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<http://www.apsnet.org/meetings/abstracts.asp>

**Grunwald, N.J.; Larsen, M.; and Goss, E.M. 2008. Genotypic diversity of *Phytophthora ramorum* in U.S. nurseries. *Phytopathology* 98:S63.**

*Phytophthora ramorum* is the causal agent of sudden oak death, responsible for the rapid decline of tanoak and coast live oak in California coastal forests. It also causes Ramorum blight in many common ornamentals, including *Rhododendron*, *Viburnum*, *Pieris*, *Syringa* and *Camellia*. Genetic variation in *P. ramorum* is structured into three clonal lineages, designated EU1, NA1, and NA2. EU1 is generally mating type A1 while all tested NA1 and NA2 isolates have been mating type A2. All three clonal lineages have been isolated from U.S. nurseries. We have been routinely genotyping *P. ramorum* isolates found in U.S. nurseries using microsatellite loci that exhibit variation within and between lineages. The clonal lineage of each genotyped isolate is posted to a public website along with additional information about the isolate, such as the host species and its county and state of origin (<http://oregonstate.edu/~grunwald/index.htm>). We have found that NA1 continues to be the most common lineage isolated from infected nursery stock in the U.S. Our genotyping revealed the first incidence of EU1 in California in 2006, where it appeared in the same nursery as NA1. In 2007 we found the two lineages on different leaves of the same plant in an Oregon nursery. EU1 was found in all three Pacific coast states in 2007, whereas the NA2 lineage was limited to Washington State. Continued genotyping of nursery isolates will be critical for monitoring migration of the clonal lineages and the emergence of any new or recombinant lineages.