. maculans* has overcome major gene resistance in commercially released cultivars. Effective control strategies require knowledge of both plant defence and fungal pathogenicity mechanisms. Pathogenicity genes are required for the development of disease and have the potential to be fungicide targets. The aim of this project is to identify and characterise pathogenicity genes in *L. maculans*. Two approaches are being used (1) forward genetics, whereby previously generated T-DNA mutants are screened for reduced pathogenicity on *B. napus* and (2) reverse genetics whereby previously generated RNA-seq data for in vitro and in planta growth of *L. maculans*, are analysed to produce a list of candidate pathogenicity genes. Two genes are being investigated; one encodes a putative glutathione synthetase gene, which is involved in the synthesis of glutathione, and the other encodes a gene with a ferritin-like superfamily domain. Glutathione synthetase (*gsh2*) is the second enzyme involved in the synthesis of glutathione (GSH), a ubiquitous tripeptide that plays many roles in the cell, including protection against free radicals and reactive oxygen species (ROS) such as hydrogen peroxide. Preliminary results show that a T-DNA mutant with 50% down regulation of *gsh2* expression cannot infect wounded cotyledons. The mutant has increased resistance to hydrogen peroxide compared to the wildtype isolate, implying that ROS are important in the infection process. The generation of ROS can be accelerated by the presence of excess iron in the cell. Iron is essential for the growth of most organisms, despite being toxic at high intracellular concentrations. The protein ferritin stores iron until it is needed. The uptake of iron is required for pathogenicity of several phytopathogenic fungi. A gene containing a ferritin-like superfamily domain in *L. maculans* is highly up-regulated *in planta* compared to *in vitro*. The role of this gene in blackleg disease is currently being determined.
Understanding blueberry rust in Australia: histology of infection by *Thekopsora minima*

Dr Rosalie Daniel  
Department of Primary Industries, NSW  
rosalie.daniel@dpi.nsw.gov.au  
Rosalie Daniel(1), Phillip Wilk(2), Len Tesoriero(1)  
(1)Department of Primary Industries, Elizabeth Macarthur Agricultural Institute, Menangle 2567, New South Wales, Australia  
(2)Department of Primary Industries, NSW Centre for Tropical Horticulture, Alstonville 2477, New South Wales, Australia

Almost 90% of Australian blueberries are produced in northern New South Wales and southern Queensland. The subtropical climate in the region, the extended growing season and evergreen cropping practices not only favour higher blueberry yields, but are also conducive to the development of fungal diseases. Blueberry rust (*Thekopsora minima*), Botrytis blossom, fruit and twig blight, (*Botrytis cinerea*) and Anthracnose fruit rot (*Colletotrichum gloeosporioides* and *C. acutatum*) are becoming more severe and persistent in blueberry orchards, particularly during wet years. Blueberry rust was first reported in Australia in November 2001 and is now a significant impediment to blueberry production. Despite its high incidence and severity, little is known about the biology and epidemiology of *T. minima* in Australia. In the field, yellow spots appear on the upper surface of new leaves. As the disease progresses, the spots become brown and yellow pustules (uredinia) develop on the lower leaf surface. Urediniospores are the main source of new infections. The entire leaf may become chlorotic and necrotic, resulting in defoliation, premature fruit drop and a late ripening crop. Teliospores develop intraepidermally on blueberry leaves. Spores can carry over on the previous season’s foliage causing greater problems in the following season. This study used histological techniques to determine the infection process of *T. minima*, the susceptibility of leaves and shoot tips at different physiological development stages and the environmental factors that are conducive to infection. A better understanding of the pathogen biology and epidemiology will promote a more targeted, effective and efficient approach to the implementation of control strategies.

Impact of *Phytophthora kernoviae* on New Zealand vegetation

Ms Judy Gardner  
Scion  
judy.gardner@scionresearch.com  
Judy Gardner(1), Elizabeth Miller(1), Peter Scott(1), Margaret Dick(1)  
(1)Scion, New Zealand Forest Research Institute Ltd. 49 Sala Street, Private Bag 3020, Rotorua 3046, New Zealand

An unidentified *Phytophthora* species, isolated from soil from a *Pinus radiata* plantation in the Waikato in the 1950s, was recently determined to be con-specific with *Phytophthora kernoviae* Brasier, Beale & S.A.Kirk, a pathogen of shrubs and trees (principally species of *Rhododendron* and *Fagus*) in Britain. *Phytophthora kernoviae* was not associated with disease on *P. radiata* in New Zealand. In an effort to determine the presence and impact of *P. kernoviae* in the Kinleith Forest, a trial was set up at one of the original Waikato isolation sites. Soil samples and vegetation were tested and *Rhododendron catawbiense* plants were used as baits in the forest. *Phytophthora kernoviae* was recovered from the soil and killed one of the *R. catawbiense* bait plants; however it was not recovered from the natural vegetation. The impact of *P. kernoviae* on trees and shrubs in New Zealand needed to be established. In a foliar pathogenicity trial, *P. kernoviae* caused disease in four out of 31 native species and three out of three exotic species. In an under bark inoculation trial, *P. kernoviae* caused active lesions in *Fagus sylvatica* and active lesions and wilting in *Annona cherimola*; however, it did not cause damage in *R. catawbiense* and 33 native species.  

Understanding blueberry rust in Australia: histology of infection by *Thekopsora minima*  

Impact of *Phytophthora kernoviae* on New Zealand vegetation
PLANT PATHOGEN INTERACTIONS

POSTER BOARD 123

Interaction between abiotic stress and fungal infection in prickly acacia

Mr Ahsanul Haque
The University of Queensland
ahsanul.haque@uqconnect.edu.au

Ahsanul Haque(1), Victor Galea(1), Ken Goulter(1), Rieks D van Klinken(2)
(1) School of Agriculture and Food Sciences, The University of Queensland, Gatton, Qld 4343, Australia
(2) CSIRO Ecosystem Sciences, GPO Box 2583, Brisbane Qld 4001, Australia

Prickly acacia (Acacia nilotica ssp. indica) is one of the Weeds of National Significance (WONS) in Australia. Recently, dieback symptoms were observed on this species in many locations across north Queensland. Preliminary field observations suggest that fungi are associated with this phenomenon, and we hypothesise that they may result in dieback when combined with other potential stressors. We conducted glasshouse and field trials (still underway) to test this stress-relationship hypothesis. In glasshouse trials we tested 18 fungal species under Botryosphaeriaceae, Dematiaceae, Dothioraceae, Juniperaceae, Patellariaceae, Pleosporaceae, Pleurostomataceae, Trichocomaceae, Umbilicariaceae, Valsaceae and Zingiberaceae families originally isolated from dieback-affected prickly acacia and previously found to be pathogenic to seedlings in laboratory assay-tests. We also included Lasiodiplodia pseudotheobromae sourced from dieback-affected parkinsonia (Parkinsonia aculeata) which had been shown to be more pathogenic to prickly acacia seedlings and juveniles than those sourced from prickly acacia, and, therefore, selected to test this hypothesis. In the glasshouse trial, the stress treatment was imposed using a pre-determined sub lethal dose of Glyphosate applied into drilled stem using a micropipette. Significantly higher levels of dieback symptoms were recorded when Lasiodiplodia pseudotheobromae was inoculated in Glyphosate-stressed plants. This experiment was followed by a trial in north Queensland to test this hypothesis under field conditions. In the field trial, Lasiodiplodia pseudotheobromae was applied using a gelatine capsule delivery system and simultaneously combined with two sub lethal doses of Glyphosate applied into drilled stem using a pressure pump. Preliminary results (6 months after inoculation) found dieback symptoms such as stem lesions, gummosis and branch death identical to glasshouse trial. Longer stem lesions were recorded when Lasiodiplodia pseudotheobromae was combined with a lower dose of Glyphosate which supports our hypothesis that stress contributes to pathogen-induced dieback. However, there was a little effect of Lasiodiplodia pseudotheobromae in presence of a higher dose of Glyphosate. Findings indicate an interaction between fungi and level of stress. Dieback severity by Lasiodiplodia pseudotheobromae was favoured when the plants were slightly stressed. On the other hand, the role of the fungi in dieback process could not be distinguished when the plants were subjected to a higher degree of stress.

PLANT PATHOGEN INTERACTIONS

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Brassica lectins act similarly to antibodies by providing a protective cell barrier against pathogenic bacteria and nematodes

Alaa Haridi
Alaa Haridi, Peer M. Schenk
Plant-Microbe Interaction Laboratory, School of Agriculture and Food Sciences, The University of Queensland, Brisbane, QLD 4072, Australia

Induced defence gene expression is an effective way for plants to allocate resources against pests and pathogens when needed. Plant lectins are proteins that bind to carbohydrates with high specificity. They have the ability to recognise and bind glycoconjugates on the surface of microorganisms and to agglutinate cells. In this study, two highly inducible members of a lectin-encoding gene family from Arabidopsis thaliana and one from canola were used as potent defence genes in transgenic Arabidopsis and tobacco plants. DNA expression using quantitative-real time PCR and protein-ligand binding assays using glycan microarrays revealed distinctive lectin gene expression patterns during plant defence responses and global carbohydrate binding profiles. These lectins possess a signal peptide and occur in two isoforms (glycosilated and unglycosilated). Lectin-1 binds to mono- and di-saccharides and accumulates in the plant cell wall forming a protective barrier against bacterial invasions by causing effective immobilisation (clumping) similarly to antibodies. Arabidopsis and tobacco plants overexpressing Lectin-1 show strong resistance to Pseudomonas syringae pv tomato and these plants also displayed resistance to root-knot nematode infection.
Does Roundup confer viral resistance?

Ms Tracey Immanuel
Plant & Food Research
tracey.immanuel@plantandfood.co.nz
Tracey Immanuel(1,2), David Greenwood(1,2), Robin MacDiarmid(1,2)
(1) Plant & Food Research, 120 Mt Albert Road, Sandringham, Auckland 1025, New Zealand
(2) The University of Auckland, Thomas Building, Building 110, 3a Symonds Street, Auckland Central 1010, New Zealand

Viruses are obligate parasites that require their host’s protein machinery in order to replicate. As demonstrated in mammals, if the host is able to inhibit protein translation, the virus is unable to replicate and infect the host organism systemically. An important mechanism for inhibiting protein translation in eukaryotic cells involves phosphorylation of the alpha subunit of the eukaryotic initiation factor 2 (eIF2α). eIF2α is phosphorylated by specific eIF2α kinases. The mammalian-encoded eIF2α kinase PKR is activated by double stranded (ds)RNA generated during virus infection. The ubiquitous eukaryote eIF2α kinase GCN2 is activated in response to nutrient limitation. PKR and GCN2 activity have been reported in plants (Immanuel et al. 2012). However, the effect of viral dsRNA on plant eIF2α phosphorylation has not been completely ascertained. What is most intriguing is that while PKR-like activity is observed in plants, no plant PKR sequence homologue has been found. PKR overexpressed in plants has been reported to confer a degree of resistance to virus infection. Arabidopsis eIF2α is not phosphorylated upon Turnip yellow mosaic virus (TYMV) or Turnip crinkle virus (TCV) infection. However, Arabidopsis eIF2α is phosphorylated in response to amino acid starvation, purine starvation, UV light, cold shock and wounding stress by GCN2. In order to induce amino acid starvation, Roundup (glyphosate) can be easily sprayed onto plants. Roundup targets the shikimate pathway and results in the inhibition of aromatic amino acid synthesis and stimulates the amino acid starvation response. Thus, Roundup treatment activates GCN2 to phosphorylate eIF2α and inhibits protein translation. As viruses require their host’s protein translation machinery, we asked the question “Can we inhibit plant viral infection by inhibiting plant protein translation via GCN2 induced phosphorylation of eIF2α?” References

Atmospheric moisture influences on conidia development in cucurbit powdery mildew fungus through host-plant morphological responses

Ms Kaori Itagaki
Osaka Prefecture University, Research Fellow of the JSPS
itagaki.kaori@gmail.com
Kaori Itagaki(1,2), Toshio Shibuya(1), Motoaki Tojo(1), Ryosuke Endo(1), Yoshiaki Kitaya(1).
(1)Graduate School of Life and Environmental Sciences, Osaka Prefecture University, Sakai, Osaka, Japan
(2)Research Fellow of the Japan Society for the Promotion of Science

This study investigated the effects of atmospheric moisture on conidia development in cucurbit powdery mildew fungus (Podosphaera xanthii) through host-plant responses, to obtain a basic knowledge for predicting the risk of powdery mildew in agricultural and horticultural crops, particularly under changing environmental conditions. Cucumber (Cucumis sativus ‘Hokushin’) seedlings were grown in growth chambers which were maintained at a low relative humidity (RH; ≈ 10%) or a high RH (≈ 90%), and an air temperature of 30°C. When the cotyledons had expanded, spores of P. xanthii were inoculated onto the adaxial surface by spraying spore inoculum. The inoculated seedlings for both treatments were placed in a growth chamber maintained at a RH of 50%, an air temperature of 30°C. Then, development in P. xanthii was evaluated 7 d after inoculation. The density of visible P. xanthii colonies on the low-RH-acclimated cotyledons was 0.69 times that of the high-RH-acclimated cotyledons. Spore germination rate of 48 h after inoculation did not differ between the treatments. The percentage of adaxial epidermal leaf cells with haustoria was lower in low-RH-acclimated cotyledons 7 d after inoculation. There was no significant difference in leaf water potential between the treatments. The low-RH-acclimated cotyledons were thicker and had greater dry mass per leaf area. From these results, it is likely the germination was not affected, but the post-germination behavior of P. xanthii such as the infection and consequent hyphal development was affected. The water status of the cotyledons is probably not the reason for the difference in conidia development between the treatments. The inhibition of conidia development on low-RH-acclimated cotyledons was probably due primarily to the changes in leaf morphology that protect against water loss and are known to be stimulated by lower atmospheric moisture. These morphological properties that contribute to protection against water loss may also be structural barriers against invasion of P. xanthii.

Finally, we conclude that atmospheric moisture influences early development of P. xanthii conidia probably through the changes in leaf morphological properties.

Investigation of host-specificity determinants in Venturia inaequalis using a comparative genomics approach

Ms Shakira Johnson
La Trobe University
sj7johnson@students.latrobe.edu.au
Shakira Johnson(1), Jason Shiller(1), Joanna Bower(2), Matt Templeton(2), Nathan Hall(1), Kim Plummer(1)
(1)La Trobe University, Bundoora, VIC, Australia
(2)Plant and Food Research, Auckland, New Zealand

Venturia inaequalis is a hemi-biotrophic fungus that causes apple scab disease. It is the most important pathogen of apple worldwide. This disease is currently controlled through fungicides and the use of resistant cultivars. Resistance responses are host-cultivar specific and follow the gene-for-gene model of resistance. V. inaequalis race 1 induces an hypersensitive resistance response on host 5, a cultivar derived from the crab apple species, Malus micromalus. The resistance response is limited to the site of fungal penetration and fungal growth is arrested. This leads to a distinct resistance phenotype characterised by ‘pinpoint pits’ (a localised cell collapse on the leaves). Comparative genomics is being used to identify race-specific effectors (comparing race 1 and 5) and to further our understanding of non-host resistance within V. inaequalis (examining resistance responses of pear to V. inaequalis).
Genetic diversity of Botrytis in New Zealand vineyards

Dr Peter Johnston
Landcare Research
johnstonp@landcareresearch.co.nz
Peter Johnston, Karyn Hoksbergen, Duckchul Park, Ross Beever
Landcare Research, Private Bag 92170, Auckland, New Zealand

Botrytis bunch rot is the most important disease of grapes in New Zealand, with high costs due to both disease control measures and grape loss. While the impact of season, climate, and management on the development of this disease in New Zealand are becoming increasingly well understood, the genetic diversity of the Botrytis population within New Zealand vineyards has until now been unexplored. B. cinerea was first reported from grapes in New Zealand by Cunningham in 1922 and has since been reported from more than 250 host species. Research in other parts of the world has shown that Botrytis populations within vineyards can vary genetically at both the species and population levels. Here we report on the phylogenetic diversity of Botrytis in New Zealand vineyards, and explore the population-level diversity within the species by sampling for the occurrence of two common Botrytis transposons, flipper and Boty. Genetic diversity of Botrytis in New Zealand vineyards was surveyed over the period 2008 to 2012 from five wine growing regions. Isolates were gathered from symptomless flower buds immediately prior to flowering and, from the same vines, from diseased fruit at harvest. Two species were found, B. cinerea and B. pseudocinerea. Phylogenetic diversity within B. cinerea in New Zealand was similar to that known from Europe, including the occurrence of isolates that appear to match genetically the recently reported Botrytis ‘Group S’. Two distinct clades were resolved within B. pseudocinerea. Isolates in both clades share the fenhexamid-resistant phenotype, both have a similar geographic and regional distribution within New Zealand, and we accept both as B. pseudocinerea. Only one of these clades has been reported from Europe from grape. However, based on matching hsp60 sequences, the second New Zealand B. pseudocinerea clade could be the same fungus reported as an endophyte of Centaurea from Europe. The taxonomic implications of this genetic diversity will be discussed.

A widespread change in the symptoms and phenology of vascular-streak dieback of cocoa in Southeast Asia and Melanesia

Dr Philip Keane
Department of Botany, La Trobe University
p.keane@latrobe.edu.au
Agus Purwantara(1), Philip Keane(1), Peter McMahon(2), David Guest(2), Arief Iswanto(3), Sri Sukamto(4), Hussin Purung(5), Smilja Lambert(6), Ayu Parawansa(7), Josephine Saul(8), Azmi Bin Che Ahmad(9)

(1)Biotechnology Research Institute for Estate Crops, Jalan Taman Kencana 1, Bogor, Indonesia.
(2)Department of Botany, La Trobe University, Bundoora, Vic 3086, Australia
(3)Faculty of Agriculture, Food and Natural Resources, University of Sydney, NSW 2006, Australia
(4)Indonesian Coffee and Cocoa Research Institute, Jalan PB Sudirman 2, Jember, Indonesia
(5)Universitas Islam Indonesia, Jln Simcharjo, Makassar, South Sulawesi, Indonesia
(6)Cocoa and Coconut Institute, Rabaul, Papua New Guinea
(7)Malaysian Cocoa Board, Kota Kinabalu, Sabah, Malaysia

Vascular-streak dieback (VSD), caused by the basidiomycete, Oncobasidium (Ceratobasidium) theobromae, kills seedlings, branches and trees of susceptible genotypes of cocoa in Southeast Asia and Melanesia, invading only xylem vessels and causing brown streaking of vascular tissue. The most distinctive symptom seen from the 1960s to about 2000 was a general chlorosis, with remnant green spots, of the first infected leaf, usually three growth flushes behind the shoot tip, followed by similar chlorosis of adjacent leaves; leaves tended to abscise soon after becoming fully chlorotic and if leaf fall occurred during wet weather, mycelium emerged from the leaf scars and formed a white corticioid basidiocarp over the scars and adjacent bark. Since about 2004, a consistent change in leaf symptoms has been observed throughout the range of the disease, from Kerala in the west, through West Malaysia and Sulawesi, East Java and Papua in Indonesia, to Papua New Guinea in the east. The formerly distinctive pattern of chlorosis with green spots is less common, with the more common symptom being the development of large dark necrotic blotches at the margins or tips of leaves, often without initial chlorosis. Diseased leaves remain attached to branches much more tenaciously than previously, making the disease appear more obvious than when leaves abscised easily. Infected leaves tend to develop cracks in the main vein through which the fungus can emerge and form basidiocarps much more commonly than on the leaf scars, accounting for the increased incidence of the disease in recent years. However, the severity of the disease in particular clones has remained unchanged. At two sites in South Sulawesi, Indonesia the Malaysian clone PBC123, selected for resistance to the disease in the 1970s remained highly resistant, sustaining fewer infections and more restricted infections of branches than some very susceptible local clones. All clones in the study sustained infections that showed a mix of original and recent symptoms. No relation between resistance and the type of symptom was observed. Observations of hyphae in xylem and basidiocarps on leaf laminae and leaf scars showed that the fungus associated with the new symptoms was identical to C. theobromae. The most likely explanation for the change in symptoms and phenology of VSD is a region-wide environmental change that affects the host response to the fungus in this new encounter disease.
PLANT PATHOGEN INTERACTIONS

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Using excised leaf discs to test field pea reaction to *Didymella pinodes*

Ms Marzena Krysinska-Kaczmarek
South Australian Research and Development Institute (SARDI)
marzena.krysinska-kaczmarek@sa.gov.au

Marzena Krysinska-Kaczmarek, Herdina, Jenny Davidson,
South Australian Research and Development Institute (SARDI), PO Box 397, Adelaide, SA 5001, Australia

*Didymella pinodes* is one of four fungal pathogens contributing to the ascochyta blight complex of field pea (*Pisum sativum*). Reaction of field pea to ascochyta blight has been evaluated in field trials and controlled environment experiments. In laboratory experiments, researchers have used detached stipules or leaves (1) as well as excised leaf discs (2) to study the interaction between *D. pinodes* and the field pea host. The advanced field pea breeding line WAPEA2211 was less susceptible to ascochyta blight than the cultivars Kaspa, Parafiel and Alma when tested in disease management field trials (3). In the current study, excised leaf discs from 4 week old field pea seedlings were used to investigate the response of WAPEA2211, Kaspa and Parafiel to *D. pinodes* isolate FT07005 in laboratory conditions. Isolate FT07005 was collected in 2007 from the disease management field trial at Turreffield, South Australia. The 1.4cm diameter excised leaf discs were placed, adaxial side up, into Petri dishes containing 0.5% water agar. Each disc was inoculated with a 10µl droplet of 5x10^5 spores/ml suspension, and control discs were inoculated with a 10µl droplet of sterile reverse osmosis water. The discs were incubated on a laboratory bench at 22°C under fluorescent and near ultraviolet lights, 12h/12h day/night, and the diameter of the lesions was measured at 3 and 7 days post inoculation. Each disc was placed in a 1.5 ml tube, DNA was extracted and used for the quantification of pathogen using real-time qPCR (2). No differences in lesion size or quantity of DNA of *D. pinodes* were observed, which may indicate that the isolate FT07005 is equally virulent on all three field pea lines tested in this study or that the excised leaf discs do not reflect field resistance of whole, intact plants. Further studies using multiple isolates of *D. pinodes* are in progress to clarify these issues.

PLANT PATHOGEN INTERACTIONS

POSTER BOARD 132

Phyllosphere microbial influence on RuBisCO activity in *Hordeum vulgare*

Ms Joyeeta Mitra
Amity University Uttar Pradesh, Noida, India
joyeetabiotech87@gmail.com

Joyeeta Mitra, P. K. Paul
Amity Institute of Biotechnology, Amity University Uttar Pradesh, Sector-125, Express Highway, NOIDA-201303, Uttar Pradesh, India

Phylloplane microbes have been attributed to affect the physiology of host plants in a number of ways. However, information is lacking on influence these microbes could have on the physiology of chloroplasts. RuBisCO, a prominent enzyme found in soluble fractions of chloroplast (stroma) is a key enzyme in Calvin cycle. In the present study, an effort was made to understand the impact of phyllosphere microbes on RuBisCO activity and Hill reaction in barley plants. *Hordeum vulgare* var. *jagriti* were raised under aseptic conditions at 25±1°C, 75% R.H. and 12H L/D photoperiod. 10 day old plants were divided into six groups of 45 plants each. They were either treated with *Drechslera graminea* only, metabolite of *Aspergillus niger* (isolated from same variety of field grown barley), *A. niger* metabolite preceding pathogen inoculation, pathogen inoculation prior to *A. niger* metabolite treatment, concomitant treatment with pathogen and fungal metabolite (1:1) and sterile distilled water (control). The activity of photosynthetic protein RuBisCO was analyzed for all groups along with estimation of Hill reaction. RuBisCO was extracted from the isolated chloroplast pellets using Tricine-PEG buffer. NADH was served as a substrate of RuBisCO. Results demonstrate that the metabolite enhance RuBisCO activity by two-folds (P≤0.01) after 72 hours of treatment. Plants inoculated with *D. graminea* had significant reduction in RuBisCO activity after 24 hours (P≤0.05). Plants inoculated with premix of pathogen and fungal metabolite showed maximum enhancement of activity. Plants treated with fungal metabolite prior or after pathogen inoculation had significant increase in enzyme activity after 72-96 hours of treatment (P≤0.01). Elevation of Hill reaction was observed after 48 hours of treatment with fungal metabolite (P≤0.01). The outcome implicates the involvement of phylloplane microfungi in the functioning of the chloroplast.
PLANT PATHOGEN INTERACTIONS

POSTER BOARD 134

The use of DNA sequence data to identify alternate hosts of rust fungi

Dr Mahajabeen Padamsee
Landcare Research
padamseem@landcareresearch.co.nz
Mahajabeen Padamsee, Eric McKenzie
Systematics Team, Landcare Research, Auckland, New Zealand

Of the approximately 250 recorded species of rust fungi in New Zealand, only half are considered native. Native rusts are found in five genera and three form genera. The three form genera (**Aecidium**, **Caeoma**, and **Uredo**) contain 31 endemic species. Most of the native rusts are thought to be autoecious (non-host-alternating) with only two confirmed heteroecious (host-alternating) species on native plants (**Puccinia caricina** and **Mikronegeria fuchsiae**). Traditionally, experimental inoculations between putative alternate hosts are required to establish whether there is a connection between rust fungi on two unrelated hosts. Such trials can be difficult to conduct with New Zealand rusts as many of them occur on alpine plants that may be protected. In a recent manuscript (Jin et al. 2010. *Phytopathology* 100:432-435), DNA analyses were used to confirm the alternate host of **Puccinia striiformis** at every step of the traditional inoculation process, which suggests that DNA analyses alone may suffice to quickly identify alternate hosts. A preliminary single locus phylogeny of New Zealand rust fungi was constructed that supported inoculation data establishing **Mikronegeria fuchsiae** as heteroecious, and suggested an alternate host for **Aecidium ranunculus-lyalli**. Multi-locus phylogenetics will allow further identification of heteroecious rust fungi.

PLANT PATHOGEN INTERACTIONS

POSTER BOARD 133

Do virus-encoded suppressors of silencing inhibit phosphorylation of eIF2alpha?

Ms Kate Olliver
New Zealand Institute of Plant and Food Research,
waitakereanimal@gmail.com
Kate Olliver(1,2), Tracey Immanuel(1), Robin MacDiarmid(1), Colleen Higgins(1)
(1)Plant and Food Research, Auckland, New Zealand
(2)Auckland University of Technology, Auckland, New Zealand

Eukaryotic cells protect themselves against virus infection using a process called RNA silencing. To counter this and allow infection to occur, plant viruses encode at least one suppressor of RNA silencing (VSR). Virus infection of vertebrate cells activates Protein Kinase R (PKR), which phosphorylates the alpha subunit of eukaryotic translation initiation factor 2 (eIF2α). This phosphorylation inhibits protein production by the host cell, and thereby virus replication, as the virus requires the host cell protein translation machinery. Some vertebrate-infecting viruses encode an inhibitor of PKR activity which inhibits phosphorylation of eIF2α and thereby allows virus replication (Davies et al, 1993); these same inhibitors of PKR activity were also shown to have VSR activity (Bucher et al, 2003, Hatada, et al 1999). It is unknown whether plant virus-encoded VSRs can also affect phosphorylation of eIF2α. This project investigates whether plant viruses encoded VSRs can also inhibit eIF2α phosphorylation by both plant and animal eIF2α kinases. To determine whether plant VSRs inhibit eIF2α kinases, the ratio of phosphorylated to non-phosphorylated eIF2α is measured via western blot. Chemiluminescence of equal volumes of protein were used to determine the amount of phosphorylated eIF2α present in plant samples. In addition, known VSRs and eIF2α kinases were transiently expressed in Nicotiana benthamiana in overlapping areas to determine whether VSRs directly inhibit eIF2α kinase activity. Leaf tissue from areas infiltrated with a VSR, an eIF2α kinase, or both was used in the method described above to determine whether eIF2α phosphorylation was inhibited by the presence of a VSR.
Biological and molecular characteristics of five different *Cherry leaf roll virus* isolates from New Zealand

Prof Michael Pearson  
University of Auckland  
m.pearson@auckland.ac.nz  
Elizabeth Woo, Michael Pearson  
School of Biological Sciences, University of Auckland, Auckland, New Zealand

*Cherry leaf roll virus* (CLRV) has a global distribution, infects a wide range of plant species and can have a significant economic impact. Hence, the virus is of serious concern to phytosanitary authorities worldwide. Natural hosts include woody species such as cherry (*Prunus avium*) and walnut (*Juglans regia*), herbaceous species such as rhubarb (*Rheum rhaponticum*), and chives (*Allium tuberosum*), ornamental species such as lilac (*Syringa vulgaris*), and hydrangea (*Hydrangea macrophylla*), and weeds such as sorrel (*Rumex acetosella*). CLRV is transmitted naturally through seeds and pollen, and experimentally by mechanical inoculation. However, unlike many nepoviruses, CLRV does not appear to be transmitted by soil-inhabiting nematodes. CLRV has been documented to cause severe and detrimental effects on various cash crops, fruit trees and woodland plants. CLRV is known to be transmitted by soil-inhabiting nematodes. CLRV has been documented to cause severe and detrimental effects on various cash crops, fruit trees and woodland plants. CLRV is known to be transmitted by soil-inhabiting nematodes.

Four of the five CLRV isolates, from *Malus domestica*, *Ribes rubrum*, *Rumex obtusifolius* and *Vaccinium darrowii*, showed greater than 80% seed transmission while the isolate from *Rubus idaeus* was not seed transmissible. Based on symptoms and seed transmission, the isolates appear to be biologically distinct strains of CLRV but there was no obvious correlation between sequence and symptomatology.

Dieback-affected and healthy *Mimosa pigra* stands have similar fungal endophyte communities in the Northern Territory, Australia

Ms Aniline Sacdalan  
The University of Queensland  
aniline.sacdalan@uqconnect.edu.au  
Aniline Sacdalan(1), Victor Galea(1), Ken Goulter(1), Louis Elliott(2), Rieks D. van Klinken(2)

(1) School of Agriculture and Food Sciences, The University of Queensland, Gatton, QLD 4343  
(2) Department of Land Resource Management, Palmerston, Northern Territory 0831  
CSIRO Ecosystem Sciences, GPO Box 2583, Brisbane QLD 4001

*Mimosa pigra* L. (Fabaceae), one of the most troublesome weeds in northern Australia, has been the target of biological efforts for 30 years, but still remains a serious problem. *M. pigra* is also a subject to a sporadic dieback phenomenon first reported in 1988 on the Adelaide River floodplains. This phenomenon is associated with reddish-brown lesions originating from the leaf axil, yellowing of the leaves and subsequent stem death. Previous work consistently isolated the fungus *Botryodiplodia theobromae* Pat. (= *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl.) from plants that exhibited these dieback symptoms. We used field surveys to test whether fungal endophyte communities in *M. pigra* differ with dieback symptoms. A culture-based approach was used to survey the fungal communities in stems collected from the twenty-two non-randomly selected sites representing the different levels of dieback expression (from healthy to recovering dieback rating sites) observed in the Mary and Daly River catchments of northern Australia. Stems were collected during the early wet and dry season in 2012. Fungal cultures were isolated from extensively surface sterilised tissue pieces placed on four types of media (PDA, V8A, MA and WA) and then grouped on the bases of cultural morphology and sporulation. A total of 987 isolates were recovered from 189 stem samples. All stem pieces contained either one or two fungal endophytes. The most frequently isolates taxa common across all sites were from the genera *Phomopsis* sp., *Pestalotiopsis* -type, from the family Botryosphaeriaceae (including *L. theobromae*) and Sterilia Mycelia. *Alternaria, Cladosporium, Colletotrichum, Epicoccum, Fusarium, Phycomyces*, and *Trichoderma* were isolated at very low frequencies. Endophytic communities were not significantly different in healthy and dieback-affected sites and between seasons when compared using Shannon-Wiener indices. This preliminary study demonstrated that *M. pigra* harbors abundant and diverse fungal endophytic communities. However, the lack of differences in fungal communities between *M. pigra* populations with different levels of dieback expression is surprising. Further work is therefore required to conclusively confirm any role fungi may have in causing the dieback phenomenon.
Calcium-dependent protein kinases (CPKs) are plant proteins that directly bind calcium ions before phosphorylating substrates involved in metabolism, osmosis, hormone response, and stress-signalling pathways. A comprehensive genome-wide analysis of CPKs from algae to higher plants has been used to identify the most conserved members of this gene family, which form Group IIB. These CPKs have the highest degree of sequence conservation between species but show functional distinction between paralogues within a genome, unlike other CPK groups which do not show any pattern in function. In Arabidopsis, CPKs that belong to this group are AtCPK3, 17 and 34. Based on microarray and the few functional studies, AtCPK3 responds to osmotic stresses and bacterial elicitors, but very little is known about its involvement during infection by different plant pathogens. AtCPK17 and 34 on the other hand are undetectable throughout the plant except in floral tissues, where they are highly expressed; these are involved in pollen development but no stress response association has been reported for these two CPKs. A similar pattern in function is seen in Group IIB CPKs in rice and poplar. We investigated the function of AtCPK3 and its orthologues in rice (OsCPK1 and 15) and kiwifruit (AcCPK16), in response to bacterial *Pseudomonas syringae* DC3000, fungal *Botrytis cinerea* and viral infections. Leaf samples were taken at 0, 1, 2, 6, 10 days post inoculation (dpi) for *P. syringae* and *B. cinerea*, and 0, 2, 3, 7, 14, 21 and 28 dpi for virus infections. The transcript accumulation of AtCPK3 and its orthologues was measured using reverse-transcriptase quantitative PCR (RT-qPCR). Transgenic Arabidopsis and kiwifruit lines that over-express and/or are ablated of AtCPK3 and AcCPK16, respectively, have been generated or acquired (AtCPK3 T-DNA knockout lines were acquired from Salk Institute). Phenotypic analysis of these lines in response to infection includes symptom severity scores, plant (inflorescence) height, number of leaves, leaf rosette diameter and dry weight. AtCPK3 and its orthologues may present good target genes for a study of biotic and abiotic stress tolerance that is applicable to a broad range of plant species.
Peach latent mosaic viroid mutates rapidly in peach seedlings

Dr Arezou Yazarlou
University of Adelaide
arezou.yazarlou@adelaide.edu.au

Arezou Yazarlou, John W Randles
The University of Adelaide, School of Agriculture, Food and Wine, Waite Campus, Urmbrae, SA 5064, Australia

Viroids are circular infectious RNAs that range in size from 246 to 399 nucleotides, do not code for any proteins, and use host plant machinery for replication, processing and transport. They present signals to the host machinery by their structure and sequence. They replicate by a rolling circle mechanism with specific sequence motifs within the viroid molecule controlling replication, symptom severity and interference with plant RNA silencing machinery. Structure and sequence are used for classifying these minimal plant pathogens. Peach latent mosaic viroid (PLMVd, Pelamoviroid, Avsunviroidae) is established in Australasia. We maintained a field isolate in 2 grafted peach seedlings for 12 years, and found that the sequences recovered from each of these showed 92% similarity only. This result confirmed the known quick generation of sequence heterogeneity in natural PLMVd infections. We decided to determine the speed at which sequence heterogeneity was generated by inoculating two recombinant viroid clones derived from the grafted peaches to peach seedlings (cv Nemaguard), maintaining the inoculated seedlings at 30°C for 30 days. PLMVd was detected by RT-PCR at 21 days in 7/9 seedlings, and symptoms appeared at 28 days. Reisolation, cloning and sequencing from 6 plants showed that the progeny viroid differed from the parent viroid clone in both genome size and sequence. Each clone differed from the parent clone by 20 mutations in this single passage. The mutations were distributed unevenly, and did not occur in known conserved ‘hammerhead arm’ and ‘kissing loop’ regions of the viroid. The branched structure of the viroid is stabilized by a pseudoknot between 2 kissing loops. These results, with an average of 20 substitutions for each clone observed within one passage, and apparent protection from mutation of specific regions, lead to the following conclusions: (i) the generation of mutants estimated at a rate of $6.5 \times 10^{11}$ nt/site/year is about 1000-fold higher than for RNA viruses; (ii) variants of PLMVd occur independently of the sequence in the initiating infection, and therefore pathogenic forms may appear rapidly; (iii) primers for detection of PLMVd infection in plant health programs need to be derived from conserved regions of the viroid sequence.

An intraspecific recombinant begomovirus from the Nile Basin

Dr Mohammed Alsaleh
King Saud University
malsaleh@yahoo.com

Mohammed Al-Saleh(1), Ibrahim AlShahwan(1), Omer Abdalla(1), Mahmoud Amer(1), Judy Brown(2), Ali Idris(3)
(1) Department of Plant Protection, King Saud University, Riyadh, Saudi Arabia
(2) School of Plant Sciences, The University of Arizona, Tucson, AZ 85721, USA
(3) Center for Desert Agriculture, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia

Tomato leaf curl Sudan virus (ToLCSDV) is a single stranded DNA begomovirus of tomato causes downward leaf curl, plant yellowing and stunting, and contributes significantly to yield reduction in the Nile Basin agro-ecosystems. These disease symptoms resembling those caused by Tomato yellow leaf curl virus, a widespread and a better studied begomovirus originated in the Middle East. Recently, tomato samples exhibiting similar symptoms were collected from Gezira, Sudan. The complete genome of 2766 bases from these samples was amplified using rolling circle amplification, cloned and sequenced for a new variant of ToLCSDV that shared the highest nucleotide identity with Shambat strain at 96%. These new variants shared 88% and 90% identity with Omani and Yemeni strains of ToLCSDV, respectively, strains cloned from the arid and semiarid southern region of the Arabian Peninsula. Analysis of the complete sequence revealed that this new variant is a natural recombinant between two previously reported strains of ToLCSDV. Agro-infiltration of the cloned genome shown to be infectious based on symptom development and detection of the virus in the convenient model host Nicotiana benthamiana 7-10 days post-inoculation. Phylogenetic analysis partitioned ToLCSDV strains based on their geographical origin.
Genetically diverse phytoplasmas strains cause devastation of sesame crop in Northern and Southern India

Mr Sachin Kumar
University of Delhi
sach_inom@yahoo.co.in

Sachin Kumar(1), Vibhuti Singh(1), Suman Lakhanpaul(1), Kangila Venkataramana Bhat(2).

(1)Plant Molecular Genetics Laboratory, Department of Botany, University of Delhi, Delhi-110007, India
(2)National Research Centre on DNA Fingerprinting, National Bureau of Plant Genetic Resources, New Delhi-110011, India

Sesame (Sesamum indicum) is a common host of phytoplasma (a group of wall-less plant pathogenic bacteria, Mollicutes) which causes disease ‘phyllody’. To determine the taxonomic status of phytoplasma affecting sesame in different eco-geographical regions in India collections were made from Northern and Southern parts of the country (2007-2010). Nested-Polymerase Chain Reaction assays targeting partial 16S ribosomal DNA regions of phytoplasma showed all symptomatic plants to be positive for phytoplasma. Subsequent, restriction fragment profiling (using HpaI, MseI and TaqI), sequencing and phylogenetic analysis of these products revealed diversity in the phytoplasma isolates affecting the sesame crop. Isolates from North India predominantly belonged to group 16SrI-B (’Candidatus’ Phytoplasma asteris), except the 2007 phytoplasma isolate which stood distinct as a group 16SrII member. Sesame phyllody phytoplasma from south showed the presence of three different 16SrII strains, 16SrII-A, 16SrII-C and 16SrII-D. This is the first report of an intricate phytoplasmal diversity attributed to widely distributed host sesame from India.
Real-time PCR and High-Resolution Melting Analysis for differentiation of Phytophthora species

Dr Rebecca McDougal
Scion, 49 Sala Street, Rotorua, 3046, New Zealand.

New Phytophthora species are being isolated and described at an increasing rate. However, identification of Phytophthora species can be time-consuming and culturing is not always successful. High-resolution melting analysis (HRMA) is a rapid, high-throughput method that can differentiate species based on the DNA sequence of a PCR amplicon. During real-time PCR amplification a fluorescent dye is incorporated into the double-stranded DNA, intercalating between every nucleotide. When subjected to a temperature gradient the double-stranded DNA molecule “melts” and releases the fluorescence. The melting profile of different DNA sequences is reflected in the fluorescence released over time, and can be expressed as the optimal melting temperature. Here we describe a method developed for rapid, high-throughput identification of Phytophthora species, using HRMA. The focus of this study is concerned primarily with Phytophthora species associated with forest diseases, for diagnostic and biosecurity purposes. These species include Phytophthora of national and international concern to commercial and exotic tree species. The ability to quickly diagnose overseas threats like P. ramorum, P. pseudosyringae and P. pinifolia is a high priority for this project. This method is being developed for use by the Forest Health Reference Laboratory at Scion, where a diagnostic service for woody plants is provided (as part of the High Risk Site Surveillance program) to the Ministry for Primary Industries and the forest industry. Using HRMA, we have screened genetic regions including the HSP90, beta-tubulin, enolase, and elongation factor genes. This revealed that a region of the beta-tubulin gene shows promise for differentiation of Phytophthora species.

Checking Possibility of Designing Specific Primer for Fusarium oxysporum f. sp. sesami, the Causal Agent of Yellows and Wilt of Sesame in Fars Province in Iran by Using β-tubulin Gene Sequencing

Dr Seddiq Mohammadi
Shiraz Islamic Azad University, Iran
Mohammadi.pp@gmail.com

Seddiq Mohammadi(1), Rasul Zare(2), mohammadd Razavi(3)

(1)Department of Plant Pathology, Collage of Agricultural Sciences, Shiraz Islamic Azad University, Shiraz, Iran
(2)Department of Botany, Iranian Research Institute of Plant Protection, Tehran, Iran
(3)Department of Plant Pathology, Iranian Research Institute of Plant Protection, Tehran, Iran

Fusarium oxysporum f. sp. sesami the causal agent of Sesame yellows and wilts disease, is one of the most destructive disease which is a major production constraint in cultivation of this crop. For determining of β-tubulin gene sequencing and checking possibility of designing specific primer for diagnosis of this formae specialis in Fars Province, pathogen was isolated from sesame plants in major sesame growing area. After pathogenesis test, DNA was extracted. For multiplying of β-tubulin gene two primers BtmycF and BtmycR were used. Product of β-tubulin gene multiplying sequenced after purification. Result of sequencing was determined in gene bank by BLASTN (ver.2.2.17) and was confirmed its correctness. Sequencing of this part of genome was aligned with other formae specialis and other species of Fusarium oxysporum. Phylogenetic tree was diagramed according to compare of about 220 bp of β-tubulin region according to Neighbour-Joining method. Bands that formed for all isolates were 550 bp. All isolates of Fusarium oxysporum f. sp. sesami located in one group. Isolates derived in two groups by 50 present of Bootstrap value. Isolates of Fasa, Estahban and Noorabad were located in Group A and Isolates of Darab, Neyriz and other isolates of Fasa were located in Group B. There were no genetic difference between isolates of Group A but Isolates of Group B had genetic difference. Fusarium oxysporum f. sp. sesami and Fusarium oxysporum f. sp. ircicis were closer than Fusarium oxysporum f. sp. phaseoli from genetically. This gene had able to separate this formae special from other formae specialis of Fusarium oxysporum that were β-tubulin gene sequencing in gene bank. So it seems β-tubulin gene sequencing can provide possibility of designing specific primer for diagnosis of Fusarium oxysporum f. sp. sesami. Key words: Fusarium oxysporum f. sp. sesami, β-tubulin gene and specific primer.
**Rep-PCR based Genetic Diversity of Macrophomina phaseolina Isolated from Sesame Plants in Different Regions of Iran**

Dr Naser Safaie  
Tarbiat Modares University  
nsafaie@modares.ac.ir  
Naser Safaie(1), Mohsen Naderpour(1)

Department of Plant Pathology, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran  
Phone:+982148292346  
FAX:+982148292200

Macrophomina phaseolina (Tassi) Goid the causal agent of charcoal rot is a soilborne pathogen of global distribution and a wide host range of more than 500 species from 75 plant families. The genetic diversity of 90 M. phaseolina isolates from sesame plants in 11 provinces of Iran was studied. All isolates were taxonomically identified with species-specific primers. NTSYSpc 2.0 software, Jaccard similarity coefficient and UPGMA approach were applied in data analyses with each marker. Using five rep-PCR primers applied in genetic diversity studies, 83 loci were overall amplified out from that 92.77% were polymorphic. The highest percentage of polymorphism was obtained with two REP2-I and ERIC 1R primers (100%) and the lowest percentage of polymorphism was found with ERIC 2I (75%). The highest polymorphism information content was found with ERIC 1R and ERIC 2I (0.37) and the lowest was obtained with ERIC 2I (1.96). No considerable relationship was found between genetic diversity and geographical origin of the isolates, however, the best geographical origin-based grouping was resulted using UPGMA cluster analysis methodology with the sum of indices leading to the generally close grouping of the isolates of the same or adjacent geographical origin. Iranian populations of the pathogen exhibited high genetic diversity similar to those in other countries. Results from this investigation are of potential applications in the management of sesame charcoal rot as well as in the evaluation of the resistance of sesame genotypes against the disease.

**Phenological, morphological, pathological and genetical diversity of Iranian isolates of Alternaria alternata, the causal agent of early blight disease of potato**

Dr Abbas Sharzei  
University of Tehran  
asharze@ut.ac.ir  
Elham Sadeghi(1), Mehdi Nasr Esfahani(2), Abbas Sharzei(3)

(1)Department of Plant Pathology, Marvdasht Branch, Islamic Azad University, Marvdasht, Iran  
(2)Agricultural and Natural Resources Research Center, Isfahan, Iran  
(3)Department of Entomology and Plant Pathology, Aburaihan Campus, University of Tehran, Iran

Early blight, caused by Alternaria alternata, is one of the most important fungal diseases of potato. In this study, various isolates were collected from major potato growing regions of Iran, including Isfahan, Ardabil, Fars and Hamadan provinces. The colony colour, spore length, width and number of cells were determined for each isolate on PDA and CMA at four pH ranges. Pathogenicity tests under greenhouse conditions showed that the isolates are significantly different in this regard. To determine the genetic diversity, DNA of each isolate was extracted and PCR amplified with 15 primers. After agarose gel electrophoresis, the genomic bands were analyzed and data matrix prepared by using NT SYS-PC software. Statistical analysis results showed that clustering of the isolates based on the primer OPP-16 (5’-CCAAGCTGCC-3’) is the most similar to their clustering based on virulence. Therefore, this primer can be used to detect the virulence of each isolate.
Identification of Setophoma terrestris, the causal agent of onion pink root rot, based on ITS-rDNA sequencing

Dr Abbas Sharzei  
University of Tehran  
asharze@ut.ac.ir  
Maryam Bastani(a), Abdorahman Fassihiani(a), Abbas Sharzei(b)  
(a)Department of Plant Protection, Marvdasht Branch, Islamic Azad University, Marvdasht, Iran  
(b)Department of Entomology and Plant Pathology, Aburaihan Campus, University of Tehran, Iran

Pink root rot, caused by Setophoma terrestris, is one of the contributing factors in onion yield reduction in Fars province, Iran. Characterization of this pathogen is mainly based on morphological criteria. The fungus is a slow growing pathogen and rarely sporulates in culture media; hence, isolation and identification based on routine mycological techniques, due to the presence of other fast growing saprophytes and onion pathogens, requires high experience. In this study, both morphological and molecular techniques based on polymerase chain reaction were used to detect the pathogen. For ITS-rDNA sequencing, the fungal isolates were grown on PDA for 10-14 days. DNA was extracted from 10 isolates with morphological criteria. The fungus is a slow growing pathogen and rarely sporulates in culture media; hence, isolation and identification based on routine mycological techniques, due to the presence of other fast growing saprophytes and onion pathogens, requires high experience. In this study, both morphological and molecular techniques based on polymerase chain reaction were used to detect the pathogen. For ITS-rDNA sequencing, the fungal isolates were grown on PDA for 10-14 days. DNA was extracted from 10 isolates with morphological criteria corresponding to S. terrestris, using extraction kit. Regions of ITS1, 2, 5.8 S and a portion of the 28S rDNA genes were amplified using ITS4 and ITS5 universal primer set. The amplified fragments, of ca 600 bp, were purified, cloned, sequenced and compared to the sequences from GenBank. The ITS-rDNA sequences of S. terrestris isolates from onion fields in Fars province showed 99% homology to each other and 93.5% homology to the sequences from other isolates of the species. Use of this molecular technique could facilitate rapid and accurate detection of this fungus.

Biodiversity of Trichoderma and Hypocrea species in New Zealand

Dr Johanna Steyaert  
Bio-Protection Research Centre, Lincoln University  
johanna.steyaert@lincoln.ac.nz  
Johanna Steyaert(1), Mark Braithwaite(2), Kristen McLean(3), Peter Johnston(4), Robert Hill(5), Shelley Ball(6), Alison Stewart(7), John Bissett(5)  
(1)Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand  
(2)Landcare Research, Private Bag 92170, Auckland Mail Centre, Auckland 1142, New Zealand  
(3)Natural Resources Canada, 580 Booth Street, Ottawa, Ontario K1A 0E4, Canada  
(4)Marrone Bio Innovations, 2121 Second St, Davis, California 95618, USA  
(5)Agriculture and Agri-Food Canada, 960 Carling Ave, Ottawa, Ontario K1A 0C6, Canada

A taxonomic study of New Zealand Trichoderma/Hypocrea species in the Bio-Protection Research Centre and Landcare Research fungal culture and herbarium collections was completed. Sixty-five species of Trichoderma were identified, including 16 species which appear to represent undescribed taxa. The New Zealand species are positioned within nearly every major Trichoderma clade, with terminal lineages of the Harzianum clade, Citrina clade, and Trichoderma section well represented. This wide diversity of species suggests that a broad spectrum of ancestral Trichoderma species from the super-continent Gondwana may have survived the marine transgression of the New Zealand land mass. Subsequently, populations may also have been supplemented and maintained by trans-oceanic dispersal mechanisms, such as ocean currents and animal migrations from Australia and the subtropical land areas north of New Zealand. The New Zealand Trichoderma species were isolated from above ground (e.g. wood, bark, leaves) and below ground (roots, soil) sources. From above ground substrates, ten Hypocrea species were reported only from New Zealand. A further seven species were known only from New Zealand and Australia. Below ground, the most common Trichoderma species isolated in New Zealand was an undescribed sister species to the cosmopolitan Trichoderma atroviride, which also occurs in New Zealand. The Trichoderma below-ground isolates had a much higher proportion of species occurring outside New Zealand with a broad, pan-tropical or subtropical distribution. This pattern of distribution is indicative of frequent introductions either by natural mechanisms within the local region or by the activities of humans such as colonisation and the movement of soil and plant material. The diversity of Trichoderma species in New Zealand, their taxonomic relationships, distribution, ecology, and possible origins will be discussed.
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