



CALIFORNIA OAK MORTALITY TASK FORCE REPORT DECEMBER 2022

MONITORING – NEW *PHYTOPHTHORA RAMORUM* DETECTION IN LINCOLN CITY, OR

The Oregon Department of Agriculture (ODA), in partnership with the United States Department of Agriculture (USDA) Animal and Plant Health Inspection Service (APHIS), has confirmed the presence of *Phytophthora ramorum* at a botanical garden and private residence in Lincoln City, Oregon. ODA has intensively sampled the locations and is developing a mitigation plan. ODA and USDA APHIS suspect that the pathogen was introduced into Lincoln City through the planting of infested nursery stock several years ago. One rhododendron sample from the site has been provisionally identified as the EU1 lineage. This detection is well over 150 miles from Port Orford, OR, the northernmost known wildland detection of *P. ramorum*.

REGULATIONS

For the first time, *P. ramorum* has been detected on *Polystichum munitum* (common names western swordfern or sword fern). The host has been added to the USDA *P. ramorum* associated host list; see [USDA APHIS | Phytophthora ramorum](#).



Figure 1. *Phytophthora ramorum* symptoms on western swordfern at a residence in Oregon. Photo: Annie Debauw, ODA.

This new associated host was verified following USDA APHIS confirmatory testing at the PPQ Plant Pathogen Confirmatory Diagnostics Laboratory in Beltsville, MD. Positive determinations were confirmed using the USDA validated diagnostic protocols for real-time PCR, conventional PCR and DNA sequencing. Koch's Postulates have not been completed.

The *P. ramorum* positive western swordfern is located at a residence in Lincoln City, OR and is very close to several heavily infected rhododendrons on the property. The lineage of the positive fern sample has not yet been determined. The infected rhododendrons are not associated with recent nursery trade.

No plants from the residence have been moved. USDA APHIS PPQ and Oregon Department of Agriculture delimited the site and mitigation options are being determined. For more information contact, Patrick Shiel, patrick.j.shiel@usda.gov.



Eighty-one plant species have been added to the USDA APHIS Lists of Proven Hosts of and Plants Associated with *Phytophthora ramorum*: 30 plant species are new to the proven host plant taxa list, and 51 plant species have been added to the associated plant taxa list regulated for *P. ramorum*. Among the added species are more than 15 California manzanita (*Arctostaphylos*) species. Dated September 2022, the updated list is posted at [USDA APHIS | Phytophthora ramorum](https://www.usda.gov/aphis/pep/phytophthora-ramorum).

MONITORING - 2022 SOD BLITZ FINDINGS

In California, citizen scientist detections of *P. ramorum* are at their lowest level in more than 15 years. This is one of the key findings from the 2022 SOD Blitz led by Matteo Garbelotto, UC Berkeley. Notably, this year, the survey found the EU1 lineage in Del Norte Co. on two samples near the previous EU1 detection first reported in 2020. County-level maps, tables with results, and a recording detailing *P. ramorum* status from San Luis Obispo through to Del Norte Co. are available at https://nature.berkeley.edu/matteolab/?page_id=148.

NURSERIES AND MANAGED LANDSCAPES

Oregon Department of Agriculture *P. ramorum* Nursery Program update. Currently, there are seven nurseries participating in the Oregon *P. ramorum* Nursery Program. Six of the nurseries are interstate shippers under federal compliance agreements (7 CFR 301.92). Those nurseries are in the following counties: Washington (2), Columbia (1), Linn (1) and Marion (2). One nursery is an intrastate retail nursery in Clackamas County under a state compliance agreement (both 7 CFR 301.92 and OAR 603-052-1230).

Fall compliance inspections were completed by mid-November. The intrastate retail nursery in Clackamas Co. and two other nurseries were found to be negative for *P. ramorum*. The nursery in Columbia Co. has fulfilled the program requirements and will be released from the program in mid-December. During its fall compliance inspection, one nursery was found to have two *Magnolia grandiflora* plants positive for *P. ramorum*. The delimitation discovered three additional positive *Magnolia grandiflora* plants. Delimitation work has been completed, and impacted plants are scheduled for incineration. The nursery grounds will not contain host plants until solarization work is completed in summer 2023. Fall compliance inspection results are pending for three nurseries. For more information, please contact Chris Benemann, chris.benemann@oda.oregon.gov, or Kaitlin Gerber, kaitlin.gerber@oda.oregon.gov.



Figure 2. Symptoms on *P. ramorum* positive *Magnolia grandiflora* plants. Credit: ODA.



Washington State Department of Agriculture *P. ramorum* program update. Since June, the Washington State Department of Agriculture (WSDA) has conducted two trace-forward investigations from out-of-state positive nurseries. At one residential site in Pacific Co., a trace-forward camellia tested positive for *P. ramorum*, as did soil adjacent to the plant. Under the Confirmed Residential Protocol, the camellia was destroyed and the soil steamed by Washington State University. Monitoring of this site will occur for two years post-release.

During a separate trace-forward event, WSDA received limited customer information. This made contact difficult, so follow-up only occurred at 64 of 164 receiving locations, which were all residential. Over several months, WSDA inspectors and USDA APHIS staff assisted one another to make contact and inspect the trace-forward sites. Samples were collected at 13 residential locations. All samples tested negative for *P. ramorum*. This event was the largest trace-forward WSDA has ever participated in.

Additionally, the fall certification survey was conducted at Washington's only regulated interstate shipping nursery in late September. All plant and water samples were negative for *P. ramorum*. For more information contact Scott Brooks, SBrooks@agr.wa.gov.

RESEARCH

Bates, G.; Cohen, G.; Martos, P. and Segarra, I. 2022. Burn severity and community structure affect tanoak and California bay laurel regrowth. California Ecology and Conservation Research. 6(2): <https://doi.org/10.21973/N3C37D>.

Disturbances, both biotic and abiotic, play an integral role in shaping the species composition of ecological communities. Recently, the compounding disturbances of fire and sudden oak death have affected forests in California's Big Sur region. Sudden oak death (SOD), caused by the non-native pathogen *P. ramorum*, has led to large-scale mortality in tanoak (*Notholithocarpus densiflorus*) populations and finds reservoirs for transmission in California bay laurels (*Umbellularia californica*). In this study, we investigated how the post-fire regrowth rates of tanoak and bay laurels in *P. ramorum*-infested forests are affected by individual tree burn severity and surrounding heterospecific community density, as well as how the surrounding tanoak and bay laurels densities affect tanoak regrowth. We measured trunk scorch height and soil ash depth to determine tree burn severity, number, and height of the tallest resprout of focal trees as a proxy for growth rate; total trees in the 10-meter radius as a proxy for density; and the number of tanoaks and bay laurels (key *P. ramorum* hosts) in the 10-meter radius to investigate the effect of host density. We found that a higher scorch height was associated with taller resprouts, and heterospecific density decreased resprout height. Although tanoak regrowth positively correlates with increased burn severity, bay laurels were found to have a faster regrowth rate than tanoaks, indicating that fire is insufficient at decreasing *P. ramorum* transmission throughout the ecosystem and may lead to further bay laurel expansion in SOD-impacted forests. [This research was conducted by undergraduates at the University of California, Landels-Hill Big Creek Reserve.]



Daniels, H.A.; Bulman, L. and LeBoldus, J.M. 2022. Natural and artificial inoculation of radiata pine boles and seedlings with *Phytophthora ramorum*, causal agent of sudden oak death, reveals low host potential. Forest Pathology. e12774. Early view. <https://doi.org/10.1111/efp.12774>.

Radiata pine is an important plantation tree; more than 4 million ha are planted globally, and 90% of planted forests in Aotearoa New Zealand are radiata pine. It is susceptible to several root and foliar diseases caused by *Phytophthora* species, and is potentially susceptible to *Phytophthora ramorum*, the pathogen responsible for sudden oak death in the United States and Europe. A series of experiments were conducted to determine the potential risk of *P. ramorum* infection to radiata pine logs and seedlings in the context of forest harvest and replanting. In a natural inoculation experiment, bolts of radiata pine, Douglas-fir and tanoak were exposed to *P. ramorum* inoculum produced from sporulating tanoak canopies infected with either the NA1 or EU1 lineage of *P. ramorum*. The experiment occurred at four sites, two NA1 and two EU1, across 2 years. Four per cent of radiata pine bolts, 8% of tanoak bolts and 0% Douglas-fir bolts tested positive for *P. ramorum*. Artificial inoculations of bolts of the same species revealed a significant effect of lineage ($p = .0024$), species ($p < .0001$) and their interaction ($p = .0027$) on lesion length. Species was the only parameter that had a significant impact on average lesion length ($p < .0001$) and sporulation ($p = .00144$) from seedlings. No sporangia were observed on radiata pine seedlings ($n = 60$); few were observed on tanoak and Douglas-fir. Although radiata pine can be colonized by *P. ramorum*, without a sporulating host in proximity it does not appear to be at high risk from this pathogen.

Dun, H.F.; Hung, T.H.; Green, S. and MacKay, J.J. 2022. Comparative transcriptomic responses of European and Japanese larches to infection by *Phytophthora ramorum*. BMC Plant Biology. 22: 480. <https://doi.org/10.1186/s12870-022-03806-3>.

Background and objectives. *Phytophthora ramorum* severely affects both European larch (EL) and Japanese larch (JL) trees as indicated by high levels of mortality particularly in the UK. Field observations suggested that EL is less severely affected and so may be less susceptible to *P. ramorum* than JL; however, controlled inoculations have produced inconsistent or non-statistically significant differences. The present study aimed to compare RNA transcript accumulation profiles in EL and JL in response to inoculation with *P. ramorum* to improve our understanding of their defense responses. **Methodology.** RNA-sequencing was carried out on bark tissues following the inoculation with *P. ramorum* of potted saplings in both EL and JL carried out under controlled environment conditions, with sampling at 1, 3, 10, and 25 days post inoculation in infected and control plants. **Results.** All of the inoculated trees rapidly developed lesions but no statistically significant differences were found in lesion lengths between EL and JL. RNA-Sequencing comparing control and inoculate saplings identified key differences in differentially expressed genes (DEGs) between the two larch species. European larch had rapid induction of defense genes within 24 hours of infection followed by sustained expression until 25 days after inoculation. Results in JL were more varied; upregulation was stronger but more transient and represented fewer defense pathways. Gene enrichment analyses highlighted differences in jasmonate signaling and regulation including NPR1 upregulation in EL only, and specific aspects of secondary metabolism. Some DEGs were represented by multiple responsive copies including lipoxygenase, chalcone synthase and nucleotide-binding, leucine-rich-repeat genes. **Conclusion.** The variations between EL and JL in responsive DEGs of interest as



potentially related to differences seen in the field should be considered in the selection of trees for planting and future breeding.

RELATED RESEARCH

Kronmiller, B.A.; Feau, N.; Shen, D.; Tabima, J.F.; Ali, S.S.; Armitage, A.D., ... and Grunwald, N. J. 2022. Comparative genomic analysis of 31 *Phytophthora* genomes reveal genome plasticity and horizontal gene transfer. *Molecular Plant-Microbe Interactions*. Early View. <https://doi.org/10.1094/MPMI-06-22-0133-R>.

Marques, I.G. and Garbelotto, M. 2022. Testing the pathogenicity of three *Phytophthora* species on California hosts commonly used in restoration. *Journal of Plant Pathology*. <https://doi.org/10.1007/s42161-022-01231-x>.

RESOURCES

Recordings of the 2022 California Oak Mortality Task Force meeting held November 8-10th, are now available. Posted on the suddenoakdeath.org and calphytos.org websites, as well as below, are the links to the recordings from each of the sessions. Nov. 8th highlights international updates and research; Nov. 9th provides an update on the current status of *P. ramorum* and sudden oak death; and Nov. 10th explores soilborne *Phytophthoras* in restoration areas and nurseries.

- [Nov 8, 2022 recording](#)
- [Nov 9, 2022 recording](#)
- [Nov 10, 2022 recording](#)

Please provide any feedback, questions, or suggestions for future meetings to Janice Alexander, jalexander@ucanr.edu.

2022. Book of Abstracts. IUFRO Conference Division 7 – Forest Health, Pathology and Entomology, September 6 – 9, 2022, Lisbon, Portugal. <https://www.iufro.org/fileadmin/material/publications/proceedings-archive/70000-all-div7-lisbon22.pdf>

Abstracts from 224 oral presentations and 98 posters represent forest pathology and entomology research from 41 countries and five continents. Findings concerning *Phytophthora* in diverse ecosystems are included as well as abstracts on climate effects on forests, biosurveillance, management, and more.

2022. Book of Abstracts. The 21st annual meeting of the Oomycete Molecular Genetics Network (OMGN). *Phytophthora* Research Centre, Mendel University, Brno, Czech Republic, August 22 – 25, 2022. http://www.phytophthora.org/coajdfadlf/uploads/2019/09/Book_OMGN2022_31Aug2022.pdf

Phytophthora research presented by 89 participants from 16 countries includes cell biology, signaling and metabolism; effectors, virulence, and pathogenicity; host-pathogen interaction and resistance mechanisms; diversity, taxonomy, and population studies; and ecology, metagenomics, and microbial interactions.