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.