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BOOK OF ABSTRACTS



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national stakeholders. Our first objective is to provide candidate priority locations for epidemic surveillance based on global risk analysis of wheat cropland and trade networks. For example, locations with high cropland connectivity in Kansas, Nebraska and North Dakota in the USA, and in each wheat production region, are identified as likely important for pathogen spread. Pathogen introduction risk via wheat trade networks, if there is inadequate phytosanitary testing, is higher in countries such as the United Arab Emirates, the Netherlands, and the USA. Our second objective is to provide a global biogeographic analysis of 100 economically important wheat pathogens based on their reported geographic distribution. Although pathogen richness peaks in countries with high wheat cropland extent, early epidemic emergence events have been more frequent in the native range of wheat than elsewhere. These findings provide starting points for building global epidemic surveillance and mitigation systems to support sustainable wheat production.

P5.1-042

EXPLORING THE DIVERSITY AND PREVALENCE OF PSEUDOMONAS SYRINGAE IN SWEET CHERRY ORCHARDS OF NEW ZEALAND

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Text

Bacterial canker of cherry, caused by *Pseudomonas syringae* pathovars, is a major constraint to cherry growing in New Zealand and particularly in Central Otago, the primary growing area for cherries. To gain a better understanding of the disease's epidemiology, *Pseudomonas* spp. isolates were collected from symptomatic and asymptomatic cherry tissue from 23 commercial Central Otago cherry orchards in 2015. Isolates were classified into different taxonomic groups using phylogeny based on the *gltA* gene sequence for all strains (250) and Multi Locus Sequence Analysis (MLSA) of four housekeeping genes for 35 strains. The two main taxonomic groups were *P. syringae* pv. *syringae* (Pss) and *P. syringae* pv. *morsprunorum* race 1 (Psm1), in Phylogroup 2 (PG2) and Phylogroup 3 (PG3), respectively. The third group comprised non-pathogenic strains classified as *Pseudomonas* spp. Strains of Psm1 formed a monophyletic group, representing an almost clonal population. There was more variation detected within strains of Pss, although they were restricted to group PG2b. Non-pathogenic *P. spp.* and pathogenic Pss and Psm1 strains coexisted in the same orchard. It was concluded that Pss is the predominant pathovar in Central Otago. This is the first detailed study of the *P. syringae* species complex in cherry orchards in New Zealand and provides the basis for future epidemiology studies.

P5.1-043

COMPLEMENTARY APPROACHES TO QUANTIFY AND CHARACTERIZE INOCULA DYNAMICS AND LEAF INFECTION AT PLOT LEVEL: CASE OF BLACK LEAF STREAK DISEASE

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Text

Black Leaf Streak Disease is a major leaf disease of banana caused by the airborne ascomycete *Pseudocercospora fijiensis*. A better understanding of the disease epidemiology would help to find alternatives to fungicides. According to empirical knowledge, plant infection is mainly due to the inoculum from outside the plot (external inoculum, supposedly ascospores) whereas the inoculum within the plot (internal inoculum, supposedly mainly conidia) plays a minor role. We propose to implement two complementary and original experimental approaches to (i) characterize and quantify the external and internal inocula of a plot, and (ii) to identify which leaves are infected by each inoculum. The study is carried out in Guadeloupe, on two experimental plots planted either with a susceptible or a partially resistant cultivar to reduce ascospore production. For the first aim, we install six Burkard multi-vial cyclone samplers above and under canopy to catch respectively the external and internal inocula. Then, we quantify conidia by microscopy and ascospores with quantitative PCR. For the second aim, we describe the leaf infection due to the external and internal inocula by comparing with image analysis the number of lesions produced on leaves, protected or not from the inocula with spore proof nets. The inocula and infection dynamics will be related to the cultivar and the microclimate. This study is the first contribution to understand the role of each inoculum in the leaves' infection.

P5.1-044

GRAPEVINE TRUNK DISEASE PATHOGENS IN ROOTSTOCK MOTHER VINES: A POTENTIAL THREAT TO THE SOUTH AFRICAN GRAPEVINE INDUSTRY

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Text

Rootstock mother vines are known as sources of grapevine trunk disease (GTD) pathogen inoculum. Vines become infected through pruning wounds and spread to canes which are used as propagation material. The risks associated with ageing mother plants are unknown as most of these infected canes appear visually healthy. The aim of the study was to characterize GTD pathogens from mother vines and one-year-old canes harvested from these vines. Fungal isolations were made from 1900 mother vines of different ages and 2050 one-year-old canes. Isolates were identified based on morphology, species-specific PCRs and amplifying and sequencing relevant gene regions of representative isolates. From mother vines, *Phaeoconiella chlamydospora* occurred at the highest incidence (25.9%), followed by Botryosphaeriaceae spp. (18.6%; predominantly *Diplodia seriata*), Basidiomycetes (12.4%; predominantly *Fomitiporia* sp.) and *Phaeoacremonium* (5.9%; predominantly *P. minimum*). All major GTD pathogens occurred in mother vines as young as 4-years-old, including wood rotting Basidiomycetes. This is of great concern since wood rotting fungi could drastically reduce the productive lifespan of mother vines. A total of 4.0%