

Genetic Variation in Fraser Fir Mortality Due to Phytophthora Root Rot

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Fraser fir (*Abies fraseri* (Pursh.) Poir.), native to a small number of isolated ridgetops in North Carolina, Tennessee, and Virginia, is widely grown in the Southern Appalachians for the fresh-cut Christmas tree market. This species is the primary Christmas tree grown in North Carolina, which accounts for more than 12 percent of real Christmas trees produced in the United States and ranks second in the total number of trees harvested and first in the dollars made per tree. In 1999, for example, 1,600 North Carolina growers sold 3.7 million trees worth a reported value of more than \$92 million (N.C. Department of Agriculture and Consumer Services 2003).

Phytophthora root rot presents a serious economic limitation to Christmas tree growers, with the majority of root rot damage caused by *Phytophthora cinnamomi* Rands. In 1997 and 1998, a survey of 58 Fraser fir field sites in North Carolina found an average Phytophthora root rot incidence of 9 percent, with *P. cinnamomi* accounting for 91 percent of the Phytophthora isolates recovered (Benson and Grand 2000). Phytophthora root rot in Fraser fir typically occurs in sites with poorly drained soils (Grand and Lapp 1974, Kuhlman and Hendrix 1963). Determining whether Phytophthora root rot resistance exists in Fraser fir, and then selectively breeding to increase that resistance, would be highly useful to Christmas tree growers in the Southern Appalachians. This is especially true given that Fraser fir growers have typically used unimproved and mostly unselected seed sources (Arnold *et al.* 1994).

Species that occur in disjunct subpopulations are expected to have high inter-population genetic divergence resulting from genetic drift, reduced gene flow, elevated inbreeding, and differing selection pressures experienced among isolated populations (Young *et al.* 1996). Such variation in Fraser fir natural subpopulations could be associated with varying amounts of resistance to Phytophthora. While resistance to the pathogen has not been established in a genetic field test setting, recent field tests have indicated significant genetic variability within the species for other traits, specifically growth and form characteristics (Arnold *et al.* 1994, Jett *et al.* 1993, and Li *et al.* 1988). A recent greenhouse Phytophthora inoculation of Fraser fir seedlings found slight differences among seed sources, with highest occurring in the Roan Mountain source, the lowest in the Mount Mitchell source, and an intermediate amount occurring in the Richland Balsam source (Frampton and Benson 2003, in press).

In 2000, a progeny test of three-year-old Fraser fir seedlings in Avery County, North Carolina, became infested by *P. cinnamomi*. We analyzed seedling mortality at the test

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site with three objectives: 1) quantifying the genetic variation within the six major Fraser fir subpopulations and 94 open-pollinated families in the study for potential *Phytophthora* root rot resistance, 2) estimating genetic parameters for root rot mortality; and 3) exploring the feasibility of using a Geographic Information System (GIS) neighborhood analysis as a tool for separating potential genetic resistance to *Phytophthora* from uneven exposure to the pathogen in a field setting. Specifically, neighborhood analyses generated by the GIS package ArcView (ESRI 1999) were used to generate data on the proportion of dead trees within a given distance of each tree in a field test; that information was then used as a covariate in the genetic analyses of variance.

The differences in mortality among the six sources of Fraser fir were small in the third year following root rot exposure, ranging from 38.4 percent for the Roan Mountain source to 45.8 percent for the Mount Mitchell source. A greater amount of variability existed among the 94 families, from a low of 21.4 percent mortality to a high of 62.1 percent.

We used the statistics package ASReml (Gilmour *et al.* 2002) to generate variance terms and heritability estimates for mortality, because ASReml could both logistically transform the binomial mortality data and conduct a residual maximum likelihood (REML) analysis. In our mixed linear model, seed source, source-block interaction, and family within source were considered random effects, and blocks were treated as fixed effects.

Family within source was the only variance component significantly different from zero, and accounted for about 5 percent of the variation in the mortality data. When the populations were analyzed separately, family variance was significant in only the Balsam Mountains, Mount Mitchell, and Roan Mountain sources. Across all populations, narrow-sense family mean heritability was 0.63 and individual heritability was 0.20.

The results from these analyses, and from future analyses of additional mortality at the site, will be compared to results from a greenhouse inoculation test in progress during the summer of 2003. In this test, Fraser fir from 120 families and all six seed sources are being inoculated with a single *P. cinnamomi* isolate.

Our GIS analysis generated information on the proportion of dead trees near each individual in the plot. When we used this data as a covariate term in our genetic analysis of variance, the results did not produce different variance estimates and genetic parameters than without the use of the GIS-generated neighborhood mortality data. This may indicate that the single-tree non-contiguous plot design for the field study successfully reduced differences in *Phytophthora* exposure among Fraser fir families. The neighborhood analysis approach, however, may result in more precise genetic parameter estimates in other experimental designs.

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