

## Variation in Susceptibility to the EU1 and NA1 Lineages of *Phytophthora ramorum* among Southern Oregon Tanoak Families<sup>1</sup>

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### Abstract

*Phytophthora ramorum*, the cause of Sudden Oak Death (SOD), is an oomycete pathogen that has invaded coastal California and southern Oregon mixed-hardwood forests. In southern Oregon forests, tanoak (*Notholithocarpus densiflorus*) is the most susceptible species developing lethal stem cankers and sporulating from infected leaves and branches. Two lineages (NA1 and EU1) of *P. ramorum* occur in Oregon forests. The first step in a successful tanoak breeding program is to determine if variation in resistance to these two lineages exists. The objectives of this study are to: (i) characterize the variability in resistance of *N. densiflorus* among families using lesion length; and (ii) determine whether lineage, isolate, family, or their interactions significantly affect variation in lesion length. In a growth chamber experiment approximately 1,000 seedlings from 14 tanoak families were inoculated with 3 isolates of the NA1 lineage and 3 isolates of the EU1 lineage. Stem lesions were measured seven days after inoculation.

Averaged across all tanoak families, there were no significant differences in lesion length between the EU1 and NA1 lineages; however, there were significant differences among the six isolates tested. The averages for each family by isolate combination show an overall pattern of increased average lesion length for EU1 isolates. The majority (89%) of the variation in lesion length is explained by isolate (lineage). The family by isolate (lineage) interaction suggests that more than one isolate may be needed in order to screen for resistance to *P. ramorum*. In addition, for a resistance screening program to be successful, a reliable method to vegetatively propagate tanoak needs to be developed.

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