SUDDEN OAK DEATH AND *PHYTOPHTHORA RAMORUM:* AN UPDATE ON RESEARCH WITH IMPLICATIONS FOR REGULATIONS AND MANAGEMENT

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ABSTRACT

In 2006, Sudden Oak Death mortality, caused by the exotic, invasive plant pathogen *Phytophthora ramorum* (Werres, Cock, & Man in't Veld), surged along the central California coast from Monterey County north to Humboldt County. The recent increase in tanoak (*Lithocarpus densiflorus* [Hook. & Arn.] Rehder) and coast live oak (*Quercus agrifolia* [Nee]) mortality has been driven by two consecutive wet springs, which greatly increased spore loads (Rizzo, pers. comm), followed by exceptionally hot summers. This pattern of mortality has just recently been understood and is explained by the pathogen's ability to ramify through the xylem, thereby disrupting water relations (Brown and Brasier 2007, Parke et al. 2006b). It is becoming clear that the mode of action for *P. ramorum* is that of a wilt disease. Trees are not killed by girdling cankers, but rather by an impaired ability to meet their water needs.

After 5 years of research, funded primarily via the U.S. Forest Service Sudden Oak Death/*P. ramorum* extramural, competitive, research program, scientists are making significant new discoveries. Some research highlights and their management implications are listed below. For more information on these investigations, and on Sudden Oak Death, go to the California Oak Mortality Task Force Web site at www.suddenoakdeath.org.

Finding: The natural infection of tanoak seedling roots by *P. ramorum* was first detected (Parke et al. 2006a).

Implications: *P. ramorum* may enter plants by moving from the soil through roots. *P. ramorum* movement may not be limited to aboveground, aerial dispersal. *P. ramorum* may be present in fine roots of tanoak, as well as boles.

Finding: Camellia buds harbor *P. ramorum* (Tjosvold et al. 2006).

Implications: Camellia buds need to be inspected for symptoms. On camellia, *P. ramorum* infections may persist in the buds rather than leaves, as was previously thought, because infected leaves abscise fairly quickly once infected. Buds may play a greater role in pathogen survival and spread than previously realized.

Finding: *P. siskiyouensis* (Reeser and EM Hansen), a new *Phytophthora* species, has been recovered from soil and water in southwest Oregon (Reeser et al. 2006).

Implications: Many new *Phytophthora* species are being discovered. Will they cause widespread disease in a forest somewhere in the world? Was this species present and previously undetected, or is it new?

Finding: Multiple molecular analyses have identified distinct lineages of *P. ramorum* throughout its known range in forests and nurseries and demonstrate that it was introduced to both the United States and Europe (Ivors et al. 2006.

Implications: *P. ramorum* is moving in nursery stock. It is not native to the United States or Europe. Three distinct evolutionary lineages have been introduced to U.S. nurseries. One of the three lineages has become established in California and Oregon forests, and another lineage has become established in several European forests. The third lineage has not yet been found in a forest.

Finding: The *P. ramorum* genome was annotated revealing an exceptionally large repertoire of secreted proteins

(Tyler et al. 2006**)**. *P. ramorum's* genome was sequenced less than 4 years after the organism was discovered, the shortest time for any species. *P. ramorum* has 15,743 genes, while *P. sojae* ([Kaufm. & Gerd.], soybean *Phytophthora*) has 19,027 genes.

Implications: *P. ramorum,* like other *Phytophthoras*, has a diverse array of proteins with which to attack plants. *Phytophthora* species are Stramenopiles and belong to a kingdom distinct from plants, fungi, and animals. They are closely related to diatoms, brown algae, and Saprolegnia, a salmon parasite**.**

Literature Cited

Brown, A.V.: Brasier, C.M. 2007. **Colonization of tree xylem by *Phytophthora ramorum*, *P. kernoviae* and other *Phytophthora* species**. Plant Pathology. 56: 227–241.

Ivors, K.; Garbelotto, M.; Vries, I.D.E.; Ruyter-Spira, C.; Heckkert, B.TE.; Rosenzweig, N.; Bonants, P. 2006. **Microsatellite markers identify three lineages of *Phytophthora ramorum* in US nurseries, yet single lineages in US forest and European nursery populations.** Molecular Ecology. 15: 1493–1505.

Parke, J.L.; Bienapfl, J.; Oh, E.; Rizzo, D.; Hansen, E.; Buckles, G.; Lee, C.; Valachovic, Y. 2006a. **Natural infection of tanoak seedling roots by *Phytophthora ramorum.*** Phytopathology. 96: S90.

Parke, J.L.; Oh, E.;Voelker, S.; Ochiai, N.; Hansen, E. 2006b. ***Phytophthora ramorum* reduces xylem sapflow and specific conductivity of sapwood in mature tanoak.** Phytopathology. 96: S90.

Reeser, P.W.; Sutton, W.C.; Hansen, E.M. 2006. ***Phytophthora siskiyouensis,* a new species from soil and water in southwest Oregon.** Phytopathology. 96: S97.

Tjosvold, S.A.; Chambers, D.L.; Thomas, S.L.; Blomquist, C.L. 2006. **First report of *Phytophthora ramorum* infecting *Camellia* flower buds in North America.** Online at: http://www.plantmangementnetwork.org/php/elements/sum.asp?id=5447 & photo = 3089. Plant Health Progress DOI:10.1094/PHP-2006-0825-01-BR.

Tyler, B.M.; Tripathy, S.; et. al. 2006. **Genome sequences uncover evolutionary origins and mechanisms of pathogenesis.** Science. 313 (5791): 1261-1266.