This article was listed in Forest Nursery Notes, Summer 2007

107. Searching for *Phytophthora ramorum*: three years of surveying New York State and northeastern nurseries for the sudden oak death pathogen. Snover-Clift, K. L., Clement, P., and Jensen-Tracy, S. Phytopathology 97(7)Suppl:S109. 2007.

utility of this model as a research and educational tool, and demonstrates its applicability as a tool in the analysis and diagnosis of observed epidemics.

Phylogenetic analysis of Corynespora isolates from diverse hosts and locations

- L. J. Smith (2), L. E. Datnoff (2), J. A. Rollins (2), K. Pernezny (1), R. L. SCHLUB (3)
- (1) University of Florida, Belle Glade, FL. USA; (2) University of Florida, Gainesville, FL, USA; (3) University of Guam, Mangilao, Guam, USA Phytopathology 97:S109

Species of Corynespora have been distinguished by host substrate and morphological variation. However, morphological variability within single spore isolates has been observed depending on host, substrate and environment. Nineteen isolates of C. cassiicola from diverse hosts and 2 geographic locations were used to screen for variable sequence data useful for phylogenetic analysis. C. viticis was used as an outgroup for relative genetic distance. The nuclear ITS1, 5.8S and ITS2 locus were sequenced revealing only 2 informative polymorphic sites among the 20 isolates. Likewise, the glyceraldehyde-3-phosphate dehydrogenase gene was highly conserved with only 1 informative site. C. viticis had identical sequences to five of the C. cassiicola isolates, suggesting that C. viticis may not be a distinct species. To investigate whether genetic diversity within the species is associated with host or geographic location, additional isolates were collected and sequence data were obtained from three hypervariable nuclear loci, including one microsatellite region. These data provide evidence for distinct phylogenetic lineages and clonal reproduction based on gene tree congruence across loci. We suggest that species distinctions within Corynespora should be based on morphological distinctions on standardized substrates that correlate with molecular data.

PCR-based detection of Sclerotinia minor

D. L. SMITH (1), M. A. Cubeta (1), T. Toda (1), B. B. Shew (1) (1) Dept. Plant Path., NC State University, Raleigh, NC, USA

Phytopathology 97:S109

In North Carolina, *Sclerotinia minor* causes a major disease of peanut. The closely related species *S. sclerotiorum* and *Botrytis cinerea* are common in peanut fields but rarely damage the crop. Regions within the intergenic spacer

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Searching for *Phytophthora ramorum*: Three years of surveying New York State and Northeastern nurseries for the sudden oak death pathogen

K. L. SNOVER-CLIFT (1), P. Clement (1), S. Jensen-Tracy (1)

(1) Cornell University

Phytopathology 97:S109

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The discovery of *Phytophthora ramorum* on Camellia in a large production nursery in California in March 2004 prompted trace forward and national survey sampling of containerized ornamental plants shipped across the country. The Plant Disease Diagnostic Clinic (PDDC) at Cornell University tested plant material from three major surveys over a three year period. From 2004 through 2006, the PDDC processed 2681 samples comprised of 284 NPDN trace forward, 2035 NYS National Survey, and 362 US Forestry nursery perimeter samples. Additionally, the Tiffany Creek Preserve has been monitored due to a questionable positive test result on a mature Red Oak (Ouercus rubra) in June 2004. This result caused additional testing of trees, soil and water from the Preserve until the results were consistently negative twice a year for two years. Testing methods included the use of a commercial Enzyme-Linked ImmunoSorbant Assay (ELISA) test kit and double nested Polymerase Chain Reaction (PCR). Over the three year period, 327 of 2319 samples tested positive for a Phytophthora species with ELISA. PCR testing was conducted on these samples to determine if the Phytophthora species present was P. ramorum. All forestry samples were processed using PCR. No P. ramorum was found in any of our testing and the Tiffany Creek Preserve was deemed free of P. ramorum.

The discovery of Plum pox virus in New York State

K. L. SNOVER-CLIFT (2), P. Clement (2), R. Jablonski (3), M. Tiffany (1) (1) Agdia, Inc.; (2) Cornell University; (3) NYS Department of Agriculture and Markets

Phytopathology 97:S109

Plum pox, also known as Sharka, is a viral disease of stone fruit trees such as plum, peach, and apricot. It has been a devastating disease in Europe since the early 1900s. In recent years the disease has spread to the Americas, first being found in Chile in 1992, in Pennsylvania in 1999, in Ontario and Nova Scotia in 2000, and in Argentina in 2004. Surveys have been conducted in New York

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