



2012 Southern Division Meeting Abstracts

Abstracts presented at the APS Southern Division meeting in Birmingham, Alabama, February 5–6, 2012. The abstracts are arranged alphabetically, by first author's name.

Characterization and detection of a new *Botrytis* species from blackberry

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Phytopathology 102:S2.7

Botrytis spp. cause blossom and fruit diseases on many crops, including blackberry. In 2011, 404 isolates from blackberry and strawberry were collected from North and South Carolina and single spore colonies were characterized. Two distinct species, *B. cinerea* and another undescribed species, were identified based on examination of the coding G3PDH, HSP60 and RPB2 genes and based on morphological characters. The new species formed pale yellow to white colonies with short aerial mycelia and produced black sclerotia on PDA at 20°C. Phylogenetic analysis based on combined DNA sequence data showed that the novel *Botrytis* sp. is most closely related to *B. fabiopsis*, the causal agent of gray mold disease of broad bean, and *B. galanthina* from snow drop. Its conidia, however, are smaller than conidia of *B. fabiopsis* and *B. galanthina* and sequence analysis of genes encoding necrosis and ethylene-inducing proteins (NEPs) also indicated that the novel *Botrytis* spp. is distinct. The new species is pathogenic on broad bean leaves, indicating a broad host range and providing further evidence for its biological distance from *B. galanthina*. Inoculation of blackberry fruit with conidia caused typical gray mold symptoms but compared to *B. cinerea* the latent period was significantly longer. A PCR method was developed to distinguish *B. cinerea* from *B. caroliniana*, however, some cultural characteristics can also be used for rapid distinction.

Identification and characterization of expressed resistance gene analogs (RGAs) from peanut (*Arachis hypogaea* L.) expressed sequence tags (ESTs)

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Phytopathology 102:S2.7

Cultivated peanut (*Arachis hypogaea* L.) is an important food legume grown worldwide for providing edible oil and protein. However, due to scarcity of genetic diversity, peanut is very vulnerable to a variety of pathogens, such as rust (*Puccinia arachidis* Speg.), early leaf spot (*Cercospora arachidicola* S. Hori), late leaf spot (*Cercosporidium personatum* Berk. & M.A. Curtis), and Tomato spotted wilt virus (TSWV). Large number of peanut ESTs (225,264 ESTs by 11-11-2011) has been developed in recent years by peanut community, providing resources for gene identification and marker development. Based on the homology to typical pathogen resistance genes and the conservative domains/features, we identified 401 resistance gene analogs (RGAs), using a stringent BLAST search. By using 54 known R-gene protein sequences, we screened peanut EST database and identified 995 ESTs targeting different classes of known R genes. Among the 995 ESTs, 559 (56%) are from cultivated peanut (ten genotypes) and 436 (44%) are from three wild peanut genotypes. After assembly, 401 unigenes including 152 contigs and 249 singletons were identified and considered as peanut expressed RGAs. These expressed RGAs are comprised of 75, 196, 89, 27, and 14 RGAs representing for NBS-LRR, protein kinase (PK), LRR-PK/TM, Toxin reductase, and other domain encoding R genes, respectively. The expressed RGAs identified in this study provide a large sequence dataset for RGA-tagged potential markers that could be developed further for use in mapping and ultimately cloning disease resistance genes in peanuts.

Characterization and genetic analysis of rhizobacteria antagonistic to plant pathogens

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Phytopathology 102:S2.7

Numerous antagonistic bacteria have been isolated from suppressive soils in Mississippi. These bacteria showed significant inhibitory activity to some plant pathogenic fungi and bacteria. Preliminary analyses indicated that these bacterial isolates belong to the genera *Burkholderia*, *Pseudomonas*, *Bacillus*, *Enterobacter*, and *Streptomyces*. Further characterization and genetic analysis of the bacteria are under way. Strain MS14 was determined to be a member of