P-05

An update on the Fusarium spp. involved in SDS

Martin Chilvers^{*}, Department of Plant, Soil, and Microbial Sciences, Michigan State University, Michigan, USA

Jie Wang, Department of Field Crop Pathology, Michigan State University, Michigan, USA

Janette Jacobs, Department of Plant, Soil, and Microbial Sciences, Michigan State University, Michigan, USA

Linda Hanson, Department of Plant, Soil, and Microbial Sciences, Michigan State University, Michigan, USA

Soybean sudden death syndrome (SDS), caused by the fungus Fusarium virguliforme, is one of the top five diseases threatening soybean production in the US. SDS was first reported in Arkansas in 1971, and has subsequently been reported in adjacent states with an apparent pattern of dispersal. To date, most major US soybean producing states, with the exception of North Dakota have confirmed the presence of SDS, and that it is caused by F. virguliforme. Contrary to the wide distribution of F. virguliforme in the US, multiple species of the Fusarium solani species complex have been associated with SDS in South America. It has been proposed that South America may be the center of origin of *F. virguliforme*. In attempt to test this hypothesis and understand the genetic diversity of F. virguliforme we conducted multilocus microsatellite genotyping on a collection of 539 F. virguliforme isolates from both South and North America, including 60 isolates from Argentina. High genotypic diversity and diverse population structure composition of the Arkansas population supported the hypothesis that Arkansas is the center of origin in the US. The distribution of *F. virguliforme* in the US was not in isolation by distance as detected in a Mantel test, suggesting a rapid and recent expansion of this pathogen in the US. The hypothesis that South America is the center of origin was supported by the coalescence based migrate analysis; however, genotypic diversity and population structure of the Argentinean populations were less diverse than the Arkansas population. Suggesting that the Argentinean population cannot explain the genotypic diversity and population structure composition detected in the US. In addition, during recent surveys we have identified additional species of the Fusarium solani species complex causing SDS and/or root rot in the US, including F. brasiliense, F. cuneirostrum and F. phaseoli.