

SRSFC FINAL REPORT

Identification of the source of *Phytophthora cactorum* infections in strawberry fields

Principal investigators

Guido Schnabel, Hongwen Huang, Desmond Layne, and Steve Jeffers. First and last authors: Department of Plant Pathology, Clemson University; second and third author: Department of Horticulture, Clemson University.

Objectives

1. Develop a method for detection of genetic variability in *P. cactorum* isolates.
2. Profile the genetic diversity in *P. cactorum* isolated from major tip, plug, and strawberry fruit producing areas of Canada and the United States and from hosts other than strawberry.

Methods

P. cactorum sources. For this study we used fungal strains that were part of a collection maintained by S. Jeffers. In addition, we obtained strains from other scientists outside South Carolina and from plant material (bare root plants or plugs) shipped from US nurseries. AFLP (Amplified Restriction Fragment Polymorphism) was used to determine the genetic diversity of *P. cactorum*. It is probably the technique with the highest sensitivity to detect genetic variation. Other techniques have failed to find genetic variation within the *P. cactorum* species (Hantula, etc. 1997; 2000).

Results and Conclusions

The AFLP analysis produced a large number of reproducible and unambiguous markers for fingerprinting *P. cactorum* isolates. Eight *EcoR* I +2 /*Mse* I +1 primer pair combinations resolved 264 reliably scored markers. Across all 53 isolates evaluated, 226 markers (85.6%) were polymorphic and gave 48 unique AFLP profiles. With this technique it is now possible to create a unique DNA fingerprint database of *P. cactorum* isolates that may help to track down the origin of disease outbreaks and to study the population dynamics in *P. cactorum*.

Genetic relationships among the *P. cactorum* isolates from strawberry and other host plant species were examined by UPGMA cluster analysis (Fig. 1). The dendrogram revealed two distinct clusters, one containing South Carolina and Canadian populations and one containing all other populations. This suggests that South Carolina isolates may have derived from nurseries in Canada rather than from an indigenous population. In support of this conclusion is the unexpectedly high genetic diversity within South Carolina isolates. A population derived from one location would have been less diverse due to the homothallic nature of this fungus. Canada is the biggest supplier of plant tips for the southeastern United States. The tips are shipped to southern bare root and plug producers from which growers receive planting material.

Impact Statement

With this database of fingerprints the origin of new outbreaks of *P. cactorum* can be assessed. In addition, the strong evidence that the crown rot disease may have come from Canada will aid in the development of strategies to eliminate this inoculum source.

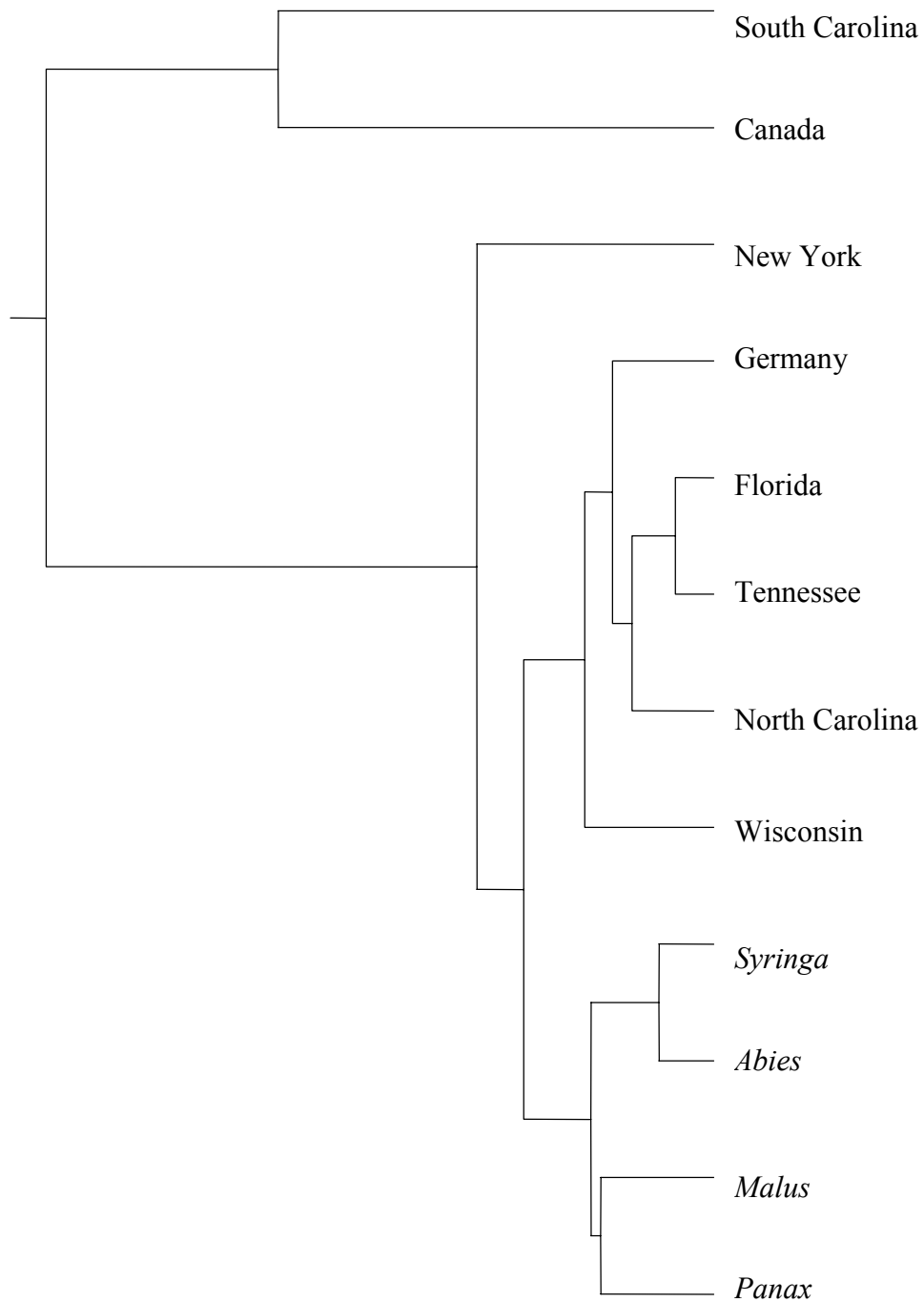


Figure 1: Unweighted pair-group mean analysis (UPGMA) dendrogram of amplified fragment length polymorphism (AFLP) genetic distance based on Nei's (1978) genetic distance among eight *P. cactorum* populations from strawberries and isolates from other host plant species.