From Forest Nursery Notes, Summer 2009

145. Initial assessment of genotypic diversity of *Phytophthora ramorum* associated with Washington state ornamental nurseries. (ABSTRACT). Dart, N. L., Chastagner, G. A., and Coats, K. Phytopathology 99:S181. 2009.

Initial assessment of genotypic diversity of *Phytophthora ramorum* associated with Washington state ornamental nurseries

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Phytopathology 99:S181

Isolates (65 total) of *P. ramorum* were obtained with help of Washington Department of Agriculture from 13 nurseries, two streams, and one landscape situation in Washington state and genotyped using 4 previously developed microsatellite markers (Prospero, 2007). Three previously described lineages, known as EU1, NA1 and NA2, (Ivors, 2007) were detected in Washington nurseries. The NA1 lineage was the most common, occurring in seven retail nurseries, one wholesale nursery, one landscape situation, and both streams. The NA2 lineage was detected in three retail and one wholesale nursery, while the EU1 lineage was detected at a single wholesale nursery. At one nursery, both the NA1 and EU1 lineages were isolated from different branches on the same rhododendron plant. DNA fingerprinting identified six unique genotypes among the NA1 lineage isolates and two unique genotypes among the NA2 lineage isolates. High heterozygosity coupled with the clonal population structure, suggests that *P. ramorum* has not undergone sexual recombination in Washington state nurseries. High levels of genotypic diversity observed at three nurseries and lack of sexual recombination suggests multiple introduction events have occurred at Washington nurseries. The fingerprinting results have also provided some insights to potential sources of inoculum that infested the two streams. In one instance isolates obtained from an infested stream matched isolates associated with an infested nursery on the stream. However, in the other situation the isolate collected from an urban stream had a rare fingerprint and the source of the stream infestation is uncertain.