**Distribution of *Phytophthora quercina* and other Oak-root *Phytophthora* Pathogens in the Midpeninsula Regional Open Space District*[[1]](#footnote-1)***

**Ebba Peterson,*2* Joyce Eberhart,*3* Neelam Redekar,*3* Jennifer Parke,*2,3* and Amanda Mills*4***

**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*-clusterand the *P. uliginosa*-clusterwere 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 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

**Bourret, T**. **2018**. Efforts to detect exotic *Phytophthora* species reveal unexpected diversity. PhD dissertation. UC Davis.

**Jung, T.; Hansen, E.M; Winton, L; Oswald, W. Delatour, C**. **2002**. Three new species of *Phytophthora* from European oak forests. Mycological Research. 106(4): 397-411.

**Jung, T.; Cooke, C.E.L.; Blaschke, H.; Duncan, J.M. and Oßwald, W.** 1**999**. *Phytophthora quercina* sp. nov., causing root rot of European oaks. Mycological Research. 103(7): 785-798.

1. A version of the paper was presented at the Seventh Sudden Oak Death Science and Management Symposium, June 25-27, 2019, San Francisco, California.

   *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. [↑](#footnote-ref-1)