# DIVERSITY WITHIN A POPULATION OF *PHYTOPHTHORA CINNAMOMI* FROM ORNAMENTAL CROPS IN SOUTH CAROLINA

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*Phytophthora cinnamomi* is a devastating pathogen that can infect over 900 hosts, including many urban and forest trees. It is the most common species of *Phytophthora* isolated from woody ornamental crops in South Carolina, but little is known about variability among isolates of *P. cinnamomi* that attack these plants. Therefore, 142 isolates of *P. cinnamomi* recovered from samples submitted to the Clemson University Plant Problem Clinic between 1996 and 2011 were characterized for growth rate, mycelium growth habit, mefenoxam sensitivity, and mating type. Average growth on PARPH-V8 selective medium was 60 mm in 72 h at 25Â°C in the dark. Mycelium growth habit on PARPH-V8 was classified as aerial, sparse, dwarf, or appressed; 85% of isolates had aerial mycelium. All isolates were sensitive to the fungicide mefenoxam at 100 ppm. The population was composed of 129 A2 and 13 A1 isolates with six A1 isolates recovered from camellia. DNA was extracted and the ITS region was sequenced. ITS had low diversity; only two genotypes were different from the majority of the population. One genotype consisted of an isolate of *P. cinnamomi* var. parvispora, and the other genotype included four morphologically diverse isolates. Consequently, there was high genetic uniformity in the ITS region for this population. Four other loci were sequenced for a subset of 61 representative isolates. Cluster analysis of the genotypes at each locus revealed five distinct groups. Dwarf isolates were genetically and morphologically distinct from the majority of isolates, which clustered in one group. The isolate of *P. cinnamomi* var. parvispora also was genetically and morphologically distinct from other isolates. Two other groups of isolates were genetically distinct but were not morphologically distinct based on the characters we evaluated. Host-pathogen relationships for this population were compared to reports in the literature, and 33 new host associations were found.