Welcome

The Organising Committee of the 9th Australasian Soilborne Diseases Symposium (9thASDS) welcomes plant pathologists, interested researchers and industry representatives to Lincoln University.

The 9thASDS continues a burgeoning tradition of similar Symposia, which have been held biennially (more or less) since 1999. The first Symposium began the tradition, where Dr Rob Magarey expressed the hope that “the First Australasian Soilborne Diseases Symposium will not be the last.” He and his supporting Organising Committee established what has become an institution within the auspices of the Australasian Plant Pathology Society. The 9thASDS Organising Committee is honoured to be able to continue to build on the foundations established by Rob Magarey and his colleagues.

The 9thASDS brings researchers from “all quarters” of the world to Lincoln University (particularly from Australia and New Zealand, but also from most of the world continents). We can enjoy the excellent Lincoln University venue, to support knowledge exchange, personal interactions and collaborative endeavour. The invited speakers who will outline latest knowledge developments in specific aspects of soil biology and pathology form a very impressive cohort of relevant expertise, experience and research achievements. Our focus is in a facet of plant pathology where plant diseases continue to provide severe challenges for plant health in crop production and heritage plant communities. The pathogens we deal with, the complexities of soil environments, and the very important economic and cultural consequences of diseases of plant roots, make our sector of the plant pathology discipline particularly challenging. The 9thASDS will be another very worthwhile event for our branch of the biological sciences.

A feature of the delegate list for this Symposium is the number of postgraduate student researchers attending and presenting their results. This is an encouraging sign for the wellbeing of our research disciplines, and we wish them well for their educational endeavours and future contributions.

I here record particular appreciation for the contributions of members of the 9thASDS Organising Committee, including the Lincoln University Conference and Event Management personnel, for their efforts over the last 2 years as we have worked towards this Symposium. I also acknowledge the financial and in-kind assistance of the Symposium sponsors, whose contributions have helped to bring the invited speakers to the Symposium.

I wish all 9thASDS attendees a very enjoyable and worthwhile stay at Lincoln and New Zealand.

Professor Richard E Falloon
Chairperson, 9thASDS Organising Committee
9th Australasian Soilborne Diseases Symposium

Symposium Organising Committee

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Donna Gibson, Robert Lamberts, Richard Falloon, Lincoln University

Footnote: As a result of the earthquake of 14 November 2016, this symposium was relocated from Hanmer Springs to Lincoln University.
Programme

Monday 14 November 2016

2.00 pm  Depart Sudima Hotel, Christchurch Airport

5.30-7.00 pm  Welcome Reception

Wednesday 16 November 2016

6.30 pm  Symposium Dinner

Thursday 17 November 2016

2.00 pm  Depart, Lincoln University

[Correct at time of print]
Tuesday 15 November 2016

8.30 am Symposium Opening

Soil health

Invited paper
8.45 am Going back to the roots: microbiology and chemistry at the plant-soil interface
Jos M Raaijmakers

Offered oral papers
9.30 am Functional composition of a disease suppressive community in an agricultural soil
Vadakattu Gupta, Christopher Penton, Jiarong Guo, Stephen Neate, Michael Gillings, Kathy Ophel-Keller, Paul Greenfield and James Tiedje
9.45 am Measuring soil health: free living nematode communities offer soil health insights
Sarah J Collins & Katherine J Linsell
10.00 am Characterising the growth and disease expression of Phytophthora agathidicida within soils of contrasting land uses
Kai Lewis, Amanda Black, Nick Waipara, Peter Scott & Nori Williams

Offered poster paper
Putative powdery scab suppressive potato field soils in Victoria, Australia
Tonya J Wiechel & Nigel S Crump

10.15-10.45 am Morning tea

Pathogen distribution and disease epidemiology

Offered oral papers
10.45 am Regional distribution of soilborne diseases in cereal crops in Australia
Vadakattu Gupta, Marcus Hicks, Alan McKay, David Gobbett, Jackie Ozman & Roger Lawes
11.00 am Exploring the influence of environment on the yield response of wheat affected by crown rot
Clayton Forknall, Steven Simpfendorfer & Alison Kelly
11.15 am The contribution of soilborne disease to sub-optimum yields of process potatoes in Canterbury, New Zealand
Sarah Sinton, Richard Falloon, Farhat Shah, Steven Dellow & Alex Michel
11.30 am Role of pathogens in the pea black spot disease complex in causing severe epicotyl and root disease on field pea (Pisum sativum)
Hieu S Tran, Ming Pei You, Tanveer N Khan & Martin J Barbetti

Offered poster papers
Soilborne fungal pathogens (Rhizoctonia solani and Fusarium oxysporum) are threats to fodder beet production in New Zealand
Farhat Shah, Sooje Chng & Shane Maley
Genotyping of potato cyst nematode in Victoria
Jacky Edwards, Arati Agarwal, John Wainer, Mark Blacket, Rudolf F de Boer, Tonya J Wiechel, Maggie D Triska & Michael Renton

11.45-1.30 pm Lunch
Disease management

Invited paper
1.30 pm  Management of soilborne diseases  
Steven B Johnson

Offered oral papers
2.15 pm  Soil fumigation for control of violet root rot in carrots  
Ian J Horner, Ellena G Hough & Brent M Fisher
2.30 pm  Enhancement of natural resistance of Capsicum annuum L. against anthracnose through selected postharvest treatments  
C Mahendranathan, NKB Adikaram & T Jayasingam
3.00 pm  Management of Pythium leak of potato from field to storage in Idaho, USA  
Phillip S Wharton, Isela Carrillo, Katie L Fairchild & James Woodhall

3.15-3.45 pm  Afternoon tea
3.45 pm  Biofumigation potential of Brassica crops for control of soilborne disease of potato caused by Rhizoctonia solani  
Le P Thanh, Richard E Falloon, Hayley J Ridgway & E Eirian Jones
4.00 pm  An integrated research-to-practice approach to soilborne disease threats in the Australian vegetable industry  
Kelvin Montagu, Gordon Rogers, Doris Blaesing, Len Tesoriero, Marc Hinderager, Donn Lucas, Kathy Ophel-Keller, Michael Rettke & Julie Finnigan
4.15 pm  Alternatives to the management of apple replant disease in South Africa  
M Nyoni, M Mazzola & A McLeod
4.30 pm  Verticillium dahliae affects tomato root morphology and plant defence responses  
Rita Grosch, Anja Buhtz & Dietmar Schwarz

Offered poster papers
Detection of mefenoxam resistance in Pythium ultimum on barley in Southern Idaho, USA  
Sandesh Dangi, James Woodhall, Katie L Fairchild, Juliet Marshall & Phillip S Wharton
Resistance of weeds from the Australian northern grain region to the root lesion nematodes, Pratylenchus thornei and Pratylenchus neglectus  
Kirsty Owen, Kerry Bell & John Thompson
Evaluation of biological and novel seed and in-furrow treatments for the control of Rhizoctonia diseases of potato  
Phillip S Wharton, James Woodhall, Isela Carrillo & Katie L Fairchild
Neem leaves protect chickpea from charcoal rot (Macrophomina phaseolina)  
Ali Morzoog Salman & David Backhouse
Lack of efficacy of methyl bromide to eliminate live root knot nematodes (Meloidogyne spp.) from fresh ginger rhizomes  
Jennifer Cobon, Mike Smith & Pauline Wyatt
Wednesday 16 November 2016

Biological control

Invited paper
8.30 am  Bridging the plant microbiome and biocontrol of soilborne pathogens with multi-omics  
Gabriele Berg

Offered oral papers
9.15 am  Forage production following Trichoderma atroviride application in the presence of soilborne pathogens  
Wadia DR Kandula, John G Hampton, Janaki Kandula, Carmen SP Teixiera & Leila Dadian
9.30 am  Can cold tolerant variants of Trichoderma atroviride wild type isolates enhance control of soilborne pathogens?  
Janaki Kandula, Wadia DR Kandula, John G Hampton, Harmanjeet Kaur & Adele Scott
9.45 am  Biodegradation of basal stem rot-affected oil palm stumps by white-rot Hymenomycetes: potential disease management by prevention of inoculum spread  
Yuvarani Naidu, Yasmeen Siddiqui, Mohd Yusof Rafi, Halimi Mohd Saud & Abu Seman Idris
10.00 am  Soil health indicators to aid management of soilborne disease in ginger production  
Anthony B Pattison, Jenny A Cobon, Tegan L Kukulies, Anna McBeath, Mike K Smith & Rob Abbas

10.15-11.00 am  Morning tea

11.00 am  Arbuscular mycorrhizal fungi enhance growth and modify essential oil content in Leptospermum scoparium (mānuka)  
Wisnu Adi Wicaksono, Catherine E Sansom, E Eirian Jones, Nigel B Perry, Jana Monk & Hayley J Ridgway
11.15 am  Potato root exudates contain stimulants of resting spore germination of Spongospora subterranea  
Mark A Balendres, David S Nichols, Robert S Tegg & Calum R Wilson
11.30 am  Development of an integrated management system to suppress Fusarium wilt of bananas  
Anthony B Pattison, Stewart J Lindsay, David East, Katelyn Ferro, Anna McBeath, Tegan L Kukulies, Shanara McComoskie, Trevor Parker, Peter Trevorrow, Kathy Grice & Lucy Tran Nguyen

Offered poster papers

Use of root endophytic Trichoderma isolates for bioprotection of oil palm against Ganoderma disease in Sarawak, Malaysia  
Robert Hill, Flor Agbayani, Nicholas Cummings, Audrey Okang, Rogellio Valdez, Mark Walker & Ivan Chirino-Valle
Influence of tomato root exudates on antagonism of Fusarium oxysporum f. sp. lycopersici by non-pathogenic Fusarium oxysporum  
Hayder Ali & David Backhouse
Assessment of the biocontrol efficacy of nematode trapping fungi against root-knot nematodes  
Karli M Groves, PUS Peiris, Phillip H Brown & Yujuan Li
Trichoderma isolates for biocontrol of Rhizoctonia stem canker of potato  
Usamah Alshimaysawe, David Backhouse & Paul Kristiansen

11.45-12.15 pm  Poster viewing and discussion
12.15-1.00 pm  Lunch
Biosecurity

Invited paper
1.00 pm  Can high throughput sequencing be used in biosecurity? A case study of Phytophthora in Australia  
Treena Burgess

Invited paper
1.45 pm  The challenges and opportunities in protecting New Zealand’s biodiversity and taonga plant species from invasive soilborne plant pathogens  
Nick Waipara

2.45-3.15 pm  Afternoon tea

Host resistance for disease management

Offered oral papers
3.15 pm  Variety resistance and pre-sowing Pratylenchus thornei population densities affect post-harvest nematode populations in wheat and barley  
Joshua P Fanning, Karyn Reeves & Grant Hollaway

3.30 pm  Selection of genotypes for resistance and tolerance to pathogens: a combined statistical analysis of yield and disease response  
Alison Kelly, Bethany Macdonald, Cassandra Percy & Phil Davies

3.45 pm  A genome-wide association approach to identifying new resistance loci to common root rot in contemporary barley breeding programmes  
Stephen M Neate & Sanjaya Gyawali

4.00 pm  Different winter cereal reactions to root and crown rot pathogens  
Ahmed Saad, Anke Martin, Noel Knight, Alison Kelly & Cassandra Percy

4.15 pm  Testing kauri (Agathis australis) for resistance to Phytophthora agathidicida  
Stanley Bellgard, Chantal Probst & Nari Williams

4.30 pm  Screening Agathis australis (kauri) genotypes for resistance to Phytophthora agathidicida  
Peter Scott, Echo Herewini, Martin Bader & Nari Williams

Offered poster papers
Resistance screening of pea varieties to Fusarium root rot in New Zealand  
Rachael M Warren, David Goulden, Ruth C Butler & Soonie F Chng

Using Normalised Difference Vegetation Index (NDVI) to select wheat genotypes for tolerance to the root-lesion nematode Pratylenchus thornei  
Neil Robinson, Jason Sheedy, Michael Mumford, Alison Kelly & John Thompson
Thursday 17 November 2016

New technologies, pathogen detection and diagnostics

Invited paper
9.00 am Risk-based detection and diagnosis of plant pathogens using new technologies
Andrew Pitman

Offered oral papers
9.45 am Species identification and genetic diversity analysis of the pathogen causing crown rot of wheat in China
He Xiaolun, Zhou Haifeng, Ding Shengli, Chen Linlin, Yuan Hongxia & Li Honglian
10.00 am What happens to the DNA of Rhizoctonia solani and Pratylenchus neglectus in soil under different storage conditions over time?
Daniel Hüberli, Sarah Collins & Carla Wilkinson
10.15 am Detection and infectivity of Peronospora sp. in the soil environment of poppy crops
Amy Lucas, Tamilarasan Thangavel, Suzie J Jones, Jason B Scott & Calum R Wilson

10.30-11.00 am Morning tea

11.00 am Rhizoctonia solani: the root of yield decline in oilseed rape (Brassica napus)?
Alexander W McCormack, Matthew A Back, Simon G Edwards & Peter R Mills
11.15 am Root rot disease complex of process peas in Canterbury, New Zealand
Bhanupratap R Vanga, Soo Hee Chng, Rachael M Warren, Ruth C Butler, David Goulden & Syama Chatterton
11.30 am New insights into the infection of potato by Pythium ultimum, from real-time PCR and isothermal detection methods
James Woodhall, Sandesh Dangi, Katie Fairchild & Phillip S Wharton
11.45 am Pathogenicity of Verticillium dahliae and Verticillium albo-atrum on potato cultivars Denali and Russet Burbank in Australia
MY Shin, TJ Wiechel, NS Crump & PWJ Taylor
12.00 noon Efficient sampling for assessing crown rot in wheat
Bethany Macdonald, Cassandra Percy & Alison Kelly
12.15 pm A flexible design to generate yield loss response curves for the root lesion nematode (Pratylenchus thornei) for wheat cultivars differing in nematode tolerance
Kirsty Owen, Clayton Forknall, Karyn Reeves, John Thompson & Grant Holloway

Offered poster papers
Characterising isolates of Rhizoctonia recovered from crops in the Pacific Northwest USA
James Woodhall, James Rutter, Katie Fairchild & Phillip S Wharton
Initial identification of fungal pathogens of a beetroot (Beta vulgaris L.) seed crop in New Zealand
Nitesh Chand, E Eirian Jones, Hayley J Ridgway & Seona G Casonato

12.30 pm Symposium closing
12.45-1.30 pm Lunch
2.00 pm Bus departs Heritage Hanmer Springs
Invited speakers

Professor Jos Raaijmakers is head of the Microbial Ecology Department of the Netherlands Institute of Ecology (NIOO-KNAW) and Professor at Leiden University, the Netherlands. The research programme of his department aims to understand the diversity of microbial communities and microbial activities in terrestrial and aquatic ecosystems. Both systems ecology and reductionist approaches are adopted to identify biotic and abiotic factors involved in microbiome assembly and activity. His research group focuses on how plant-associated microorganisms impact on plant root architecture, plant chemistry and tolerance to soilborne pathogens.

The overall goal of his current research is unravelling the diversity, dynamics and functions of microorganisms associated with plants. This is elucidating the genomic, genetic and metabolic potential of bacterial genera and species living on or in plant tissues. The functions of the plant microbiome studied in detail include protection of plants against biotic stress (pests, diseases), and modulation of root architecture, plant development, plant secondary metabolism and nutrition. Ongoing projects involve model plants, natural plant species and crops important for agriculture and the bio-based economy. His group has also initiated research to investigate microbiomes in aquatic environments. Understanding the influence of environmental conditions on the dynamics, assembly and activities of plant and fish microbiomes will help to design strategies to limit the proliferation and spread of pathogens in natural and man-made ecosystems. Next to these fundamental scientific aspects, his programme also contributes to the discovery of new antibiotic compounds and the development of novel disease control strategies to reduce pesticide use or control intractable diseases. Research in Prof Raaijmakers’ department also involves other major themes in microbial ecology, including: microbial functional diversity and dynamics in biogeochemical cycling (N, P, C) and greenhouse gas emissions (methane, nitrous oxide); bacteria/fungi interactions; decomposition of organic matter and plant biomass; volatiles in microbe/microbe communication; and metagenomics and network analyses of soil and plant microbiomes.
Assoc Prof Treena Burgess studies the biology, ecology and genetics of beneficial and detrimental microorganisms in natural ecosystems, plantation forestry and horticulture, with a focus on biodiversity and biosecurity issues. She has made significant contributions especially in pathogen population genetics, where she has designed several microsatellite markers sets that were among the first developed for fungal pathogens. She has explored cryptic speciation, pathogen movement, survival and establishment, particularly relating to forest biosecurity. Her recent research has focused on the molecular systematics and evolutionary biology of Phytophthora. She was instrumental in the recognition of 16 new species from Western Australia, and has discovered a group of Phytophthora hybrids. Many of the new Phytophthora species are endemic to Western Australia and have potential as plant community engineers, acting as causes of pre- and post-emergence damping off of endemic flora. Her recent research is using high throughput sequencing to uncover the diversity and distribution of Phytophthora across Australia and South Africa. This has involved collection of rhizosphere soil from throughout Australia (700 locations to date) and assessing their Phytophthora communities. The study has revolutionized knowledge of the diversity and distribution of Phytophthora, limits to the survival of some species and the extent of widespread invasions. Her recent publications include description of a model for the current and projected global distribution of Phytophthora cinnamomi, based on high throughput sequencing data.

Prof Gabriele Berg obtained her diploma in biology from Rostock University (Germany) in 1986 and completed a PhD degree in microbiology from the same university. She then spent one year (1987) at the University in Greifswald studying biotechnology and mycology. In 2003, she was awarded a Heisenberg grant from the Deutsche Forschungsgemeinschaft. She was appointed Professor of Environmental Biotechnology at Graz University of Technology, Austria, in 2005. Her research interests focus on microbial ecology, especially to develop understanding of plant-associated microbial communities and their interaction with plants and pathogens. Another main focus is to translate research results into new biotechnological concepts for the environment as well as for human health, for example biological control of plant and human pathogens. She has published in more than 200 peer-reviewed papers and has developed several patents. She has received numerous awards in recognition of her research achievements, including the Science2Business Award Austria and “ÖGUT Umweltpreis” (2011) and the Fast Forward Award Styria (2015).
Dr Steve Johnson is an Extension Professor and Extension Potato Specialist with the University of Maine, where he has been employed for the past 28 years. He has a BS degree from the University of Wisconsin-Madison, a MS degree from the University of Maine at Orono and a PhD from the University of Florida, all in plant pathology. He spent a 6 month sabbatical leave in Australia working on potato diseases and a similar period in New Zealand, working on potato diseases. With his interests in international agriculture, he has been a volunteer scientist in Eastern Europe and in Central America. He has served as divisional President for the American Phytopathological Society and in various leadership committee positions in the Potato Association of America. Twice receiving the Maine Potato Board’s President’s Award, he is widely recognized nationally and internationally for his expertise in potato disease control. His research and extension efforts are focused on practical applications for managing disease problems. He is currently leading and co-operating in numerous regional and national projects on disease control covering several crops. His major responsibilities in Maine are potato diseases, but he also has research and extension programmes for barley, garlic, carrot, and onion.

Dr Andrew Pitman obtained his PhD in molecular microbiology at the University of Wales Swansea and has 15 years’ post graduate experience in plant pathology. He leads the Microbial Systems Team in Plant Protection at the New Zealand Institute for Plant & Food Research (Lincoln, New Zealand), and is also Adjunct Associate Professor in the Bio-Protection Research Centre at Lincoln University. His current research spans the full spectrum of plant pathology studies, including fundamental molecular plant/pathogen interactions, greenhouse and field research. His most recently had foci have been on potato pathology and biosecurity. As the leader for potato bioprotection research at Plant & Food Research, he works closely with the New Zealand potato industry in their response to the discovery of Candidatus Liberibacter solanacearum and its associated disease zebra chip, providing knowledge and advice for seed growers dealing with this invasive pest/pathogen complex. His research has also assessed methods for the detection of soilborne pathogens such as Rhizoctonia solani, and their use as risk assessment tools for the potato industry. He continues to study the interactions of potato with the soil-dwelling bacterial pathogens belonging to the genus Pectobacterium (formally Erwinia) using genomics, transcriptomics and other molecular biology tools. This work is laying new foundations for developing disease-resistant cultivars within the Plant & Food Research potato breeding programme.
Dr Nick Waipara has a background in bioprotection-based research, specialising in plant pathology, environmental microbiology, and integrated management of soilborne diseases. His current work includes biosecurity research that underpins regional and national pest management programmes, with objectives to reduce risks and threats posed by pest plants, invertebrates, mammalian predators and invasive plant pathogens. This includes research for the New Zealand Kauri Dieback Programme (Kia ToiTū He Kauri). This is an adaptive disease management research initiative prioritised to mitigate the impacts of the Unwanted Organism, *Phytophthora agathidicida*, and its significant effects on the kauri forest ecosystem. Dr Waipara is also a Kaihautū, within the Science Leadership Group of Ngā Koiora Tuku Iho, New Zealand’s Biological Heritage Science Challenge. This role is alongside the Māori champion within the Bio-Protection Research Centre at Lincoln University. This new research consortium is facilitating and implementing investigations which incorporate mātauranga Māori to help improve management of biosecurity threats to New Zealand’s primary production and native ecosystems.
Soil health
Invited paper

Going back to the roots: microbiology and chemistry at the plant-soil interface

Prof Jos M Raaijmakers

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Plants are colonized by an astounding number of microorganisms that can reach cell densities much greater than the number of plant cells. Various studies have shown that specific members of the plant microbiome can have profound effects on plant growth and development, nutrition and tolerance to diseases and abiotic stress. For the vast majority of plant-associated microbes, however, there is limited knowledge on the mechanisms involved in modulation of plant growth and health. Novel ‘omics technologies have provided more in-depth understanding of the diversity and functioning of the plant microbiome and significant advances are being made to uncover the multitrophic interactions on plant surfaces. To better understand this intriguing complexity, systems ecology and reductionists’ approaches are both needed to identify biotic and abiotic factors involved in microbiome assembly and activity. Here, new results are presented on how soil and rhizosphere bacteria impact on plant root architecture, plant chemistry and tolerance to soilborne pathogens. We show that members of the \( \gamma \)-Proteobacteria protect plants from pathogen infection by the production of chlorinated peptides, and alter root architecture and plant growth via modulation of sulfur assimilation. For the \( \beta \)-Proteobacteria, comparative genomics, genetics, and chemical analyses revealed that specific volatile organic compounds (VOCs) affect plant growth and health. An overview will be given on the wealth of yet unknown functions of the plant microbiome and the striking similarities with the human microbiome.
Functional composition of a disease suppressive community in an agricultural soil

Vadakattu Gupta1, Christopher Penton2, Jiarong Guo3, Stephen Neate4, Michael Gillings5, Kathy Ophel-Keller6, Paul Greenfield7 & James Tiedje3

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Biological suppression of soilborne diseases has been found under various Australian agricultural environments. Improved understanding of genetic mechanisms and metabolic pathways involved with reduced disease incidence will greatly assist development of cropping practices with increased levels of natural disease suppression. In a targeted polyphasic approach, we compared functional attributes of microbial communities using metagenomic sequencing (HiSeq), catabolic diversity and potential (CLPP), composition and abundance of specific functional groups (nifH and chitinase gene harbouring microbes) of field and bioassay experimental soils in South Australia with high (SP) and low (NSP) disease suppression potential (DSP). Differences in taxonomic composition of bacteria and fungi (amplicon sequencing) were also measured. Metagenomic sequencing data showed significant differences in a number of functional attributes related to "Stress response", "Disease and defense" and "Nitrogen metabolism" between SP and NSP soils. Community metabolic diversity indices were generally greater in SP soils compared to that in NSP soils. SP soils supported large populations of nifH-gene and chitinase gene harbouring bacteria, with significant variation in nifH community composition. A diverse array of microbial (bacterial and fungal) communities are involved in the continued effective expression of disease suppression in field environments. Molecular Ecological Network analysis suggested that the suppressive community network is less condensed with greater modularity i.e. characterized by a higher functional redundancy with “small-world” interactions, whereas the non-suppressive community network is much more centralised. This indicates that the process would require interactions among multiple taxa for functional continuity and temporal stability.
Measuring soil health: free living nematode communities offer soil health insights

Sarah J Collins1 & Katherine J Linsell2

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Measuring the community structure of nematodes in soil provides a powerful tool for quantifying soil health. Quantitative real time PCR (qPCR) tests designed by SARDI provide an efficient tool for nematode community analyses. The qPCR tests quantify free-living (bacterial, fungal, predatory and omnivorous feeders) and plant parasitic nematodes. Representation in soils of these nematode feeding types indicates complexity and structure of the soil microbial community. Two independent field experiments in Western Australia used the qPCR tests to assess if a) soil amendments; or b) soil amendments combined with other management practices impact soil health in broadacre farming regimes. The Duli grower group in Cadoux applied composted refuse waste at 0, 5 and 10 t ha⁻¹ to 2 ha plots at three farms in 2014. Plots were subsequently treated according to each farmer’s normal crop rotations for three subsequent growing seasons. At Buntine, 20 t ha⁻¹ treatments of barley, oat and canola chaff were applied by Liebe Group to plots between 2003 and 2010. Different tillage, stubble management and organic matter applications were then employed over three seasons from 2010. In both experiments, soil amendments significantly affected nematode communities, with increased bacterivores, fungivores and omnivores suggesting the microbial community was more enriched and better structured in the amended soils. Soilborne diseases caused by Rhizoctonia and crown rot were reduced in composted plots at Cadoux. These experiments show that soil health was improved by the soil amendments at these broadacre farming sites regardless of specific soil type, cropping rotation or tillage practices.
Characterising the growth and disease expression of *Phytophthora agathidicida* within the soils of contrasting land-uses

Kai Lewis¹, Amanda Black¹, Leo Condron¹, Nick Waipara², Peter Scott³ & Nari Williams³

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New Zealand kauri (*Agathis australis*) is an iconic tree species of cultural significance, and an important forest ecosystem engineer and timber resource. The recently named *Phytophthora agathidicida* is hypothesized as the causal agent of kauri dieback, an aggressive root and collar rot disease which affects kauri trees of all ages. This soilborne pathogen infects roots and damages tissues which distribute water and nutrients within the tree. Surveillance studies between 2008 and 2016 have shown the widespread distribution of the disease (especially in the Auckland-Waitakare region of New Zealand). This illustrates the threat to the long-term survival of kauri. The present study is attempting to characterize the biotic/abiotic factors (e.g. microbial activity, C:N, particle analysis) of soils from contrasting land uses (e.g. indigenous kauri forest, pasture land, commercial pine forest), and provide understanding of growth response and gene expression of *P. agathidicida* within them. We suggest that the growth response of the pathogen changes between land uses and soil depths, and that RNA expression will reflect these differences. An observational study of *P. agathidicida* in each soil sample is being conducted to obtain response curves over an 8 day period. Preliminary results suggest that there is a difference in sporangium production between soil depths and an increasing trend over the observational days. Currently, data is being collected to confirm these results, and to determine their subsequent impacts on land management practices.
Putative powdery scab suppressive potato field soils in Victoria, Australia

Tonya J Wiechel1 & Nigel S Crump2

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Powdery scab of potato is an endemic disease caused by an obligate soilborne pathogen Spongospora subterranea. Symptoms include root hair infection, gall formation on roots and stolons and scab lesions on the surfaces of the potato tubers. Powdery scab causes significant yield and quality losses in fresh, processing and seed potato production. There are currently no reliable disease control measures for these diseases. Soils suppressive to pathogens have low levels of disease in spite of the presence of pathogen inoculum, susceptible hosts and conditions favourable for disease expression. Developing disease suppressive soils for Spongospora diseases represents a means for their management. Over 2 growing seasons, field monitoring was carried out to identify putative powdery scab suppressive soils in Victoria. Soil samples (114) were collected from potato fields prior to planting, and qPCR assays for S. subterranea (Predicta Pt) were applied to DNA extracted from soils to determine amounts of pathogen present. Disease risk categories were then applied. Each season, a disinfected cv. Desiree seed tuber line was planted in each field where the soil was collected. At harvest, potato tubers were visually assessed for powdery scab symptoms. Soils were considered indicatively suppressive if they had disease incidence of 10% or less but high inoculum level risk, measured by PreDicta Pt. From this survey 24 soils were identified as putatively suppressive for powdery scab. Examples of indicative powdery scab suppressive soils were found in four potato growing regions. Further investigations are required to confirm and identify the mechanisms of disease suppression.
Pathogen distribution and disease epidemiology
Regional distribution of soilborne diseases in cereal crops in Australia

Vadakattu Gupta1, Marcus Hicks1, Alan McKay2, David Gobbett1, Jackie Ozman1 & Roger Lawes3

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Soilborne root diseases are major constraints for Australian cereal production, with >$400 million annual costs. Cereals cropped continuously are at high risk from soilborne diseases. A multi-disciplinary national project was initiated in 2014 to understand the extent of yield gap in rainfed cereal crops, and identify factors driving yield limitations across Eastern, Southern and Western grain production regions. During the 2015 crop season, wheat and barley plant samples were collected at GS31 stage from paired fields at 120 farms (50 plants from five GPS locations on a 100M transect). Roots were scored for the presence and severity of diseases and overall seminal and crown root health (0-5 scale). Eight soilborne root diseases were recorded, and only a few fields (<20%) had plants without disease symptoms. Multiple diseases in a single field were commonly observed. Significant levels of most soilborne pathogens (PredictaB DNA test) were found in the pre-crop soil samples. Root rot diseases caused by *Rhizoctonia solani* AG8, *Fusarium pseudogrosminearum, Pythium* spp. and root lesion nematode were the most common. Take-all and *Bipolaris* root rot were also observed in multiple regions. Brown root rot (*Phoma scleroitedes*) less commonly recorded, mainly in fields in Eyre Peninsula (SA) and northern Western Australia. These observations coupled with water-limited yield estimations indicate that root diseases may be cause significant portions of the yield gaps in wheat and barley crops. In-crop root assessments are compared with pre-crop pathogen DNA inoculum data to identify links with soil and environmental factors affecting disease impacts.
Exploring the influence of environment on the yield response of wheat affected by crown rot

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Production losses due to foliar, crown and root diseases are major constraints in wheat and barley cropping in Australia. Losses are best quantified using response curves that relate grain yield to a measure of disease. A national project, funded by the Grains Research and Development Corporation, has coordinated the development of response curves to determine potential yield losses caused by disease on Australian wheat and barley varieties. Crown rot, caused by *Fusarium pseudograminearum*, is one of the yield-limiting wheat diseases under study in this project. Four field trials were conducted in New South Wales in 2014, where five wheat varieties were exposed to varying levels of crown rot, established through six levels of applied inoculum. Grain yields and crown rot index, a weighted average based on incidence and level of stem browning, were measured in trial plots. Response curves for yield against disease were developed using a bivariate linear mixed model. The regression nature of this model can be used to estimate the yield response (slope) and yield potential (intercept) for each variety, in each trial. Yield response and potential were used for comparison of varieties across the trials to explore potential environment interactions. This information can assist growers in varietal selection decisions to maximise returns in the presence of crown rot.
The contribution of soilborne disease to sub-optimum yields of process potatoes in Canterbury, New Zealand

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Potato crops yielding less than 55 t ha⁻¹ result in financial loss for growers. Modelling suggests that yields of 90 t ha⁻¹ should be achievable. Previous research indicated that soilborne Spongospora root diseases and Rhizoctonia stem canker, along with compacted soils restricting water uptake, are the main yield limiting factors in Canterbury potato crops. In the 2014–15 growing season, three irrigated process potato crops (=25 ha each) were regularly monitored, by measuring soil moisture (to 800 mm depth), rainfall and irrigation, plant health and yield. Net field yields were 49, 61 and 70 t ha⁻¹ (mean = 60 t ha⁻¹). The least producing crop (cv. ‘Russet Burbank’, potatoes grown 6 years previously), had high incidence and severity of soilborne diseases, causing premature crop death. There were no root restriction zones in the soil, and water supply was adequate, indicating that the soilborne diseases were the likely cause of the 36 t ha⁻¹ yield loss. Soilborne diseases were less in the other two crops. A yield gap of 23 t ha⁻¹ in one crop (cv ‘Russet Burbank’) was principally caused by inadequate water supply, intensified by a root restricting cultivation pan at 250 mm depth in the soil. The third crop grew in a field (cv ‘Innovator’, no potatoes in the previous 10 years) that was once divided in two. One original half of the field yielded to potential (90 t ha⁻¹), whereas the other half averaged 70 t ha⁻¹. Water was not limiting but contrasting crop history may have influenced yield.
Role of pathogens in the pea black spot disease complex in causing severe epicotyl and root disease on field pea (*Pisum sativum*)

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Black spot on leaves and stems of pea (caused by *Didymella pinodes*, *Phoma pinodella* and *P. koolunga*) is well described, but the roles of these pathogens as causes of root disease in field pea plants has been little explored. Two pea varieties (Kaspa; WAPEA2211) were inoculated with four individual isolates of each of the three pathogens by mixing infested millet seed into the potting mix prior to sowing. Plants were grown under controlled conditions for 5 weeks and then assessed for disease on epicotyls and roots. *Phoma koolunga* caused significant epicotyl and root rot. Despite the lower disease level on epicotyls and roots in comparison to that caused by *D. pinodes* and *P. pinodella*, two isolates of *P. koolunga* caused severe tap root rot. This is the first demonstration of *P. koolunga* as a cause of below ground disease, and the important roles of *D. pinodes* and *P. pinodella* as causes of disease on epicotyls and roots is confirmed. *Didymella pinodes* isolates caused consistently severe disease on epicotyls, and tap and lateral roots. *Phoma pinodella* isolates affected lateral and tap roots. The relative roles of these three black spot pathogens as all peas plant tissues (above and below ground) has been confirmed, indicating much greater adverse impacts on field pea than previously assumed. These results also highlight the significant challenges for breeders who need to develop cultivars with effective resistance against all three of black spot pathogens, and also against disease on above and below ground plant tissues.
Soilborne fungal pathogens (*Rhizoctonia solani* and *Fusarium oxysporum*) are threats to fodder beet production in New Zealand

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Fodder beet (*Beta vulgaris*, L.) is one of the most important forage crops for feeding animals in New Zealand. This crop can produce potential dry matter (DM) yields of more than 25 t ha\(^{-1}\). The area of fodder beet production in New Zealand has increased significantly to meet winter feeding requirements for dairy cattle and other grazing animals. Fodder beet yields are affected by biotic and abiotic factors. Soilborne fungal pathogens, causing crown and root rots, are important yield-limiting factors. During the 2015/16 growing season, diseased root samples were collected from crops in the South and North Islands. Infected samples were examined in the laboratory and incubated in a moist chamber. Pathogens were isolated from the samples and DNA was extracted from pure cultures. Internal Transcriber Spacer (ITS) fragments were amplified using ITS4 and ITS5 primer pairs. Amplified fragments were sequenced and the sequences were compared with those deposited in GenBank. BLAST comparisons indicated that the ITS fragments were most similar to *Rhizoctonia solani* AG 2-2 and *Fusarium oxysporum*. In some cases both of these fungi were isolated from individual samples. These results indicate that these pathogens may play interactive roles in crown and root rot of fodder beet. Knowledge of the primary pathogens of this crop can be used as a basis for determining their effects on yields, and for choice of disease resistant cultivars and appropriate crop rotations to reduce adverse disease effects.
Genotyping of potato cyst nematode in Victoria, Australia

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Potato cyst nematodes (PCN) are damaging soil-borne quarantine pests of potatoes in many parts of the world. There are two recognised species, 
*Globodera pallida* and *G. rostochiensis*, of which only *G. rostochiensis* is present in Australia. PCN was first discovered in Australia in 1986 in a suburb of Perth, Western Australia, was subsequently eradicated and area freedom reinstated. In Victoria, PCN was first detected in February 1991 in Wandin, east of Melbourne. Since then it has been found in small pockets in Gembrook (1991), Emerald, Keysborough and Boneo (1992), Kooweerup/Cora Lynn (2003) and Thorpdale (2008), also east of Melbourne. Strict quarantine controls have been in place since each detection. In 2007, it was speculated that there may have been up to 7 separate introductions of PCN into Victoria. In this investigation, we utilised the PCN cyst reference collection held by Crop Health Services, Agriculture Victoria, to examine the genetic variability of Victorian PCN populations to investigate the potential historical implication for geographic spread of any sequence variability. DNA was extracted from single larvae dissected from cysts and screened using seven polymorphic microsatellite markers in two multiplex PCR assays. A hierarchical sampling strategy was used, comparing variability of larvae within cysts (23), within paddocks (34) and between regions (4). Preliminary results indicate that there is very little variation, contrary to the 2007 study, suggesting that there was only a single introduction into Victoria and that PCN has been subsequently spread from one district to another.
Disease management
Invited paper

Management of soilborne diseases

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Soilborne diseases are concerns in almost every crop production system in the world. Historically controlled with crop rotation, yield and quality losses caused by soilborne diseases, especially in high value crops, are an increasingly important. While a great deal of research effort has been directed toward management of soilborne disease, changes at the grower level have been slow to come. Maximizing profitability, often in the short term, has driven most farming operations. This has resulted in highly efficient and profitable enterprises that are now relying on high input levels of technology, irrigation, fertilizers and pesticides. The scale of farming operations has grown in response to the increased costs of inputs. Grower production changes toward monocultures have been disruptive activities for soil conditions and soil microflora. Solutions from research into rotation crops, soil amendments, nutrients, and soil biology are being sought to manage soilborne diseases in a changing landscape of agricultural production. However, changes to agricultural production systems, be they pesticide use, crop rotation, or fertility, may have side effects. Soil parameters affecting productivity as well as soil biology can be affected by production changes, with not all effects being desirable or intended. Potatoes as a high value, high input crop affected by many important soilborne diseases, which provide many examples of phytopathological principles for disease control. The real-life challenge of grower adoption is an aspect of soilborne disease management that needs to be addressed.
Soil fumigation for control of violet root rot in carrots

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Carrot violet root rot (VRR), caused by Rhizoctonia crocorum, causes substantial economic losses in the Ohakune region, New Zealand. Pre-plant soil fumigation with joint applications of chloropicrin/dichloropropene (Triform®60) plus metam sodium (Fumasol™) can control the disease, but the cost of annual treatment is high. Trials were carried out in a VRR-infested site to test the carry-over effects from previous growing season fumigation, and whether fumigation in successive seasons was beneficial. Plots that had been fumigated with high rates of Triform60 (60 g m⁻²) and Fumasol (70 mL m⁻²), or left untreated the previous season were split, and either re-fumigated with low rates of Triform60 (33 g m⁻²) plus Fumasol (30 mL m⁻²) or left untreated in Year 2. In control plots left untreated in both years, disease incidence was 41% in Year 1 and 64% in Year 2, indicating greater disease pressure in plots left untreated in Year 1. Plots fumigated in Year 1 then re-fumigated in Year 2 had very low disease incidence (2% in both years). Plots fumigated in Year 1 but left untreated in Year 2 showed some carry-over of benefit, with 16% disease in Year 2, significantly less than plots untreated in both years. In plots left untreated in Year 1 then treated with the low rates of Triform60/Fumasol in Year 2, disease incidence was 29%, but reduced to 7% if the higher fumigant rates were used. This indicates that with high disease pressure, high fumigant rates are required. With low disease pressure, lower fumigant rates provided good control.
Enhancement of natural resistance of *Capsicum annuum* L. against anthracnose through selected postharvest treatments

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*Colletotrichum acutatum* was shown to be associated with chili (*Capsicum annuum* L.) anthracnose for the first time in Sri Lanka. Selected pre- and post-harvest treatments were examined for enhancement of natural resistance of chili against anthracnose, and to improve post-harvest quality. The chemical elicitor, potassium silicate, was applied as pre- and post-harvest treatments at a series of concentrations: 0 (control), 100, 200, 400 or 1000 mg L⁻¹. Potassium silicate (silicon), applied at 200 mg L⁻¹ as a monthly pre-harvest soil drench to field grown plants, commencing from initiation of flowering, reduced anthracnose when the harvested fruits were challenge-inoculated with *C. acutatum*. Postharvest application of potassium silicate at the same concentration reduced anthracnose lesion area by 25-100%, compared to the untreated controls. Post-harvest spray treatment of chili with potassium silicate at 200mg L⁻¹ at the mature, green stage reduced the severity of anthracnose by 34-100% during ripening. Spore germination assays revealed that potassium silicate has no antifungal effect on conidia of *C. acutatum*. Potassium silicate treated fruits, when inoculated with *C. acutatum* after harvest, showed greater accumulation of phytoalexins and enhanced β-1,3-glucanase activity in the tissues. Phytoalexins and Pathogenesis-Related (PR) Proteins such as β-1,3-glucanase are considered to play important roles in plant disease resistance.
Management of *Pythium* Leak of potato from field to storage in Idaho, USA

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Pythium leak, caused by *Pythium ultimum*, has been a major storage disease problem in the Pacific Northwest (PNW) and Idaho potato production areas for many years, but in recent years reported losses have increased. In storage, *Pythium*-infected tubers rot quickly and create wet areas which enhances tuber breakdown, leading to severe losses. Current measures for controlling *Pythium* include fungicide applications of mefenoxam in-furrow and to foliage. Recently, mefenoxam resistant strains of *P. ultimum* have been found in PNW potato production areas. Despite the risk of resistance and the cost of mefenoxam, it is still widely used in potato production in this region due to its efficacy in managing Pythium leak and the lack of effective alternative compounds. Pythium leak is most often seen at harvest or during storage. Also recently, however, extensive damage has been found weeks ahead of harvest, particularly in fields with high levels of fungicide resistance. This indicates higher disease risk from resistant isolates than sensitive ones. Fungicide efficacy trials in were carried out to evaluate new reduced risk fungicides for the control of *Pythium* leak in the field and going into storage. Several new foliar fungicides were identified which had good efficacy against *P. ultimum*, along with an effective postharvest treatment for control of Pythium leak in storage.
Biofumigation potential of *Brassica* crops for control of soilborne disease of potato caused by *Rhizoctonia solani*

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Biofumigation using *Brassica* crops is a promising alternative to agrochemicals for control of potato disease caused by *Rhizoctonia solani*. A dual Petri plate study determined the effects of macerated tissues from ten different *Brassica* types, including mustards (‘Caliente 199’, brown, white), ‘Nemat’ arugula, radishes (‘Lunch’, fodder), kale (‘Corka’), rapeseed, forage rape and leafy turnip, on mycelial growth of ten *R. solani* isolates from Anastomosis Groups (AG) 3PT and AG-2-1, which predominantly infect potatoes in New Zealand. The most effective *Brassica* plant types were selected to evaluate the effects of tissue amount (with/without soil incorporation), type (shoots or roots) and flowering times on inhibition of *R. solani* AG-3PT and AG-2-1 isolates. Macerated tissue of all the ten *Brassica* types suppressed mycelial growth of all *R. solani* isolates. ‘Caliente’ and brown mustards completely inhibited mycelial growth (100%), followed by ‘Nemat’ (98%) and kale and leafy turnip (89-90%). *Brassica* tissues at 5-10 g/dish (or 5-10% in soil) were the most effective, but soil incorporation of *Brassica* tissues decreased efficiency. All ‘Caliente’ tissues, and harvested at three flowering times, completely inhibited mycelial growth of all *R. solani* isolates. ‘Caliente’ and brown mustards completely inhibited mycelial growth (100%), followed by ‘Nemat’ (98%) and kale and leafy turnip (89-90%). *Brassica* tissues at 5-10 g/dish (or 5-10% in soil) were the most effective, but soil incorporation of *Brassica* tissues decreased efficiency. All ‘Caliente’ tissues, and harvested at three flowering times, completely inhibited mycelial growth of all *R. solani* isolates. ‘Caliente’ and brown mustards completely inhibited mycelial growth (100%), followed by ‘Nemat’ (98%) and kale and leafy turnip (89-90%). *Brassica* tissues at 5-10 g/dish (or 5-10% in soil) were the most effective, but soil incorporation of *Brassica* tissues decreased efficiency. All ‘Caliente’ tissues, and harvested at three flowering times, completely inhibited mycelial growth of all *R. solani* isolates. ‘Caliente’ and brown mustards completely inhibited mycelial growth (100%), followed by ‘Nemat’ (98%) and kale and leafy turnip (89-90%).

Selected *Brassica* crops have potential as biofumigants to control Rhizoctonia diseases of potato, but biofumigation efficiency is likely to depend on *Brassica* type, tissue amount and type, plant growth stage, and *R. solani* AG group.
An integrated research-to-practice approach to soilborne disease threats in the Australian vegetable industry

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Soilborne diseases are major threats to vegetable production, costing Australia’s $4 billion vegetable industry approx. $120 million p.a. These diseases have been identified as the top challenge for soil management and crop protection in recent surveys of growers and agronomists. There are five groups of soilborne pathogens groups that continue to be a major problem for vegetable growers: Sclerotinia spp. (S. sclerotiorum and S. minor), Fusarium spp. (F. oxysporum and F. solani), water moulds (primarily Pythium spp.), nematodes and Rhizoctonia spp. Management of these diseases has become increasingly complex due to the decline in chemical control options, combined with increasingly intensive production and consumer demands for “perfect” produce. The industry has responded by funding three projects to provide an integrated research→practice→research approach. Two research projects are currently; 1. developing and testing disease management systems that work at a whole-farm level, and 2. validating molecular diagnostics assays for vegetables pathogens for assessing risk at a paddock level. These projects are strongly linked to the Soil Wealth and Integrated Crop Protection extension projects, which include 14 demonstration sites. A key to this approach is partnering with growers and advisors, as the system experts, to integrate risk management and control measures into the wide diversity of vegetable production systems. An example of this approach is the Soilborne Disease Masterclass, where growers, agronomists and research are brought together to translate the key principles and new research results into integrated control measures for vegetable production systems.
Alternatives to the management of apple replant disease in South Africa

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Apple replant disease (ARD) is a phenomenon where the growth of young apple trees is impaired when replanted onto old apple orchard soils. This soilborne disease is incited by multiple agents including specific species of fungi (Dactylonectria, Ilyonectria and Rhizoctonia spp.), oomycetes (Pythium and Phytophthora spp.) and nematodes (Pratylenchus). In South Africa, ARD management consists of chemical fumigation, which is unsustainable and doesn’t provide prolonged disease protection due to strip fumigation. Furthermore, fumigation cannot control ARD pathogens associated with planting material, which is known to be problematic in South Africa. Four orchard trials evaluated the efficacy of two fumigants varying in chloropicrin and 1,3-dichloropropene content, and semi-selective chemicals (fenamiphos, metalaxyl, imidacloprid and potassium phosphonate) applied to fumigated and non-treated soil. In all four orchards, tree growth responses in the different treatments showed similar trends after two to three growing seasons. All fumigants were equally effective and significantly improved tree growth relative to the non-treated controls. When used independently, tree growth attained using the semi-selective chemical treatment did not differ significantly compared to any of the fumigation treatments. The exception was one orchard where the semi-selective chemicals tended to be less effective than some, but not all, of the fumigant or fumigant plus semi-selective treatments. Application of semi-selective chemicals to trees grown on fumigated soil did not improve tree growth significantly relative to the fumigated only treatments. ARD pathogen characterization and quantification studies are currently in progress.
Verticillium dahliae affects tomato root morphology and plant defense responses

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Vascular wilt, caused by Verticillium dahliae, is responsible for economically important plant diseases on a wide range of annual crop plants including solanaceous species. The pathogen invades host plants via root tips, root wounds or lateral roots, and spreads systemically throughout plant tissues. A functional root system appropriate in size is essential for water and nutrient supply to aerial plant parts. Effects of pathogens on host root morphology have been little considered, although root surface area can affect the number of potential root-pathogen contacts. Root growth and especially root surface area are very important in the progress of diseases caused by root pathogens. This study focused on the evaluation of effects of V. dahliae on root morphological characteristics of tomato, including consideration of plant growth and defense responses of roots and leaves. Investigations were carried out over a growing period of up to 4 weeks post-inoculation. Infection by the pathogen suppressed tomato growth and leaf area, and reduced photosynthesis and stomatal conductance. The up-regulation of pathogen-related genes occurred in response to pathogen invasion. However, this response did not prevent colonization of the roots by V. dahliae. High variability in pathogen population density was found within the root system resulting in a significant increase of the specific root length and surface area. Root surface area correlated with water use efficiency. Morphological changes of the roots represent plant adaptive responses to pathogen colonization, evolved to sustain the supply of water and nutrients during pathogenesis.
Detection of mefenoxam resistance in *Pythium ultimum* on barley in Southern Idaho, USA

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Pythium root rot, caused by *Pythium* spp. is a serious soilborne disease of wheat and barley and has been a major problem in Idaho wheat and barley production areas for many years. In recent years, however, reported losses have increased. Currently, seed treatments containing mefanoxam are the only treatment option available for management of this disease. Recently, there have been reports of loss of efficacy of these products. In June 2016, plant samples displaying root rot were collected from wheat and barley fields in southern Idaho and tested using Loop-Mediated Amplification (LAMP) for *Pythium* infection. *Pythium ultimum* was detected in all of the symptomatic root samples and isolation from infected tissue resulted in six *P. ultimum* isolates. Isolates were tested to evaluate whether they were mefenoxam resistant using the spiral plate method. Most of the isolates (4) were found to be insensitive to the mefenoxam. In the PNW, barley and wheat are rotated with potato. *Pythium* leak caused by *P. ultimum* is also a major disease of potato in the Pacific Northwest of the USA, and the presence of resistant *Pythium* isolates may also have implications for control of Pythium leak in potatoes.
Resistance of weeds from the Australian northern grain region to the root lesion nematodes, *Pratylenchus thornei* and *Pratylenchus neglectus*

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There is very little known about the resistance/susceptibility of common weed species in the Australian northern grain region to the root lesion nematodes, *Pratylenchus thornei* and *P. neglectus*. In two glasshouse experiments (planted in July and August), ten weed species collected from the region were tested. These were: *Avena* spp. (wild oats), *Chloris truncata* (windmill grass), *C. virgata* (feathertop Rhodes grass), *Conyza bonariensis* (fleabane), *Echinochloa colona* (awnless barnyard grass), *Fallopia convolvulus* (climbing buckwheat), *Hibiscus trionum* (bladder ketmia), *Sisymbrium thellungii* (African turnip weed), *Sonchus oleraceus* (sow thistle) and *Urochloa panicoides* (liverseed grass). For *P. thornei*, most of the grass weeds were resistant (R) to moderately-resistant (MR) in both experiments. However, resistance ratings varied between experiments for awnless barnyard grass (changed from R to moderately-susceptible (MS)) and for wild oats (changed MR to MS-S). The ratings differed for African turnip weed (MS), climbing buckwheat (MS-S) and bladder ketmia (MR), but these treatments had limited replication. For *P. neglectus*, all weed species were R to MR in both experiments with the exception of liverseed grass which was MR-MS in the first experiment, but MR in a second experiment. Understanding the roles of planting time and seasonal effects on the rate and timing of germination and plant growth, and genetic variation within populations of weed species is warranted for future experiments. Targeted weed control, particularly of weed species susceptible to these nematodes, will support their management and contribute to better understanding of changes in populations of root-lesion nematodes when weeds are poorly controlled.
Evaluation of biological and novel seed and in-furrow treatments for the control of *Rhizoctonia* diseases of potato

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*Rhizoctonia solani* is an important pathogen of potato, causing qualitative and quantitative losses. It has been associated with black scurf, elephant hide on potato tubers and stem canker on plants. Isolates of *R. solani* are classified into several anastomosis groups (AGs), of which AG3-PT is most commonly associated with potato diseases. The most successful control of seed tuber- and soil-borne *Rhizoctonia* diseases is achieved by the application of effective fungicide seed tuber and/or in-furrow treatments. Biofungicides, alone and in combination with reduced risk fungicides, was evaluated for control of *Rhizoctonia* diseases. Results showed that applying a seed treatment or in-furrow treatment was effective for controlling these diseases. However, the use of both together was most effective in controlling disease. Biofungicides were more effective when applied in combination with a reduced risk fungicide than when applied alone.
Neem leaves protect chickpea from charcoal rot (*Macrophomina phaseolina*)

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The effects of neem (*Azadirachta indica*) extract on charcoal rot of chickpea, caused by *Macrophomina phaseolina*, were examined. Neem seed oil promoted mycelial growth of the fungus but leaf extracts were toxic. In pot experiments, adding neem leaf powder at 0.5% w/w to soil protected chickpea plants of Desi and Kabuli varieties from infection by *M. phaseolina*, and resulted in growth similar to uninoculated controls. There was a slight phytotoxic effect of neem leaf powder in the absence of the pathogen. Mycorrhizal colonization, and the number of *Rhizobium* nodules per plant, were not affected by neem treatment. However, the total dry weight of nodules was doubled by neem application, both with and without inoculation of seeds with Group N *Rhizobium*. Neem leaf extracts have potential as treatments for managing charcoal rot of chickpea, but further work is required to optimize application methods and to reduce phytotoxic effects.
Lack of efficacy of methyl bromide to eliminate live root knot nematodes (*Meloidogyne* spp.) from fresh ginger rhizomes

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Australia has general requirements for all fruit and vegetables requiring consignments to be free of live insects, disease symptoms, trash, contaminant seeds and other debris on arrival in this country. Imported ginger is subject to mandatory fumigation with methyl bromide for burrowing nematode, *Radopholus similis*. Consignments were found to contain live root knot nematodes, following mandated fumigation with methyl bromide at 32 g m⁻³ for 3 h at ≥21°C, indicating that the treatment is ineffective against internal feeding parasites. Ginger rhizomes infested with root knot nematodes were placed within six 10 kg cartons of ginger. Three pieces of infested ginger were each placed at the bottom left, centre or top right of each carton, and the cartons, together with another 10 cartons of “filler” ginger, were fumigated in a research-scale chamber (1.1 m³). The methyl bromide fumigation treatments, verified by gas chromatography of chamber headspace, were: 32 g m⁻³ at 22°C; 40 g m⁻³ at 17°C; and 48 g m⁻³ at 12°C, all for 3 h. Additional ginger rhizomes were left unfumigated as untreated experimental controls. After fumigation and venting for >24 h, the rhizomes were peeled, sliced finely and placed in a misting chamber for a total of 7 d to extract all nematodes. Nematodes were collected and counted on days 1, 4 and 7 on a 38 micron sieve, with the aid of a microscope to accurately determine live nematodes. Initial results showed that live nematodes were readily recovered from each of the treatments 7 d after fumigation.
Biological control
Invited paper

Bridging the plant microbiome and biocontrol of soilborne pathogens with multi-omics

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The microbiome is crucial for plant growth and health. Recent insights reveal close, mainly symbiotic, relationships of microorganisms and plants and high levels of structural and functional diversity within plant microbiomes. These studies have also brought deep insights that now allow specific applications in biological control of soilborne diseases. The rhizosphere microbiome has been identified as a strong and plant-specific network, consisting of bacteria, archaea and fungi with interacting with soilborne pathogens. New knowledge and technologies can have an impacts on: 1) the detection of new biocontrol agents; 2) the optimization of fermentation and formulation processes for biological control agents; 3) stabilization of the biocontrol effects under field conditions; and 4) risk assessment studies for biocontrol agents. Examples will be presented and discussed for the biological control of soilborne pathogens, including *Rhizoctonia solani* and *Verticillium dahliae*. 
Forage production following *Trichoderma atroviride* application in the presence of soilborne pathogens

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Forage production may be constrained by soilborne pathogens, and biological control may offer options to reduce these losses. Granule and prill formulations of a mixture of *Trichoderma atroviride* isolates were tested in a field in which plants suffered biotic stress induced by soilborne pathogens. Seeds of perennial ryegrass (*Lolium perenne* cv. One50), kale (*Brassica oleracea* cv. Sovereign) and forage rape (*B. napus* cv. Goliath) were sown in spring 2013, with each species constituting a separate experiment. Treatments were control (bare seed), bare seed plus granule or bare seed plus prill, with each treatment replicated nine times in 8 × 2.1 m plots, in a randomised block experimental design. Application rates for the granules and prills were 15kg ha⁻¹. Seedling emergence and plant dry matter (DM) production were measured. Kale seedling emergence was increased by both *Trichoderma* treatments because of reduced seedling death caused by *Rhizoctonia solani*, and this resulted in increased DM (mean increase = 1746 kg ha⁻¹) at harvest in late autumn 2014. Forage rape was more tolerant of *R. solani* and neither seedling emergence nor DM production were affected. Perennial ryegrass seedling emergence did not differ among the treatments, but for six of eight DM cuts from summer of 2014 to summer 2015, both *Trichoderma* treatments increased plant growth (total mean increase = 1884 kg DM ha⁻¹ greater than the control). At this site, and in the presence of biotic stress, both *Trichoderma* treatments improved plant production for two of the three forage crops.
Can cold tolerant variants of *Trichoderma atroviride* wild type isolates enhance control of soilborne pathogens?

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Activity of the biological control agent *Trichoderma atroviride* can be reduced in cold, wet soils which are common for late autumn/early spring crop sowings in New Zealand. Cold tolerant variants of four *T. atroviride* isolates were developed by intra-strain protoplast fusion. Their ability to control soilborne pathogens of kale (*Brassica oleracea* cv. Gruner) was compared against that of the original wild-type isolates in glasshouse and field experiments, when applied as mixtures to seed. In the glasshouse (mean daily temperature 18°C), kale seeds were sown into a field soil known to contain fungal pathogens. Rhizosphere colonisation by *Trichoderma* was greater for the cold tolerant variants than the wild-type. Both treatments increased seedling emergence and plant dry matter compared with the untreated seed control, but there were no differences between the wild-type and cold tolerant treatments. In a field experiment (grass minimum temperature < 10°C for the week following sowing), rhizosphere colonisation was greater for the cold tolerant variants than the wild-type. Seedling emergence averaged 60% and did not differ among treatments. By 70 and 153 days after sowing (DAS), however, the cold tolerant variants gave more plants m⁻² than the other two treatments. At 70 DAS the cold tolerant variants gave greater root but not shoot dry weight than the wild type, but final dry matter yields did not differ between the *Trichoderma* treatments, both of which produced a 22% greater yield than the control. Further assessment of these cold tolerant variants in differing agro-ecological environments is warranted.
Biodegradation of basal stem rot-affected oil palm stumps by white-rot Hymenomycetes: potential disease management by prevention of inoculum spread

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Sustainability of oil palm production in South-East Asia, especially in Indonesia and Malaysia, is jeopardized by Ganoderma boninense, the fungus which causes basal stem rot (BSR) in oil palm. Root-to-root contact is a major mode of disease spread, and oil palm debris left unattended in fields is an important sources of infection. Management of basal stem rot includes the expulsion of as much of this debris as possible, particularly before replanting. Antagonistic white-rot hymenomycetes and their extracellular lignocellulolytic systems were assessed to determine their biodegradation potential. Two of these fungi, Lentinus tigrinus FBJG3 and Pycnoporus sanguineus FBR, secrete hydrolytic, oxidative and amylolytic enzymes. These isolates reduced wood mass, respectively, by 79% and 77% after 120 days of biodegradation periods. Pycnoporus sanguineus FBR selectively removed wood lignin, whereas L. tigrinus FBJG3 preferentially degraded wood polysaccharides prior to lignin degradation. Scanning electron microscopy revealed the ingression and colonization of fungal mycelium with clamp connections within the wood vessels and the parenchymatic tissues. The formation of pores were clearly evident in the parenchymatic tissue and appeared as round spots. This study provides knowledge of the lignocellulosates degradation mechanisms and processes in these white-rot hymenomycetes, and provides a basis of biotechnological approaches in degrading oil palm-generated crop debris, under natural conditions. Use of these biodegrading organisms could effectively reduce G. boninense inoculum potential during oil palm replantation.
Soil health indicators to aid management of soilborne disease in ginger production

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Ginger production is an important agricultural industry in Queensland, valued at approx. $30 million p.a. However, soilborne diseases caused by Pythium spp. (Pyth), Fusarium oxysporum f.sp. zingiberi (Foz), and root-knot nematodes (Meloidogyne spp.) (RKN) pose serious limitations to production. Observations on losses caused by soilborne diseases indicated that inherent soil conditions and management practices are major contributors to disease incidence. A step-wise discriminant analysis of results from a 3 year survey of “good” and “poor” ginger growing areas found that nine soil indicators; clay, organic carbon, potassium, phosphorus, β-glucosidase enzyme activity, soil nematode bacterivore (c-p2), enrichment index and the plant-parasitic nematodes RKN and Pratylenchus sp. could be used to group soils. The indicators were each assigned a score depending on whether more, less or optimum indicator parameters were considered better for soil health. For Pratylenchus sp., presence and absence were used, while for RKN, a threshold value (1 RKN g⁻¹ soil) was used to calculate scoring functions. There was overlap in the good and poor scores, particularly in the 2013-14 season, but improvement in the discrimination between good and poor fields in subsequent years. By constructing the soil health scoring function, the impact of farm management practices on ginger growth and suppression of Pyth, Foz and RKN could be determined. Practices investigated for changes in soil health indicators included; fumigation, or addition of microbial inoculants, urea, lime, molasses or woodchips. The incorporation of woodchips into ginger-growing soil increased soil health parameters, improved ginger growth and tended to suppressed Foz and RKN.
Arbuscular mycorrhizal fungi enhance growth and modify essential 

oil content in *Leptospermum scoparium* (mānuka)

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Arbuscular mycorrhizal fungi (AMF) can improve plant health by providing available nutrients and protecting plants from phytopathogens. These symbionts can also directly influence soil microbial communities, by releasing substrates for microbial growth, or indirectly by modifying soil structure which affects microbial communities. AMF have also been shown to modify essential oil production in some plants. Mānuka is a New Zealand native medicinal plant valued for essential oils that have antimicrobial properties. There is, however, only limited knowledge of the AMF partners of this plant, and their effects on the essential oils in mānuka are unknown. This is the first study to investigate AMF structure in mānuka by culture dependent (trap culture) and independent approaches (DGGE). The effects of different AMF species on growth and essential oil composition of a single regional chemotype of mānuka were investigated. Leaf essential oil compositions and yields were determined by GC-MS analyses. Six of seven AMF increased mānuka growth compared to experimental controls. Effects of AMF inoculation on essential oil composition qualitatively and quantitatively varied depending on the AMF strain. Three AMF species (*Acaulospora* sp. M4, *Acaulospora* sp. MPC47 and *Scutellospora* sp. MPC13) modified essential oil composition qualitatively, and three other species (*Acaulospora* sp. M2, *Glomus* sp. MPC8 and *Scutellospora* sp. MPC13) modified essential oil composition quantitatively. AMF influenced Gammaproteobacteria communities in the roots of mānuka plants, which may have contributed to essential oil modification. Overall, AMF can improve the growth of mānuka and affect essential oil composition.
Potato root exudates contain stimulants of resting spore germination of *Spongospora subterranea*

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Root exudates play important roles in the soil chemical ecology influencing rhizosphere microbiota. It was suspected that root exudates from host and non-host plants could stimulate resting spore germination of *Spongospora subterranea*, the powdery scab pathogen of potato. Empirical evidence for stimulation has not been available, and the identity of specific stimulatory compounds was unknown. This study showed that potato root exudates stimulate *S. subterranea* resting spore germination. Treating pathogen sporosori with exudates and specific individual constituent components (certain amino acids, sugars, organic acids and other low molecular weight organic compounds) resulted in release or greater numbers of zoospores at an earlier time than water experimental controls. Given that several identified stimulatory compounds are commonly found in exudates of diverse plant species, we indirectly support observations of non-host stimulation of resting spore germination. This study has provided new knowledge of *S. subterranea* resting spore biology and chemical ecology that may be useful in formulating new disease management strategies.
Development of an integrated management system to suppress Fusarium wilt of bananas

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Fusarium wilt (FW) of bananas, caused by \textit{Fusarium oxysporum} f. sp. \textit{cubense} (Foc), has become widespread in Southeast Asia. FW has recently been detected on a single property in the main banana producing region of Queensland. Farm quarantine of the affected property and on-farm biosecurity of unaffected properties have restricted the spread of the disease. However, to ensure the viability of the Australian banana industry, management practices are required for the three scenarios that banana growers may encounter; namely: 1. no FW present, requiring practices required to remain disease free; 2. FW has been detected requiring practices to limit the spread of the disease; and 3. FW has become widespread requiring remediation practices. Training on disease epidemiology, disease spread pathways and effective farm biosecurity practices has been disseminated to 85\% of banana growers. Early FW detection methods using remote, proximal sensing and soil DNA testing are under development. Eradication procedures of infected plants and techniques to enhance the decomposition of the banana pseudostems may reduce the return of Foc inoculum to the soil. Vegetated ground covers that reduce soil movement may also increase Foc antagonists, providing increased competition. The removal of alternative hosts that act as Foc refugia potentially reduces pathogen survival. In plantations where FW has become widespread, crop rotation to reduce Foc inoculum is required before replanting with clean planting material, using cultivars with enhanced resistance. The addition of FW suppressive management practices, in areas infested with Foc, will enable banana growers to remain economically viable.
Use of root endophytic *Trichoderma* isolates for bioprotection of oil palm against *Ganoderma* disease in Sarawak, Malaysia

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*Trichoderma* can be an effective biocontrol agent against soilborne plant pathogens, particularly those causing root rots. In pot trials with oil palm seedlings, effective *Trichoderma* strains isolated from local healthy plants were found to successfully antagonise *Ganoderma boninense*, protecting the seedlings from damage by the disease. Incidence of leaf spot diseases was also reduced in palms treated with the best *Trichoderma* strains. Five *Trichoderma* isolates were shown to decrease the production of *Ganoderma* fruiting bodies. Inhibition of the pathogen was confirmed by destructive sampling and examination of roots, and *Ganoderma* inoculum in trial pots. Field trials demonstrated significant improvement in the survival, vigour, and growth of palms inoculated with the best *Trichoderma* strains. *Trichoderma* application was also shown to improve recovery and initial growth of overgrown oil palm seedlings. *Trichoderma* inoculation of oil palm seedlings has now been adopted as the new standard operating practice by a key oil palm production company.
Influence of tomato root exudates on antagonism of *Fusarium oxysporum* f. sp. *lycopersici* by non-pathogenic *Fusarium oxysporum*

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The effects of tomato root exudates on growth of *Fusarium oxysporum* f. sp. *lycopersici* (Fol) and antagonism by non-pathogenic *F. oxysporum* (F1, F4) were tested. Inhibition of Fol by F1 and F4 in dual culture was greatest on Hoagland solution containing root exudate compared with Hoagland solution and Hoagland solution plus sugar. Hoagland solution plus sugar gave the greatest dry weight of all fungi in liquid culture compared with Hoagland solution plus root exudate and Hoagland solution alone. The effects of sugars and organic acids typically found in tomato root exudates on fungal growth and inhibition of Fol was tested. The greatest inhibition of growth of Fol by F1 and F4 was recorded on lactose compared with other sugars, and on malic acid compared with other organic acids. Adding sugars or organic acids in a pot trial did not alter the interactions between the non-pathogens and Fol. The results indicate that root exudates play an important role in the interaction of pathogen and non-pathogen but that this may be due to components of the exudate other than sugars and organic acids.
Assessment of the biocontrol efficacy of nematode trapping fungi against root-knot nematodes

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Root-knot nematodes (*Meloidogyne* spp.) are the most economically damaging plant parasitic nematodes, due to both their worldwide distribution and extensive host range. Fungal biocontrol is a rapidly developing research area, and there is growing interest in the exploitation of fungi for controlling root-knot nematodes. In this study, two nematode trapping fungi, *Arthrobotrys dactyloides* and *Arthrobotrys oligospora*, isolated from Queensland soils, were encapsulated in kaolin-alginate granules. Their efficacy for controlling root-knot nematodes was assessed by applying these granules into heated and non-heated field soil in a soil microcosm experiment. After applying the granules, significantly less root-knot nematodes were recovered from both heated and non-heated soils than from control treatments, which indicated that both fungi have biocontrol potential to suppress root-knot nematodes. Compared to control treatments, granule application of both fungi reduced nematode numbers by a greater extent in the heated soil than the non-heated soil. This may have been due to biological factors in the field soil that affected the biocontrol efficacy of the nematode trapping fungi, such as competition for nutrients or predation by other microorganisms. Further research is required to understand the interactions between these fungal granule products and other microorganisms in the field soil to improve their efficacy for controlling root-knot nematodes under natural field conditions.
Trichoderma isolates for biocontrol of Rhizoctonia stem canker of potato

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Trichoderma isolates from potato soil were tested for their ability to control Rhizoctonia solani AG-3 on potato plants in glasshouse experiments and as competitors of the pathogen. Two isolates (T. harzianum, T5 and T. hamatum, T8) greatly suppressed pathogen growth and promoted plant growth. In pot trials, strain T8 produced significantly greater plant growth parameters with reduced disease incidence compared with the other treatments. In experiments with ‘Desiree’ potato plants originating from tissue culture, T5 and T8 increased the shoot dry weight of infected plants by, respectively, 2.1 and 2.4 times. In hydroponic plant culture, adding spore suspensions of T8 into the nutrient solution with toothpick inoculation of the pathogen into the stems of potato plants significantly inhibited disease and increased plant biomass. Results to date suggest that these isolates of Trichoderma inhibit activity of the pathogen, promote growth of potato plants, and may also induce systemic host resistance. Overall, the data indicate that T. hamatum strain T8 had superior potential for reduction of the pathogen and improving potato plant growth and yield.
Biosecurity
Invited paper

Can high throughput sequencing be used in biosecurity? A case study of Phytophthora in Australia

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The introduction and subsequent impact of Phytophthora cinnamomi within natural vegetation is one of the major conservation issues for biodiversity in Australia. Recently, many new Phytophthora species have been described from Australia’s natural ecosystems, but their distribution, origin, and potential impact remain unknown. This is concerning because if they are present due to breaches in biosecurity we need to understand the pathways of introduction. Historical bias in Phytophthora detection has been toward sites showing symptoms of disease, and traditional isolation methods show variable effectiveness for detecting different Phytophthora species. However, new techniques based on the sampling of environmental DNA and metabarcoding are now available through the use of high throughput sequencing (HTS). Phytophthora diversity and distribution in Australia has been defined using metabarcoding of soil samples, and the diversity detected using this technique has been compared with that available in curated databases. This study revealed high Phytophthora richness within natural vegetation and a difference between land use types (agriculture vs natural ecosystems). The additional HTS records provide a valuable baseline resource for future studies. Many of the Phytophthora species now uncovered in Australia’s natural ecosystems are newly described. Until more is known the precautionary principle needs to be followed regarding the spread and conservation management of these new species in Australia’s unique ecosystems. There are many unanswered questions, but of great importance is evaluation of the invasiveness of different Phytophthora species. New technologies can be used to establish baseline databases and then set up monitoring and surveillance protocols for the detection of new pathogen incursions.
Invited paper

The challenges and opportunities in protecting New Zealand’s biodiversity and taonga plant species from invasive soilborne plant pathogens

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The health and resilience of New Zealand’s soils, and their dependent ecosystems, are under increasing threat from anthropomorphic disturbance and degradation, fragmentation, environmental stressors, and invasive soilborne pathogens. The ongoing spread of these pathogens that are already well-established within the country is further exacerbated by the potential threats of new biosecurity incursions. Predicted climate change scenarios will also expose New Zealand to a suite of new and emerging global pest threats, additional to changes in future distributions, susceptibility and local abundance of current soilborne pathogens. A number of long-term disease management programmes and initiatives have been implemented in response to new soilborne pathogen threats. These include; targeted and passive surveillance; identification of risk pathways; and vector control to reduce and contain disease spread. These operational interventions are underpinned by research and innovation to address key knowledge gaps and increase the control toolbox. Building and improving a resilient biosecurity system is a constant challenge, while also ensuring public support for the adaptive management of soilborne pathogens through effective communication and engagement strategies that account for community values and perspectives. This paper summarises current case studies, such as a number of Phytophthora species associated with decline and mortality of native taonga (treasured) plant species, where the challenges facing New Zealand’s long-term management of soilborne pathogens has been mitigated with innovation and opportunities to increase public awareness and community participation. This has included new and traditional indigenous knowledge (mātauranga Māori), and cultural practices (Tikanga) with Tangata Whenua (Māori).
Host resistance for disease management
Variety resistance and pre-sowing *Pratylenchus thornei* population densities affect post-harvest nematode populations in wheat and barley

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In south eastern Australia, the root lesion nematode *Pratylenchus thornei* is estimated to cause yield losses valued at AUD$12 million p.a. To reduce these losses, control of nematodes is achieved through cultivation of resistant varieties. However, the interacting effects of variety resistance and pre-sowing nematode population density on the post-harvest nematode density are insufficiently understood. Four 2 year experiments were conducted in the Wimmera region during 2011-2015. In the first year, a range of nematode densities were established using three cereal varieties, with contrasting resistance/susceptibility. In the second year, pre-sowing nematode densities were quantified using qPCR (PreDicta B) and then plots were sown to five cereal varieties with contrasting resistance to *P. thornei*. Nematode densities were also quantified post-harvest. Orthogonal regression analysis was applied to combined experimental data to determine the relationships between pre-sowing and post-harvest *P. thornei* densities in relation to variety resistance/susceptibility. Susceptible varieties always increased the nematode population densities within the range of pre-sowing densities in the experiment (from 1 to 180 *P. thornei* g\(^{-1}\) soil). The rate of multiplication decreased with increasing pre-sowing nematode densities. In contrast, moderately resistant to moderately susceptible cereal varieties increased nematode densities up to 16 *P. thornei* g\(^{-1}\) soil. However, when pre-sowing nematode densities were above this threshold, the post-harvest nematode densities were less than pre-sowing densities. This study has demonstrated low nematode population densities can be maintained if growers reduce the use of susceptible varieties, thereby reducing yield losses in subsequent nematode intolerant crops.
Selection of genotypes for resistance and tolerance to pathogens: a combined statistical analysis of yield and disease response

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Phenotyping for the effects of disease on genotypes from a plant breeding programme requires measurement of both the growth of the pathogen and the subsequent effect of the pathogen on grain production. Resistance is measured as the severity of the disease symptoms in host plants, and tolerance is measured through grain yield at harvest. Experiments to test the resistance and tolerance of genotypes typically consist of replicated field trials with treatments including an untreated control (uninoculated) and an imposed disease level (inoculated with the respective pathogen). Different genotypes are grown under these two conditions with the aim of selecting genotypes possessing combined traits of resistance and tolerance to disease. A method for the selection of genotypes for resistance and tolerance to crown rot in wheat, caused by the fungal pathogen *Fusarium pseudograminearum*, is presented through a combined analysis of yield and disease response across inoculated and uninoculated plots. The regression nature of the analysis allows derivation and selection for three traits of interest. Firstly, yield responsiveness of genotypes under inoculated and uninoculated conditions can be compared. Secondly, severity of disease symptoms in inoculated plots can be used to select genotypes with superior resistance. Thirdly, yield advantage in the presence of disease taken from the response in yield against measured disease in the inoculated plots can be used to select for genotype tolerance, independently of resistance. This method is shown to be superior to traditional approaches of determining yield differences or percentage yield loss calculations.
A genome-wide association approach to identifying new resistance loci to common root rot in contemporary barley breeding programmes

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Control of many soilborne diseases in broad acre cereals is achieved by the use of rotation, fungicides or crop management. The more environmentally benign approach of using genetic resistance is used less frequently. The biggest impediment to the use of resistance is often the need to identify and assemble many genes of small effect. This is a very important problem in malting barley, where the many required essential quality traits restrict the use of wild or unadapted lines in a breeding programme. Little is known about the genetics of resistance to common root rot (CRR) in barley. A genome-wide association study (GWAS) was used to map genes for CRR resistance using 768 adapted barley breeding lines from the USA spring barley breeding programs. The lines were phenotyped in the field with a background of the CRR pathogen, and genotyped with 3072 single nucleotide polymorphism (SNP) markers. Five quantitative trait loci (QTL) associated with common root rot resistance, CRR-3H-28-51, CRR-5H-180-195, CRR-6H-30-64, CRR-6H-91-97, and CRR-7H-50-86 were detected, respectively, on chromosomes 3H, 5H, 6H, 6H, and 7H. The phenotypic variation explained ranged from 3.9 to 5.2%. Only one QTL, CRR-5H-180-195, was in a region in which resistance QTL had previously been found. GWAS using advanced and adapted breeding lines has identified five small effect QTL for resistance to CRR that can be accumulated in breeding programmes without the linkage drag associated with unadapted lines jeopardizing essential quality traits.
Different winter cereal reactions to root and crown rot pathogens

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Crown rot of cereals in Australia is predominantly caused by \textit{Fusarium pseudograminearum} (\textit{Fp}), with \textit{Fusarium culmorum} (\textit{Fc}) important in southern regions. \textit{Fusarium graminearum} (\textit{Fg}) is an important pathogen worldwide and has also been reported to cause crown rot in wheat. Common root rot is caused by \textit{Bipolaris sorokiniana} (\textit{Bs}) in Australia and can also be associated internationally with other \textit{Fusarium} species. The ability of these pathogens to cause crown rot and common root rot on different hosts is not fully understood. Bread wheat (cv. Livingston), durum wheat (cv. Hyperno), barley (cv. Grimmett), triticale (cv. Endeavour) and oat (cv. Genie) were inoculated with two isolates each of the four pathogens (\textit{Fp}, \textit{Fc}, \textit{Fg} and \textit{Bs}) to determine the impact of these pathogens on each host. Seedlings were harvested at 21 d after inoculation and the sub-crown internode and 1\textsuperscript{st} three leaf sheaths of each seedling were visually rated for disease severity using a 0 - 100\% scale. Plant height and shoot biomass were recorded. Significant pathogen/genotype/isolate interactions were detected in the severity of disease on the sub-crown internodes and leaf sheaths. Overall, Livingston and Grimmett were most severely diseased. Hyperno and Endeavour were more diseased on leaf sheaths than the control, only when infected with \textit{Fp}. Significant pathogen/genotype interactions were recorded for height and shoot biomass. While Genie showed low disease levels, height was reduced by each pathogen. This study reports significant variation in host responses among winter cereals exposed to crown rot and root rot pathogens.
Testing kauri (*Agathis australis*) for resistance to *Phytophthora agathidicida*

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*Phytophthora agathidicida* is a newly-described, exotic pathogen causing kauri dieback in the north island of New Zealand. The decline was first noted on Great Barrier Island in 1972, but the disorder was only recognised in 2006 on mainland New Zealand. A multi-agency response was initiated in 2009, and in 2014, research began to assess disease resistance within the remnant kauri forest stands under the “Healthy Trees Healthy Future” programme. Non-destructive, low-impact experimental approaches have been applied, to obtain progenies from parent trees that display differential disease responses. Shoots were pruned from target trees and 1-year-old shoots were selected. Ten randomly selected leaves from each shoot were inoculated with *P. agathidicida* grown on V8 juice agar, and five leaves were inoculated with V8-juice agar (controls). After 10 d, the leaves were photographed for Winfolia analysis, lesion lengths were scored, and isolations were made from set distances beyond the inoculation points. Ten shoot pieces were each inoculated mid-way along the stem with a millet seed infected with *P. agathidicida*, and five shoot pieces were inoculated with millet seeds (controls). After 28 d, the shoots were dissected and post hoc evaluations of the test material included; i) plating to *Phytophthora* selective media, ii) preserving material for cytological investigations (via fluorescent in situ hybridization), and iii) cryostoring tissues for downstream, “omics” – analyses. The results from the leaf and shoot assays were compared to determine if there were concordances between the levels of differential disease resistance observed from these ex situ assays.
Screening *Agathis australis* (kauri) genotypes for resistance to *Phytophthora agathidicida*

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*Phytophthora agathidicida* is responsible for a devastating decline of *Agathis australis* (kauri) within its endemic range in the North Island of New Zealand. This significant soilborne pathogen causes primary, secondary and tertiary root damage and significant stem bleeding basal cankers on host trees. The pathogen is easily spread through the movement of contaminated soil water and organic material. Work is currently being conducted to protect non-infested forests and reduce the spread of *P. agathidicida*. Further research is required to understand the vulnerability of the host species and, where appropriate, identify genotypes of kauri that can be made available for restoration. Kauri seeds from infected and non-infected forests have been collected in collaboration with local iwi (Maori groups). This germplasm will be used for conserving and propagating genetic material in tissue culture libraries, optimizing pathogenicity screening protocols, identifying genetic signatures of resistance, and scaling up of a resistance screening programme. To accelerate pathogenicity screening, root and leaf inoculation assays were conducted for over 35 unique kauri genotypes. A spectrum of susceptible to comparatively more resistant genotypes was identified. This shows promise that resistance to *P. agathidicida* will be identified. The next key stage is to understand the level of variability in resistance within kauri families and across populations/regions, and to determine how robust these screening assays are with mature trees.
Resistance screening of pea varieties to *Fusarium* root rot in New Zealand

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Root rot is an important fungal disease of pea (*Pisum sativum* L.). In a recent survey of 51 process pea fields across Canterbury, New Zealand, *Fusarium avenaceum* and *Fusarium solani* were isolated most frequently, implicating them in the development of root rot. Management of Fusarium root rot is difficult as *Fusarium* spores can persist in soil and survive on plant debris. The use of resistant cultivars is seen as a long-term solution for effective management of Fusarium root rot. This study evaluated 41 pea lines from the Plant & Food Research pea germplasm collection for their resistance to *F. avenaceum* f. sp. *pisi* and *F. solani* f. sp. *pisi*, under glasshouse conditions. This was to provide a basis for selecting host material which can be incorporated into pea breeding programmes. Plants were assessed for root rot severity on a 0-4 scale and their biomasses were recorded. Ten accession lines showed moderate levels of resistance to *F. solani*, while 11 lines provided a high level of resistance to *F. avenaceum*, a rating comparable to the un-inoculated control. These lines had varying shoot to root dry weight ratios when compared to uninoculated controls. Selected lines are currently undergoing evaluation for their potential resistance against Fusarium root rot under field conditions.
Using Normalised Difference Vegetation Index (NDVI) to select wheat genotypes for tolerance to the root-lesion nematode *Pratylenchus thornei*

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*Pratylenchus thornei*, the prevalent root-lesion nematode in Australian’s northern grain region, can reduce grain yields from intolerant wheat cultivars by up to 70%. Australian plant breeders continue to incorporate genetic tolerance into commercial wheat cultivars to protect crops from *P. thornei* damage. This study aimed to determine if the NDVI, or GreenSeeker™, can be used as a tool to select tolerant germplasm. The 2-year experiment studied wheat cultivars of varying tolerances to *P. thornei*. Replicated strip-plots were established in the preceding year using resistant and susceptible wheat cultivars to establish, respectively, low and high *P. thornei* populations. Thirty-six genotypes were sown in these plots in the following season. GreenSeeker™ measurements were performed regularly throughout the season, and grain yield was measured at maturity. Two cultivars (EGA Hume (intolerant) and EGA Gregory (tolerant)) had different responses when compared at two nematode population densities. The greenness of EGA Hume decreased by 16%, while that of EGA Gregory increased slightly with higher nematode population densities. Similarly EGA Hume lost 17.5% of its yield compared with only 4.3% for EGA Gregory when grown on the higher *P. thornei* densities. Initial analyses suggest that for EGA Hume, approx. 70-80 d after sowing NDVI is more effective for measuring tolerance. GreenSeeker™ will be a useful tool to assist plant breeders and other researchers estimate *P. thornei* tolerance. Further analyses are required to understand the relationship between NDVI and grain yield at different sensing times and its application to other intolerant grain crop species.
New technologies, pathogen detection and diagnostics
Invited paper

Risk-based detection and diagnosis of plant pathogens using new technologies

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Detection and diagnosis of plant pathogens for disease management and biosecurity rely heavily on the use of classical and molecular tools that categorise pathogens by taxonomic means. Arguments abound about the best methods for taxonomically-related identification, but regardless of the techniques used, often the risks associated with a pathogen remain ambiguous. Next generation nucleotide sequencing (NGS) techniques, in conjunction with other tools, provide new opportunities to understand population variation, mechanisms of virulence and how these combine to provide threats to host plants. With such information we now have the potential to decipher the risks associated with single pathogen strains in the context of the local microflora. This paper explores the application of NGS techniques to enhance understanding of pathogen populations and virulence. The potential of these methods to assist development of risk-based detection tools for plant pathogens is examined in the context of small laboratories with minimal resources. Case studies are presented to demonstrate how NGS can be used to develop diagnostics for important pathogens in orchard cropping systems in New Zealand. These define microbial organisms taxonomically, but can also assist in establishing their threats to crop production. We aim to show that these techniques can provide insights not revealed using simple taxonomic detection and diagnostic tools, and that they can be utilised without considerable time and resource investments.
Species identification and genetic diversity analysis of the pathogen causing crown rot of wheat in China

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Crown rot of wheat is a recently occurring and rapidly increasing soilborne disease in China. Samples of diseased wheat plants were collected in 2012 and 2015, from the Huang-Huai region, the main winter wheat growing area in China, including Henan, Hebei, Shanxi, Anhui, Jiangsu and Shandong provinces. More than 1200 fungal isolates from diseased plants were identified, indicating that Fusarium pseudograminearum was the dominant pathogen in the north of the Huang-Huai area, and F. graminearum dominated in the south. Fusarium proliferatum, F. equiseti, F. tricinctum, F. oxysporum, and F. culmorum were also isolated with the low frequency. The genetic diversity of 261 F. pseudograminearum collected isolates was analysed with URP-PCR markers. The number of migrants per generation among eight geographical populations was 2.8362, which indicated frequent genetic exchange. All isolates were clustered in two groups (similarity coefficient of 0.962). Group 1 included five geographical populations, i.e. Northern Henan, mid Henan, Eastern Henan, Western Henan and Southern Henan. Group 2 included three geographical populations, i.e. Hebei, Shandong and Shanxi. The pathogenicity of 34 representative isolates of F. pseudograminearum was tested in greenhouse assays, demonstrating very significant differences in pathogenicity. The isolate XX114-9A displayed the strongest pathogenicity with 100% incidence, while isolate FC136-2A was the weakest with 25% incidence. There was no significant relationship between pathogenicity and geographical origin of isolates.
What happens to the DNA of *Rhizoctonia solani* and *Pratylenchus neglectus* in soil under different storage conditions over time?

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*Rhizoctonia solani* AG8 and root lesion nematode (*Pratylenchus neglectus*) are two of the most yield-depleting soilborne pathogens/pests on broadacre crops in Western Australia. *PreDicta B*, a qPCR based test, can be used to assess amounts of *R. solani* and *P. neglectus* in the soil to guide best management strategies. Soils samples are often stored refrigerated or at ambient temperature prior to sending for DNA testing. This study investigated effects of storage time and temperature on the integrity of *R. solani* and *P. neglectus* DNA in dried or paddock moisture soils. Soil was collected from a cereal paddock known to be naturally infested with *R. solani* and *P. neglectus*. Dried and moist soil samples were stored at either ambient (av. 20°C) or refrigerated (4°C) conditions for 0, 7, 14, 28 or 119 d prior to testing for DNA levels. For *R. solani*, there were no significant treatment differences between times 0, 7 and 14 d. At 28 and 119 days, however, there were significant reductions in the pathogen DNA levels at both storage temperatures and soil moistures. For *P. neglectus*, DNA levels declined for both dry and moist samples stored at ambient conditions, while for samples stored at 4°C, DNA levels did not decline with time. Soil samples, regardless of storage temperature, need to be sent within 14 days of sampling for the most accurate measurement of *R. solani* levels, while for *P. neglectus*, DNA integrity is maintained when soil is stored at 4°C for long periods (at least 119 d).
Detection and infectivity of Peronospora sp. in the soil environment of poppy crops

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Opium poppy (Papaver somniferum) is a commercially important crop, grown for its alkaloid compounds, including morphine and thebaine. Downy mildew is a major disease constraint to the Australian poppy industry. This diseases is caused by infections with one of two Peronospora species; P. meconopsidis which following infection induces localised necrotic lesions on leaves, and P. somniferi, which is responsible for chlorosis, systemic stunting and deformation of infected plants. Despite their importance, the epidemiological knowledge about critical sources of inoculum of these pathogens is limited. Our study sought to confirm the presence inoculum in soil and in crop debris, and to determine capacity for seedling infection from these sources. Species-specific qPCR tests were developed using Taqman probes to detect and quantify the level of the pathogens in soil samples. Soils collected from three growing regions in Tasmania were tested using these probes. These soils were then used into a glasshouse bioassay to evaluate the potential for soil to plant transmission. Both of the downy mildew pathogens are present in soil/crop debris. Planting poppy into such soil can subsequently lead to downy mildew development in poppy seedlings.
**Rhizoctonia solani**: the root of yield decline in oilseed rape (*Brassica napus*)?

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Oilseed rape (OSR, *Brassica napus*) is an important global source of vegetable oils for food, fuel and industrial use. Europe is the largest producer, with the United Kingdom, France and Germany being the main contributors due to high crop yields. Within recent years, however, productivity has become limited, with United Kingdom crops failing to reach their full potential. This is linked to an increase in soilborne pathogens under intensive cropping systems. The current study aims to elucidate which pathogenic fungal species are present within OSR crops, and examine their effects on plant health as individuals and in combinations with other fungi. Fifty individual OSR field sites were selected from across England covering different cropping intensities, agronomic and environmental situations. Root material from each growing crop was collected and used for DNA extraction before sequencing the ITS1 region using an Illumina MiSeq, to identify the fungal species associated with each site. The majority of sequences belonged to soil generalists and saprobes, along with some pathogenic species. *Rhizoctonia solani* was the most frequently observed pathogen, and was further studied by sub group-specific real-time PCR to classify the anastomosis groups (AG) present. This demonstrated that AG2-1 was the dominant AG followed by AGs 8 and 5. Our results suggest that agronomic factors may have limited impacts on the fungal species found within the roots of OSR in England. The pathogenic species *R. solani* was also identified as a potential agent for yield decline and is recognised for causing disease in other OSR regions of the world.
Root rot disease complex of process peas in Canterbury, New Zealand

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Process peas (Pisum sativum) are one of the most important vegetable crops grown in New Zealand. In 2015, 8250 ha were planted, producing approx. 66,500 tonnes, valued at $27 million in domestic sales and $85 million for export. Peas suffer from root and collar rot diseases caused by a complex of soilborne pathogens. More than 20 soil pathogens, including species of Aphanomyces, Pythium, Fusarium, Ascochyta, Phoma and Rhizoctonia, have been implicated as the causal agents of root rot in pea crops. To determine the pathogens that are most prevalent in pea crops in New Zealand, we assessed 51 pea fields in the Canterbury region in the 2014/15 growing season, and collected 60 plants from each field for further analyses. The roots of the collected plants were washed and visually scored for root and collar rot. The presence of different soil microorganisms were characterised, using microbiological and molecular methods. Twenty-seven different microorganisms were identified. Phoma pinodella was the most frequently isolated pathogen, followed by a complex of Fusarium species (F. solani, F. avenaceum, F. oxysporum, F. graminearum, and F. culmorum). Many of these microorganisms are known to cause root and foot rot of peas and many other crops. These results collectively suggest that a Fusarium complex and P. pinodella pose threats to pea cultivation in New Zealand. Improved management practices along with resistant pea cultivars are required to combat the pea root rot disease complex.
New insights into the infection of potato by *Pythium ultimum*, from real-time PCR and isothermal detection methods

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*Pythium ultimum* is a soilborne plant pathogen causing damping off and root rot diseases in a wide range of crops and ornamental species. In potatoes, it is one of the main causes of leak (watery wound rot). *Pythium* infecting potato seed tubers can result in delayed emergence and poor stands. The disease can also develop in storage resulting in rotten tubers which appear discoloured and water soaked. Since similar symptoms can be caused by other pathogens, rapid and robust tests are required to detect the pathogen in plant material and soil. Several LAMP and real-time PCR assays were designed for *P. ultimum* and evaluated for specificity and sensitivity. For this study the Genie 3C platform (OptiGene, United Kingdom) was used. This offers portable, battery powered real-time analysis for either PCR or LAMP. TaqMan assays had the lowest limit of detection and the most tolerance to inhibition from humic acid. TaqMan was therefore most suitable for detecting the pathogen in soil. LAMP assays were suitable for in-field detection in plant material and could be used with a simple DNA extraction method for quick and reliable on-site tests for *P. ultimum* in symptomatic tuber material. Both TaqMan and LAMP assays were used to investigate the onset of infection in tubers. This determined that infection usually resulted in symptoms 2 days after inoculation. In addition, pathogen DNA levels were typically greatest in the eyes of tubers, followed by the periderms and were least in the medullae.
Pathogenicity of *Verticillium dahliae* and *Verticillium albo-atrum* on potato cultivars Denali and Russet Burbank in Australia

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Verticillium wilt is an important disease of potato, primarily caused by the soilborne fungi *Verticillium dahliae* and *V. albo-atrum*. In Australia, *V. dahliae* is the more important of these pathogens as it is widespread across fields in south-eastern Australia, whereas *V. albo-atrum*, has only recently been detected in a few fields in Victoria and Tasmania. Little is understood about the significance and epidemiology of *V. albo-atrum* in Australia. Glasshouse pathogenicity tests were conducted by immersing roots of the resistant cultivar Denali and susceptible cultivar Russet Burbank in spore suspensions (5 x 10^4 spores mL^-1) of *V. dahliae* and *V. albo-atrum* for 5 min. The experimental control treatment consisted of dipping plant roots in sterile distilled water. Each treatment had five replicates. Disease symptom severity was assessed weekly using a 0-5 qualitative scale, where 0 = healthy, 1 = chlorosis of leaves, 2 = moderate (30-50%) wilt with chlorosis, 3 = moderate wilt and necrosis, 4 = severe (>50%) wilt and necrosis and 5 = plant death. Plants were also destructively sampled at 2, 5 and 9 weeks after inoculation and different host tissues were cultured on ethanol potassium amoxicillin agar to determine the incidence of pathogens. Overall, *V. dahliae* was more pathogenic than *V. albo-atrum* in both cultivars. *Verticillium dahliae* led to earlier symptom expression and exhibited more accelerated progression of disease severity. This pathogen also consistently colonised greater proportions of infected stem tissues. The cultivar Denali was more resistant than Russet Burbank to both *Verticillium* species.
Efficient sampling for assessing crown rot in wheat

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Crown rot is a soilborne disease caused by *Fusarium pseudograminearum* which infects cereal crops grown in Australia. Assessing the severity of crown rot in wheat is a key component for identifying and selecting genetic material that shows resistance or tolerance to the disease. The current sampling procedure for estimating the severity of the disease involves rating multiple tillers on each of up to 20 plants randomly sampled from each field plot. Sampling and subsequent disease assessment is a time consuming and expensive process. The aim of this investigation, funded by the Grains Research and Development Corporation, was to determine the sampling strategy that provides the most accurate and precise measure of the crown rot infection, with minimal sampling effort. Three replicated field trials were conducted in which every tiller on every plant was assessed for crown rot severity. The data from each trial were then sub-sampled using various sampling scenarios consisting of different numbers of plant and tiller combinations, e.g. three tillers on five plants. The data set from each sampling scenario was then analysed and the resulting estimates of genetic effects were compared for accuracy and precision to those generated using the full data set. From this study, recommendations can be made to reduce the sampling effort involved in assessing crown rot severity, while maintaining accuracy and precision of genotype comparisons.
A flexible design to generate yield loss response curves for the root lesion nematode (*Pratylenchus thornei*) for wheat cultivars differing in nematode tolerance

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In the Australian northern grain region, the root lesion nematode (*Pratylenchus thornei*) causes up to 65% yield losses in intolerant wheat cultivars. A pilot experiment was conducted to establish methods to quantify, using response curves, relationships between initial nematode population densities and grain yields, in wheat cultivars with differing tolerance to *P. thornei*. A 2-year field experiment established differing *P. thornei* densities in year 1 using four wheat cultivars ranging from susceptible to moderately resistant in a randomised block design. In year 2, six wheat cultivars (Lincoln and Strzelecki (intolerant), Lang and Spitfire (moderately intolerant) and EGA Gregory and Suntop (tolerant)) were grown on the range of *P. thornei* densities. Samples collected at 0–30 cm soil depth before planting in year 2 provided an opportunity to re-allocate the second-year treatments to ensure each was exposed to a uniform range of populations (from ≈1 to 49 *P. thornei* g⁻¹ soil).

Using a bivariate linear mixed model, significant negative responses between yield and *P. thornei* densities were detected for the intolerant second-year cultivars. Maximum yield loss was, respectively, 61, 53, and 25% for cvs. Lincoln, Strzelecki and Lang. For the more tolerant cultivars (Spitfire, EGA Gregory and Suntop) significant yield responses were not detected. Re-randomising the second-year treatments based upon the observed nematode densities before planting ensured that each cultivar was planted on a similar range of *P. thornei* densities. Similar, repeated experiments will be conducted nationally to better understand the interaction of root lesion nematode populations, cultivar tolerance and yield losses.
Characterising isolates of *Rhizoctonia* recovered from crops in the Pacific Northwest USA

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*Rhizoctonia* is a species complex comprising multiple anastomosis groups (AGs) and subgroups, many of which are important pathogens of many crops worldwide. In 2016 a Plant Clinic was opened at Parma in southwest Idaho and received numerous samples displaying symptoms associated with *Rhizoctonia* from various crops including hop, bean, potato, mint, raspberry and mustard. *Rhizoctonia* was successfully isolated from all hosts and the AG of each isolate was determined by sequencing the rDNA ITS region and subsequent analysis of the resulting sequence. In addition, plants were re-inoculated with a pure culture of the *Rhizoctonia* isolate to confirm Koch’s postulates. The disease symptoms and the AGs of the *Rhizoctonia* isolates are described, along with the importance of considering the AG of the *Rhizoctonia* isolates present. This knowledge can be important when considering the effectiveness of crop rotation strategies for minimising effects of diseases caused by this species complex.
Initial identification of fungal pathogens of a beetroot (*Beta vulgaris*) seed crop in New Zealand

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New Zealand produces approx. 50% of the world’s beetroot seed. Suitable climate, excellent industry infrastructure and the expertise of skilled growers make it possible to produce high quality seeds at a relatively low cost in this country. However, New Zealand beetroot seed growers lose significant amounts of produce due to beetroot diseases, on which there has been limited research. This preliminary study addresses this knowledge gap, and has been carried out at a beetroot seed growing farm in Rakaia, Canterbury. The study aimed to determine fungal pathogens that are associated with disease symptoms. Initial results indicate the major fungal pathogens isolated from the bulbs of beetroot plants were *Fusarium* spp., *Phoma* spp. and *Alternaria* spp. Bulb rot symptoms were not observed in the field at the time of collection. Additionally, Cercospora leaf spot (*Cercospora* spp.), Phoma leaf spot (*Phoma* spp.), Alternaria leaf spot (*Alternaria* spp.), and downy mildew (*Peronospora* sp.) were observed on leaves of beetroot plants. Further surveys will be undertaken at different sites to collate more information on the causal agents of beetroot diseases in New Zealand.
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