



Oral Technical Session: Fungal Biology 1

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Distribution and detection of *Botrytis* species of blackberry and strawberry in the Southeast United States.

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Botrytis spp. cause blossom blight and fruit rot on many crops, including strawberry and blackberry. In 2011, 400 isolates from blackberry and strawberry fields were collected from North and South Carolina and single-spore colonies were obtained and characterized. Two distinct species, *B. cinerea* Pers. and another newly described *Botrytis* species – *Botrytis caroliniana* X.P. Li & G. Schnabel, were identified based on examination of the coding G3PDH, HSP60, RPB2 and NEP1 genes and based on morphological characters. A PCR method was developed to distinguish *B. cinerea* from *B. caroliniana* but cultural characteristics can also be used for rapid distinction. Without exception, *B. cinerea* isolates sporulated on potato dextrose agar and kings medium B, while *B. caroliniana* isolates did not. The new species is pathogenic on blackberry, strawberry, broad beans and tomatoes, which is the second *Botrytis* species that has a broad host range besides *Botrytis cinerea*. Isolates from both species were subjected to cyprodinil, fenhexamid, fludioxonil, pyraclostrobin, boscalid, thiophanate-methyl and iprodione sensitivity evaluations using germination assays and several different fungicide resistance phenotypes were discovered.

Keywords: Fungus, Fruits-Nuts, Cane Berry

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Erysiphe necator, the causal agent of grapevine powdery mildew, overwinters as chasmothecia in many grapevine growing regions. In the following spring, chasmothecia discharge ascospores that cause primary infections and trigger powdery mildew epidemics. In organic viticulture, only sulphur and biocontrol agents (BCAs) are available to control this disease, and the efficacy of these products must be maximized to obtain acceptable control. The possibility of including sanitation (via application of a BCA against the overwintering chasmothecia) in powdery mildew control was evaluated over a 4-year period in experimental vineyards. A biocontrol product "AQ10" that contained *Ampelomyces quisqualis* and that was applied twice (before and after harvest, i.e., during the formation and maturation of the chasmothecia), halved disease severity on bunches until the pea-sized berries stage in the following season. When sanitation with *A. quisqualis* was coupled with early season (i.e., between bud break and fruit set) sulphur applications scheduled according to the output of a mathematical model predicting ascospore infection based on weather data, disease severity on bunches was reduced by 98% (vs. an 80% reduction with sulphur sprays alone). In conclusion, the use of sanitation with *A. quisqualis* and a weather-driven model for ascospore infection can increase the efficacy of sulphur for control of powdery mildew in organic viticulture.

A unique genomic region of the *Cochliobolus sativus* pathotype 2 isolates carries genes for high virulence on barley cv. Bowman
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Cochliobolus sativus (Anamorph: *Bipolaris sorokiniana*) is the causal agent of several important diseases, including spot blotch, common root rot, and black point, in cereal crops. Three pathotypes (0, 1, and 2) with differential virulence patterns on three barley genotypes (Bowman, ND5883 and NDB112) were identified. The pathotype 2 isolates showed high virulence on barley cv. Bowman but exhibited low virulence on the other two barley genotypes. Our previous studies indicated that the high virulence of the *C. sativus* pathotype 2 isolate ND90Pr was controlled by a single locus *VHv1* and genes for nonribosomal peptide synthetases (NRPSs) and/or polyketide synthases (PKSs) were involved in the biosynthesis of the unknown virulence factor. In this study, we identified a genomic region (approximately 137 kb in size) unique to ND90Pr based on genome sequence analysis in comparison with non-pathotype 2 isolates of *C. sativus*. This unique region contains an AFLP marker co-segregating with *VHv1* and thus is the location of the gene(s) conferring high virulence on Bowman. Of 43 predicted genes in this region, 17 had predicted annotations including two genes encoding for nonribosomal peptide synthetases (NRPSs). One of the genes for NRPSs was knocked out and the knockout mutants were significantly reduced in virulence on cv. Bowman, suggesting that it is involved in high virulence of the pathogen. Molecular and functional characterization of the genes related to virulence in this region will be presented.

Sensitivity of *Monilinia fructicola* to sterol demethylation inhibitors and analysis of *CYP51* promoter insertions in Michigan populations
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American brown rot (ABR; *Monilinia fructicola*) is a serious disease problem affecting stone fruit. The most effective class of fungicides for ABR management is the sterol demethylation inhibitors (DMIs); however, resistance has been reported in the southeastern US, NY, NJ, and OH. Recent publications suggest a PCR-based survey to detect a novel 376-bp insert

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Effects of piperidine alkaloids from the red imported fire ant on cucumber damping-off caused by *Pythium ultimum* in the greenhouse
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Pythium ultimum Trow is a plant pathogen that causes significant yield losses to many economically important crops. Chemical seed treatment has been used for disease control. In searching for alternatives, the venom alkaloids from the red imported fire ant were employed to control cucumber damping-off caused by *P. ultimum* in the greenhouse as seed and drench treatments. Seed soaking treatments did not provide control effects. Drenching treatment significantly improved the seedling emergence and seedling height of cucumber in the greenhouse. This is the first report using piperidine alkaloids from the red imported fire ant to control plant disease caused by *P. ultimum* in greenhouse. These findings may lead to the development of a new group of fungicides.

A new soybean rust resistance gene identified in PI 567102B
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Soybean rust (SBR) is one of the most destructive diseases of soybean. It is caused by *Phakopsora pachyrhizi* Syd. and P. Syd. Durable resistance to *P. pachyrhizi* is the most effective long-term strategy to control SBR. The objective of this study was to investigate the genetics of resistance to *P. pachyrhizi* in soybean accession PI 567102B. This accession was previously identified as resistant to SBR in Paraguay and to *P. pachyrhizi* isolates from seven states (Alabama, Florida, Georgia, Louisiana, Mississippi, South Carolina, and Texas) in the USA. Analysis of two independent populations, one in which F_2 phenotypes were inferred from F_2 -derived F_3 ($F_{2,3}$) families and the other in which F_2 plants had phenotypes measured directly, showed that the resistance in PI 567102B was controlled by a single dominant gene.