

Distribution of *Phytophthora quercina* and Other Oak-root *Phytophthora* Pathogens in the Midpeninsula Regional Open Space District¹

Ebba Peterson,² Joyce Eberhart,³ Neelam Redekar,³ Jennifer Parke,^{2,3} and Amanda Mills⁴

Abstract

Surveys of native wildlands worldwide to determine *Phytophthora* diversity have found a surprisingly large assortment of root disease-causing species, many of which may contribute to the phenomenon of oak decline. Many species of concern, for example *P. cinnamomi*, are widely distributed throughout the San Francisco Bay Area. Others, notably *P. quercina* and *P. uliginosa*, may additionally contribute to oak decline in Europe (Jung and others 1999, 2002), but are not thought to be widely distributed in the western United States.

To determine *Phytophthora* diversity and distribution in the Midpeninsula Regional Open Space District (MROSD), we collected soil from 30 planted restoration sites, 12 planned restoration sites and 29 adjacent, minimally disturbed non-planted areas in December 2017 and 2018. In addition to baiting, we extracted DNA from a 10 g subsample of each soil. The ITS1 region was amplified and PCR products were submitted for Illumina MiSeq high-throughput sequencing. During the 2018 sampling, we additionally returned and re-sampled sites with strong DNA-only detections of the *P. quercina*-cluster (which may be *P. quercina* and/or *P. versiformis*) and the *P. uliginosa*-cluster (which may be either *P. uliginosa* and/or *P. europaea*) in an attempt to bait these species from soils.

Phytophthora was detected at all 9 MROSD preserves sampled. The *P. quercina*-cluster and the *P. uliginosa*-cluster were widespread, being detected via Illumina MiSeq in either 6 or 5 preserves, respectively. Nearly all detections were from non-planted areas, found in association with overstory oak or tanoak.

We were unable to obtain any isolates matching *P. quercina* or closely related species. To confirm the identity of *P. quercina* in the DNA extracts, we additionally sequenced these extracts

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² Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331.

³ Dept. of Crop and Soil Science, Oregon State University, Corvallis, OR 97331.

⁴ Midpeninsula Regional Open Space District, Los Altos, CA 94022.

Corresponding author: E. Peterson, peterebb@science.oregonstate.edu.

with the MinION sequencer, which provides longer (1,000 bp) read lengths. This revealed this OTU was an approximate 90% match to the *P. quercina*-cluster and likely represents a taxon not present in our database. In 2018, we recovered three isolates from two preserves with ITS1 sequences poorly matching to *P. europaea*. Subsequent sequencing of the COX region revealed these isolates are *P. sp.* ‘cadmea’ which was only recently recovered by Bourret (2018) in a neighboring county. This new taxon has not been evaluated for its risk to native flora.

Illumina MiSeq high-throughput sequencing is a useful tool to study the distribution of hard to bait taxa; however, DNA-only detections are difficult to interpret without isolates to confirm their identity, viability, and pathogenicity.

Literature Cited

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