

New developments in the control of black Sigatoka and Fusarium wilt in banana

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Banana production rely mainly on one clonal cultivar, Cavendish, which is world-wide grown and therefore highly prone to diseases. Major diseases are *Mycosphaerella fijiensis* and *M. musicola*, which are controlled by a wide range of fungicides coming from 10 different classes. The agronomic conditions in which bananas are cultivated demand frequent applications. In principal multi-site fungicides are used frequently and site specific systemic fungicides are added in critical phases of the disease epidemics. In many regions resistance to various fungicide classes has developed and needed to adapt the use recommendations. Resistance is found for BMC, QoI, DMI and SDHI (even if not widely spread) fungicides in many areas and therefore restrictive guidelines were agreed. Other fungicide classes are free from significant resistance evolutions, but precautions measures are agreed. Recently biologicals have been introduced into the spray program. An overview on the fungicide classes and associated resistance, geographical spread and known mechanisms will be given, describing the consequences for the use pattern of fungicides. Panama disease caused by *Fusarium oxysporum* f. sp. *cubense* TR4 race is recently re-occurring threat to many banana cultivars, including Cavendish. This race is spreading within Asia and endangering other major banana growing countries. Since no direct control measures are available, a range of indirect measures are in place to limit further spread. Research activities have been started to investigate the pathogen, the host resistance and direct control. A project together with the University of Wageningen has been initiated to elucidate the possible usage of fungicides towards *Fusarium oxysporum* f. sp. *cubense*.

Plant pathogenic and toxigenic Fusarium species - their taxonomy, systematics and nomenclature in the molecular age

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The fungal genus *Fusarium* contains some of the most economically and socially important species of plant pathogens affecting agriculture and horticulture. It also contains numerous species that are important mycotoxin producers and some that are increasing in importance as pathogens of humans. Some of the plant diseases, such as head blight of wheat and Fusarium wilt of bananas, are amongst the most important diseases of these hosts and have not only caused enormous losses in production around the world but have also had a huge impact on the communities that depend on these crops. The genus is a complex, polyphyletic grouping whose taxonomy has always been controversial with species numbers ranging from over a 1000 at the beginning of the 1900s, down to 9 in the 1950s and '60s and currently anything from nearly 100 to 500. The generic boundaries are also currently a point of debate. This talk will provide an overview of *Fusarium*, its phylogeny and biogeography and the mechanisms involved in speciation and the evolution of pathogenicity.

Towards deciphering host resistance to phytonematodes: Transcriptome analysis of a coffee incompatible response to *Meloidogyne incognita*

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The root-knot nematode (RKN) *Meloidogyne incognita* is considered one of the most economically damaging pathogen in coffee crops. Breeding introgression strategies with R genes result in resistance breaking, while chemicals nematicides are considered harmful. We had previously observed that the development of *M. incognita* in *Coffea arabica* is prevented by the necrosis of the host cells at 6 days after infection (dpi) in (R) roots, while the feeding sites are being established by the formation of giant cells in (S). Samples from these contrasting materials were sequenced by RNAseq Illumina HiSeq 4000, generating over 800 million 2x100 nt length reads. Differential expression analysis and GO enrichment results point out that some gene families are strongly deregulated in the resistance response. These genes could be important players in the coffee-RKN incompatible interaction and may be potentially used in biotechnological approaches to nematode control.

Improved surveillance of diseases using nano-pore sequencing

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Next generation sequencing (NGS) has revolutionised plant pathogen diagnostics, as prices continue to fall and applications continue to expand. At the forefront of this revolution are the detection, diagnosis and characterisation of plant viruses. In 2011 a new disease emerged in maize production in Kenya. Whilst early attempts to provide a diagnosis using conventional methods failed, NGS was used to rapidly identify suspect viruses (*Maize chlorotic mottle virus* and *Sugarcane mosaic virus*) which were later confirmed using PCR testing, whilst mechanical inoculation satisfied Koch's postulate. The rapid identification of the causal agents of an emerging disease (maize lethal necrosis) enabled rapid development and deployment of qPCR tests in local labs enabling diagnosis of suspected outbreaks and seed testing. The genomes analysed from Kenya, South Sudan, Rwanda and Ethiopia shows that the isolates of MCMV recovered are highly conserved, whilst the sequence of ScMV is divergent and in some cases other potyviruses are present. This suggests that the spread of MCMV is driving the disease epidemic, whilst potyviruses are a frequent local infection. Follow-on testing suggests that in some locations the disease symptoms in the field are being confused with those caused by other viruses. The most commonly detected of these was the recently characterised 'maize yellow mosaic virus' at a number of locations. These data show the value of incorporating NGS into routine diagnostics, especially in outbreak situations. The use of nanopore sequencing (Oxford Nanopore) was explored which may be more suited to resource poor settings. The results show that despite the increased error rate, the technology can be used to provide valuable genome sequence data and cloud based analysis supports use by non-specialists and negates the need for elaborate IT infrastructure.

Aldaulactone, a new phytotoxin involved in *Alternaria dauci* - *Daucus carota* interaction

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The mechanisms of quantitative aggressiveness and partial resistance have not been extensively studied and are prevalent in most plant – necrotrophic pathogen interactions, including the *Daucus carota* – *Alternaria dauci* interaction. In those, pathogens often produce phytotoxic secondary metabolites. In the work presented here, we explored the link between *A. dauci* aggressiveness and toxin production. In a first set of experiments, we uncovered a link between aggressiveness and fungal exudates toxicity on *in vitro* cultured carrot cells. These results were obtained with cells from the *A. dauci* susceptible genotype H1. Cells from the partially resistant genotypes K3 and I2 were only affected by exudates from the most aggressive *A. dauci* strain, ITA002. We made the hypothesis that toxicity of the fungal exudates was correlated with the amount of toxic compounds produced by the fungus. Interestingly, apolar fungal exudates production was correlated with strain aggressiveness. We analyzed the apolar fungal exudates using HPLC, and correlations

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