



Ebba Peterson¹, Joyce Eberhart², Neelam Redekar², Amanda Mills³, and Jennifer Parke^{1,2}

¹ Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331

² Dept. of Crop and Soil Science, Oregon State University, Corvallis, OR 97331

³ Midpeninsula Regional Open Space District, Los Altos, CA 94022

contact: peterebb@science.oregonstate.edu

Distribution of *Phytophthora quercina* and other oak-root *Phytophthora* pathogens in the Midpeninsula Regional Open Space District



Introduction & Methods

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 et al. 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 20 planted restoration sites and 18 adjacent, minimally disturbed non-planted areas in December 2017. 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.

Illumina MiSeq generates short (300 bp) DNA fragments of all oomycetes in the sample. Each unique DNA sequence is called an operational taxonomic unit (OTU), which can then be identified through comparison to a reference database of known species. In some cases, differentiating between spp. cannot be done at the ITS1 region or species distinctions are under review (in which case they are called a **complex**); in other cases multiple species are identical over the 300 bp region (in which case Illumina cannot distinguish between them and they are called a **cluster**).

In December 2018 we sampled 19 new sites (10 planted and 9 unplanted). During this time we additionally returned and re-sampled sites with strong DNA-only detections of *P. quercina* and the *P. uliginosa*-cluster (which may be either *P. uliginosa* and/or *P. europaea*) in an attempt to bait these species from soils.

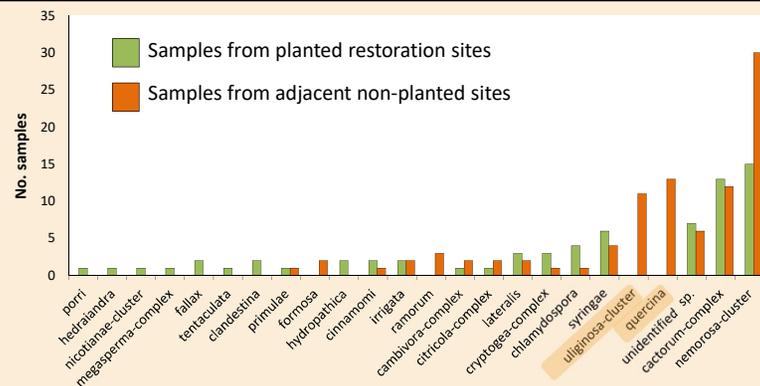


Fig. 1. Number of samples in which each *Phytophthora* OTU was detected via Illumina MiSeq sequencing. We sequenced a total of 88 samples from planted restoration areas and 94 samples from adjacent, non-planted areas collected in 2017.

The *P. uliginosa*-cluster may be either *P. uliginosa* and/or *P. europaea*.

Acknowledgements

This project was funded by the Midpeninsula Regional Open Space District. We would like to thank MROSD staff, especially Jamie Hawk, Coty Sifuentes-Winter, and Cindy Roessler.

References

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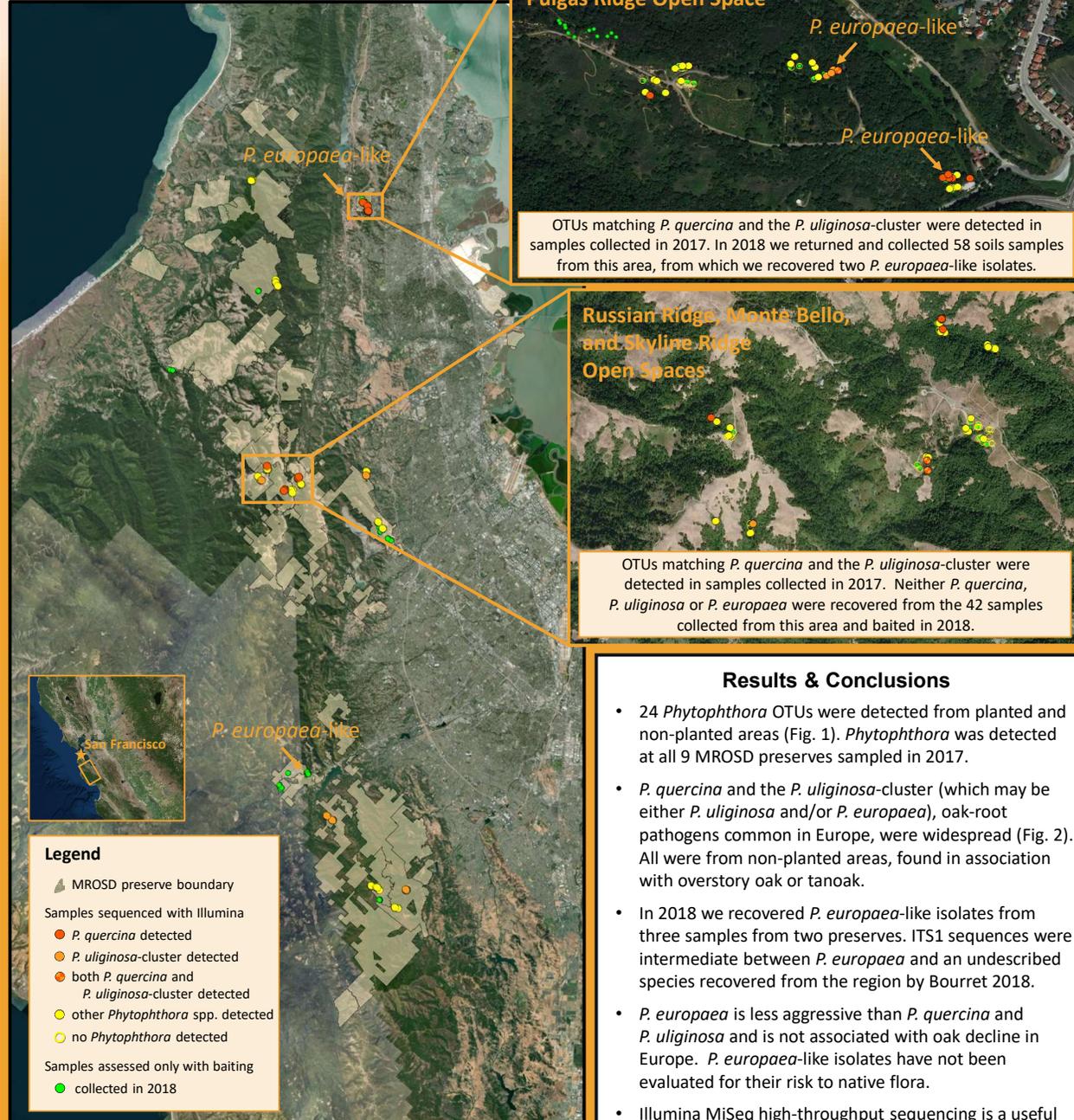
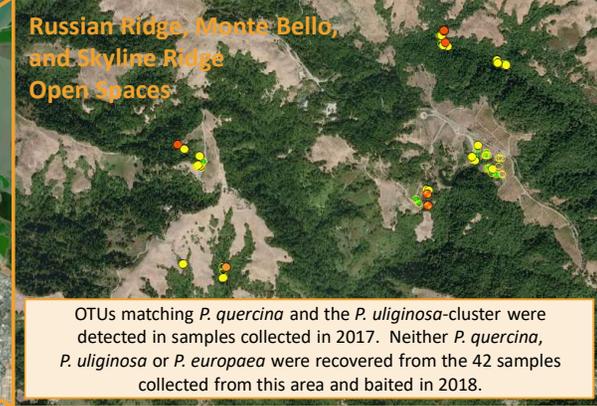
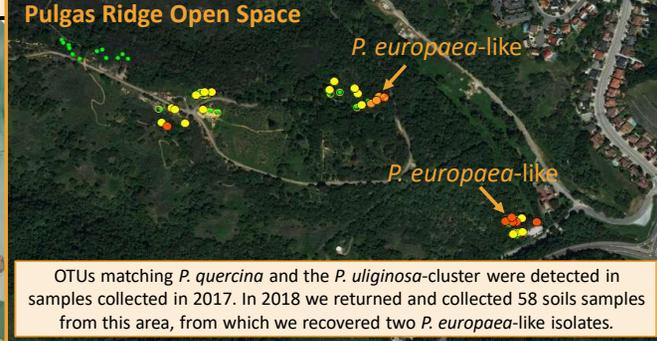


Fig. 2. Distribution of *P. quercina* and the *P. uliginosa*-cluster detections via Illumina MiSeq sequencing of DNA extracted from soil samples collected in 2017. Baiting of samples collected in 2018 (green circles) yielded *P. europaea*-like isolates from three samples collected at two preserves.



Results & Conclusions

- 24 *Phytophthora* OTUs were detected from planted and non-planted areas (Fig. 1). *Phytophthora* was detected at all 9 MROSD preserves sampled in 2017.
- P. quercina* and the *P. uliginosa*-cluster (which may be either *P. uliginosa* and/or *P. europaea*), oak-root pathogens common in Europe, were widespread (Fig. 2). All were from non-planted areas, found in association with overstory oak or tanoak.
- In 2018 we recovered *P. europaea*-like isolates from three samples from two preserves. ITS1 sequences were intermediate between *P. europaea* and an undescribed species recovered from the region by Bourret 2018.
- P. europaea* is less aggressive than *P. quercina* and *P. uliginosa* and is not associated with oak decline in Europe. *P. europaea*-like isolates have not been evaluated for their risk to native flora.
- Illumina MiSeq high-throughput sequencing is a useful tool to study the distribution of hard to bait species (such as *P. quercina*); however, DNA-only detections are difficult to interpret without isolates to confirm their identity, viability, and pathogenicity.