Effect of mutations to *FST1* in *Fusarium verticillioides* on functionality and the regulation of gene expression

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Phytopathology 103(Suppl. 2):S2.104

Fusarium verticillioides is a fungal pathogen that causes seedling, stalk, and kernel diseases of maize. The pathogen also produces the mycotoxin fumonisin in infected kernels. This study focuses on *FST1*, a gene that impacts fumonisin B1 (FB1) biosynthesis, resistance to reactive oxygen, pathogenicity, and macroconidia production. *FST1* encodes a protein with 12 putative transmembrane domains and has a central loop and a C-terminus that are predicted to project into the cytoplasm. We have hypothesized that the central loop and C-terminus structures are involved in the functionality of Fst1. Constructs of *FST1* containing deletions in the coding regions of the central loop and C-terminus were transformed into a strain lacking a functional *FST1*. All the constructed failed to complement the strain, suggesting that the structure of both regions of the protein is critical for function. We also analyzed the impact of *FST1* on the secretome during colonization of kernels. A comparison of the transcriptome of the wild type and the Δ*fst1* mutant six days after inoculation of maize kernels revealed that expression of 2227 genes in the mutant were significantly ($P<0.05$) different than wild type. Of the 1412 genes that are predicted to encode secreted proteins, expression of 256 were significantly altered (≥ 2 fold) in the mutant strain. Among these genes was the reduced expression of an extracellular peroxidase, likely involve in resistance to reactive oxygen.

Aflatoxin B_1 contamination of groundnut *Arachis hypogaea* L. in eastern Zambia

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Phytopathology 103(Suppl. 2):S2.104

Groundnut is a rich source of protein and it is the second most widely grown crop in eastern Zambia. A survey was conducted in 2012 to determine the incidence of aflatoxin B_1 contamination in groundnuts from several districts important in groundnut production in eastern Zambia. Nyimba and Mambwe districts are in the Luangwa Valley and are comparatively hotter and drier than Chipata and Petauke districts which lie in the cooler plateau. 399, 1 kg unshelled groundnut samples were collected from farmers' fields and also from homesteads upto 1 month after harvest. Aflatoxin B_1 was assayed in each shelled sample by weighing and comminuting 100 g subsample and extracting aflatoxin from six 20 g aliquots. ELISA was used to estimate aflatoxin levels and the six values averaged to give the sample contamination. 34 and 27% of samples from Nyimba (maximum=4,980 ppb and arithmetic mean [AM] =1.1) and Mambwe (maximum=69 ppb and AM=0.7), respectively, had aflatoxin levels greater than 20 ppb. In comparison, 38 and 28% of samples from Petauke (maximum=3,258 ppb and AM=0.9) and Chipata (maximum=1,077, and AM= 0.8), respectively, had aflatoxin levels greater than 20 ppb. At the beginning of the season, priority is given to planting maize and cotton, while planting groundnut is delayed, increasing the risk of the crop being exposed to end-of-season drought. The aflatoxin contamination levels we report are a barrier to trade and the well being of consumers.

Effect of temperature and wetness period on guava stylar end-rot monocycle

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Phytopathology 103(Suppl. 2):S2.104

The guava (*Psidium guajava*) stylar end-rot, which *Fusicoccum aesculi* is one of the causal agent, can reaches 40% of incidence in post-harvest in Brazil. This work studied the favorable environmental conditions for the development of disease. Isolates of *F. aesculi* were collected on symptomatic fruits and the specie was confirmed by morphological characterization and phylogenetic analysis of the ITS and β-tubulin regions. Germination of conidia was evaluated at temperatures of 10, 15, 20, 25, 30, 35, and 40°C in combination with 4, 6, 12, 24, and 48 h of wetness period. Guava fruits cv. Kumagai were inoculated with conidial suspensions of *F. aesculi* and maintained at temperatures of 15, 20, 25, 30, and 35°C and wetness periods of 6, 12, 24, and 48 h. We evaluated the incubation period, the diameter of the lesion seven days after inoculation and the growth rate of the lesion. The optimum temperature for the conidia germination was 30°C and the maximum germination occurred after 24 h wetness period. The optimum temperature for growth of the lesion was 30°C and wetness period of 48 h increased the disease severity. The lowest incubation period (3 days) occurred at temperature of 30°C and wetness period of 48 h. The growth rate of lesion estimated by the monomolecular model was 0.3/day. The favorable environment conditions for development disease is high temperatures and prolonged wetness period.

Phylogenetic overview of the Boletineae

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Phytopathology 103(Suppl. 2):S2.104

Boletes are a morphologically diverse group of fungi that are mainly ectomycorrhizal and have successfully colonized all the continents, except for Antarica. The wide diversity found in the boletes makes it an excellent group to test evolutionary rates and trends of morphological and ecological changes. The relationships of selected genera, representing the largest and most common genera of the Boletineae [Boletales], were studied using nuc-lsu, *tef1*, and RPB1, producing the most comprehensive phylogeny to date. With the exception of *Hyndomerulius pinastri*, the Boletineae, Paxillaceae and Boletaceae were strongly supported. The majority of traditional, morphologically described genera were not recovered as monophyletic unless using the most narrow description available (i.e. using the description of the section of a genus that contains the type species). Specifically, *Boletus* species were found throughout the phylogeny, but Singer's *Boletus* section *Boletus* was monophyletic. Further sampling is required to identify lineages of *Boletus* species that are not members of Singer's section *Boletus* and test if subgeneric groups described previously may be described as genera. The phylogeny implies nearly every genus is in need of reorganization. Additionally, the phylogeny indicates multiple, independent evolutions of secotioid and gasteroid forms (including sequestrate forms) and lineages that may be transitions from an ectomycorrhizal nutritional strategy.

Transcriptomic, proteomic, and nutritional analyses of potato tissues infected with '*Candidatus* Liberibacter solanacearum'

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Phytopathology 103(Suppl. 2):S2.104

Zebra chip (ZC) is an emerging destructive disease of potato and is associated with the phloem-limited α-proteobacterium, '*Candidatus* Liberibacter solanacearum' (Lso). In this study, RNA-Seq, 2-DE, mass spectrometry and qRT-PCR analyses identified over 100 differentially produced gene transcripts and proteins in above-ground (AG) and below-ground (BG) potato tissues upon Lso infection. Interestingly, in spite of an Lso-mediated down-regulation of photosynthesis-related genes/proteins, over 80% of the differentially produced gene transcripts/proteins were up-regulated in AG tissues. This was accompanied by an increase in nutrient concentrations of K, Mn, Fe and Cu in both AG and BG tissues in response to Lso infection. Furthermore, there was a strong induction of proteinase inhibitors in AG tissues upon Lso infection. In contrast, the expression of proteinase inhibitors was markedly suppressed in Lso-infected BG tissues. In general, results suggest that ZC disease development involves an Lso-mediated down-regulation of photosynthesis accompanied by an ineffective and potentially inefficient up-regulation of stress response-, metabolism-, and housekeeping-related gene transcripts/proteins with concomitant increases in nutrient accumulation. This study presents a first approach of a holistic investigation of the global transcriptomic, proteomic and nutritional response of potato plants to Lso infection.

Management of *Meloidogyne incognita* with tall fescue grass rotations prior to peach orchard establishment

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Phytopathology 103(Suppl. 2):S2.104

Root-knot nematodes (*Meloidogyne* spp.) are important pests of peach in the USA. Preplant fumigant nematicides have been used to control *Meloidogyne* spp. associated with Southeastern peach production. Unfortunately, growers have increasingly faced economic challenges, making it difficult for them to afford application costs of preplant nematicides. Finding an alternative to control root-knot nematode is warranted. Previous studies indicated that Jesup (Max-Q) tall fescue grass is a nonhost for *M. incognita* and *M. hapla*. In 2005, the effects of 1- and 2-yr fescue rotations for the management of *M. incognita* were initiated in Georgia. Prior to orchard establishment in 2009, both fescue rotations (2005-2008) and preplant Telone II (1,3-dichloropropene) fumiga-