Session 01: New Problems

Climate change and soilborne diseases

Bruna Batista[1]

1. Western Sydney University, Brisbane, QLD, Australia

Available scientific evidence and simulation models suggest that the ongoing changes in climate patterns have the potential to threaten the already vulnerable global food security in multiple ways, including exacerbating soilborne diseases that affect staple crops. In this presentation, I will discuss the main mechanisms by which the changing climate can increase the severity and dispersion of soilborne diseases globally. I will show that the current approaches to monitoring and managing soilborne pathogen outbreaks are constrained by the focus on the one pathogen – one disease classical concept. Expanding studies to include other key aspects of the disease, such as the dynamics of soil microbiomes and their interactions with the pathogen and with the host plants, can provide better scientific knowledge to improve predictive tools and develop sustainable solutions to control soilborne diseases.

Genomic studies on *Macrophomina phaseolina* and *M. tecta* associated with broadacre crops in Australia and implications for charcoal rot disease management

Barsha Poudel[1], Dante Adorada[1], Adam Sparks[2], Natalie Moore[3], Sam Blanch[3], Niloofar Vaghefi[4]

1. Centre for Crop Health, University of Southern Queensland, Toowoomba, Queensland

2. Department of Primary Industries and Regional Development, Perth, Western Australia

3. New South Wales Department of Primary Industries, Grafton, New South Wales

4. University of Melbourne, Parkville, VICTORIA, Australia

Charcoal rot, caused by *Macrophomina* species, is an important root and stalk disease of many broadacre, horticultural, and vegetable crops, worldwide. The genus *Macrophomina* accommodates five species, but in Australia, only three species, namely, *M. phaseolina*, *M. pseudophaseolina*, and *M. tecta*, have been detected in association with charcoal rot on broadacre crops thus far. The aim of this study was to investigate the genetic diversity and structure of *Macrophomina* spp. populations in the northern grains region and understand potential host-association of pathogen genotypes on broadacre crops. The host range of a pathogen has a major impact on the development, distribution and management of disease; therefore, understanding the underlying molecular mechanisms and evolutionary forces shaping host range of *Macrophomina* species is crucial in managing charcoal rot. A total of 256 isolates collected from mungbean, soybean, and sorghum (2020 to 2021) were genotyped through RAD-Seq technology for genome-wide marker discovery and population genomics analyses. Results indicated the presence of two *Macrophomina* species; *M. tecta* and *M. phaseolina* in NSW and Qld, with significant differences in genetic diversity and host association of the two species. *Macrophomina tecta* population showed significantly lower genetic and genotypic diversity compared to *M. phaseolina* and was detected at higher frequency in association with sorghum crops. These results, together with comparative genomic analyses that detected accumulation of DNA transposons in *Macrophomina* isolates associated with sorghum, is suggestive of potential host adaptation of *M. tecta* on sorghum. Implication for charcoal rot epidemiology and management on broadacre crops are discussed.

A new disease of cotton caused by novel *Eutypella* species, its distribution and management

Linda Smith[1], Paul Greenfield[2], Dinesh Kafle[1], Linda Scheikowski[3], Gupta Vadakattu[4]

1. Department of Agriculture and Fisheries, Brisbane, QLD, Australia

2. Commonwealth Scientific and Industrial Research Organisation , Lindfield, NSW, Australia

3. Department Of Agriculture and Fisheries, Toowoomba, Queensland, Australia

4. Commonwealth Scientific and Industrial Research Organisation , Urrbrae, SA, Australia

In the 2017/18 season, a single small patch of cotton plants in a field in Central Queensland were observed to suddenly wilt and die. The disease reoccurred in the same location in subsequent cotton plantings, increasing to approximately 1 h in 2020. Fungal species were recovered from discoloured vascular tissue of dead plants and Koch's postulates conducted to determine if they contributed to their death. Isolations were consistently dominated by one fungus based on culture morphology. Identification was established on sequences of the internal transcribed spacer region of ribosomal DNA and revealed that all the isolates had high homology to *Eutypella scoparia*. Further analyses revealed that there were two distinct *Eutypella* species present in the isolates. Community profiling of diseased root samples showed that two operational taxonomic units related to *E. scoparia* were the most abundant fungi accounting for 45 to 99% of all sequences. Pathogenicity tests showed that a *Eutypella* isolate when inoculated into the stem of healthy *G. hirsutum* caused cankerous growth and necrosis of vascular tissue, typical of trunk disease. The fungus caused a red-brown streaking of the vascular tissue like that observed in diseased field plants. This study shows that the fungal isolates, which form a distinct group within the *Eutypella*, are associated with the root and stem of dying cotton and were the dominant fungi of diseased roots. This is the first known case of *Eutypella* affecting cotton worldwide and is considered an expansion of this genus' host range. Cotton disease surveys in Queensland confirmed this disease, called reoccurring wilt, to be widespread in the Dawson Callide region and present in a small number of fields in Emerald and St George. For early detection and potential spread of *Eutypella* sp. via aerial spores, the use of spore traps is being investigated. A variety trial conducted in the 2021/22 season showed there was no difference in resistance to the disease between four commonly grown varieties. The challenge now is to understand the lifecycle of *Eutypella* sp. and its management.

Ilyonectria capensis, *Dactylonectria estremocensis* and *Dactylonectria pinicola* are pathogens of *Pinus radiata* cuttings and seedlings

Tonya J Wiechel[1], R Aldaoud[1], Q Dinh[1], J Edwards[1], R Mann[1], D Smith[2]

1. Agriculture Victoria, Bundoora, VIC, Australia

2. Biosecurity and Agricultural Services, Agriculture Victoria, Cranbourne, Vic , Australia

In 2019/20, pine production in Victoria was 3870,000 m^3 across 224,000 ha. In Victoria, the pine industry had an estimated farm-gate value of approximately $344M. Pine plantations are predominantly found in four production regions: green triangle; central Victoria, west and south Gippsland and North East Victoria. In early 2021, Agriculture Victoria was notified that many pine cuttings/seedlings at a nursery were suffering serious dieback and damping off. Samples of the declining plants were sent to the Victorian Government diagnostic laboratory. Soilborne fungi, *Cylindrocarpon* sp. were isolated and further identified as *Ilyonectria capensis, Dactylonectria estremocensis and Dactylonectria pinicola* by sequencing 3 genes (ITS, TEF1 and Histone3). *I. capensis*, *D. estremocensis* and *pinicola* have not been previously isolated from *Pinus radiata* in Victoria.

Pathogenicity trials were performed on clean cuttings and one-year-old seedlings against all three pathogens. The aims of this study were to 1) evaluate the pathogenicity of newly isolated species *I. capensis* (VPRI 44054), *D. estremocensis* (VPRI 44094), *D. pinicola* (VPRI 44086) to pine plants by inoculating cuttings and one-year old seedlings 2) re isolate the putative pathogens from diseased tissue and 3) subject those isolates to DNA multi-marker sequence analyses for formal identification. *I. capensis* was the most pathogenic on cuttings and *D. pinicola* was the most pathogenic on seedlings. Seedlings were less susceptible to disease than cuttings. The pathogens were re-isolated from diseased tissue of both the cuttings and seedlings demonstrating Koch's postulates.

Detection and impact of *Phytophthora cinnamomi* and *P. multivora* in macadamias.

Olumide Jeff-Ego[1], Olufemi A. Akinsanmi[1]

1. The University of Queensland, QAAFI, Dutton Park, QUEENSLAND, Australia

Phytophthora cinnamomi is a major soilborne pathogen causing stem canker and root rot in macadamia worldwide. Recent detection of *P. multivora* as a causal agent of from stem canker in macadamia trees in Australia, is a concern to the industry. In addition, there is no information of the contribution of *P. multivora* to Phytophthora root rot pathosystem in macadamia. Therefore, this study sought to compare disease severity caused by *P. multivora* and *P. cinnamomi* on stem, root and leaf; in five commercial macadamia cultivars. Additionally, we examined the effect of both *Phytophthora* species on open-pollinated seedlings and their maternal parents.

Results showed that both *Phytophthora* species caused varied levels of leaf lesion, stem canker and root rot in the five macadamia cultivars. However, root infections caused by *P. cinnamomi* were more severe than *P. multivora* infections, whereas, severity of stem infections was similar in both *Phytophthora* species. Among the cultivars, cv. HAES 816 was the most susceptible to both *Phytophthora* species in the maternal parents and seedling progeny for root rot and stem canker severities. Significant (P<0.001) correlations were observed between the using the *in vivo* leaf lesion of the maternal parent and the decline in root biomass and stem lesion of the seedlings in the *in planta* assays. A moderate narrow-sense heritability (h^2) was estimated for root disease severity parameters to be a range of 0.26 - 0.49 and a small h^2 = 0.18 was estimated for stem diameter gain in open-pollinated seedlings. Our findings indicate significant variation in phenotypic traits for *Phytophthora* infection in open-pollinated seedlings in macadamia, which could be explored for breeding for disease resistance.

Session 02: Diagnostics

Molecular quantification of low populations of root-knot nematode (*Meloidogyne* spp.) in soil samples from fields to be planted to highly susceptible vegetable crops

Neil L Wilson[1], Graham R Stirling[2]

1. Metagen Pty. Ltd., Gatton, QLD, Australia

2. Biological Crop Protection, Brisbane, QLD, Australia

When root and tuber crops such as potato, sweet potato and carrot are grown in sandy soils or well-structured ferrosols, root-knot nematode (RKN, *Meloidogyne* spp.) often causes serious damage and markedly reduces yields. Most growers use RKN-resistant rotation crops and various cultural control methods to reduce nematode populations, but because the damage threshold is very low (1-10 nematodes/200 mL soil) and diagnostic services cannot reliably quantify populations of this magnitude, a nematicide is usually applied as an insurance measure. To help ensure that expensive nematicides are not applied unnecessarily, research was undertaken to develop better methods of quantifying low RKN populations. Soil was collected from 16 fallowed fields in Bundaberg and gall counts on tomato bioassay plants showed that the number of viable RKN ranged from 0 to 303 nematodes/2 L soil. Morphological counts of nematodes extracted from duplicate 2 L samples showed a good relationship between numbers of RKN and the gall count (R^2 = 0.86). DNA was extracted from nematode suspensions and RKN abundance was assessed with a qPCR assay using RKN-specific primers (RKN-qPCR). The probable number of RKN individuals in each sample was determined by comparison of qPCR Ct values to a standard curve produced using known numbers of RKN. There was a good relationship between the RKN-qPCR Ct values and both the RKN count (R^2 = 0.78) and the number of galls in the bioassay (R^2 =0.67). However, when duplicate 500 g samples were processed by SARDI using its PreDicta Pt method, there was no relationship between the DNA reading and either the RKN count or gall count (R^2 = 0.01 and 0.07, respectively). As few people have the skills required to identify and count RKN J2 in samples containing thousands of free-living nematodes, and PreDicta Pt is not suitable for quantifying the low RKN populations that often occur in pre-plant samples from vegetable-growing soils, we argue that the future lies in extracting nematodes from large volumes of soil and quantifying RKN using the RKN-qPCR methodology.

The current status of *Phytophthora* spp. in Australian almond orchards

Brittany Oswald[1], Suzanne F McKay[1, 2], Len Tesoriero[3], Simone Kreidl[4], Son Quang Dinh[4], Jacky Edwards[4, 5], Mark Sosnowski[1, 2]

1. PIRSA, Urrbrae, SOUTH AUSTRALIA, Australia

2. School of Agriculture, Food and Wine, The University of Adelaide, Urrbrae, South Australia, Australia

3. NSW Department of Primary Industries, Ourimbah, New South Wales, Australia

4. Agriculture Victoria Research, AgriBio Centre for AgriBiosciences, Bundoora, Victoria, Australia

5. School of Applied Systems Biology, La Trobe University, Bundoora, Victoria, Australia

Phytophthora spp. can be highly aggressive pathogens to almond, causing root rot, crown rot, and trunk cankers. Symptoms include limb dieback, chlorosis, gummosis, discolouration and woody tissue death, root necrosis, tree decline and eventual tree death. A 2018 grower census revealed that Phytophthora diseases were prevalent and reportedly having an impact on

orchard profitability in all almond growing regions. During disease surveys from 2018-2020, root and trunk samples taken from symptomatic trees from orchards in South Australia, Victoria, and New South Wales yielded numerous *Phytophthora* isolates. Species were identified as *Phytophthora acarina, Phytophthora cactorum, Phytophthora hedaiandra, Phytophthora multivora, Phytophthora niederhauserii* and *Phytophthora syringae, using* ITS (ITS4 and DC6) and Cox1 (FM84 and FM77) primers. Historically, *P. niederhauserii,* and *P. acerina* have been rarely reported, and this constitutes the first report of *P. hedraiandra* on almonds in Australia. A preliminary pathogenicity experiment was conducted on almond trees (cv. Price) in August 2020 and repeated in February 2021 at the Waite Campus in Adelaide. Species available at the time of the experiments included *P. cactorum, P. acerina* and *P. niederhauserii*. A *Phytopythium* sp., isolated from symptomatic almond roots, was also included. One-year-old branches were inoculated with mycelial agar plugs, incubated for 6 weeks, and lesion length recorded, followed by re-isolation to confirm Koch's postulates. Results showed that all three *Phytophthora* species were pathogenic, whilst the *Phytopythium* was not. Current research is evaluating pathogenicity of all six species identified in Australia. In future, it will be important to establish the prevalence of *Phytophthora* spp., the impact they are having on orchard productivity, and to develop more management options for the Australian almond industry. This research was conducted as part of project AL16005 funded by Hort Innovation using the almond research and development levy and funds from the Australian Government.

Identification and pathogenicity of *Pythium* on pyrethrum (*Tanacetum cinerariifolium*) plant in Australia

Yuzhu Liu[1], Peter Ades[2], Alexander Idnurm[3], Paul Taylor[1]

1. Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Melbourne, Victoria, Australia

2. Faculty of Science,, The University of Melbourne, Parkville, Melbourne, Victoria, Australia

3. School of BioSciences, The University of Melbourne, Parkville, Melbourne, Victoria, Australia

Pyrethrum (*Tanacetum cinerariifolium*) cultivation in Australia suffers from a persistent yield decline which in part is caused by a complex of soil-borne pathogens. There has been no research on the relationship between *Pythium* spp. and pyrethrum yield decline. During surveys between 2018 to 2021, 13 known *Pythium* spp. and two putative new *Pythium* species were recovered from crown and root tissues of infected pyrethrum plants and from soils from 16 sites in Tasmania and Victoria, Australia. Identification of *Pythium* spp. was based on morphological characters and multigene phylogenetic analyses using ITS, Cox-1 and Cox-2 gene sequences. *Pythium ultimum* var. *ultimum* was the most abundant in soils, while *P. sylvaticum* and one *Pythium* sp. nov. were most abundant in pyrethrum plants. In glasshouse post-germination bioassays, seven *Pythium* species were pathogenic to pyrethrum seedlings with *P. irregulare* and *P. ultimum* var. *ultimum* being the most aggressive, causing seedling damping-off and significant plant biomass reduction. The results suggest that *Pythium* species could be contributing to yield decline in pyrethrum in Australia. This is the first report of *Pythium* species as pathogens of pyrethrum globally.

Diversity, pathogenicity and management of *Berkeleyomyces rouxiae* causing black root rot of cotton seedlings in New South Wales

Duy LE[1], Beth Shakeshaft[2], Chi Nguyen[1], Alison Young[2]

1. NSW Department of Primary Industries, Narrabri, NSW, Australia

2. NSW Department of Primary Industries, Yanco, NSW, Australia

Black root rot (BRR) is of a major constraint of cotton production in New South Wales (NSW), Australia. BRR is caused by a soilborne fungus *Berkelyomyces rouxiae* (previously known as *Thielaviopsis basicola*), that was reported for the first time in 1990 in northern NSW. The disease is now widespread across the state. There has been a significant investment in characterization and management of the disease in the past 30 plus years. A collection of over 200 isolates that were recovered from BRR-diseased cotton seedlings sampled across NSW in the past four seasons was subjected to multi-sequence analyses of the ITS, RPB2 and MCM7 genes for their diversity. Cotton-*B. rouxiae* isolates were highly uniform and clustered well together in a maximum likelihood analysis though both mating type idiomorphs were detected within the population. In vitro assays failed to induce sexual reproduction through pairing isolates carrying opposite mating types. Five representative isolates arbitrarily selected in five main cotton growing valleys in NSW exhibited a relatively mild virulence on cotton seedlings (disease severity rated <40%) in the first pathogenicity assay. These tested isolates appeared highly virulent in subsequent second and third assays, especially for those isolates recovered from southern NSW. This observation was deemed to associate with the pathogen virulence itself since the relationship between inoculum loads and disease severity was weak (R^2 = 0.11). Among control options that we have assessed to date, only seeds either treated with acibenzolar-S-methyl or drenched with myclobutanil reduced the disease severity by approximately 23% and 15%, respectively in our pot trials. Field trials revealed in-furrow application of myclobutanil could lower the disease severity, but the results varied between cropping seasons.

Session 03: Breeding and genetics

Breeding technologies to fast-track the development of crops with improved tolerance to soilborne diseases

Shanice Van Haeften[1], Samir Alahmad[1], Brendan Fu[2], Eric Dinglasan[1], Yichen Kang[1], Hannah Robinson[1], Daniel Smith[2], Kai P Voss-Fels[1], David R Jordan[3], Millicent Smith[1, 3], Colin Douglas[4], Elizabeth Aitken[2], Andrew K Borrell[3], Scott Chapman[1, 2], Andries B Potgieter[5], Lee Hickey[1]

1. Queensland Alliance for Agriculture and Food Innovation , The University of Queensland, St Lucia, QLD, Australia

2. School of Agriculture and Food Sciences, Faculty of Science, The University of Queensland, Gatton, QLD, Australia

3. Centre for Crop Science, QAAFI, UQ, Hermitage Research Facility, Warwick, QLD, Australia

4. Department of Agriculture and Fisheries Queensland, Bundaberg, QLD, Australia

5. Centre for Crop Science, QAAFI, The University of Queensland, Gatton, QLD, Australia

Soilborne diseases in crops are caused by a range of pests and pathogens and impose a major biological constraint for agricultural productivity in Australia. Through plant breeding, new crop varieties can be developed with improved tolerance. However, traditional methods are slow and breeding crops with improved tolerance to soilborne diseases is particularly challenging due to a number of factors: 1) limitations and bottlenecks associated with traditional phenotyping approaches, 2) a lack of resistance alleles in modern germplasm, and 3) the genetic controls of tolerance mechanisms are often complex. In this presentation, we highlight new technologies and innovations that can help fast-track the development of future crops tolerant to soilborne diseases. This includes camera-mounted UAVs to support indirect phenotyping and selection of canopy proxy traits, speed breeding technology to accelerate tissue culture pipelines and generation turnover in pre-breeding and breeding programs seeking to introgress exotic alleles for tolerance, and a new breeding framework that uses artificial intelligence to rapidly stack chromosomal blocks for tolerance and performance in production systems constrained by soilborne diseases. We provide examples for Fusarium disease tolerance across a range of crops, including Fusarium crown rot of durum wheat, Fusarium wilt of mungbean and Fusarium wilt of banana.

QTL mapping flavonoid accumulation in chickpea (*C. aretinium L.* & *C. echinospermum*) infected with Phytophthora root rot (*P. medicaginis*)

Nicole Dron[1], Tim Sutton[3, 2], Jason Ng[4], Ulrike Mathesius[4], Julian Taylor[2], Beata Sznajder[2], Kristy Hobson[1]

1. NSW Department of Primary Industries, Tamworth, NSW, Australia

2. School of Agriculture, Food and Wine, University of Adelaide, Adelaide, SA, Australia

3. South Australian Research and Development Institute, Adelaide, SA, Australia

4. Australian National University, Canberra, ACT, Australia

Plant root exudates contain metabolites that play an important part in plant-microbe interactions within the rhizosphere, particularly important in leguminous chickpea. Flavonoid and isoflavonoid compounds modulate nitrogen fixing nodulation and are linked to improved levels of plant disease resistance, as reported in soybean (*Glycine max*) with *Phytophthora sojae* (Zhou et al., 2018). Phytophthora root rot (PRR) of chickpea caused the soil-borne

oomycete *P. medicaginis*, results in significant losses to the Australian chickpea industry annually. This study explored the influence of *P. medicaginis* infection on the specific accumulation of 43 target flavonoids in chickpea (*C. aretinium L.* & *C. echinospermum*). Following eight days mycelial-oospore *P. medicaginis* infection using a hydroponic system, 12 flavonoids were detected and demonstrated up to 8.8-fold increase in accumulation when compared to the uninfected control. Differential accumulation occurred between the moderately resistant wild *Cicer* back cross 04067-81-2-1-1 and *C. aretinum* moderately susceptible Yorker. Using an F6 biparental population of 142 recombinant inbred lines (RIL) derived from 04067-81-2-1-1 and Yorker, 12 putative QTL were identified for iso/flavonoids: formononetin, maackiain, biochanin A, genistein (genistein-7-O-glucoside) and morin accumulation following *P. medicaginis* infection. QTL analysis showed that two previously published QTL of the same RIL population for field PRR resistance (*QYBprrsi01* and *QYBprrsi01*) co-located closely with putative QTL for morin (*QYBmoprr02*) on chromosome 3 and (*QYBmoprr04*) on chromosome 6, respectively (Amalraj et al., 2019). The physical mapping of PRR resistance and reported antioxidant morin QTL to comparable genomic regions provides novel evidence that they're potentially the same functional genes. An additional 14 QTL for 12 detected flavonoids were also identified. This information can be used to link key metabolites involved in PRR resistance and flanking markers which can in future facilitate breeding for resistance to PRR in chickpea.

1. AMALRAJ, A., TAYLOR, J., BITHELL, S., LI, Y., MOORE, K., HOBSON, K. & SUTTON, T. 2019. Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (Cicer arietinum L.) and wild (Cicer echinospermum PH Davis) chickpea. Theoretical and Applied Genetics, 132, 1017-1033.
2. ZHOU, Y., HUANG, J.-L., ZHANG, X.-L., ZHU, L.-M., WANG, X.-F., GUO, N., ZHAO, J.-M. & XING, H. 2018. Overexpression of chalcone isomerase (CHI) increases resistance against Phytophthora sojae in soybean. Journal of Plant Biology, 61, 309-319.

Occurrence of fungicide resistance in *Rhizoctonia solani* and its effects on management of Rhizoctonia diseases of potato in Idaho.

Phillip Wharton[1], Katie L Malek[1], Alan Malek[1], Shelbie Anderson[1], James W Woodhall[2]

1. Dept. Entomology, Plant Pathology and Nematology, University of Idaho, Aberdeen, Idaho, USA

2. Dept. Entomology, Plant Pathology and Nematology, University of Idaho, Parma, Idaho, USA

Rhizoctonia solani is an important pathogen of potato, causing qualitative and quantitative losses. It has been associated with black scurf and 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. In 2020, a fungicide sensitivity survey was conducted to determine the effectiveness of known fungicides against different AGs of *R. solani* isolated from field crops growing in Idaho. Thirty-one isolates were collected and screened for resistance to nine different fungicides. Fungicide sensitivity testing was done using spiral plate dilution gradients. Fungicide solutions were applied to PDA in a 2.5-log dilution in a continuous radial concentration gradient using a spiral plater. Fungal inoculum was placed in radial lines across the gradient. Plates were incubated for 4 days before being assessed. Fungicide sensitivity was expressed as an EC_{50}, the fungicide concentration at which a fungal isolate's radial growth was equal to 50% of the average growth of the isolate on non-amended PDA. Results showed that *R. solani* isolates were sensitive to most of the fungicides tested with the exception of pencycuron. Of the six isolates of *R. solani* tested that showed resistance to pencycuron, none were AG3-PT isolates collected from potato. Field trials were carried out in 2020 and 2021 with pencycuron and other fungicides to determine if there has been a loss of

efficacy of these fungicides in the control of Rhizoctonia diseases of potato. Results showed that seed tuber and/or in-furrow applications of registered fungicides are still effective in controlling Rhizoctonia disease of potato in Idaho.

Double trouble: investigating the interaction of soilborne pathogens in wheat, using three-dimensional response surfaces

Bethany Rognoni[1], Kirsty Owen[2], Cassandra Percy[2], Lucas Peitton[1], Clayton Forknall[1]

1. Queensland Department Of Agriculture And Fisheries, Toowoomba, Queensland, Australia

2. Institute for Life Sciences and the Environment, University of Southern Queensland, Toowoomba, Queensland, Australia

Plant diseases caused by soilborne pathogens can be devastating for cereal crop growth, resulting in adverse impacts on crop productivity. Typically, experimentation quantifies the impact of one pathogen on crop response variables such as grain yield and grain quality. However, in practice, growers are faced with disease complexes, where multiple soilborne pathogens can be present in the farming system.

Fusarium pseudograminearum, which causes crown rot, *Bipolaris sorokiniana*, which causes common root rot, and *Pratylenchus thornei*, a root-lesion nematode, are all major yield-limiting soilborne pathogens of wheat in the northern Australian grain growing region. These pathogens also commonly co-occur in this region. For example, of the 35% of paddocks with medium-high levels of *P. thornei*, 44% of those paddocks also had *F. pseudograminearum* at medium-high levels.

To investigate the potential interaction between selected pairs of these soilborne pathogens, a robust and novel statistical method was implemented. This required the development of a bespoke experimental design approach, before applying a state-of-the-art analysis technique using tensor cubic smoothing splines in a linear mixed model framework.

This statistical methodology was applied to two experiments conducted in south-east Queensland, in which two wheat varieties were tested. The first experiment explored responses to established continuums of *F. pseudograminearum* and *P. thornei*, while the second explored responses to established continuums of *F. pseudograminearum* and *B. sorokiniana*. As a result, three-dimensional response surfaces were generated, formed using two explanatory pathogen continuum variables, along with a response variable of interest such as yield. These response surfaces provided insight into how these pathogens simultaneously affected the response variables. Additionally, the method provided insight into pathogen dynamics, including changes in population densities of the co-occurring pathogens and disease severity. Altogether, the application of the techniques described enabled a more robust exploration of soilborne disease interactions than previously conducted.

Session 04: Engagement

Building resilience in community through engagement

A T Marsh[1], J M Green[2], L Ford[2], R Wallace[3], K Guthadjaka[3]

1. The New Zealand Institute for Plant & Food Research, Palmerston North, MANAWATU, New Zealand

2. The New Zealand Institute for Plant & Food Research Limited, Auckland, New Zealand

3. The Northern Institute at Charles Darwin University, Darwin, NT, Australia

Indigenous communities in both Australia and New Zealand are constantly facing threats from both naturally occurring incursions and the human-mediated spread of existing pests, diseases and weeds. These incursions can have disastrous effects on commercial, traditional subsistence and niche-market cropping systems, the latter often occurring in relatively remote communities. For response programmes to be implemented, it is essential that effective communication, understanding and cooperation is achieved between agencies charged with controlling the incursions and communities affected by them.

The overall aim of the project was:

To enhance the ability of indigenous communities and relevant regulatory authorities and industries to better manage social, cultural, environmental and economic impacts of threats to industry and community, and to participate in strategies by describing and evaluating bicultural engagement models that build empowerment and ownership in indigenous communities and their response to those threats.

The project was undertaken by a multicultural team drawn from the Institute for Plant and Food Research, New Zealand and the Northern Institute, Charles Darwin University, Australia. Because traditional cultural values, behaviours and protocols were recognised as essential elements of effective engagement, the team included respected elders (kaumatua) from both countries to provide guidance, support and validation on cultural issues.

Team members in each country used participatory action research to document procedure and identify key principles to the process. The careful collection of traditional knowledge from elders in both Māori and Aboriginal communities created trust, understanding and a willingness to share details the research teams could relate to and embed in the models. This methodology has resulted in models for engagement developed by indigenous communities for indigenous communities, thereby increasing the probability of adoption and success.

The work provides a knowledge base that can be utilised and implemented as procedure by government, agencies and industry. This has not been done before.

The extension response to Panama Disease Tropical Race 4 in north Queensland

Shanara Veivers[1], Tegan Kukulies[1], Stewart Lindsay[1], John Bagshaw[2], Shane Dullahide[2], Sarah Simpson[2], Naomi King[2]

1. Department of Agriculture and Fisheries, Boogan, Queensland, Australia

2. Formerly Australian Banana Growers Council, Rocklea, Queensland, Australia

Fusarium wilt - also known as Panama disease - is caused by the soilborne fungus *Fusarium oxysporum* f.sp. *cubense (Foc)* and is regarded as one of the most destructive diseases of banana. Panama disease Tropical Race 4 (TR4) was identified for the first time in Queensland on a commercial banana property in the Tully Valley in March 2015. The wet tropics of Far North Queensland, including Tully, produces 96% of Australia's total banana crop worth approximately

$600 million annually, and sustains many regional coastal communities. Currently, there are no known economically viable options for effectively managing the disease. The implementation of effective on-farm biosecurity practices is essential for limiting the spread of the disease. Following the detection of TR4, a multi-faceted multi-agency research, development and extension program supported the investigation of short, medium and long term research objectives to limit the spread of the disease and support the industry into the future as the disease spreads. At the heart of the initial response, a multidisciplinary team of extension practitioners, research scientists, and key industry stakeholders used a mixed method learning and engagement approach to conduct training and biosecurity planning with commercial banana farms in north Queensland. The extension response consisted of a) interactive and personalised on-farm biosecurity workshops; b) one-on-one farm visits; c) regular extension events e.g., meetings, field days and R&D updates; d) development of Panama disease TR4 information and communications material, and; e) peer-to-peer sharing of effective on-farm biosecurity grower practices. Evaluation activities conducted throughout the response shows that the multidisciplinary, multi-agency R,D&E approach to the outbreak of Panama disease TR4 in Queensland played a fundamental role in improving knowledge and understanding of the disease as well as the implementation and adoption of robust science-based on-farm biosecurity practices to reduce the spread of the disease.

Cover crops for managing soilborne diseases in vegetable production - the good, the bad and the ugly.

Kelvin Montagu[1], Marc Hinderager[1], Len Tesoriero[2], Calum Wilson[3]

1. Applied Horticultural Research, Eveleigh, NEW SOUTH WALES, Australia

2. Crop Doc Consulting Pty Ltd, Gosford

3. TIA Vegetable Centre, Hobart

Soilborne diseases present an ongoing challenge to the Australian vegetable industry, with an estimated $120 million in losses annually. Cover crops are an important soil management tool and can be useful in managing the risk of soilbourne diseases. But for soilbourne disease management cover crops must be chosen carefully to get the good and avoid the bad and ugly.

In this presentation we identify the good, the bad and the ugly of cover crops for soilborne diseases important in vegetable cropping including *Rhizoctonia solani*, *Pythium* spp, *Sclerotinia sclerotiorum, S. minor*, *Fusarium oxysporum*, *Sclerotium rolfsii*, *Verticillium dahliae*, and *Thielaviopsis basicola.*

A literature review collated results from 81 publications looking at the impact of cover crops on soilborne disease incidence, with “Good”, “Bad” and the “indifferent” used to indicate cover crops which reduced, increased or had no effect, respectively, on disease incidence compared to a bare fallow. This simplistic categorisation did not take into account the many factors including crop genetics, environmental conditions, pathogen load, cultural practices and the general health of the soil, that influence how a soilborne disease impacts on crop health and yield. These factors are paddock specific and need to be used in conjunction with the cover crop information to assess the disease risk. The “ugly” of cover crops are those biofumigant varieties which if managed poorly can increase disease incidence during their growth, and not reduce the disease on incorporation.

With mixed cover crops growing in popularity, we also discuss the implications for soilborne disease management.

Distribution and Genetic Diversity of the Fusarium Wilt Disease in Laos

Khonesavanh Chittarath[1]

1. ., Cambodia

Fusarium wilt, caused by the fungus Fusarium oxysporum f. sp. cubense (Foc), poses a major threat to global banana production. The tropical race 4 (TR4) variant of Foc is a highly virulent form with a large host range, and severely affects Cavendish bananas. Foc TR4 was recently observed within Laos, after Chinese private companies expanded Cavendish production to the region. In this study, extensive surveys conducted across Laos show that Foc TR4 is still mainly constricted to the northern regions of country and is limited to Cavendish cultivation settings. In Laos, Foc TR4 is associated with large-scale Cavendish plantations owned by or involved with Chinese companies through which infected planting material could have been imported. Foc TR4 was not recorded on banana cultivars other than Cavendish. The extensively cultivated 'Pisang Awak' cultivar was solely infected by VCGs belonging to Foc race 1 and 2, with a high occurrence of VCG 0123 across Laos. Substantial diversity of Foc VCGs was recorded (VCGs 0123, 0124, 01218 and 01221) from northern to southern regions in country, suggesting that Fusarium wilt is well established in the region. Interviews with farmers indicated that the local knowledge of Fusarium wilt epidemiology and options for disease management was limited. Clear communication efforts on disease epidemiology and management with emphasis on biosecurity practices need to be improved in order to prevent further spread of Foc TR4 to mixed variety smallholder settings.

Pyrolysis of oil palm wastes as a possible sanitation measure against the fungal disease basal stem rot

Jitka Kochanek[1], Emad Jaber[2], Evah Tokilala[2], Agnieszka Mudge[3]

1. Australian Institute for Bioengineering and Nanotechnology, The University of Queensland, St Lucia, QLD, Australia

2. PNG Oil Palm Research Association, Dami Research Station, West New Britain Province, Papua New Guinea

3. The University of Queensland, St Lucia, QLD, Australia

Oil palm (*Elaeis guineensis* Jacq.) is a long-term perennial crop of great economic importance to many countries in tropical Asia/Oceania, providing export revenue and much needed income to both large plantations and smallholders. Unfortunately, basal stem rot (BSR), caused by the fungus *Ganoderma boninense* Pat., poses a major threat to the oil palm industry and hence to farmers' livelihoods. A potential long-term control measure for this disease would be through improved cultural practices. In a related project we have confirmed that oil palm residues from previous planting (windrowed logs and stumps) are a source of inoculum for new planting thus continuing the disease cycle. Therefore, a disease management measure would be to remove old logs and stumps from the field. This is costly and time consuming, especially to the smallholder. Thus, we investigated pyrolysis of oil palm residues (logs, fronds and empty fruit bunches) using two technologies (low and medium cost) as a way to convert oil palm residue into biochar, a charcoal like material. We demonstrated that biochar made with both technologies promoted growth of vegetable seedlings in a commercial nursery, indicating that oil palm residue is a good clean feedstock for pyrolysis. Biochar from oil palm residues has the potential to close the circular economy by converting waste into a higher value product. Furthermore, pyrolysis promises to break the disease cycle by sanitation of diseased plant material.

Session 05: Flash Talks / Posters

QTL mapping of waterlogging tolerance traits in chickpea (*C. aretinium L.* & *C. echinospermum*) and the genetic relationship with QTL conferring Phytophthora root rot (*P. medicaginis*) resistance

Nicole Dron[1], Tim Sutton[2, 3], Julian Taylor[3], Beata Sznajder[3], Kristy Hobson[1]

1. NSW Department of Primary Industries, Tamworth, NSW, Australia

2. South Australian Research and Development Institute, Adelaide, SA, Australia

3. School of Agriculture, Food and Wine, University of Adelaide, Adelaide, SA, Australia

Waterlogging is an important precondition for severe Phytophthora root rot (PRR) development in chickpea. The pathogen itself can sporulate rapidly in transient flooding conditions; whilst under waterlogging conditions the plant itself undergoes structural and physiological modification increasing plant stress and disease susceptibility. Levels of waterlogging tolerance in chickpea are inherently low. However, PRR moderately susceptible chickpea cultivar Yorker demonstrated an increase in early adventitious root growth from the epicotyl region compared to the PRR moderately resistant interspecific backcross genotype 04067-81-2-1-1, which maintained a greater root depth under waterlogging (Dron et al., 2021). Soil-borne *Phytophthora* spp. are attracted to branch sites and leached exudates, hence why selection for primary root depth under waterlogging may improve PRR resistance compared with root replacement traits. This study explored the genetic relationship between waterlogging tolerance traits and PRR disease resistance in chickpea seedlings. Using an F6 biparental population of 156 recombinant inbred lines derived a wild *Cicer* back cross 04067-81-2-1-1 and *C. aretinum* Yorker. Following 14 days of soil saturation, waterlogging tolerance QTL were identified for traits including: dry root weight (DRW), dry shoot weight (DSW), plant height (PH), primary root length (PRL) and adventitious root count (RC) or root recovery. Three previously published QTL for field PRR resistance *QYBprrsi01*, *QRBprrsi02* and *QRBprrsi03* co-located closely with the waterlogging QTL for DRW, PRL and RC, respectively (Amalraj et al., 2019). The physical mapping of PRR resistance and waterlogging tolerance QTL to similar genomic regions on the Kabuli v1.0 chickpea reference genome provides novel evidence that they're potentially the same functional genes. Six additional unique QTL for waterlogging were also identified. This information can be used to link key traits and flanking markers which can in future facilitate breeding for resistance to both waterlogging and PRR disease in chickpea.

1. AMALRAJ, A., TAYLOR, J., BITHELL, S., LI, Y., MOORE, K., HOBSON, K. & SUTTON, T. 2019. Mapping resistance to Phytophthora root rot identifies independent loci from cultivated (Cicer arietinum L.) and wild (Cicer echinospermum PH Davis) chickpea. Theoretical and Applied Genetics, 132, 1017-1033.
2. DRON, N. M., SUTTON, T., SIMPFENDORFER, S., HARDEN, S. & HOBSON, K. 2021. Phenotyping for waterlogging tolerance as a proxy for Phytophthora medicaginis resistance in chickpea. Plant Health Progress, 287-293.

Glasshouse screening to identify rotation crops resistant to reniform nematode (*Rotylenchus reniformis*) for the sweetpotato industry

Jennifer Cobon[1], Wayne ONeill[1], Tim Shuey[1]

1. DAF, Agriscience Qld, Brisbane, QLD, Australia

Plant-parasitic nematodes are a major constraint to sweetpotato production, causing considerable losses in yield and quality, with current estimates suggesting they cost the Australian industry $20M per year.

Reniform nematode (*Rotylenchulus reniformis)* is recognised worldwide as a major plant-parasitic pest of sweetpotato and was present at 10% of surveyed sites across the Australian sweetpotato production area. They mainly occurred on crops in the warmer regions of central Queensland and Bundaberg. However, one site in SE Queensland and one site in Cudgen NSW were also infested with *R. reniformis* (53 and 365 per 200 g dry soil respectively).

Nematodes can be managed by removing host plants, in this case sweetpotatoes and susceptible weeds, growing resistant rotation crops and replanting with clean planting material. Resistant rotation crops do not support nematode feeding and/or reproduction. This reduces plant-parasitic nematode abundance and increases productivity in the following sweetpotato crop, while reducing the negative impact of nematode damage on the quality of storage roots.

To guarantee a constant supply of nematodes for experimentation, reniform nematode was cultured in the glasshouse onto tomato plants from a single egg mass obtained from a field-infested sweetpotato. Glasshouse experiments were undertaken to establish a suitable potting media for resistance screening. A range of potential crops that may be useful rotations for sweetpotato growers were then assessed in glasshouse trials for resistance to reniform nematode.

A well-managed crop rotation phase in the cropping cycle can mean that sustainable sweetpotato production is not constrained by *R. reniformis* and other plant-parasitic nematodes.

Studies of antagonist effect of *Trichoderma harzianum* (biological control agent) against *Fusarium oxysporum* (wilt disease causal agent) in laboratory condition (i*n vitro*)

Gomathinayagam K Subramanian[1], Rekha S Murugesan[2], Shanmugaiha V Velusamay[2]

1. University of Guyana Berbice Campus, Berbice, GUYANA

2. Microbial Technology, Madurai Kamarj University, Madurai, Tamil Nadu, India

Biological control of plant diseases is gaining momentum in recent years since use of chemical pesticides lead to various health's hazardous to human beings (Brent, 1995; Sharma *et al.*, 1998). In the last two decades, numerous biological disease control agents are being examined and the use of microorganism based bio pesticides is being increased for the management of various crop diseases.

Trichoderma harzianum is a potential fungus, showing antagonistic activity against plant pathogenic fungi (Peng and Sutton, 1991; Kumar and Jha, 2002). *T. harzianum* is a soil fungus and also exist in dead matter and living tissues as saprophyte and parasite, respectively, T. *harzianum* is a weak pathogen and upon infection, induces host plant resistance and also plays a major role in growth promotion of plants.

Tomato is one of the most widely grown garden and cash crops in Guyana, and elsewhere. As a very nutritious and tasty fruit, it is used fresh in salads, processed into juices and condiments, and cooked in stews. Tomatoes can be grown throughout the country, but do well in areas

where the soils are loose, deep, free-draining, rich in nutrients and with a pH range of slightly acidic to slightly alkaline (5.5 - 7.5). Sandy and loamy soils should be enriched with organic matter - manures or compost. They can be cultivated throughout the year but grow better during the dry seasons.

The crop grows well in open plots, but can also be grown in protected, enclosed farming structures. They respond well to sunlight as they harden and become properly established. However, they are very sensitive to water availability and can easily wilt when the soil is dry or can become asphyxiated when the roots are water-logged. Frequent, light irrigation is required to avoid any form of water stress (Tomato Crop Information Brochure Guyana 2017).

The present studies to check antagonistic effect *Trichoderma harzinum* against tomatoes will disease cause pathogens *Fusarium oxysporum* in *in vitro* condition.

Key words: *Trichoderma harzinum, Fusarium oxysporum*, antagonistic, biological control, *in vitro*

Investigating the microbial activity in the rhizosphere and bulk soil from declining and healthy avocado trees.

Denis Brendan Roe[1], Akila Devi Prabhakaran[2], Elizabeth Dann[2]

1. School of Agriculture and Food Sciences, University of Queensland, Brisbane, Queensland, Australia

2. Center for Horticultural Sciences, Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Brisbane, Queensland, Australia

Phytophthora root rot (PRR) caused by the soilborne pathogen *Phytophthora cinnamomi* (Pc), is one of the major productivity constraints in the avocado (*Persea americana*) industry. Feeder roots, rhizosphere (0-5cm) and bulk (10-20cm) soil samples were collected in June 2021 from healthy and declining avocado trees. *Dactylonectria* sp., but not *P. cinnamomi* was isolated from roots on selective media at high frequencies from all treatments. However, lupin baiting experiments confirmed that *P. cinnamomi* was abundant in the soil with all treatments showing high percentages (above 75%) of seedlings wilted, with subsequent plating onto 3P media confirming Pc. The rate of decomposition of cotton squares buried in soil samples, and microbial activity determined by substrate induced respiration (MicroResp^{TM} assay) were measured. There were significantly higher rates of decomposition of cotton squares (lower cotton dry weights) from rhizosphere soil samples compared to bulk soil samples. Microbial respiration of all rhizosphere soil was significantly higher than the bulk soil. There were no significant differences in cotton decomposition or microbial respiration between soil collected from the declining and healthy trees. There was a significant correlation between the simple cotton decomposition and MicroResp^{TM} assays (R^2=0.57). Results from further soil and root collections in December 2021 and April 2022 are being processed and will be presented.

Disease management of *Fusarium oxysporum* and *Pythium irregulare* causing root decline of processing tomatoes

Hanyue Feng[1], Paul Taylor[1], Niloofar Vaghefi[1], Sigfredo Fuentes[1], Claudia Gonzalez Viejo[1]

1. University of Melbourne, Melbourne, VIC, Australia

In recent years, soil borne diseases have caused serious root damage and growth reduction in processing tomatoes in Victoria, Australia. Various *Fusarium* and *Pythium* species were isolated from necrotic roots and collar tissues of diseased plants, with the most abundant and aggressive being *F. oxysporum*, *P. irregulare* and *P. ultimum.* Glasshouse pathogenicity bioassays are being

developed and optimized to enable varietal screening of different tomato cultivars to identify resistance, and to study host-pathogen interactions under different biotic stresses. These trials also include measuring plant physiological parameters using e-nose, NIR and Li-Cor to construct machine learning models for more accurate monitoring and prediction of plant health conditions at early growth stages. The efficacy of a commercial biostimulant was also assessed to suppress pathogens in the soil and stimulate root growth and overall biomass production. Preliminary results with *F. oxysporum* showed varietal differences in resistance with one cultivar being able to tolerate low level of pathogen inoculum without reduction in root growth. Whereas the other cultivar was highly sensitive with root growth largely reduced even at the lowest level of pathogen inoculum. Rate of photosynthesis, transpiration, and production of volatile compounds such as ammonia, hydrogen, and methane etc. between healthy plants and inoculated plants were also significantly different. The application of biostimulant to the soil improved plant root growth and overall biomass production, however from *in-vitro* toxicity tests, direct inhibition/antibiosis against both pathogens was not observed.

Key words: root rot, oomycete, yield decline, soilborne disease, remote sensing, biocontrol

---

Molecular characterization and diversity of *Fusarium* spp. from sorghum

Niroshini Gunasinghe[1], Niloofar Vaghefi[2, 3], David Jordan[4, 5], Alan Cruickshank[4], Emma Mace[4], Anke Martin[1]

1. Centre for Crop Health, University of Southern Queensland, Toowoomba, QLD, Australia

2. School of Agriculture and Food, Parkville, VIC 3010, University of Melbourne, Melbourne, Victoria, Australia

3. Centre for Crop Health, University of Southern Queensland, Toowoomba, QLD, Australia

4. Department of Agriculture, Forestry & Fisheries, Queensland, QLD, Australia

5. Centre for Crop Science, University of Queensland, Brisbane, QLD, Australia

Sorghum (*Sorghum bicolor*) is the fifth most important cereal crop in the world and the dominating summer crop in Queensland, where more than half the area planted to summer crops is planted to sorghum. It is used mainly for feed for livestock and as a dietary staple for 500 million people in over 30 countries across the world. Stalk rot caused by *Fusarium* spp. results in significant economic losses to the sorghum industry. The disease incurs yield losses due to poor grain fills and may contribute to lodging. This study aimed to identify locally dominant *Fusarium* species and assess their diversity in Queensland. Sorghum samples were collected from nine different fields in major sorghum-producing regions in southern Queensland (Qld) and northern New South Wales (NSW). A total of 203 *Fusarium* spp. were isolated from symptomatic or asymptomatic tissue, and phylogenetic analyses were conducted using partial sequences of the translation elongation factor 1 (*TEF1-α*) and RNA polymerase II beta subunit (*RPB2*) genes. The majority of isolates (80%) belonged to the Fusarium Fujikuroi Species Complex (FFSC) and the remaining isolates belonged to the Fusarium Oxysporum Species Complex (FOSC) (19%) and Fusarium Chlamydosporum Species Complex (FCSC) (1%). Within the FFSC species complex, *F. thapsinum* was isolated at the highest frequency (46%) across all regions. The second and third most abundant species were *F. verticillioides* and *F. nygamai* comprising 10% and 8%, respectively. Isolates recovered from the asymptomatic tissues showed a similar pattern of abundance and belonged to two species complexes, namely FFSC and FOSC. Outputs from this study shed light on the diversity of *Fusarium* species affecting sorghum crops in Qld and NSW, and will further be used to develop a method for phenotyping disease resistance/tolerance.

Session 06: Integrated Management

Exploring the soil virosphere

Joanne B Emerson[1]

1. University of California, Davis, Davis, CA, United States

Viruses have been recognized as abundant but virtually unknown members of the soil microbiome. With a focus on dsDNA bacteriophages in natural and agricultural soils, early results in the burgeoning field of soil viral community ecology will be presented. Using shotgun viral metagenomic (viromic) approaches to recover and sequence the viral size fraction, tens of thousands of viral 'species' have been recovered from a wide range of soils, consistently indicating substantial viral diversity across terrestrial ecosystems. Soil viral communities are often strongly spatially structured, even over short distances. In agricultural soils, early results suggest that viral communities can differ over space, time, and across soil compartments (*e.g.*, bulk soil vs. rhizosphere). The emerging paradigm is of a highly active and dynamic soil virosphere with the potential for substantial contributions to soil and plant health in both natural and managed ecosystems.

Suppression of carpogenic germination and viability of sclerotia of *Sclerotinia sclerotiorum* by Perlka and *Coniothyrium minitans*

Madhavi Dassanayaka[1], **Eirian Jones**[1], **Seona Casonato**[1]

1. Department of Pest-management and Conservation, Faculty of Agriculture and Life Sciences, Lincoln University, Lincoln, Canterbury, New Zealand

The fungal pathogen, *Sclerotinia sclerotiorum,* devastates a broad range of hosts. Sclerotial germination of *S. sclerotiorum* is reportedly suppressed by Perlka, a multi-purpose fertilizer whilst *Coniothyrium minitans* is a sclerotial parasite. This research evaluated the suppression of carpogenic germination and viability of *S. sclerotiorum* sclerotia, by Perlka and *C. minitans* alone and in combination. Clear plastic boxes (500 mL) were filled with 1) potting compost (with 30% w/w moisture) amended with two different field rates of Perlka, 300 Kg/ha and 400 Kg/ha, or 2) potting compost amended with only Perlka (400 Kg/ha) or *C. minitans* (isolate LUPP418 at 10^6 spores g^{-1}) and in combination. Controls consisted of unamended potting compost in each experiment. In each box, mesh bags containing five sclerotia were buried into the potting compost and five free sclerotia were pressed into the substrate surface. Boxes were incubated at 18^{o}C (14L: 10D light). Carpogenic germination of surface sclerotia were recorded regularly up to 15 weeks. Buried sclerotia were recovered after 15 weeks, surface sterilized and cultured on Potato Dextrose Agar for viability assessment. Perlka treatment at 400 Kg/ha and 300 Kg/ha resulted in 100.0% and 80.5% suppression of carpogenic germination, respectively compared to the control with germinated sclerotia (83.0%). Of the recovered sclerotia, 97.5% were viable in both treatments. Perlka and *C. minitans* treatments alone, and in combination, resulted in complete inhibition of sclerotial germination in comparison to the control with 84.6% carpogenically germinated sclerotia. *Coniothyrium minitans* alone reduced the sclerotia viability by 97.0%, and in combination with Perlka, by 95.0% compared to the Perlka only and unamended control. Perlka successfully controls carpogenic germination of sclerotia but *C. minitans* resulted in reduced sclerotial viability providing improved long term disease suppression.

Ecology of reniform nematodes in Australian cotton soil

Dinesh Kafle[1], Tim Shuey[1], Dean Brooks[2], Jennifer Cobon[1], Linda Scheikowski[3], Linda Smith[1]

1. Department of Agriculture and Fisheries, Brisbane, QLD, Australia

2. Commonwealth Scientific and Industrial Research Organisation , Dutton Park, Qld, Australia

3. Department Of Agriculture And Fisheries, Toowoomba, Queensland, Australia

The reniform nematode (*Rotylenchulus reniformis*) is a major plant-parasite of cotton worldwide which accounts for up to 11% of the total loss of cotton yield due to a disease in the USA. Annual surveys conducted by the Queensland Department of Agriculture and Fisheries (DAF) show that reniform nematodes' presence has been limited to the Central Queensland region so far but there is a risk of their spread to other cotton-growing regions. We conducted several field, laboratory, and greenhouse trials to understand reniform ecology in the Australian soil so that appropriate management tools can be devised. First, we analysed the genetic diversity of the reniform nematode population found in different crops in Australia and those found in cotton-growing regions globally. Molecular analysis clarified that the reniform isolates from different crops in Australia and those of international origins are similar. We conducted three different glasshouse experiments to assess the vertical movement of nematodes in a vertisol soil; host/non-host suitability of different field crops; and the effect of different reniform nematode populations on the growth and yield of different cotton varieties. The vertical movement trial showed that reniform nematodes move upwards in the soil profile in presence of a food source (growing cotton roots). Interestingly, in some of the fields, the highest population was found at the depth of 70-100 cm below the soil surface. These results clearly show that the reniform can live and survive deep in the soil profile thereby providing a reservoir of nematodes that can move upward towards the host once the seedling starts to grow. The host/non-host trial conformed that corn, wheat, forage, and grain sorghum are non-hosts of reniform nematode and thus are suitable as rotation crops. The reniform population trial showed that a higher population of reniform nematode can significantly reduce the biomass and yield of cotton and this reduction was variety dependent. These results show that reniform nematodes are a serious problem for the cotton industry, therefore, it needs more consideration from the scientific community and the growers.

Screening *Tasmannia lanceolata* for resistance against *Phytophthora cinnamomi* dieback

Chiranthika Sinhalagoda[1], Matthew Wilson[1], David Cahill[2], Kara Barry[1]

1. University of Tasmania, Sandy Bay, TAS, Australia

2. Deakin University, Geelong, VIC, Australia

Tasmannia lanceolata (native pepper) is wild harvested, and the species has been reported as susceptible to *Phytophthora cinnamomi*. However, surveys in plantations suggest that clones differ in susceptibility and the key objective of this study was to identify native pepper clones resistant to *P. cinnamomi*, and the defence mechanisms responsible. Plant material from over 70 genotypes was collected from native stands throughout Tasmania from June-October 2020, and 47 clones were successfully propagated as cuttings. Two disease screening experiments were conducted in "soil-free plant growth system" units, with four replicates of each clone placed in separate control and inoculated units. *P. cinnamomi* zoospores (1×10^5 zoospores/mL) were applied to all root tips of all plants in the inoculation units. Successful inoculation and infection were confirmed via observation of symptoms on simultaneously inoculated lupin roots and re-

isolation of the pathogen from native pepper roots. Image analysis and machine learning was used to quantify root infection and discolouration. In the first experiment with 47 clones and one isolate of *P. cinnamomi*, the pathogen could not be re-isolated from 17 clones, which were tentatively considered less susceptible (LS) than the other 30 clones, which were tentatively considered more susceptible (MS). In the second experiment, 2 of the MS clones and 5 of the LS clones were included and challenged with two different isolates of *P. cinnamomi*. Re-isolation results for these clones were identical to experiment 1 and the same for both *P. cinnamomi* isolates. The putative defence compounds callose, lignin, hydrogen peroxide and peroxidase were assessed visually and quantitatively in the clones used for experiment 2 and their abundance was found to be significantly ($P<0.05$) affected by both clone and inoculation treatment. The constitutive and induced levels of these compounds could have a role in defence of native pepper and their detection a new way of selecting clones tolerant/resistant to *P. cinnamomi*.

Soilborne pests and diseases affecting both coffee and black pepper in Central Highlands in Vietnam: a complex consortium of pathogenic fungi, oomycetes, and nematodes.

Nguyen Van Long[1, 2], Hermann Laetitia[1, 3], Dinh Le Thao[4], Venugopal Abhi[5], Nguyen Chung[4], Enez Aydin[5], Katz Mathias[3, 6], Liem Van[4], Lucas Bernigaud-Samatan[3, 6], Lambert Brau[1], Didier Lesueur[1, 3, 7, 8, 9]

1. School of Life and Environmental Sciences, Faculty of Science, Engineering and Built Environment, Deakin University, Melbourne, VIC, Australia

2. Pepper Research and Development Center (PRDC), The Western Highlands Agriculture and Forestry Science Institute (WASI), Pleiku, Province of Gai Lai, Vietnam

3. Alliance of Biodiversity International and International Center for Tropical Agriculture (CIAT), Asia hub, Common Microbial Biotechnology Platform (CMBP), Hanoi, Vietnam

4. Plant Protection Research Institute (PPRI), Vietnam Academy of Agricultural Sciences (VAAS), Vac Tu Liem, Hanoi, Vietnam

5. Centre for Regional and Rural Futures (CeRRF), Faculty of Science, Engineering and Built Environment, Deakin University, Melbourne, VIC, Australia

6. AgroParisTech, Paris, France

7. Centre de Coopération Internationale en Recherche Agronomique pour le Développent (CIRAD), UMR Eco&Sols, Hanoi, Vietnam

8. Eco&Sols, University of Montpellier (UMR), , CIRAD, Institut National de la Recherche Agronomique (INRAE), Institut de Recherche pour le Développent (IRD), Montpellier SupAgro, Montpellier, France

9. Chinese Academy of Tropical Agricultural Sciences (CATAS), , Rubber Research Institute, Haikou, China

Vietnam is the world's 1st and 2nd largest exporter of black pepper and coffee robusta, respectively. However, due to intensive management practices, soil health has gradually reduced, resulting in production of both commodities being seriously affected by Soil Borne Pests and Diseases (SBPDs). About 300,000 ha of coffee plantations must be renewed, but all attempts to replant them have failed due to high populations of SBPD (mainly attributed to nematodes) in severely degraded soils. During the early years after its introduction, black pepper yields have exceeded the Vietnamese government's expectations even in areas with poor soils. However, farmers now observe a decrease in pepper yield. Pathogenic oomycetes including *Phytophthora capsici* and *P. tropicalis* were previously considered to be the only agents responsible for reduced pepper yields in the region. In the frame of the V-Scope project funded by the Australian Centre for International Agricultural Research (ACIAR), our team investigate SBPDs responsible for destruction of plantations of both black pepper and coffee in 3 Provinces

(Gai Lai, Dak Lak and Dak Nong). Our results show that in addition to *Phytophthora*, other groups such as *Pythium*, *Phytopythium* and *Fusarium* are also causing damages in black pepper plantations. Nematodes (*Meloidogyne* and *Pratylenchus*) were also found to affect both commodities and analysis of secondary data suggests that the populations of nematodes may be increased when coffee trees are intercropped with jackfruit and black pepper. Moreover, by using quantitative PCR, we found that *Phytophthora* and *Fusarium* were also present in black pepper plantations showing no symptoms, suggesting complex interactions between soil health, pathogen presence and plant damages. Overall, understanding the complex relationship between agricultural management practices and the consortium of SBPDs is crucial to restore soil health, control the SBPD populations and improve yields of coffee and pepper.

Session 07: Systems

Pink rot of potatoes – impact of soil factors on disease expression and understanding field detection of the recalcitrant causal agent, *P. erythroseptica*.

Robert Tegg[1], Michael Rettke[2], Bill Cotching[3], Calum R Wilson[1]

1. University of Tasmania, NEW TOWN, TAS, Australia

2. SARDI, PIRSA, Urrbrae, South Australia, Australia

3. Soil Management Consultant, Scarborough, Queensland, Australia

Phytophthora erythroseptica is a soil borne oomycete and the primary causal agent of pink rot in potatoes (*Solanum tuberosum*). The disease is characterized by pink colouration of the cut tubers and a distinctly unpleasant odour. The rapid rotting of the tubers, whether in ground or in storage, results in significant yield losses and product downgrades or rejection. Pink rot is a disease of increasing importance, particularly in key potato production regions of Tasmania, and to a lesser extent, small regions on mainland Australia.

Currently disease management relies on the use of soil-applied fungicide treatments although recent work has revealed evidence of fungicide resistance breaking strains of the pathogen in Tasmania (Chitrangi et al. 2019). This highlights the need for a more integrated approach to disease management.

This research project studied the dynamics of pathogen inoculum and soil factors that impacted pink rot disease expression from 20 commercial potato field sites across two growing seasons in Tasmania. Detection of the pathogen *P. erythroseptica* was heavily dependant on seasonal conditions with the pathogen detected rarely at most sites prior to planting of commercial crops. As the season progressed detection increased and were likely associated with higher soil temperatures and conducive moisture conditions. Pink rot disease was recorded from greater than half of the sites studied with significant crop losses observed. Greater severity of disease was observed where topsoil depth was shallower, and compaction and soil quality ratings were poor. Additionally, low lying areas were more prone to disease in most cases.

Findings suggest that soil factors play an important role in determining extent and severity of pink rot disease although there are still major knowledge gaps that remain in predicting and understanding this recalcitrant potato disease.

1. Chitrangi, R., et al. 2019. Pink rot of potato, a re-emerging problem in Tasmania: isolate diversity, fungicide resistance, pathogenicity & population dynamics. EAPR Pathology & Pests Symposium, Switzerland, 2 Sep 2019.

Phytophthora root rot inoculum decline in Australian chickpea cropping systems

Sean Bithell[1], Kevin Moore[1], Alan McKay[2], Steven Harden[1], David Backhouse[3], Andre Drenth[4], Steve Simpfendorfer[1]

1. NSW DPI, Calala, NSW, Australia

2. South Australian Research and Development Institute, South Australia, Adelaide, South Australia, Australia, Australia

3. University of New England, Armidale, NSW, Australia

4. University of Queensland, Brisbane, Queensland, Australia

Phytophthora root rot (PRR), caused by *Phytophthora medicaginis*, is an important root disease of chickpeas in Australia. A soil DNA and a plant bioassay were used to investigate changes in *P. medicaginis* inoculum levels in chickpea cropping systems. A survey conducted in eastern Australia detected *P. medicaginis* DNA in 26% of soil samples collected from within chickpea and break crops, 79% of these samples produced both PRR symptoms in the bioassay and *P. medicaginis* isolates from symptomatic plants.

Phytophthora medicaginis DNA concentrations in soil declined substantially following premature death of the very susceptible variety Sonali. Studies using the susceptible variety PBA HatTrick indicated the most labile fraction of *P. medicaginis* inoculum was associated with soil and the root fraction contained the majority of inoculum. Inoculum decayed exponentially at 5°C, dropping 50% over 2.3 months and 90% over 16.4 months.

Both in-crop and post-harvest inoculum declines were implicated in the inability to detect *P. medicaginis* DNA in half of field replicates four months after harvest. Bioassay disease incidence results did not significantly correlate with *P. medicaginis* DNA concentrations in split soil samples. Our findings showed that levels of *P. medicaginis* inoculum in chickpea cropping systems are difficult to quantify accurately, vary over time, and differ among methods used such as our baiting bioassay and qPCR on DNA from soil samples. These two methods are best used to investigate host-pathogen interactions and appear to have limited use as a predictor of disease incidence prior to planting chickpea crops.

Can mechanical soil amelioration reduce nematode pests and soilborne pathogens in broadacre crops?

Sarah J Collins[1], George Mwenda[1], Carla Wilkinson[1], Sultan Mia[1], Catherine Borger[1], Andrew van Burgel[1], Stephen Davies[1]

1. Department of Primary Industries and Regional Development, Western Australia, Perth, WA, Australia

Mechanical soil amelioration is widely adopted by broadacre growers in WA as a 'once in a decade' strategy to ameliorate edaphic and biotic constraints like compaction, topsoil water repellence and herbicide-resistant weeds. Techniques include deep soil mixing (e.g. ripping and spading), soil inversion (e.g. mouldboarding or one-way plough) and deep ripping. All techniques lead to various degrees of soil mixing, changing the soil's physical profile and redistributing the top 10cm of soil. In WA, most major soilborne pathogens, nematode pests and weed seeds occur in the top 10cm of the soil, but little is known about how the mixing process from amelioration affects their diversity, distribution and long-term survival.

Over three seasons, levels and expression of rhizoctonia bare patch (*Rhizoctonia solani* AG8), root lesion nematodes (RLN; *Pratylenchus neglectus* & *P. quasitereoides*) and cereal cyst nematode (CCN; *Heterodera avenae*) in cereal and canola crops were monitored in increments to 40cm soil depth at two sites. Changes in weed species incidence and density, soil physical and chemical properties, root health and grain yield were also assessed.

The effects of soil amelioration varied depending on organism, tillage technique, crop and soil type. Soil inversion proved to be the most effective treatment over two cereal (2019 & 2020) followed by canola (2021) cropping seasons at both sites. It increased yields and reduced *Rhizoctonia solani* (AG8) and CCN at 0-10cm depth. However, both RLN species recolonized the topsoil over time. Cereal plants from plots where the soil profile had been inverted had consistently better root systems than the other treatments, particularly deep

ripped and the un-ameliorated controls. Soil inversion also reduced weed density and subsequent panicle production of surviving plants. Conversely, all amelioration treatments increased levels of *R. solani*, both RLNs and CCN at 10-30cm depth where they are not usually found in un-ameliorated soil.

Integrated Management of Root-knot Nematode in Sweetpotato

Wayne O'Neill[1], Jennifer Cobon[1], Tim Shuey[1], Rachael Langenbaker[2], Sandra Dennien[3]

1. Department of Agriculture and Fisheries, Brisbane, QLD, Australia

2. Department of Agriculture and Fisheries, Bundaberg, QLD, Australia

3. Department of Agriculture and Fisheries, Gatton, QLD, Australia

Plant-parasitic nematodes are important pests of sweetpotato, costing the industry an estimated $20 M per year in Australia. Root-knot nematodes are responsible for the majority of losses and are widely distributed throughout the growing regions. Two long-term field trials have been established in Bundaberg to assess the ability of rotation crops, organic amendments and novel management practices to control nematodes and improve soil health.

One field trial is close to current grower best practice and includes a nematode resistant rotation and different amendment treatments, as well as nematicide and nil controls. The other trial is more experimental and is being used to assess a variety of rotation crops and organic amendments. It also has a longer rotation phase and early bed formation, where beds are reformed just after harvest and are not intensively cultivated prior to planting.

Although results vary from one crop cycle to the next, organic amendment treatments are showing a trend for suppression of root-knot nematode and an increase in free-living nematode populations in both trials. For example, one treatment in the best practice trial (an incorporated band of chicken manure + sawdust) had significantly less root-knot nematodes than all other treatments at the second crop harvest (mean of 226 root-knot per 200g dry soil compared with 739 for nematicide), and significantly more free-living nematodes (mean of 8718 per 200g of dry soil compared with 2124 for the nil control).

In the experimental trial, treatments which received a double amendment (incorporated band of organic matter after harvest and a second application in a furrow prior to planting) consistently had the lowest root-knot numbers at harvest, although these results have not been significant to date. The legume sunn hemp proved to be a very effective rotation crop for reducing root-knot populations.

The trials are ongoing, and treatments will be monitored through further crop cycles for efficacy as well as effects on yield and quality.

Session 08: Microbiome

Agricultural microbiomes and pathogen ecology

Paul Dennis[1], Olwen Paterson[1], Anna-Belle Clarke[1], Rebecca Lyons[1], Henry G.W. Birt[1], Anil Raghavendra[1], Jeff Daniells[2], Adam Skarshewski[1], Robert Hoelzle[1], Young Song[1], Scott Lieske[1], Ryan Orr[3], Paul Nelson[3], Yolima Carrillo[4], Hazel L Gaza[2], Anthony B Pattison[2]

1. School of Earth and Environmental Sciences, The University of Queensland, St Lucia, QLD, Australia

2. Centre for Wet Tropics Agriculture, Department of Agriculture and Fisheries, South Johnstone, QLD, Australia

3. James Cook University, Cairns, QLD, Australia

4. Hawkesbury Institute for the Environment, Western Sydney University, Sydney, NSW, Australia

The Innisfail-Tully region of Queensland's wet tropics is the heartland of Australia's banana industry and has been on high alert since the 2015 detection of Fusarium Wilt on a commercial Cavendish farm. In response, efforts to obtain new resistant varieties have been boosted and biosecurity measures have helped to slow the spread of the disease. In addition, efforts to identify other management strategies that could enhance disease resilience have been intensified.

Within the region, almost all land, except urban and military, may be classified as rainforest, pasture, sugarcane, or banana. We have demonstrated that land use strongly influences the biomass and composition of soil microbial communities with consequences for the severity of Fusarium Wilt and the likelihood of its causal agent (*Fusarium oxysporum* f. sp. *cubense* (*Foc*)) being able to colonise. Relative to other land uses, for example, banana soils have less microbial biomass, more *F. oxysporum*, fewer fungivorous nematodes, and are more likely to be colonised by *Foc*. Furthermore, bananas grown in banana soils exhibit more severe disease symptoms. Interestingly, these observations are not consistent with those for wild banana soils, indicating that improvements in management of banana plantations could improve soil health and contribute to disease prevention and containment.

To date, we have evaluated the impacts of fertilisers, herbicides, and ground covers on the microbiome of banana plants and soils. We have found that disease severity is negatively associated with the presence of ground covers and may be exacerbated by high rates of nitrogen addition. Furthermore, we have defined a core microbiome of *Musa* spp. comprising 36 bacterial and 21 fungal taxa that are present irrespective of genotype and edaphic conditions. We are evaluating their ecological preferences and potential functions using metagenomics, and have isolated c. 60% of the core bacteria, of which roughly half appear to inhibit *Foc*.

Our work is helping to identify management approaches that leverage plant and soil microbiomes to improve soil health and protect Australia's banana industry from threats such as Fusarium Wilt.

Assigning function to the core microbiome of banana (*Musa* spp.) using genome-centric metagenomics

Anna-Belle Clarke[1], Tony Pattison[2], Hazel Gaza[2], Henry Birt[1], Olwen Paterson[1], Rebecca Lyons[1], Robert Hoelzle[1], Paul Dennis[1]

1. The University of Queensland, Fairfield, QLD, Australia

2. Department of Agriculture and Fisheries, South Johnston, QLD, Australia

Management of banana (*Musa* spp.) microbiomes may offer novel solutions to production constraints but is challenging due to their high diversity and variability across environments. To

help circumvent these issues we identified the core microbiome of banana, which comprises 36 bacterial taxa that are assumed to be important for host fitness due to their persistent nature. To better understand the potential functions of these taxa we annotated and interrogated metagenome assembled genomes (MAGs) obtained via the assembly and binning of 323 Gbp of shotgun sequences derived from 50 banana rhizosphere samples. In total 473 MAGs were recovered, including 92% (33/36) of the core taxa. Core taxa included genes that encode diverse functions including biogeochemical cycling, plant growth modulation, and defence. Gene-centric analyses of the same dataset indicate a core and accessory set of genes and their encoded functions. This work contributes to the development of microbiome management strategies that aim to improve *Musa* spp. production through enhanced growth and reduced disease pressure.

Assigning function to the core microbiome of *Musa* spp.

Olwen M Paterson[1], Antony B Pattison[2], Anna-Belle C Clarke[1], Robert D Hoelzle[1], Rebecca Lyons[1], Hazel L Gaza[2], Henry WG Birt[1], Paul G Dennis[1]

1. School of Earth and Environmental Sciences, University of Queensland, Brisbane, QLD, Australia

2. Department of Agriculture and Fisheries, Centre for Wet Tropics Agriculture, South Johnstone, QLD, Australia

In 2015 *Fusarium oxysporum* f. sp. cubense (Foc) Tropical Race 4 (TR4) was detected on a banana farm in North Queensland. Since then, we have greatly enhanced our knowledge of the microorganisms associated with banana plants and soils within the region. Importantly, we have identified 36 core bacterial taxa that are persistently associated with *Musa* spp., but their impacts on host fitness remain to be elucidated. To this end, we generated and screened c. 5,000 enrichment cultures from banana roots and leaves for the presence of core bacteria, which were isolated, stored in glycerol, and subjected to genome sequencing, and a range of bioassays. Despite the high prevalence of 'unculturables' in soils, we successfully isolated 64% (23/36) of the core bacteria. Genome analyses have revealed the presence of genes encoding diverse functions including biogeochemical cycling, plant growth promotion and the production of secondary metabolites. Using dual-culture plate assays, we have identified 10 isolates that significantly suppress Foc, and are performing functional 'omics and pot experiments to determine their modes of action and ability to reduce disease severity *in planta*. This work will yield detailed functional insights into the core microbiome of *Musa* spp. and contribute to the development of novel management options for Fusarium wilt.

Biological disease suppression: amendments affect pathogen growth and microbial communities

Gupta Vadakattu[1], Marcus Hicks[1], Stasia Kroker[1], Sabrina Morrison[2], Therse McBeath[1], Linda Smith[3], Ryan Pention[4]

1. Commonwealth Scientific and Industrial Research Organisation, GLEN OSMOND, SA, Australia

2. University of Queensland, Brisbane

3. DAF Qld, Brisbane

4. Arizona State University, Mesa, USA

The successful control of many soilborne plant diseases, such as Rhizoctonia bare patch in cereals and Verticillium wilt in cotton, involves management of the pathogen at different microsites in soil at different time periods (pre-season or in-crop) and the control of infection and incidence. Biological disease suppression can be the result of suppression of pathogen or disease incidence or both. Pathogen suppression occurs when soils become inhospitable to the

pathogen itself, whereas lack of disease incidence can be the result of the inability of pathogen to cause disease due to pathogen-microbiome interactions and/or from changes to plant's resistance to pathogen. Using short-term soil-based (7 day) and plant-bioassays (4 weeks) under controlled environment conditions, we investigated the responses in pathogen abundance (qPCR), microbial catabolic potential, diversity and composition of soil microbiomes (group specific amplicon sequencing) to the addition of C (sucrose, chitin), N (fertilizer) inputs and crop residue (wheat, sorghum, broccoli) amendments. Pathogen growth and disease expression responses were measured in wheat (*R. solani* AG) and cotton (*V. dahliae*) in suppressive and conducive soils.

Amendment effects on the growth of *R. solani* and *V. dahliae* varied and in soils with different physical and chemical properties and suppression potential. For example, the addition of simple carbon source (eg sucrose) reduced *R. solani* AG growth in all soils whereas its effect on *V. dahliae* growth varied between suppressive and conducive soils. Addition of chitin increased the growth of total fungi but the effect on the two pathogenic fungi was different. Sorghum and broccoli residues reduced *V. dahliae* growth whereas addition of N fertilizers increased the growth. Multivariate analysis of genetic diversity of bacteria, pseudomonads and soil fungi and catabolic profiles showed significant differences between different amendments and soil types. For example, addition of sorghum, broccoli, chitin increased relative abundances of soil fungi and bacteria with antibiosis, antifungal and plant growth promoting capabilities. These results suggest that understanding the intricacies of complex microbiome-pathogen interactions is important to identify amendments that can promote disease suppression capacities in agricultural soils.

Session 09: Integrated management

Effect of phosphonate and metalaxyl on avocado growth in the presence and absence of *P. cinnamomi*

Jacob Jose[1], Elizabeth Dann[1], Andre Drenth[1]

1. Queensland Alliance for Agriculture and Food Innovation, Dutton Park, QLD, Australia

Avocado root rot caused by the soilborne oomycete *Phytophthora cinnamomi* is the greatest limiting biotic factor in avocado production worldwide. Phosphonate-based chemical control is a valuable component in the integrated disease management strategy. The crop protectant is highly systemic and is believed to have multiple modes of action which have not been thoroughly investigated in avocado. Metalaxyl, which is another systemic fungicide but with single site activity, is also commonly used at planting. This study aims to investigate the effect of phosphonate and metalaxyl on the growth of avocado – inoculated or not inoculated with *P. cinnamomi*. Results from glasshouse trials demonstrate that phosphonate foliar sprays (applied at 2 time points after inoculation or mock-inoculation) did not affect any above-ground or below-ground plant growth parameters of avocado seedling in the absence of *P. cinnamomi* compared to water treated control, while the compound reduced root necrosis, and also increased plant diameter in seedlings inoculated with *P. cinnamomi* (in one of the two experiments). In *P. cinnamomi* inoculated seedlings, metalaxyl granules incorporated into the top 2 cm of the potting mix (applied at 2 time points after inoculation) increased plant diameter, leaf number, total leaf surface area, above-ground and below-ground biomass of plants, and reduced both root necrosis and frequency of *P. cinnamomi* isolated from roots, compared to water treated control. In mock-inoculated seedlings, metalaxyl treatment increased plant height, diameter and root growth compared to water treated control (in one of the two experiments). This study will help expand our current knowledge of avocado root rot and its chemical control, potentially informing industry practices to utilise phosphonate and metalaxyl more efficiently in the management of Phytophthora root rot.

Decontamination efficacy of cleaning agents against black root rot and Verticillium wilt pathogens of cotton

Chi Nguyen[1], Duy LE[1]

1. NSW Department of Primary Industries, Narrabri, NSW, Australia

Black root rot (BRR) and Verticillium wilt of cotton caused by *Berkeleyomyces rouxiae* and *Verticillium dahliae*, respectively can individually cause yield loss of 10 - 50% in New South Wales. Both diseases are now detected across the state. 'Come Clean Go Clean' is widely practised to minimise the risk of further introduction of the pathogens from one field to another through movements of soil-contaminated farm equipment and machineries. We rely on cleaning agents to effectively wash down and decontaminate the equipment/machineries. In experiment 1, two commonly commercial products along with 70% ethanol (EtOH) and 25% household bleach (HhB) were assessed for their efficacy against *B. rouxiae* and *V. dahliae* reproductive structures with and without soil contamination. We successfully manipulated formation of long tern survival structure that being microsclerotia (MS) of *V. dahliae* using potato broth, which allowed for an easy harvest and separation of MS from conidia through sieving. In separate assays, germination of MS and conidia in both presence and absence of 10% (w/v) soil contamination was completely suppressed even for a short 10 sec exposure to EtOH and HhB.

The two commercial products reduced the germination rate significantly but did not completely kill MS and conidia after 30 min exposure. In similar assays against *B. rouxiae*, both EtOh and HhB provided potent efficacy, completely suppressing germination of chlamydospores and endoconidia after 10 sec exposure. The two tested products only achieved a similar efficacy after soaking for 24. In experiment 2, eight additional cleaning products were tested and revealed that soaking for 24 h was the most effective treatment for most products (6 out 8). It is noted that both conidia and endoconidia of *V. dahliae* and *B. rouxiae*, respectively could resist the chemical treatments though they were commonly believed fragile and short-lived.

Commercial application of metham sodium to produce dieback-free gravel for road construction

Elaine Davison[1]

1. *Curtin University, Perth, WA, Australia*

Phytophthora cinnamomi (the dieback 'fungus') is an introduced soilborne pathogen that is associated with the death of native plants in the south-west of Western Australia. It is readily spread in infested soil, including gravel. Main Roads Western Australia (MRWA) only uses dieback free gravel for road construction and repair; this is in short supply. One option is to chemically treat infested gravel to kill *Phytophthora*. Field trials completed in 2011 showed that the soil fumigant metham sodium eliminates *Phytophthora* from gravel, and it is now registered by the Australian Pesticides and Veterinary Medicines Authority for this purpose. The process, however, needs to be scaled-up before it is commercially viable. A scaled-up experiment using pine plug inoculum in a 2,500 m^3 gravel stockpile treated with metham sodium during construction, showed *Phytophthora* survived in less than 6% of the inoculated plugs. A review of the experimental process indicated that modification of stockpile construction and better surface sealing would further reduce survival of *Phytophthora*, and this is now standard practice. MRWA source gravel from contractors and need a compliance test to show whether the gravel they purchase has been treated as specified in their contracts. As direct methods for showing the treated gravel is dieback-free are unsuitable, an indirect method based on microbial diversity is being investigated. A DNA based assay shows significant differences in the number and diversity of one group of bacteria in treated versus untreated gravel. These differences appear within 6 weeks of treatment and persist for at least 15 weeks. This microbial assay, together with paper records, have the potential to be used in a robust compliance system.

The correlation between soil abiotic attributes and Fusarium wilt severity of banana in Central Java

Irianti Kurniasari Irin[2, 1], Arif Wibowo[2], Siti Subandiyah[2], Anthony Pattison[3]

1. Politeknik Pembangunan Pertanian , Malang, Indonesia

2. Universitas Gadjah Mada, Yogyakarta, Indonesia

3. Department of Agriculture and Fisheries, South Johnstone, QLD, Australia

Banana is important fruit crop in Indonesia. The crop is threatened by the fast spreading disease known as Fusarium wilt, caused by *Fusarium oxysporum* f.sp. *cubense*. Severity of the disease is believed to be influenced by soil abiotic attributes and their interaction on plant defence, the growth of the pathogen and the soil microorganisms. This study was conducted to determine the relationship between soil abiotic attributes and the severity of Fusarium wilt disease in the banana growing areas. Field surveys and laboratory analysis were conducted to determine

severity of the disease and soil physicochemical condition in banana growing of Central Java, including the district of Gunung Kidul, Kulon Progo, Sleman, and Bantul. Soil physicochemical variable data were analyzed by regression and Pearson's correlation, while disease severity data was analyzed by ANOVA. The result showed that the disease severity in four districts of banana growing namely Gunung Kidul, Kulon Progo, Sleman and Bantul was low at 11.0%, 6.5%, 4.5%, and 3.7% respectively. The analysis of the regression revealed that there were positive and negative correlations between the severity and soil abiotic attributes. Soil texture including silt and clay, pH, and phosphorous availability content are positively correlated with disease severity at p=0.35 and p=0.49, p=0.15, and p=0.14, whereas total nitrogen, potassium availability, and organic carbon are negatively correlated with disease severity at p=-0.47, p=-0.34, and p=-0.07 respectively. This study provides information on the relationship between soil abiotic attributes with severity of Fusarium wilt disease regardless environmental factors and the banana cultivation. Thus, management practice oriented toward soil suppression through manipulation of pH, organic matter content and availability of nutrients can be considered for the use in the control strategy of Fusarium wilt disease.

Soil microorganisms in Allium systems

Jessie Harper[1]

1. University of Queensland, St Lucia, QLD, Australia

Soil microorganisms are a key component of agricultural systems; however, most are undescribed, and their functional roles are not understood. Intensive vegetable production systems operate under tight rotations, with intensive cultivation and high inputs. The impact that agronomic practices and soil properties have on the soil microbiome of Allium production systems is not well understood and requires investigation. A survey was conducted to characterise the current agronomic practices of allium (garlic and onion) cropping systems in Southern Queensland under both organic and conventional practices. Agronomic practices and soil characteristics were surveyed and related to the soil microbiome composition in the rhizosphere and bulk soil. The survey conducted in this research aimed to identify whether management practices and soil properties directly influence the soil microbiome and predicted functionality.

The results of the survey showed that because of soil-borne pathogens allium farmers adopt diverse long rotations of crops with allium species. The results demonstrated 57% of farms also used some form of soil microbial inoculant in allium production. More intensive cultivation was practiced on organic farms to manage weeds.

There was no difference in alpha-diversities of bacterial species in the rhizosphere between either organic and conventional systems, or for garlic and onion production systems. The taxa of fungi showed a large proportion of unassigned taxa, but the phylum Ascomycota was dominant in both rhizosphere and bulk soils. Preliminary assessment of the fungal rhizosphere soil samples showed presence of genera containing plant pathogenic species, but these could not be identified to a species level. The genera potentially contain fungal pathogens of *Allium* spp. including *Fusarium, Stemphylium, Alternaria* and *Plectosphaerella* spp. These genera were dominant taxa in the rhizosphere and these trends warrant further investigation.

Session 10: Flash Talks / Posters

Woodchip amendment can alter banana soil microbial abundance and disease suppressive potential

Hazel Gaza[1], Wayne O'Neill[2], Tim Shuey[2], Anthony Pattison[1]

1. DAF, South Johnstone, QUEENSLAND, Australia

2. Eco Sciences Precinct, DAF, Dutton Park, QLD, Australia

Cultivation of bananas has altered the soil microbial communities compared to areas retaining native vegetation. Specifically, the fugal microbial community in banana soil is less abundant and less diverse, allowing potentially pathogenic groups of fungi, such as *Fusarium oxysporum'* s, to dominate. Applying woodchips to banana soil could potentially increase soil fungi leading to greater disease suppression. Three rates equivalent to 2, 20 and 100 t/ha of woodchips from leguminous trees, *Erythrina* sp., *Gliricidia* sp., and *Leucaena* sp., were incorporated into soil used for commercial banana production. One month after adding woodchips, a Ducasse (*Musa* ABB) plant was planted into the soil. One month later, the plants were inoculated with $1x10^5$ spore suspension of *Fusarium oxysporum* f. sp. *cubense* (Foc) Race 1 (VCG 0124). Results indicated that the incorporation of woodchips did not significantly impact the growth of banana plants, except for the high rate (100 t/ha) of *Gliricidia* sp., which reduced plant height, leaf number, and leaf area. Initial results on suppression of Foc were inconclusive and require further evaluation. Woodchip incorporation significantly increased the abundance of bacteria, archaebacteria and fungi in the soil compared to non-amended soil. The 100 t/ha rate led to the greatest increase in archaebacteria, regardless of the type of woodchips used. Fungal biomass was significantly increased following the application of *Leucaena* sp., whereas bacterial biomass was enhanced considerably following the incorporation of *Erythrina* sp. An increase in the rate of woodchip application increased the proportion of omnivorous nematodes and decreased the proportion of bacterivores, with no significant impact on herbivorous, fungivorous and predatory nematodes. The incorporation of woodchips altered the microbial community of banana soil, but further investigation is required to select species and application rates that promote plant growth and enhance disease suppression.

A potential antagonist against Macrophomina phaseolina on strawberry

Apollo O Gomez[1]

1. Department of Agriculture and Fisheries, Queensland, Nambour, QUEENSLAND, Australia

Macrophomina phaseolina (Tassi) Goidanich is a soil-borne fungal pathogen of strawberry which causes a disease called charcoal rot. Significant strawberry plant losses associated with charcoal rot have been reported worldwide, including Australia. Soil fumigants do not provide effective control and there are no fungicides registered for the pathogen on strawberry. In addition, health and environmental concerns with the use of chemicals warrants the investigation of non-chemical alternatives. Several species from the fungal genus *Trichoderma* have been reported to be antagonistic to a wide range of plant pathogens. In this study, *Trichoderma* sp. isolate AG-02 was evaluated against *M. phaseolina* in a glasshouse pot trial. Certified strawberry runners (cv. Albion) were dipped in a spore suspension ($1x10^6$ spores per mL) of the isolate and were potted in *M. phaseolina*-infected potting mix. Strawberry plants were then treated with sequential drench applications of the biocontrol agent at 2, 4, 8, 12 and 16 weeks after planting. Mortality was recorded weekly for 24 weeks. Untreated control plants were not treated with the isolate. The rate of plant mortality over time occurred significantly faster on the untreated plants

compared with the plants treated with the biocontrol agent during the experimental period. At 16 weeks, 95% of untreated plants had wilted due to *M. phaseolina* compared with 63% of dipped (only) plants. At the same timepoint, plants dipped and given two or more sequential drenches recorded an average mortality of 22%. This preliminary study showed *Trichoderma* sp. isolate AG-02 may have the potential to significantly protect strawberry plants against *M. phaseolina*, hence reduce charcoal rot incidence. Field trials are currently underway to evaluate strawberry plants treated with the isolate under field conditions. Further investigations could also be extended to other soil-borne pathogens and to economically important crops affected by this devastating pathogen.

Managing pests and diseases in agricultural systems with suppressive soils.

Mary Cole[1, 2]

1. Agpath Pty Ltd, Melbourne, VIC, Australia

2. Faculty of Veterinary & Agricultural Sciences, University of Melbourne, Melbourne, VIC, Australia

Pest and disease impact in agricultural systems is largely of our own making. Monoculture of major cropping systems often with just one genetic strain of crop species encourages the overuse of synthetic chemistry to harvest an economic product.

Crops grown in soil that is biologically rich are healthier and more robust when compared with plants grown with synthetic chemistry and have less pest and disease damage because the plant tissue has a higher Brix and the soil is more microbially diverse. In a cropping or garden environment, plants attacked by insects or disease-causing pathogens, are weaker and have lower Brix readings than those left untouched.

Using a Brix meter is a useful and easy method of determining sugar/total solids levels in vegetables and fruits in the cropping system or garden. Soil providing high brix readings in the plants, demonstrates a highly diverse soil biota where suppression of disease pathogens acts in parallel with pest management. Use of compost tea as a foliar spray introduces diversity of beneficial microbes onto the plant surface minimising pathogen impact.

The same healthy soil suppresses fast growing, shallow rooted weedy species such as cape weed in our southern Australian pastures. Use of compost and compost tea improves soil biota activity while changing soil structure. The soil microbiology shifts from active bacterial domination to fungal active domination; protozoa increasing producing more plant available nitrogen and the mycorrhizal fungal pool increases providing more plant available phosphorus and calcium.

Biological farming practices can improve soil and plant health, reduce input costs thus increasing an economic return to farmers. This can be done without an increase in agricultural land. This method of farming demonstrates a better and more resilient use of current agricultural land.

1. Mary Cole. The Importance of the fungal Kingdom to healthy soils. 21/05/21. Australian National Field Days, Orange NSW AIHA regenerative Agriculture. https://us02web.zoom.us/rec/share/qBx5UaRlw8kQ5JqYQt1hSHDK0Ndly33gLnBWfvOCNRBeW0MOgp6VzPo1XN-0EtZY.wd86x61gUWfZkxWR?startTime=1620547289000
2. Mary Cole. Compost tea to manage broad leaf weedy species in agricultural systems. A case Study. Soil Science Australia & the New Zealand Society of Soil Science Joint Conference 30 Nov – 4 Dec 2020. Cairns, Australia.
3. Mary Cole. Fungal pathogens – are they of our own making. Soil Regen Summit – hope for the Future, 2022.
4. Mary Cole, Peter McCoy, Dr Elaine Ingham. SFW webinar. Panellist for Fungal Fun.
5. Mary Cole. Soil microbiology and weed control. Podcast Regen Ray. Farming Secrets. https://omny.fm/shows/secrets-of-the-soil-podcast/7-soil-microbiology-weed-management-with-compost-t.

6. Mary Cole, Dr Elaine Ingham, Colin Andrews Farming in the World of Shifting Weather Patterns. https://webinar.soilfoodweb.com/webinar-ed-farming-in-the-world-of-climate-change
7. Mary Cole. Remediating a depleted soil. City of Hume City Council. Youtube.
8. Mary Cole. Bioloigcal Farming basics. Microstart Pty Ltd.
9. Mary Cole. Smartsoil Ground cover. Farming the soil. Youtube.
10. Thomas M. Dykstra, 2019. Picky-eater insects pass on high brix plants. Acres Sept. edition.

Session 11: Microbiome/Integrated management

Innovative Research: BioClay™ for Sustainable crop protection

Neena Mitter[1]

1. QAAFI, The University Of Queensland, QUEENSLAND, Australia

Innovation driving sustainable crop protection resonating with health of planet and the future consumer is key to food and nutritional security and to meet the daily need of two trillion calories for 10 billion people by 2050. RNA based biopesticides or 'RNA vaccines' for plants as a next generation crop protection platform without the need for genetic modification is gaining momentum across the globe. It is almost like 'nature versus nature' where a gene sequence from the pathogen is used to kill the pathogen itself. We have developed BioClay™ technology to deliver RNA as biological active using clay particles as carriers. It is a non-GM, residue free, specific, and environmentally sustainable alternative to chemical pesticides. BioClay can deliver the double stranded RNA, which is the key trigger molecule of RNA interference, as a sustainable spray application without the need for genetic modification. RNAi effectors delivered as BioClay are stable, do not get washed off and provide protection to the sprayed and unsprayed leaves against the targeted virus for up to 20 days post spray. The clay degrades on the surface of the leaf alleviating concerns about residues. We have recently shown that BioClay can target multiple life cycle stages of whitefly, a pest with a very wide host range. BioClay platform is being progressed to target viruses, insect pests and fungi including pathogens such as *Verticillium*, *Fusarium* and *Phytophthora*. Real world application of RNA based biopesticides with sustainable credentials for the global consumer will be governed by factors such as cost-effective production of dsRNA , the regulatory landscape and social license to operate.

Plant-parasitic nematodes in sweetpotato production areas in Australia

Jennifer Cobon[1], **Wayne O'Neill**[1], **Tim Shuey**[1], **Rachael Langenbaker**[2], **Sandra Dennien**[3]

1. DAF, AgriScience Qld, Brisbane, QLD, Australia

2. DAF, AgriScience Qld, Bundaberg, QLD, Australia

3. DAF, AgriScience Qld, Gatton, QLD, Australia

Australian sweetpotato growers produce the world's highest yields per hectare with a current farm gate value of $90M per annum. Plant-parasitic nematodes are a major constraint to sweetpotato production. Worldwide, *Meloidogyne* spp. (root-knot nematodes), cause general un-thriftiness and yield loss, as well as blistering, bumpiness and cracking of the storage roots. Yield and quality reductions due to plant-parasitic nematodes in Australia are currently estimated to cost the industry $20M per year.

Surveys were undertaken in the main sweetpotato production regions in 2017/2018 to determine the presence and abundance of plant-parasitic nematodes. Soil was sampled from 45 sites in the Bundaberg region, 12 from the central Queensland region, 6 from South East Queensland, 3 from the Atherton Tablelands in North Queensland and 17 from Cudgen in northern NSW.

Root-knot nematode was morphologically identified at 50 of the 83 sites (60% of sites), ranging in abundance from 1 to 3,413 per 200 g dry soil. Through molecular identification, *M. javanica* and *M. incognita* were identified as the two most common root-knot nematode species present at 28% and 13% of positive sites, respectively. *Meloidogyne hapla* and *M. arenaria* were also identified at 9% and 2% of positive sites, respectively.

Rotylenchulus reniformis (reniform nematode) was present at 10% of sites, mainly in the warmer regions of central Queensland and Bundaberg. However, one site in SE Queensland and one site in Cudgen were also infested with *R. reniformis* (53 and 365 per 200 g dry soil respectively). *Pratylenchus zeae* (lesion nematode) was found at 49% of sites across all regions and was the most common lesion nematode present.

Other common plant-parasitic nematodes identified in low numbers included spiral, stubby, stunt, ring, dagger and *Rotylenchulus parvus* (another reniform nematode), suggesting sweetpotato was not a good host to these plant parasites.

Using biocontrol agents to alleviate *Rhizoctonia* bare patch in wheat production

Wajira Nandanee Gamachchige Galhena[1], Catriona Macdonald[1], Brajesh K Singh[1], Juntao Wang[1], Bruna D Batista[1]

1. Hawkesbury Institute for the Environment, Western Sydney University, Richmond, NSW, Australia

Wheat is one of the major staple foods in the world and the most important crop in Australia based on gross value of production. However, wheat production is currently constrained significantly by Rhizoctonia bare patch disease caused by the soil borne fungus *Rhizoctonia solan*i AG8. Conventional control approaches including tillage management and fungicide exhibit limited efficacy and adverse environmental effects. The combination use of microbial biocontrol agents (BCAs) together with fungicide could be a potential strategy to improve management of wheat bare patch. In this study, we investigated the efficacy of microbial BCAs isolated from wheat roots, used either alone or in combination with fungicide in alleviating Rhizoctonia bare patch on wheat. A glasshouse study was conducted using wheat to evaluate the efficacy of four BCAs over a period of five months. Of the four antagonistic strains tested a consortium of BCAs (named 2I), consisting of endophytic bacterium *Pseudomonas* TK32 and the endophytic fungus *Diaporthe* sp., demonstrated significantly higher grain yields and total biomass over the control, with 7% increment in grain yield and 3% increase in the total biomass. Combined with fungicide application, the consortium 2I increased grain yield by 15% compared to the control. It was also observed that the amount of pathogen in consortium treated soils were significantly lower than that of the control. Using biocontrol consortium 2I separately or in combination with fungicide can be a viable management option for controlling Rhizoctonia bare patch in wheat while allowing producers to use less fungicide at less economic and environmental cost.

Key words: wheat, Rhizoctonia bare patch, biocontrol agents, consortium, endophytes

---

Plant defence activation against Phytophthora root rot in phosphite primed avocado

Kelly Scarlett[1], David Guest[2], Elizabeth Dann[1]

1. The University of Queensland, Brisbane, Queensland, Australia

2. The University of Sydney, Darlington, NSW, Australia

Phytophthora cinnamomi is a major constraint to avocado productivity, causing root necrosis, reduced yields and tree mortality. A key component in the management strategy is the application of phosphite; a phloem-mobile oxyanion of phosphorous acid. While a dual mode of action of phosphite is generally accepted, evidence supports an independent dose-response relationship between the phosphite concentration required to directly reduce pathogen growth and the root concentration required to prime plant defences. However, these relationships

between *in planta* phosphite concentration and plant defence activation has only been investigated in model plants, such as in Arabidopsis where phosphite (10mM) was shown to suppress the phosphorylation of mitogen activated protein kinase 4 (MAPK4); a negative regulator of biotic stress signalling and salicylic acid accumulation. Here, we aim to assess the root phosphite concentrations required for activation of avocado cellular defences that result in suppression of *P. cinnamomi* infection. Using quantitative PCR, we measured the relative transcript abundance of a putative MAPK4 gene, as well as avocado defence-related genes coding for phenylalanine ammonia-lyase, lipoxygenase, pathogenesis-related protein 5, endochitinase, gluthathionine S-transferase and metallothionein in 3-month-old Reed seedling roots at 0 h, 3 h, 6 h, 12 h, 24 h, 48 h post infection. Preliminary analysis demonstrates down regulation of the putative MAPK4 gene expression 6 hours post infection, followed by the reduced relative expression of *P. cinnamomi* cytochrome oxidase II gene 12 hours post infection in roots containing approximately 30 mg/kg of phosphorous acid. Greater empirical evidence for the role of induced defences against *P. cinnamomi* will be beneficial to the avocado industry worldwide.

Susceptibility of some alternative crops to Verticillium dahliae

Linda Scheikowski[1]

1. DAF, Toowoomba, QUEENSLAND, Australia

The soilborne pathogen *Verticillium dahliae* Kleb. causes yield loss in many crops worldwide and is an important economic constraint to cotton (*Gossypium hirsutum* L.) production in Australia. Management options for this disease require an integrated approach and crop rotation is one option. A common rotation often includes a fallow-winter cereal crop but growers are not necessarily seeing a decline in disease levels following this rotation sequence. Given that many new plant species are succumbing to infection by *V. dahliae* worldwide, the susceptibility of crops commonly rotated with cotton in the Australian farming system has been investigated to determine the potential risk for disease carry over. Where different cultivars of wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) were inoculated in the glasshouse with two different pathotypes of *V. dahliae*, using the root-dip technique, there were differential responses within cultivars and between pathotypes. The pathogen was also recovered from seed of both cereals. The colonisation of cereal rotation crops may provide a bridge between susceptible crops and warrants further investigation under field conditions. A better understanding of relationships among cereal crops and *V. dahliae* may allow crop rotations to be used more effectively in reducing soil inoculum levels as an efficient management practice.

Session 12: Engagement

What soil borne diseases mean to the farming enterprise

Doug Phillips[1]

1. Johnstone River Produce, Boogan, QLD, Australia

Johnstone River Produce is a horticultural farming operation near Innisfail in North Queensland. Originally a cane farm, it has had a history of banana, papaya and passionfruit production in more recent times.

While, like all businesses, there are a wide range of factors that influence decision making, the focus of this presentation will be on the presence or threat of soil borne diseases and how these have significantly influenced its operations including the composition of its production.