Using Single Strand Conformational Polymophisms (Sscp) To Identify Phytophthora Species In Oregon Forests Affected By Sudden Oak Death

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Phytophthora species are abundant in streams, widespread in soils and occasional in diseased plants in the tanoak forests of SW Oregon. It is time-consuming and expensive to identify hundreds of isolates to species using morphology or ITS sequencing. We are attempting to modify a published *Phytophthora* SSCP protocol to allow quantitative matching of unknown isolates. The method uses fluorescent-labeled ITS6 and ITS7 primers and automated measurement on a slab-gel DNA sequencing machine. Ninety six samples can be processed simultaneously. We drew a blind sample of eighty unknowns from a larger collection of isolates from streams, soil, and plants, and ran a preliminary test with sixteen reference *Phytophthora* species. SSCP distinguished 13 groups of unknowns. Twenty isolates matched taxon 'Pg chlamydo,' twelve isolates matched *P. nemorosa*, seven isolates matched *P. gonapodyides*, and seven isolates matched *P. ramorum*. Several isolates from stream samples were identified as *P. nemorosa*, previously known only from tanoak cankers in our area. The remaining unmatched groups suggest a large diversity of *Phytophthora* species in natural environments. Five isolates from one unique group have been characterized by ITS sequence and culture morphology, and appear to be a new species of *Phytophthora*. Analysis of additional unknowns revealed problems separating some groups of isolates, and some concerns about repeatability. We are working to incorporate fluorescent-labeled fragments from the mitochondrial COX spacer region to increase specificity, and to isolate variables that are contributing to inconsistent results.