

Seventh Sudden Oak Death Science and Management Symposium
Healthy Plants in a World with *Phytophthora*
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Abstracts

Oral Presentation Abstracts..... 3

Poster Abstracts.....50

Oral Presentation Abstracts

(alphabetically by author's last name)

Determining the Minimum Treatment Area and Importance of Soil Moisture for Effective Soil Solarization in Nurseries

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Soil solarization is a low-cost, non-chemical method that can be highly effective in killing soilborne *Phytophthora* species in infested nurseries. This method consists of using a transparent plastic film to trap solar radiant heat. Understanding and implementing the best methods for soil solarization are critical for successful eradication of pathogens. We examined how the size of the solarization treatment area, soil moisture content, and duration of solarization affected the survival of *Phytophthora* inocula buried at 5, 15, and 30 cm.

Research sites were established in Corvallis, OR and at the National Ornamental Research Site at Dominican University of California (NORSUDUC) quarantine facility in San Rafael, CA in the summers of 2017 and 2018. At the California site, we tested survival of *P. ramorum*, and *P. pini*; at the Oregon site, we tested only *P. pini*. Each site contained 16 plots, arranged in a randomized block design with four blocks. Each block included three sizes of solarization treatment areas (0.25, 1.0, and 4.84 m²) and a non-solarized control. Half of the blocks were irrigated before solarization; the other half were not irrigated. Inoculum survival was determined after 2, 4, 6, and 12 weeks.

In 2017, each of the factors (species, depth, irrigation treatment, treatment area, and duration) significantly affected *Phytophthora* survival. Regardless of irrigation treatment, the greatest recovery of inoculum occurred in the non-solarized and 0.25 m² plots, and the lowest recovery occurred in the largest (4.84 m²) plots. At the 30 cm depth, *P. ramorum* was eliminated from both irrigated and non-irrigated treatments by two weeks in the 4.84 m² plots, whereas it persisted in 1 m² plots for up to six weeks. *P. pini* at the same depth in the 4.84 m² plots was eliminated by four weeks of solarization, but it took twelve weeks to kill it in the 1 m² plots. The smallest plots (0.25 m²) used for solarization were ineffective, with inoculum survival no different than in non-solarized soil. Similar trends were observed in 2018 trials. Effects of soil moisture on soil temperature and solarization effectiveness are still being investigated.

The impact of solarization in nurseries and restoration sites could be maximized and the associated costs reduced by optimizing treatment area, soil moisture content and duration of solarization. This research is critical for soil solarization to be an effective management tool in preventing the spread of soilborne *Phytophthora* species.

Early Host Resistance Selection and Development should have been a Primary Management Response to the Sudden Oak Death Epidemic

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In this presentation I will illustrate the theoretical foundations for a proposed drastic change in how we respond to invasive alien forest pathogens, like *Phytophthora ramorum*. This new framework is the result of an in-depth analysis of the reasons why effective management of invasive alien phytophagous insects and phytopathogens (PIPs) in forest environments remains an elusive aspiration (Showalter et al. 2018). A fundamental reason for why we continue failing is that such PIPs encounter evolutionarily naïve host trees in their new environments, which are incapable of mounting adequate resistance responses. However, it is also true that even the most undefended host populations almost always include individuals that are capable of resisting attack. Such resistance need not be absolute (immunity), but sufficient to ensure survival and reproduction of the target host, so that either natural selection can act directionally upon the traits conferring such resistance, or modern approaches can be brought to bear towards tree improvement programs that are increasingly capable of rapidly selecting and augmenting tree defenses. In the latter case, improved trees can then be used for plantings that are capable of withstanding such invasive alien PIPs. Both in-field directional selection and tree-for-planting improvement programs can be accelerated tremendously by using non-destructive resistance screening techniques such as those we have developed for the coast live oak-*P. ramorum* pathosystem. In all cases, however, to be a successful management approach, careful target selection, early implementation and sustained support are fundamental. I will illustrate a simplified proposed framework to guide future responses to invasive alien PIPs like *P. ramorum*.

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Ten new Provisional Species of *Phytophthora* and *Nothophytophthora* from California

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Phytophthora diseases in landscapes have gained prominence during the 21st century, due to an increase in *Phytophthora* surveys and a greater focus on species-level diagnostics. Concurrently, the number of known *Phytophthora* species has increased from about 60 in 1996 to more than 300 today. In addition to entirely novel species being discovered, many of the most common and well-known 20th century species have been revealed to represent species complexes and are rapidly being divided into new taxa. Beyond the increasingly large *Phytophthora*, two *Phytophthora*-like related genera, *Calycofera* and *Nothophytophthora* were described in 2017.

Herein are presented nine novel species of *Phytophthora* and one novel *Nothophytophthora* species recently isolated from California. Each species is provisionally described by demonstrating it to be phylogenetically distinct from all other named species based on analysis of ITS rDNA and COX1 mtDNA sequences, the two barcoding loci used for *Phytophthora* species-level identification. Some species appear to be cryptic species within well-known complexes; these taxa are also found outside of California based on the geographic sources of publicly deposited sequence data. For other species, there is no evidence that they have ever been previously isolated. Whether these new species represent endemic Californian pathogens, long-term residents or recent invaders is unknown.

Two novel species are presented in *Phytophthora* clade 2: *Phytophthora* sp. *aureomontensis* is a member of the *P. citricola* species complex only known from California and Oregon coastal streams. *Phytophthora* taxon eriodictyon is a member of the *P. citrophthora* species complex that appears to be moving worldwide via the nursery trade; this species is known in California only from restoration outplantings. *Phytophthora* sp. *cadmea* is a novel species in clade 7a also baited from restoration areas. *Phytophthora* taxon wysteria, also a member of clade 7 was isolated from a commonly planted ornamental. *Phytophthora* taxon agrifolia represents a novel sub-clade within the vast clade 8. Two novel species are presented in clade 9, one of which, *Phytophthora* taxon xguadalupesoil, appears to be an interspecific hybrid. *Phytophthora* taxon juncus is closely related to the only other member of clade 11, *Phytophthora lilii*, while *Phytophthora* taxon mugwort represents its own subgeneric clade, clade 13. *Nothophytophthora* taxon umbellularia is known only from a single isolate, baited from a North coast creek with a California bay laurel (*Umbellularia californica*) leaf.

Although provisional, naming these taxa and depositing their barcoding sequences into public databases provides vital information to the worldwide *Phytophthora* diagnostics community about the distribution and movement of these potentially pathogenic and invasive organisms.

More systematic work, including morphological characterizations and pathogenicity tests are needed to more fully characterize these provisional species, and live strains will be deposited in culture collections. Nevertheless, because the direct comparison of DNA sequences represents the most tractable and reliable way to compare *Phytophthora* isolates across space and time, this initial step serves to inform the scientific and regulatory communities of the existence of these species.

Sudden Oak Death in the Context of Global Tree Mortality and Regional Efforts to Limit Carbon Emissions

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An emerging body of published research, ongoing field and modeling studies, and disease management experiments are building an understanding of *Phytophthora ramorum* impacts to carbon cycling from stand-to-landscape scales. California has been recognized as a leader in policy and management efforts to limit greenhouse gas emissions. The large economy, annual greenhouse gas emissions, and the nexus of natural resource, economic, and infrastructure challenges are realistic reflections of the complexity and difficulty of enacting change at global scales. Sudden oak death is the most significant source of tree mortality in the coast and Klamath ranges of the state. The scale and severity of mortality associated with the disease is comparable to other large tree mortality events globally; thus, the disease and the collective management response also holds implications for regional, national, or global carbon emissions (Cobb et al. 2017a).

Using a large plot monitoring network and current estimates of host distribution and density, sudden oak death impacts were recently estimated to exceed 50 million killed tanoak and oak trees in California and Oregon as of 2012, likely resulting in emissions exceeding 2.5 Tg of carbon between 1995 and 2012 (Cobb et al. 2019), or about 0.6% and 7.6% of the state total emissions and combined agriculture/forestry emissions in 2016, respectively (Air Resources Board 2018). Although the total trees impacted by the disease is lower than that of the Sierra Nevada bark beetle outbreak (with about 138 million dead trees), the chronic and expanding dynamics of the disease suggest the total could become the greatest biotically-driven emissions in the state. Within disease impacted stands established pathogen populations suppress live carbon biomass accumulation while also increasing emissions from decomposition (Cobb et al. 2013, Cobb and Rizzo 2016). Disease impacts to fuels can lead to heightened carbon release from soils during wildfire, an ecosystem carbon pool that is otherwise often protected from aboveground disturbances (Cobb et al. 2016).

Despite the large scale and amounts of carbon lost due to the disease, a body of stand-scale experiments and recent modeling studies leveraging data on patterns of partial resistance in tanoak suggest a suite of management interventions can be effective in limiting or ameliorating these releases. Mastication and hand-pile treatments have been demonstrated to increase potential for regeneration of less-susceptible species, reduction of ground fuels, and to possibly slow invasion of uninvaded stands (Cobb et al. 2017b). These treatments initially increase soil carbon release from decomposition and may depress atmospheric methane (CH₄) consumption associated with increased soil moisture. It is unclear whether carbon accumulation in live trees, either due to increased growth of remaining canopy trees, or by recruitment of less-susceptible species, will exceed this release rate within a decade of treatment although growth and yield estimates suggest this will eventually occur. Carbon sequestration in uninvaded stands could be further increased and standing pools protected by utilizing patterns of partial resistance in tanoak, which recent work has shown to be present frequently among stands but always at low densities with a random distribution within stands (Cobb et al. 2018). From the perspective of the state's greenhouse gas goals, the extent and severity of sudden oak death's impacts to forests must not be ignored or discounted. Stand scale management is increasingly showing that responses can be effective and a vision – as well as clear plan – for scaling up treatments at the scale of the disease is now needed.

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Approaches to Protect Against Phytophthoras at the Presidio

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The Presidio, a 1,500 acre National Park on a former military post at the foot of the Golden Gate Bridge, is a major outdoor and cultural recreation hub in northwest San Francisco. As part of the Golden Gate National Recreation Area, it is among the most visited urban national parks, but also home to twelve species of rare, threatened or endangered plants, many associated with serpentine soils, as well as habitat for over 300 bird species and other wildlife.

In 2015, the Presidio initiated a *Phytophthora* management program to protect endangered plant species and native habitat. Dieback associated with *Phytophthora pseudocryptogea* on Raven's manzanita (*Arctostaphylos hookerii* ssp. *ravenii*), an endangered species with only one known wild individual, underscored the resources at risk given the threat of human-assisted introductions from plantings for large-scale construction and restoration projects. The program is also informed by the Presidio's native plant nursery program and underlying value of natural resource stewardship.

The *Phytophthora* management program includes mapping *Phytophthora*, and pre-plant *Phytophthora* screening of incoming landscape plants. Best management practices are used for fieldwork to promote sanitation and thereby lower the likelihood of *Phytophthora* introductions on imported soil or on workers' or visitors' shoes, and to educate staff and tourists in the role they can play in reducing the spread of plant pathogens. The program represents a significant effort, with 80% time of an IPM specialist and an intern for at least 3 months in the spring and summer and other costs associated with rejected container plant lots, construction delays, etc.

The evaluation of *Phytophthora* species on purchased, incoming landscape plants and determination of resident *Phytophthoras* in restored areas demonstrates the complexity and difficulty of managing these pathogens. Pre and post restoration sampling on eleven sites indicates that the recovery of *Phytophthora* in some areas is undesirably high. The patterns of species recovery present many questions that propel further adaptive management.

Incidence and Distribution of Resistance in a Coast Live Oak/Sudden Oak Death Pathosystem

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In coastal California, infection by the pathogen *Phytophthora ramorum*, causal agent of sudden oak death, results in extensive mortality of native oak species including coast live oak (*Quercus agrifolia*, CLO). However, apparently resistant CLO have been observed within native populations. In this study, we monitored disease progression from 2010 to 2017 in CLO artificially inoculated with *P. ramorum* and disease incidence in CLO left to become naturally infected in the same stand. After seven years, 61% of artificially inoculated CLO died while 27% appeared to be resistant (i.e. in remission, no longer showing active symptoms of *P. ramorum* infection) (N = 149). In addition, 13% of non-inoculated CLO showed symptoms of natural *P. ramorum* infection, e.g. bleeding exudate (N = 423). Canker length measured approximately one year following inoculation was a significant predictor of CLO resistance and survival ($P < 0.001$). Canker length was also used to examine the distribution of resistant and susceptible CLO across the landscape using inverse distance weighted analysis. This analysis revealed resistant and susceptible CLO are aggregated, suggesting resistance is a heritable trait. A better understanding of the amount and distribution of resistant CLO within native populations can be used to facilitate the restoration of disturbed habitats and identify sources of germplasm for future breeding efforts.

Oregon Sudden Oak Death Management Follow-up: Epidemiology

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Phytophthora ramorum, the oomycete pathogen responsible for Sudden Oak Death (SOD) in California and Oregon forests, requires constant vigilance to detect and manage. Prior to 2011, the focus of Oregon-based management was complete eradication of all disease centers through removal of infected plant material. Despite intense eradication procedures, the disease continued to spread. Current Oregon management focuses on reducing the spread of SOD within Curry County, and preventing spread to neighboring counties.

Previous research published in 2015 focused exclusively on the NA1 lineage and its population genomics. The EU1 lineage was first confirmed in a forested site in 2015, in Curry County, OR. Therefore, there's a need to reassess the effectiveness of management techniques with the discovery of this more virulent lineage. Ongoing research looks at the effectiveness of eradication/suppression efforts, including the newly discovered EU1 strain. Additionally, impacts of natural fire on eradication can be studied through the 2017 Chetco Bar Fire, which swept through portions of the Oregon Quarantine Zone and Generally Infested Area.

In addition to assessing management of SOD, a study of the relation between spatial and genetic distance is nearing completion. Using data collected since 2001, both NA1 and EU1 infections were tracked over time and space. A preliminary computational assessment of subsequent new SOD infections relative to previously eradicated infections revealed candidate samples for sequencing. Whole-genome sequencing of spatially related trees and their neighbors will reveal their level of genetic relatedness.

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Assessing the Incidence and Diversity of *Phytophthora* Species Occurring in Planned Restoration Areas of the Angeles National Forest

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The Angeles National Forest (ANF), located in the greater Los Angeles metropolitan area encompasses approximately 700,000 acres (238,230 ha), comprising a vital biodiversity hot spot. From 2002 to 2008, the ANF was affected by three major fires, the Copper (2002), Ranch (2007) and Sayre (2008). Together, these fires affected approximately 40,000 acres (16,187 ha) of coastal sage scrub, montane chaparral, grassland, riparian corridor, as well as isolated big cone Douglas- fir (*Pseudotsuga macrocarpa*) stands. Droughts and floods in the following years, plus off-road recreational off-highway vehicle use aggravated erosion and altered chaparral vegetation regeneration. As a mitigation effort, restoration attempts in these areas were initiated to plant native nursery stock.

In 2016 - 2017, prompted by concerns that *Phytophthora* species may have been introduced on restoration plantings, *Phytophthora* surveys were conducted in several restoration locations associated with utility project mitigation on ANF lands. The inadvertent outplanting of infested nursery stock is considered one of the main pathways of entry of exotic *Phytophthora* into natural areas. These preliminary surveys detected numerous *Phytophthora* species associated with outplanted native plants and at the source nurseries. The ANF has a Mediterranean climate and averages about 15 – 20 inches (28 to 50 cm) of precipitation per year with long dry periods in late spring into early fall. The ability of *Phytophthora* species to survive and become established under these conditions is not known.

To better understand the *Phytophthora* distribution on arid lands of the ANF, a survey was performed in May 2018 to determine the incidence and distribution of *Phytophthora* pathogens in burned areas of the Copper fire that were prioritized for restoration. Fifty-six soil samples were collected from 14 sites; 13 pre-restoration and one of which had already been planted with container nursery stock. Four *Phytophthora* spp. were detected from 3 sites (*P. cactorum*, *P. gonapodyides*, *P. riparia* and an undescribed *P. lacustris x riparia* hybrid). All the detections were located in or near dry creek beds. *Phytophthora* was not detected in the recently planted area. Species belonging to *Pythium* s.l. were recovered from all 14 sites, which suggests that *Pythium* may be resident to ANF lands. Sampling will be repeated seasonally in all three fires areas to determine what additional factors could be correlated with the incidence of *Phytophthora* pathogens. Further research is on-going to explore the ecological factors affecting the survival and distribution of *Phytophthora* species on arid ecosystems and fire-affected areas of the ANF.

Over Two Decades of Sudden Oak Death in California

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Phytophthora ramorum garnered international attention upon its discovery in the summer of 2000 (Rizzo et al. 2002), but thanks to genetic information collected from around the state, we know the pathogen has been in California since the 1980-1990s (Mascheretti et al. 2008). As the decades pass and the possibility of large-scale eradication passes solidly out of reach, we continue to witness the transformation of our forests. New tree mortality ebbs and flows as pathogen populations contract and expand during years of severe drought followed by seasons with adequate rainfall. Decades later, millions of trees have been lost, and the pathogen continues to spread and kill trees; yet we still have a lot to lose: habitat, carbon storage, natural beauty, as well as other cultural and ecological values.

From the forests of Monterey County along the Central Coast, to Del Norte County in northern California and into southern Oregon, the pathogen, although a clone, behaves quite differently throughout its range. We have observed wildfire interacting with the pathogen to exacerbate fire severity and create dangerous fire suppression conditions and extreme fuel mitigation issues in Monterey County (Metz et al. 2011, Cobb et al. 2016, Lee et al. 2009). In the greater San Francisco Bay Area there is extensive property damage, and park-land degradation. Along the Sonoma and Mendocino County coasts, sudden oak death impacts are combining with those of other non-native forest pathogens to unforeseen eventual effect as dominant tree species are eliminated from coastal vegetation. In the farthest north of the pathogen's range, bay laurel (*Umbellularia californica*) trees rarely harbor the pathogen but for the rest of its range, bay is implicated in driving mortality in almost every study.

Many hope that finding both mating types of *P. ramorum* in Vietnam could yield new insight into resistance mechanisms for our local tree species. Meanwhile, another lineage of *P. ramorum* arrived in the Pacific Northwest instilling fear that hybridization or mutation of an already virulent, generalist pathogen could allow for expansion into new ecosystems.

In California forests, cumulative tree mortality levels are at an unprecedented high, as is the loss of life and property due wildfire. For coastal California forests, sudden oak death further compounds the challenge to sustain trees and plants that are integral to the health and well-being of the humans, plants and animals that dwell with them.

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Accreditation to Improve Restoration Program Shows Promise for Pathogen Prevention

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In 2018, we launched a pilot project, “Accreditation to Improve Restoration and Native Plant Nursery Stock Cleanliness (AIR)” to explore whether an audit-based accreditation program could be used to increase confidence that restoration and native plant nursery stock are not infected with *Phytophthora* species. Due to capacity and cost limitations, we accepted eleven nurseries in the greater San Francisco Bay Area in the initial phase. Each participating nursery completes a self-assessment to confirm that they are producing plants with the practices outlined in the Phytophthoras in Native Habitats Work Group best management practices for restoration nursery stock (BMPs) (see http://www.suddenoakdeath.org/wp-content/uploads/2016/04/Restoration.Nsy_.Guidelines.final_.092216.pdf). These practices require the growers to dedicate a significant amount of time and attention to phytosanitation throughout their operations.

The nursery self-assessment covers all aspects of production divided into twelve categories including layout, water source, growth media (soil), propagation and sanitation. The assessment form is a shared online document that includes both nursery-supplied data and the auditors’ responses and risk ratings as well as test results. After the self-assessment is completed, the audit team visits the facilities to check for BMP compliance and assess risk pathways associated with the nursery’s infrastructure. The auditors also conduct limited testing of nursery stock for the presence of *Phytophthora* using a standardized irrigation leachate baiting method unless equivalent third-party test results are available.

The audit process helps nurseries validate their existing practices and identify areas for improvement. In general, restoration nurseries that adopted the Nursery *Phytophthora* BMPs in 2016 or earlier and had results from internal and/or third-party pathogen testing, showed good BMP compliance. Feedback from periodic testing is critical for identifying and correcting problems before they can spread. Nursery audits have provided insights into both the variety of challenges faced by different nurseries as well as the approaches that can be used to implement the BMPs. Feedback from the audit process have also been used to make AIR program improvements and identify research data gaps. For the program to be more widely adopted, a consistent source of financial support and an organization to act as the auditor need to be identified.

The Development and Application of Dynamic, Geospatial *P. ramorum* Spread Models for Oregon

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Dynamic geospatial simulations are valuable assets for exploring how an invasive pest or pathogen is likely to spread given a range of possible scenarios. In particular, they are powerful for conducting computational experiments to assess how management affects spread, as large-scale management experiments may be impractical or unethical. Further, models can be used to generate no-management “control” comparisons, which do not exist with observed datasets. Geospatial simulations such as these have been developed to examine *Phytophthora ramorum* spread and impacts in California (Meentemeyer et al. 2011, Cunniffe et al. 2016). Yet, models had not been developed for Oregon, where sudden oak death continues to pose a significant economic and environmental threat.

In collaboration with experts from Oregon State University, Oregon Department of Forestry, and the U.S. Forest Service, we have updated these *P. ramorum* models to reflect epidemiological conditions in Oregon. Most notably, evidence suggests that tanoak disproportionately affects disease patterns in Oregon (Hansen et al. 2005), so the model was updated to reflect a single-host tanoak system which accounts for disease-induced mortality. Model development is complicated by the presence of two disease strains (NA1 and EU1) and years of intensive management which can obscure natural spread patterns. By simulating both the disease spread and management simultaneously, we were able to parameterize the model for both strains. Using these derived parameters, we generated a hypothetical no-management scenario for 2001-2017 to evaluate how effective Oregon’s landscape-scale management efforts were at reducing pathogen spread.

Further, to increase the interactivity and usability of this model, we have linked it with a decision-support system called Tangible Landscape (Tonini et al. 2017). This innovative modeling tool allows users to intuitively guide models, regardless of prior experience with code or geospatial software. We present questionnaire results from a modeling workshop with Oregon stakeholders that highlight this tool’s potential to engage stakeholders in sudden oak death management and decision-making.

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Efficacy of Local Eradication Treatments against the Sudden Oak Death Epidemic in Oregon Tanoak Forests

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The sudden oak death pathogen (*Phytophthora ramorum*, SOD) has inadvertently been distributed widely across the United States but is not established in forests outside of California and Oregon. Here, it has triggered widespread concern, and, especially in Oregon, an intensive disease management program. Now we provide the first systematic evaluation of the efficacy of that effort.

In 2001, when *P. ramorum* was first discovered in Oregon, a 23 km² quarantine area was established and attempted eradication was initiated. As SOD continued to spread, the quarantine area was expanded and treatments continued. The optimum treatment calls for early detection, primarily through aerial and stream survey, with follow up ground survey and confirmation of the pathogen. Infected trees plus a surrounding 100 m or 200 m buffer of visibly healthy but susceptible trees are killed. Infected and buffer trees and other host plants are cut. In 2012 the goal of the program was restated from “eradication” to “slow the spread.”

This paper evaluates four measures of the efficacy of SOD local eradication treatments: Inoculum availability; Inoculum from tree species other than tanoak; Disease spread from treated areas; and Cumulative infested area with and without treatment. We conclude that eradication of SOD from infested sites is difficult but not impossible. The disease usually does not persist after cutting infected trees. Spread on the landscape continues because the pathogen may be present on new infections for a year or two before whole tree symptoms are visible. This limits early detection, and coupled with delays in completing eradication treatments, prolongs the chances for long distance aerial dispersal.

Local treatments demonstrably reduce local inoculum levels. The economic and ecological benefits of slowing the spread of SOD, in contrast to eliminating it, require careful cost–benefit analysis if the program is to continue.

Biosecurity and *Phytophthora* Monitoring at the Royal Botanic Garden Edinburgh

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Ex situ conservation—that is, propagating plants outside their native environment to preserve germplasm and reduce pressure on threatened species—is a crucial part of the plant conservation toolbox (Mounce et al. 2017). However, translocating plants for the sake of conservation presents a special challenge: it is impossible to move plants without also moving some number of their microbial associates, some of which may be damaging parasites on new hosts and/or in new environments. *Ex situ* conservation programs have high scientific and conservation value, but require acknowledgement and management of pest/pathogen introduction risks.

These introduction risks have been highlighted recently with the documentation of *Phytophthora* spp. movement in California conservation programs (Rooney-Latham et al. 2018) and in ornamental nurseries in Oregon (Parke et al. 2014), compounded by the heavy ecological toll worldwide of such diseases as ramorum blight and *Phytophthora austrocedri* dieback of junipers.

In response to these challenges, The Royal Botanic Garden Edinburgh (RBGE) has evaluated and revised its biosecurity practice and undertaken a monitoring program to assess its Living Collection and propagation systems for *Phytophthora* spp. as a bellwether for cryptic pathogens.

Here, we discuss RBGE's tiered risk-based approach to biosecurity monitoring and findings from pre-translocation screenings and repeated systematic sampling of planted garden environments and the separate nursery facility. We report the incidence, diversity, and spatial distribution of *Phytophthora* spp. in nursery and long-term planted environments, and discuss their importance for biosecurity practice and allocating monitoring effort.

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Intensification of Sudden Oak Death in Oregon Forests in the Absence of Eradication Treatments

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Sudden oak death, caused by *Phytophthora ramorum*, was first discovered in coastal southwest Oregon forests in July 2001. Since then an interagency team has slowed spread and intensification of the disease through a program of early detection and mandatory local eradication by cutting and burning infected and nearby tanoak (*Notholithocarpus densiflorus*) and other host plants. From 2009 through 2011, funding limitations resulted in no treatment of many infestations near the center of the quarantine area, which led to the 2012 change in the state quarantine regulations that established a Generally Infested Area (GIA) in which eradication was no longer required by law. In the absence of local eradication treatments within the GIA, disease and tanoak mortality increased rapidly.

Beginning in 2012, aerial and ground surveys were curtailed on private land inside the GIA and tanoak mortality was estimated from high-resolution color digital imagery collected in July each year from 2012 through 2018. On ten 1-ha tracking plots, mortality of overstory tanoak increased from <5% to an average of 87% during a four year period. From 2012 through 2017 the infested area (untreated) within the 151 km² GIA increased from 85 ha to more than 1,020 ha. Patterns of disease spread and intensification are discussed.

Dual Transcriptome Analysis Reveals Insights into Innate and Phosphite-Induced Resistance of Tanoak to *Phytophthora ramorum*

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Phosphites have been used in the control of sudden oak death, however, the precise mode of action of these compounds is not fully understood. In order to study the action of phosphites in the context of naturally occurring host resistance, we designed an inoculation experiment on four open-pollinated tanoak families, previously defined as partially resistant. Stems of treatment- individuals were sprayed with phosphite, and 7 days later, distal leaves were inoculated with the sudden oak death pathogen, *Phytophthora ramorum*. Leaves from treated and untreated control plants were harvested for RNA extraction before and 7 days after inoculation, and transcriptomes of both host and pathogen were analyzed. We found that tanoak families differed in the presence of innate resistance and in the response to phosphite treatment. Sets of genes associated with innate resistance and with phosphite-induced resistance showed little overlap among tree families. However, sets of genes associated with innate resistance and with phosphite-induced resistance largely overlapped within a more susceptible but phosphite-treatment responsive tanoak family, supporting the hypothesis that phosphite treatment increases the resistance of susceptible host plants to *Phytophthora* infection. In addition, our dual RNA-Seq enabled us to monitor gene regulation of the pathogen *in planta*. Genes for energy generation such as those in the TCA cycle and genes for amino acid membrane transporters were upregulated, whereas elicitor genes were downregulated when comparing genic expression of *P. ramorum* in tanoak leaves relative to genic expression of *P. ramorum* mycelium in culture. We also found that genes of the pathogen involved in detoxification, such as ATP-binding cassette (ABC) transporters and vitamin B₆ biosynthesis genes, were upregulated in phosphite-treated plants, but not in untreated plants. Upregulation of these genes has been observed for axenic culture of *P. cinnamomi* in the presence of phosphite, indicating these genes responded to the direct toxicity of phosphite. In summary, our dual RNA-Seq supports a dual mode of action of phosphite compounds, including a direct toxic effect on *P. ramorum* and an indirect enhancement of resistance in the tanoak host.

Using Citizen Science and Outreach Education to Reduce the risk of *Phytophthora ramorum* Spread in Oregon Forests

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Sudden oak death (SOD), caused by a non-native pathogen *Phytophthora ramorum* has killed hundreds of thousands of tanoak (*Notholithocarpus densiflorus*) trees in Curry County, Oregon since it was first detected in 2001. With the expansion of the *Phytophthora ramorum* state quarantine in 2015, more landowners in Curry County are now under regulations to slow the spread of sudden oak death. Some landowners are under a state quarantine for the first time and in some cases are unaware of the state sudden oak death quarantine regulations. Since 2015, the European lineage (EU1) of *P. ramorum* has been detected in 19 infested areas within the SOD quarantine boundary. In Europe, the EU1 lineage kills or damages several conifer tree species and is considered more aggressive than the North American lineage (NA1). These two developments have brought to light an increased need for outreach education of local landowners about SOD, state quarantine regulations, and the new EU1 lineage in southwestern Oregon forests. Additionally, the EU1 lineage has become the highest priority for multiple state and federal agencies, which has led to the opportunity for increased monitoring near the EU1 infestations. Oregon's SOD Program would greatly benefit from a coordinated outreach effort to train citizen scientists about the importance of early detection in order to slow the spread of the disease (Meentemeyer et al. 2015). We focused on communities along the leading edge of the disease, and held workshops to teach local residents about disease recognition, early detection methods, and effective treatment options. A citizen science project was piloted and focused on training residents to conduct multiple early detection methods for sudden oak death and to coordinate landscape-level sampling for new SOD infestations. Additionally, focusing on potentially resistant tanoak, we are training residents to identify and report healthy tanoak in infested areas. We will present project design and first year results.

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Common and Uncommon Diseases of Oak, Tanoak and Bay - New Diagnostic Tools Have Led to Important New Discoveries

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Although sudden oak death has been the primary concern for California oak woodlands over the last 20 years, other fungal pathogens of oak (*Quercus* spp.), California bay (*Umbellularia californica*), and tanoak (*Notholithocarpus densiflorus*) also occur in California. Many cosmopolitan Botryosphaeriaceae species with wide host ranges can invade oak and tanoak under stress conditions through wounds, causing perennial cankers in twigs and shoots and large bole cankers. Oak root rot caused by *Armillaria mellea* is widespread in native California soils and infected trees often exhibit cambium death and canopy dieback due to root colonization.

White mycelial fans are often seen under the bark and cambium and the distinctive mushrooms may be present during the fall and winter months on the bases of infected trees. Species of *Ganoderma* can also cause root and butt rots of oak and other hardwoods. The large characteristic conks are generally found at or near the base of the tree and usually indicate advanced wood decay (Swiecki and Bernhardt 2006). Although macromorphological characters of some of these fungal pathogens make generic identification possible in the field, species-level identification for many fungi, including those in the Botryosphaeriaceae usually requires culturing onto media followed by DNA sequence analysis.

Our increased awareness of other pathogens associated with hosts of *Phytophthora ramorum* has coincided with the increased use of DNA-based techniques for fungal species identification.

More than 2,000 new fungal species were described in 2017, and it is estimated that there are millions yet to be discovered (Niskanen et al. 2018). In 2018, a new *Tubakia* species (*Tubakia californica*) causing a foliar disease and twig dieback of Fagaceae species was described in California (Braun et al. 2018). Leaves of infected trees do not undergo typical defoliation in the fall. Instead, they remain attached, allowing the fungus to overwinter and release inoculum in close proximity to the new season's spring growth. Confirmed hosts of *T. californica* include California black oak (*Quercus kelloggii*), interior live oak (*Q. wislizeni*), coast live oak (*Q. agrifolia*), chinquapin (*Chrysolepis chrysophylla*), and tanoak. In 2010, a new leafspot disease of bay resembling Ramorum blight was documented in a Sonoma County area known to be infested with *P. ramorum*. Subtle differences in symptomology between this disease and those caused by *P. ramorum* led the collector to send the sample to the California Department of Food and Agriculture (CDFA) for identification. Culturing and PCR analysis revealed it to be a novel species of *Cylindrocladium* that has yet to be officially described. New DNA-based diagnostic tools have also detected the presence of many more Botryosphaeriaceae canker pathogens than previously known from oak, tanoak, and bay (Lynch and Eskalen 2014). *Dothiorella iberica*, *Botryosphaeria dothidea*, and multiple species of *Diplodia* and

Neofusicoccum have all been confirmed on these hosts. Nearly all these species occur on agricultural and other hardwood hosts and cross infection is likely occurring. As the Plant Pest Diagnostics Lab continues to receive more samples, we are placing greater emphasis on using molecular, sequence-based diagnostic approaches to detect existing and new pathogens. These techniques have not only improved the accuracy and reliability of the Plant Pest Diagnostics Lab's determinations but have also increased our knowledge of the diversity of fungal pathogens in California.

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Comparative Epidemiology of EU1 and NA1 Lineages of *Phytophthora ramorum* in Southwestern Oregon Tanoak forests

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Phytophthora ramorum, cause of Sudden Oak Death (SOD), is an invasive pathogen that infects over 100 species of plants and has been introduced multiple times into the coastal forests of southern Oregon and northern California. In southwestern Oregon forests, tanoak (*Notholithocarpus densiflorus*) is the most susceptible species developing lethal stem cankers and sporulating from infected leaves and branches. The NA1 lineage was first reported in Oregon in the early 2000s and in 2015 the EU1 lineage was discovered infecting tanoak in the South Fork Pistol River drainage in Curry Co., Oregon. Using an approach developed by Garbelotto et al. (2017) sporulation of each lineage was compared at six sites (3 NA1; 3 EU1). Sporulation, temperature, and relative humidity were quantified for 5, 2-week intervals in winter 2017/2018 and 2018/2019. In addition, infection frequency of tanoak, Douglas-fir (*Pseudotsuga menziesii*), western hemlock (*Tsuga heterophylla*), western larch (*Larix occidentalis*), and sitka spruce (*Picea sitchensis*) seedlings at the sites was also compared. Preliminary analysis indicates greater sporulation at EU1 sites compared to NA1; however, this did not correspond to increased infection of tanoak seedlings at EU1 versus NA1 sites. In contrast, there were differences in the infection frequency of Douglas-fir (EU1 = 37%; NA1 = 10%), western hemlock (EU1 = 10%; NA1 = 0%); sitka spruce (EU1 = 55%; NA1 = 0%); and larch (EU1 = 90%; NA1 = 13%).

Differences in the infection rate of conifer seedlings at EU1 compared to NA1 sites and the implication for the management of SOD will be discussed.

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***Phytophthora* Species Associated with Decline and Mortality of Native Vegetation in California Wildlands**

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Before *Phytophthora ramorum* was identified as the causal agent of sudden oak death in 2000, *P. lateralis*, cause of Port-Orford-Cedar root disease, was the only introduced *Phytophthora* that had been associated with widespread plant decline and mortality in California wildlands. The soil-borne *P. lateralis* is closely associated with riparian or high-rainfall sites with high soil moisture. In 2003, the well-known root pathogen *P. cinnamomi* was found to be causing extensive mortality of manzanita (*Arctostaphylos myrtifolia*, *A. vicida*) in dry upland habitats of the lower Sierra Nevada foothills. This find expanded the search image for *Phytophthora* root diseases in California wildlands. Subsequent investigations have associated *P. cinnamomi* with decline and mortality of native trees and woody shrubs in a variety of other California plant communities across a range of climate zones and soil types. As symptomatic native vegetation in additional sites have been assayed for the presence of *Phytophthora*, other soil-borne *Phytophthora* species have been associated with decline and /or mortality of native species in a variety of habitats. *P. cactorum*, *P. cambivora*, *P. crassamura*, *P. cryptogea*, *P. pseudocryptogea*, *P. pseudotsugae*, and others have been associated with symptomatic native hosts that include conifers, hardwood trees, and woody to nonwoody shrubs and perennials. Some non-*Phytophthora* oomycetes may also be involved in observed declines (e.g., *Elongisporangium* (= *Pythium*) *undulatum* and *Phytophythium* spp.). Establishing a clear connection between pathogen presence and plant symptoms is difficult. Baiting of root/soil samples has been a reliable method for detecting these soil-borne pathogens, but detection efficiency can be low and can vary seasonally. Direct isolation from affected plant tissues often yields false-negative results. Although some highly susceptible hosts die rapidly when infected, other hosts appear to have long latent periods followed by progressive decline.

Dates of pathogen introduction are generally unknown, which complicates the interpretation of symptom progress and the roles of other stressors or secondary agents that may be present. Human activities appear to be associated with introductions of these pathogens to virtually all affected sites, and in some cases, *Phytophthora* species have likely been directly introduced via infected stock used in habitat restoration or forestry activities. Management options for affected stands are few; steps to prevent further spread

are the only options in many sites. The examples discussed here illustrate that *Phytophthora* and other oomycete pathogens pose increasing threats to California forest health. Increased efforts are needed to improve detection, impact assessment, and management of these pathogens.

Status of the *Phytophthora ramorum* Epidemic across Forests of the East Bay Regional Park District, San Francisco Bay Area, California

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The East Bay Regional Park District, the largest urban park network in the United States, includes extensive coast live oak (*Quercus agrifolia*)-dominated forests at the urban-wildland interface. Parks that encompass chaparral, grasslands, riparian habitats, and hardwood and conifer forests are adjacent to one of the most heavily-populated urban regions in the country. From 2008 to 2011, we placed 535 randomly assigned, 10 m radius fixed plots in coast live oak- bay laurel (*Umbellularia californica*) stands in each of five parks to establish baseline disease conditions. The random design permits extrapolation to landscape scales. Baseline data included diameter at breast height (DBH) for all woody stems >2.5-cm, disease status of coast live oaks, and woody plant regeneration. Plots were re-assessed between 2015 and 2018 to quantify change and to develop projections for future change.

All parks exhibited increases in infection and mortality levels, with annual infection rates as high as 7.7%. Infections increased markedly following the cessation of the 2011-2015 drought. Despite general similarities in species composition, 2011 infection levels varied from 6.3% (Anthony Chabot) to 14.4% (Wildcat Canyon) and mortality varied from 4.1% (Wildcat Canyon) to 8.7% (Redwood Park). The 2015-2018 evaluations found infection levels between 8.7% (Anthony Chabot) and 27.7% (Wildcat Canyon) and mortality levels from 8.7% (Anthony Chabot) to 29.9% (Wildcat Canyon). Within-park variation in disease and mortality may reflect stand level differences in mean coast live oak DBH, but land-use history also probably affects disease levels. Larger coast live oaks show much higher levels of infection and mortality than the more abundant smaller size classes. The disproportionate loss of the largest mast-bearing trees in these forests will affect wildlife in ways we yet do not understand. In addition, the increase in fuels in these evergreen forests increases the risks of catastrophic wildfire in stands that lie to the east of large population centers.

We also conducted surveys of three more inland parks; Diablo Foothills and Pleasanton Ridge Regional Parks and Las Trampas Regional Wilderness. Diablo Foothills was assessed using randomly placed plots. Despite having much less coast live oak than blue oak (*Q. douglasii*, not a known host), 34% of the coast live oaks (N = 259) in Diablo Foothills were symptomatic in 2016. The other two parks were surveyed, but not randomly, for presence of symptomatic coast live oaks in 2018. In Las Trampas, 30.6% of coast live oaks (N = 98) were symptomatic, with 10% dead. Pleasanton Ridge showed

10% symptomatic (N = 211), with less than 1% dead. The continuing epidemic is leading to permanent changes in landscape composition and environmental services, which will require attention to management of these forests adjacent to large population centers.

Slowing the Spread of Sudden Oak Death in Oregon Forests, 2001-2018

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Sudden Oak Death (SOD), caused by *Phytophthora ramorum*, is lethal to tanoak (*Notholithocarpus densiflorus*) and threatens this species throughout its range in Oregon. In July 2001, the disease was first discovered in coastal southwest Oregon forests. Since 2001, an interagency team has been attempting to eradicate and slow the spread of disease through a program of early detection, survey and monitoring, and destruction of infected and nearby host plants. Eradication treatments, totaling approximately 2,550 ha (6,300 ac), eliminated disease from most infested sites, but the disease continued to spread slowly, mostly in a northward direction. From the initial infestations of 2001, the disease has been detected a maximum distance of 30 km (18.5 mi) to the north, 12 km (7.6 mi) to the northeast along the Chetco River, and 15 km (9.3 mi) to the southeast along the Winchuck River.

In early 2015, the EU1 clonal lineage of *P. ramorum* was detected on a single tanoak tree located approximately one mile north of a small private nursery (now closed) near the Pistol River. Genotype comparison of the tanoak and nursery isolates suggests the nursery as the probable source for the forest infestation. This is the first report of the EU1 lineage in US forests. EU1 infested trees have continued to be detected within a small geographic area just north of Pistol River resulting in 190 ha (470 ac) of eradication treatments from 2015 to the end of 2018.

In 2017, an Oregon SOD Task Force convened local, state and federal governments and agencies, local tribes, industry associations, and local residents and environmental groups. The mission of the Task Force was to develop a collaborative-based strategic action plan, including securement of additional resources to contain the NA1 pathogen of *Phytophthora ramorum* and eradicate the EU1 pathogen of *Phytophthora ramorum* in Curry County, Oregon using the best available science.

***Phytophthora* species can be Reliably Detected by Dogs both from Infested Substrates and Infected Plants**

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In recent years, reports of *Phytophthora* detections have increased from plant production facilities supplying plant stock for restoration projects (Garbelotto et al. 2018). When introduced into new natural habitats through infected plant stock, the potential for *Phytophthora* infection and spread is high. Monitoring of nursery stock is key to reducing new introductions into wildlands, however, sampling in nurseries is currently considered too expensive and complex to be performed on a large scale.

This study was undertaken to determine if it would be possible to train ecological scent detection dogs to discern *Phytophthora species* and discriminate *Phytophthora* odors from other scents in leaves and soil of infected plants. The U.C. Berkeley Forest Pathology and Mycology Lab teamed with H. T. Harvey & Associates to develop a *Phytophthora* detection dog pilot study (Swiecki et al. 2018), starting with a single dog.

The training has occurred in phases, first to expose the dog to recognize *Phytophthora* odor in a range of media. Four species of *Phytophthora* - *P. ramorum*, *P. cinnamomi*, *P. nemorosa* and *P. cactorum* – were grown in four different media – soil-water solution, soil-water-pea broth solution, local soil collected under oak trees, and commercial potting soil. The dog had a 100% detection level in blind testing consisting of 10 trials each.

Phase two of the training employed infected *Rhododendron* plants for the scent trials. *P. ramorum* and *P. nemorosa* were inoculated on leaves, while *P. cinnamomi* and *P. cactorum* were soil inoculated. The dog again had a 100% detection success level in blind testing.

We are currently running trials in phase three, i.e. discrimination of *Phytophthora* from co-occurring *Pythium* isolates, to ensure that the detection is genus specific. In addition, we are testing the dog's ability to correctly identify *Phytophthora* infection in plant species other than *Rhododendron* spp.

Results from the study so far suggest that ecological scent detection dogs may offer an innovative and reliable method to survey for *Phytophthora* in a variety of settings. Dogs could offer a rapid way to reliably detect the pathogen in a variety of controlled environments, such as nurseries; to prescreen plants before they are installed at habitat restoration sites; and possibly to identify infected naturally occurring plants and soil in the field.

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Soilborne *Phytophthora* spp. at Restoration Sites in the Midpeninsula Regional Open Space District

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The inadvertent spread of *Phytophthora* species from nurseries into native ecosystems has increased interest in assessing *Phytophthora* diversity in native plant communities. Of major concern is the inadvertent movement of *Phytophthora* spp. from native plant nurseries into vulnerable habitats during restoration outplantings. Root-infecting *Phytophthora* spp. are abundant within plant nurseries; their introduction can result in failed plantings, reduced natural regeneration, and further spread of *Phytophthora* into surrounding habitat. To assess this risk we surveyed restoration sites within the Midpeninsula Regional Open Space District (MROSD) to determine the presence and distribution of *Phytophthora* pathogens.

In December 2017 we collected soil from the base of symptomatic plants at 20 planted-restoration sites, 7 planned-restoration sites, and 18 non-planted, minimally disturbed areas adjacent to the restoration projects. Soil baits yielded *Phytophthora* species from 10 planted-restoration sites, 2 planned-restoration sites, and 8 non-planted, minimally disturbed sites. Species of concern include *P. ramorum*, *P. cinnamomi*, *P. cambivora* and *P. cactorum*, all of which are associated with plant decline in native plant communities.

To identify any additional oomycete species that might be present, we extracted DNA from 10 g of each soil sample. The ITS1 region was amplified and sequenced with the high-throughput Illumina MiSeq platform. *Phytophthora* was equally prevalent in planted and non-planted areas, however many species were only found in areas in which nursery plants were introduced. This method also detected numerous species not recovered by baiting, including *P. quercina* and *P. tentaculata*.

Phytophthora spp. are widespread within MROSD preserves, although some preserves had noticeably greater species diversity and detection frequency. Given the complex history of disturbance at restoration sites we cannot always conclusively determine which *Phytophthora* spp. were introduced via nursery-grown plants. Nevertheless, future management of MROSD preserves and restoration projects should utilize best management practices to limit the spread of *Phytophthora* to surrounding environs.

A High Throughput DNA Fingerprinting Tool for Biosurveillance of the Sudden Oak Death Pathogen *Phytophthora ramorum*

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Phytophthora ramorum has emerged repeatedly as four distinct clonal lineages in North America (lineages NA1, NA2, and EU1) and Europe (EU1 and EU2). Long-distance migration of *P. ramorum* is known to have occurred via the nursery trade. While most populations sampled in North American forests belong to the NA1 clonal lineage, nurseries have been shown to be infested with three lineages NA1, NA2 and EU1. EU1 and NA2 populations were discovered in environments around nurseries suggesting that nursery infestations could spread in the forest. It is therefore important to monitor populations for clonal lineages and screen for emergence of potential new lineages. To achieve this goal, we are developing a high throughput genomic tool that uses targeted sequencing to accurately identify species and lineage from minute amounts of pathogen material within a 24-hour time frame.

Targeted sequencing of a defined subset of the genome (<5Mb) allows PCR based enrichment of select genomic regions. This technique is powerful for environmental and outbreak samples given its robustness and speed. We selected our target genome regions in a hierarchical fashion using published gene sequences and unique markers generated by genome comparison (Feau and others 2018). Sequencing data from outbreak and survey samples can be used to accurately identify the pathogen, its lineage, and potential sources of introduction using primer panels that target unique regions.

We have developed two detection panels comprising 114 amplicons that can generate genome sequences polymorphic among *Phytophthora* species (panel I) or between *P. ramorum* lineages (panel II). We tested these panels on 28 samples and generated over 500 single nucleotide polymorphisms. We used variant calling, principal component analysis and phylogenetic assignment to accurately assign each sample to its phylogenetic clade and *P. ramorum* samples to the right lineage. This approach is scalable since each panel can be augmented as needed, and high-throughput as 384 samples can be pooled in a single reaction. The assay is suitable for *P. ramorum* outbreaks to facilitate an understanding of its spread and to enable early detection and control.

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Understanding Metabarcoding Benefits and Limitations for Analysis of *Phytophthora* Communities

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The metabarcoding approach has revolutionized the study of microbial ecology with its ability to detect microbial DNA at an unprecedented depth and coverage. This method exploits high-throughput sequencing and DNA barcoding for identification of microbial species, including novel and uncultivable microbes. The metabarcoding approach is gaining more interest in the *Phytophthora* scientific community for monitoring the existence and spread of *Phytophthora* species in diverse habitats.

With several case studies from our research in California and Oregon, we will demonstrate benefits of metabarcoding for *Phytophthora* exploration. We have employed this approach to study *Phytophthora* diversity in soils from restoration sites, commercial tree seedling nurseries, and organic vegetable farms, and from nursery irrigation water and streams. We investigated some of the operational biases associated with ITS1-amplicon metabarcoding studies using synthetic mock communities and determined the limit of detection for *Phytophthora ramorum* DNA. In some studies, we compared the metabarcoding approach with a culture-based approach (baiting) for detecting *Phytophthora* species.

We will also present limitations of the metabarcoding approach and highlight challenges we encountered. These include the existence of unresolvable taxonomic groups due to relatively short Illumina sequence lengths, detection of unculturable species, interference of cell-free (relic or environmental) DNA, PCR primer bias resulting in amplification of only a sub-population with matching priming sites, determination of the true biological threshold versus arbitrary cutoffs, and false positives due to barcode-index switching.

Understanding and mitigating metabarcoding limitations is crucial for achieving better resolution and accurate determination of the diversity of *Phytophthora* species. Despite the challenges, the metabarcoding approach continues to be a promising tool for studying *Phytophthora* ecology.

Fire and Sudden Oak Death's Effect on Species Prevalence in Big Sur, California

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Sudden Oak Death (caused by *Phytophthora ramorum*) has been present in the Big Sur region since the mid-1990s (or earlier) and is the primary agent of mortality in tanoaks (*Notholithocarpus densiflorus*) there. *P. ramorum* also causes significant mortality in coast live oak (*Quercus agrifolia*) and Shreve oak (*Quercus parvula* var. *shrevei*) as well as ramorum blight in other species including California bay laurel (*Umbellularia californica*). A body of work has shown this changes forest composition and species abundance in Big Sur. (Metz et al. 2011).

A plot network consisting of 280 plots was established in 2006 and 2007 to study the epidemiology and impacts of *P. ramorum* in Big Sur. The plots were established in forests dominated either by coast redwood (*Sequoia sempervirens*) or by mixed-evergreen species (Metz et al. 2011). The purpose of the plot network has shifted focus to include the interaction of *P. ramorum* and fire following the 2008 Basin Complex Fires, in which 97 plots burned; and the 2016 Soberanes Fire, in which 113 plots burned.

Previous work has shown that there is increased coast redwood mortality under certain conditions of disease and fire (Metz et al. 2013) and that the resprouting patterns of tanoaks and coast redwood following fire are altered by the presence of *P. ramorum* (Simler et al. 2018). However, the recovery of species following fire and the role of *P. ramorum* in changing the composition of the plant community is unknown. This analysis uses repeated plot surveys of tree diameter, species composition, and ground fuels (Browns transect fuel measurements), performed between 2006 and 2018, to improve understanding of these interactions.

This talk will explore the recovery of a few key species following fire in plots with or without evidence of *P. ramorum* invasion prior to the 2008 Basin Complex fire. We performed previous analysis on the prevalence of several common species looking at presence or absence of *P. ramorum* and fire return interval. We found a significant difference in the prevalence of California-lilac species (*Ceanothus* spp.), a known soil nitrogen fixing plant, between plots with medium or long fire return intervals where *P. ramorum* tested positive. We expect to see decreased post-fire abundance of tanoak and oak species on plots invaded by *P. ramorum* prior to burning, and that plots on which *P. ramorum* has never been isolated will have greater post-fire abundance of those species. The decrease should be independent of the time since the burn, indicating a possible change in the composition of the plant community when compared with uninfected and unburned plots. These changes should be driven by significantly higher pre-fire fuels accumulations documented at plot establishment and in 2012 and 2013 plot surveys.

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Selective Thinning of California Bay Laurel is a Cost-Effective way to Control *Phytophthora ramorum* in Mixed-Oak Woodlands

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It has been long determined that *Umbellularia californica* (California bay laurel) is the key transmissible host for the sudden oak death pathogen (SOD, *Phytophthora ramorum*) in mixed- oak woodlands, however the parameters of bay to oak disease transmission have not been fully clarified (Garbelotto et al. 2003). Here, we concisely present results of three studies: one clarifying the parameters of bay to oak transmission, and two testing whether two cost-effective approaches involving selective removal of a limited number of California bay laurel trees may reduce disease incidence in naturally infested oak stands.

Study 1 consisted of a multi-year survey of approximately 900 bay laurels and two thousand oaks (mostly *Quercus agrifolia*, coast live oak) across 63 transects in the San Francisco Public Utilities Commission (SFPUC) mixed-oak woodlands in San Mateo County. Results identified an inverse relationship between bay to oak distance and oak infection, with infection levels approaching zero as distance between bays and oaks approaches 20 m. Oak size (stem diameter), was positively correlated with likelihood of SOD infection. Study 1 also identified that bay infection levels dropped dramatically during dry years.

Study 2 (Garbelotto et al. 2017) consisted of a stand manipulation trial in which the frequency of Inoculum Pressure Events (IPE) above the threshold levels necessary to infect oaks was monitored every 3 weeks for 7 years in 64 “treatment” and in 64 “control” plots located in the Soquel Demonstration Forest (Santa Cruz County). After 2 years, all bay laurels were removed from “treatment” plots, generating bay-free buffer zones around plots of 10 and 20 m. Results showed that inoculum pressure was strongly affected by rainfall and by bay absence/presence.

IPE frequency was reduced to zero during drought years, while in wet years, IPE frequency was significantly lower in treatment than in control plots, with a stronger effect in plots with a 20 m bay-free buffer around them. Results thus provided additional experimental evidence that selectively removing bays 10 and 20 m around oaks reduces the likelihood of oak infection.

Study 3 was performed in 4 “treatment” and 4 “control” plots in SFPUC lands between 2014 and 2015, as follows. Eight plots with low bay bay disease incidence at the end of a 4-year long drought were identified. In each plot, SOD disease incidence was recorded on 25 bay laurels. The 2014 results identified all bays still carrying SOD infection during a drought, and in 2015 these bays (5 to 8 per plot) were herbicide-killed in the four

treatment plots. In 2016, despite extremely high rainfall, disease incidence was significantly lower in treatment than in control plots, and the same result was obtained in 2017. Conversely, in 2018, a dry year, disease incidence dropped to very low levels both in treatment and control plots. These results indicate that selectively removing the small numbers of bay laurels that are infected by *P. ramorum* after a prolonged drought effectively reduces SOD disease incidence. The selection of bays to be removed can be either driven by their proximity to oaks or by their infection status at the end of a drought. This finding thus provides a cost-effective way to manage SOD in mixed-oak woodlands.

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Wildfire Limits the Occurrence, Frequency, and Impacts of *Phytophthora ramorum* in the Coastal Forests of Big Sur, CA

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Ecological disturbances have clear potential to shape the dynamics of native and introduced plant diseases, via their impacts on the spatial pattern of hosts, host composition, pathogen survival, and microclimatic conditions. Yet, studies examining potential interactions between disease and disturbance are rare, or primarily focus on pathogen occurrence, rather than the additional processes of spread, infection, and host mortality that determine disease impacts. Given that anthropogenic activities have both altered disturbance regimes across the western United States and introduced ecologically-damaging, non-native plant pathogens, understanding how disease dynamics may interact with or be determined by historical and changing disturbance regimes may be of significant conservation and management importance.

The emerging infectious disease sudden oak death (SOD) impacts fire-prone coastal forests in California and Oregon, and previous studies suggest that historical and recent fire history may influence the occurrence of SOD's causal agent, *Phytophthora ramorum* (Moritz and Odion 2005, Beh et al. 2012). In this study, we leveraged a ten-year forest monitoring dataset tracking the impacts of *P. ramorum* across the Big Sur region to explore the mechanisms underlying the relationship between fire and disease. We analyzed how both long-term fire history and recent wildfires influence pathogen presence, but also other metrics of disease, including infestation intensity, re-invasion, and severity of SOD host mortality.

We found that areas that burned more frequently over the last sixty-five years were less likely to contain California bay laurel (*Umbellularia californica*) trees and had reduced SOD host basal area. In turn, more frequently burned plots were less likely to contain *P. ramorum*, had lower rates of host infection, and exhibited decreased rates of host stem mortality. Immediately following the 2008 Basin Complex fire in this region, previous research recorded a reduction in

P. ramorum occurrence in burned areas, with the pathogen primarily persisting in surviving, intact California bay laurel canopies (Beh et al. 2012). Up to 7 years following fire, we find no evidence that regenerating host vegetation plays an epidemiologically significant role and find that infestation intensity is primarily determined by this legacy of surviving hosts. Further, infection by *P. ramorum* does not appear to strongly determine host mortality in these recently-burned areas, suggesting that wildfire may reduce *P. ramorum* propagule pressure or alter microclimates to reduce SOD severity. Overall, these results suggest that severe wildfire reduces not only *P. ramorum* occurrence, but

also its spread, infestation intensity, and mortality impacts, which could have significant implications for predictions of future SOD dynamics under climate change and increasing wildfire ignitions from human activities in this region.

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Exotic *Phytophthora* species are being Systematically Introduced in California Wildlands during Restoration Projects

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This study describes the identification of several *Phytophthora* species previously found in San Francisco Bay Area nurseries (Sims et al. 2018a) from multiple sites at the urban wildland interface within the greater San Francisco Bay Area. Isolation success was highest from the three plant species: *Diplacus aurantiacus* (sticky monkey-flower), *Ceanothus thyrsiflorus* (blueblossum), and *Frangula californica* (California coffeeberry), growing in restoration sites and in adjacent disturbed sites. Isolation success was zero in control undisturbed “natural” areas adjacent to infested sites. In order to confirm plant production facilities were the source of the *Phytophthora* strains isolated from restoration sites, genetic and phenotypic analyses were performed on *Phytophthora crassamura*, one of the most common species identified during the course of this and other studies. Results indicated that field isolates were genetically identical to those found in plant production nurseries. Resistance to fungicides such as phosphites and mefenoxam was identified in a select number of isolates found both in plant production facilities and wildland sites, which further corroborates a “nursery” origin for the wildland infestations (Sims et al. 2018b). Spatial landscape-level analysis identified patterns of *Phytophthora* spread consistent with an outward expansion from sites that were planted and with topography, although the presence of some species was not associated with water accumulation patterns. *Phytophthora* species assemblages were site-specific and possibly related to site type, nursery where the plants were grown, and time since planting. To our knowledge, this is one of the first studies providing robust evidence that exotic *Phytophthora* species are being systematically introduced through the use of infected plants in restoration projects.

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Bark Scribing as a Treatment for Sudden Oak Death: A Case Study in Why Controls Matter

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Over the past two decades, many treatment methodologies have been proposed to therapeutically treat oaks infected with *Phytophthora ramorum*, causal agent of sudden oak death. Because of the coastal distribution of *P. ramorum*, one of the species at greatest mortality risk is coast live oak, *Quercus agrifolia*. Bark scribing, a treatment technique listed by the University of California Integrated Pest Management program to treat *Phytophthora* infected citrus trees, seemed to show promise, especially as it had a treatment history going back nearly 100 years. We therefore endeavored to test the technique on *Q. agrifolia*.

Detecting lesion size in the bark of infected trees is a challenge without cutting into the bark. An attempt at using thermography to non-invasively detect lesion size in naturally infected oaks failed. Another approach is to introduce live inoculum at known rates into the bark of healthy trees. However, mature trees would be required for this study because young trees differ in their infection response. Finding enough uninfected mature trees to do the work took time, as it is somewhat difficult to find property owners willing to potentially sacrifice enough healthy coast live oaks to be statistically significant. In the interim, uncontrolled bark scribing pilot studies using over 200 naturally infected trees suggested that treated oaks had a better than 80% survival rate in the field.

Controlled, replicated studies done on branches of mature oaks show that the situation is much more complicated than expected. Of the approximately sixty trees used in the study, about one third resisted the pathogen so effectively that no growth occurred in either the treatment inoculations, the control inoculations, or both, and in most of these cases no living isolate of the pathogen could be recovered (though residual pathogen DNA could be detected via PCR in many of these lesions). Another sixth or so of the trees were killed by the inoculation, and therefore could not be used for this study. The remaining half of the oaks showed no significant difference between treatments and controls at the 95% confidence level.

Our interpretation of the results is that oaks are surprisingly good at killing *P. ramorum*, even if the trees do not always survive infection. Our findings have been corroborated by other researchers, using other field techniques. Thus, when practitioners utilize tools such as bark scribing to treat infections, results cannot be reliably interpreted from the survival rates of treated trees alone. Furthermore, our results cast doubt upon the purported efficacy of bark scribing as a treatment technique, even in such “proven” systems as citrus (Grafton-Cardwell et al. 2008). It turns out that this technique does not have adequately controlled research studies to back up its purported efficacy in citrus systems.

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Evaluating Threats Posed by Exotic *Phytophthora* species to Sensitive Plant Communities in the Santa Clara Natural Community Conservation Plan Area

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Root rots caused by exotic *Phytophthora* species have been associated with dying and declining vegetation in a number of native plant communities in the Bay Area and elsewhere in northern California. This project focused on detecting *Phytophthora* species that are currently affecting or have the potential to seriously affect populations of covered plants in the Santa Clara Natural Community Conservation Plan (NCCP) area. A key component of the NCCP was the creation of a 19,000 ha reserve network within the plan area that was intended to safeguard protected and conserved species and habitats for the length of the plan (50 years). We used a GIS-based analysis to determine where at-risk priority habitat types might be exposed to contamination from potential *Phytophthora* sources within the NCCP reserve system and conducted targeted sampling to detect *Phytophthora* species. High-priority vegetation included rare and threatened species, as well as vegetation complexes that were poorly represented in the plan area. We collected 189 root/soil samples from reserve system areas with high-priority vegetation types; 68 samples were collected from the three existing populations of the endangered Coyote ceanothus (*Ceanothus ferrisiae*). One of these populations is threatened by an extensive but still localized, multispecies *Phytophthora* infestation that was likely initiated by a restoration planting of infected Coyote ceanothus nursery stock.

Phytophthora species were detected in 67% of 21 water samples collected across all sampled locations. These included spring-fed ponds where contamination may have been introduced via grazing livestock. Forty-four root/soil samples were collected from sites that are periodically flooded, and 124 root/soil samples were from uplands or flats and lowlands not subject to inundation. *Phytophthora* species were recovered from 59% of the periodically flooded sites, and 9% of samples of natural vegetation from drier upland and flat/lowland sites. In all, 20 *Phytophthora* taxa were recovered, including several undescribed species.

Our baseline sampling indicated that *Phytophthora* infestations were generally uncommon in and near reserve system lands. Most detected infestations were associated with common *Phytophthora* sources such as plantings of nursery stock, previous agricultural areas, and contaminated watercourses. Spread from sources was associated with roads, trails, development and grading activities, and livestock grazing. Management of the reserve system to minimize threats posed by *Phytophthora* should prioritize preventing introduction of additional *Phytophthora* species into habitat areas and preventing spread from existing infestations into additional areas.

Long-term Performance of Sudden Oak Death Management Treatments in Northern California Locations

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Sudden oak death (SOD), caused by *Phytophthora ramorum*, was first diagnosed as the cause of a lethal canker disease of coast live oak (*Quercus agrifolia*), California black oak (*Q. kelloggii*), and tanoak (*Notholithocarpus densiflorus*) in 2000. Between 2005 and 2009, we initiated a number of studies to test strategies for reducing SOD impacts in stands of tanoak and susceptible oaks. In oak forests, California bay (*Umbellularia californica*) is the primary source of *P. ramorum* inoculum that infects oaks. We evaluated the effectiveness of removing California bay, either on an area-wide basis or locally around individual oaks on the development and progress of SOD in coast live oak, Shreve oak (*Q. parvula* var. *shrevei*), and canyon live oak (*Q. chrysolepis*). Since these plots were initiated in 2008/2009, California bay removal treatments around susceptible oaks has proved to be very effective in preventing new infections in comparison to matched untreated controls.

Although the presence of California bay enhances disease development in tanoak stands, the development of *P. ramorum* inoculum on tanoak twigs and leaves requires different strategies for managing SOD in tanoak stands. The systemic chemical, potassium phosphite has been identified as a possible chemical treatment for control of SOD in susceptible oaks and tanoaks.

Starting in 2005, we initiated a series of studies to determine if trunk spray applications of this chemical could prevent infection or suppress SOD development to a practical degree in tanoak stands. Stands selected for treatment were free of SOD but close to areas where *P. ramorum* was present, and California bay was not present in the treated or control plots. Annual applications of potassium phosphite initiated years before *P. ramorum* was detected in the study areas did not prevent treated trees from becoming infected with SOD. In treated stands that were invaded by *P. ramorum*, disease development and mortality were not suppressed by phosphite application. Even though *P. ramorum* had been detected in the vicinity of all study plots at the start of the studies, little or no progress of SOD into either treated or control plots has been detected in multiple locations. Drought conditions that persisted from 2012 through 2016 greatly slowed the advancement of *P. ramorum* in these extensive stands of susceptible tanoaks. Our data indicate that the invasion of tanoak stands by *P. ramorum*, even within areas considered to be infested, is subject to considerable variation over space and time and is strongly affected by rainfall. As a result, large differences in disease levels can develop between nearby plots due to chance alone that could incorrectly be attributed to treatment effects. Over short time horizons, tests showing no treatment effect are more readily interpreted than those that appear to show a treatment effect. A high-confidence protective treatment

effect cannot be obtained without long-term observations that clearly show treated areas have resisted disease while all adjacent areas have succumbed.

Impacts of and Responses to Sudden Oak Death on Marin Watershed Lands

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The Marin Municipal Water District (MMWD) stewards 22,000 acres of watershed lands in Marin County. Recognized as a biodiversity hotspot, with over 1,000 plant taxa in more than 100 recognized communities, it is one of the first introduction sites of *Phytophthora ramorum* in California. In part to understand and monitor this new threat, MMWD completed its first Vegetation Classification and Map in 2005 with support from California Native Plant Society, California Department of Fish and Wildlife, and Aerial Information Systems (AIS). A 2010 re-map of forested areas with support from the USDA Forest Service and AIS showed the progression of SOD and shift in vegetation types within impacted areas, and a 2015 map tracks increasing canopy gaps and additional impacts to oak woodlands (AIS 2015). Ground sampling and maintenance records reveal new hosts (Rooney-Latham et al. 2016), community shifts, threat interactions, and increasing costs and fire danger from dead and downed trees. Responses to forest disease vary based on severity, location, and vegetation type impacted, but include cutting dead and down trees and altering planting palettes.

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Poster Abstracts

(alphabetically by author's last name)

Observations of *Castanea sativa* as a Host of *Phytophthora ramorum* in England over a Decade

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Forestry Commission England aerial surveillance operations to detect *Phytophthora ramorum* between 2009 and 2014 were primarily focused on identifying infected larch (*Larix* spp.), although sweet chestnut (*Castanea sativa*) has been recognized as a sporulating host of *P. ramorum* since the mid-2000s (Denman et al. 2006). During follow-up ground investigations, infected sweet chestnut was confirmed and considered an incidental host on 23 sites (54 laboratory positives), with individual trees or small discrete stands of sweet chestnut affected but always in close proximity to other infected sporulating hosts (usually *Rhododendron ponticum* and larch). Observed symptoms of sweet chestnut comprised foliar wilting, leaves with blackened petioles, discolored mid-ribs, and/or 'water-soaked' or discolored leaf margins. These symptoms were most common on abundant epicormic growth low on the stems of mature trees.

In 2014 an area of sweet chestnut showing general symptoms of decline and crown dieback was noted. The site was in south-west England with known historic *P. ramorum* infection, so survey flights specifically targeting areas of sweet chestnut were added to the surveillance program in 2015. Between 2015 and 2017, 182 sweet chestnut woodland sites (predominantly in south-west England) were identified with crown dieback and mortality, ranging in severity from individual trees through to approximately $\geq 30\%$ trees affected. Follow-up ground investigations inspected trees for symptoms consistent with *P. ramorum* infection. Many of the sites were found to contain sweet chestnut trees with symptoms which yielded positive lateral flow test results, and laboratory testing of samples from 82 of the sites yielded 150 positive *P. ramorum* results, either based on isolation of *P. ramorum* (EU1) cultures and/or rtPCR confirmation. In addition to foliar symptoms, new symptoms observed included premature abscission of symptomatic leaves from the crown, cankers on epicormic shoots, and in some cases extensive cankers affecting branches and stems of mature trees. An apparent co-occurrence of symptoms with rapid or chronic crown dieback was observed.

In 64 cases, confirmed sweet chestnut infection was in a location with a current or historic presence of *P. ramorum* in larch or rhododendron. Dieback appeared to have progressed in recent years in spite of the removal of the other sporulating hosts on these sites. In a further 18 cases however, infected sweet chestnut trees with crown decline were confirmed in locations where any infected larch and rhododendron could be several km distant (up to 7.5 km in one instance). This suggests long distance aerial transmission of *P. ramorum* to sweet chestnut, and that the disease can also cycle on sweet chestnut in the absence of any other sporulating hosts.

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Characterization of Hybrids between *Phytophthora lacustris* and *P. riparia*

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Studies of hybrid organisms often reveal two types of interspecific hybridization: polyploid hybridization, where the number of chromosomes changes during or immediately following hybridization, and homoploid hybridization, where the number of chromosomes is unchanged. Homoploid hybridization is thought to occur only between very closely-related species, while polyploidy can allow for the persistence of what would normally be a sterile or unstable cross between more distantly related species. Polyploid hybrids may not be able to interbreed with their parents, persisting through time as reproductively isolated species, while homoploids are likely to be able to back-cross, sometimes leading to a “hybrid swarm” of individuals related in varying degrees to the two parent species, blurring the lines between them. Polyploid hybridization has been well-documented in the plant-pathogenic genus *Phytophthora* (Phylum Oomycota), where it can lead to the formation of hybrid species with different host ranges and degrees of virulence than the parent species.

In California, two closely-related species of *Phytophthora*, *P. lacustris* and *P. riparia* are commonly isolated from freshwater environments, along with individuals that appear to be hybrids between the two species. Using a population of stream isolates obtained during sudden oak death monitoring activities, a traditional cloning approach was employed in an attempt to characterize the nature of these *P. lacustris* X *riparia* hybrids and to determine if a hybrid swarm is present. Results and their implications are discussed.

Intraspecific Diversity of Californian Clade 3 *Phytophthora* Isolates

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Within the large plant-pathogenic genus *Phytophthora*, lies an enigmatic phylogenetic cluster of five species known as “clade 3.” Conflicting studies have suggested that this group of species may be native to Europe or North America. At the turn of the 20th century, clade 3 was known only from a single species, *P. ilicis*, which had been isolated in North America and Europe. In 2002, a second species, *P. psychrophila* was described from declining European oak forests. In 2003, two additional species were introduced, with *P. nemorosa* found only in North America and *P. pseudosyringae* from both Europe and North America. In 2013, *P. pluvialis*, another North American species was added.

Despite being distantly related to *P. ramorum*, the sudden oak death (SOD) pathogen, *P. nemorosa* and *P. pseudosyringae* cause indistinguishable symptoms on native Californian hosts, albeit with less frequency and virulence. Because SOD is an emerging disease caused by a non-native pathogen, this led to speculation that *P. nemorosa* and *P. pseudosyringae* were also introduced to North America. In 2009, a study of genome-wide diversity of the two species suggested highly clonal populations, and (for *P. pseudosyringae*), that the North American isolates were derived from the European population. The 2009 study, combined with a lack of association with landscape-level disease in Europe and a lack of aggressiveness on native European hosts led to a 2015 assessment that *P. ilicis*, *P. pseudosyringae* and *P. psychrophila* were the only species of *Phytophthora* (out of about 60 categorized) native to Europe.

Phytophthora nemorosa and *P. pluvialis* have still never been documented in Europe. Originally described only from Oregon, *P. pluvialis* was found causing significant disease in *Pinus radiata* (Monterey or radiata pine) plantations in New Zealand as well as native stands of *Pseudotsuga menziesii* (Douglas-fir) in Oregon; this New Zealand occurrence represented the first documentation of clade 3 outside of North America or Europe. A worldwide collection of *P. pluvialis* strains from Oregon, California and New Zealand suggested that the New Zealand population was derived from North America, although these results do not necessarily indicate this is the native range of *P. pluvialis*. Most recently, *P. pseudosyringae* was isolated from South America.

Another source of evidence regarding geographic origins is the diversity of sequences derived from *Phytophthora* clade 3 isolates available in public databases, the expectation being that the greatest genetic diversity will be found in the native range. So-called “barcoding sequences” including the ITS rDNA and various sections of the mitochondrial cox2-cox1 region are commonly deposited for *Phytophthora* isolates, allowing for the identification and comparison of isolates across space and time. A 2017 study demonstrated that all five clade 3 species are either common or uncommon but consistent in *Phytophthora* surveys of Oregon natural

ecosystems, and that more intraspecific diversity can be found across Oregonian than European isolates. This evidence is consistent with the notion that at least some species in clade 3 may, in fact, be native to North America.

We obtained barcoding sequences from more than one hundred Californian isolates in *Phytophthora* clade 3, comprising four of the five species. These isolates were obtained from various UC Davis, Rizzo Lab projects sampling California natural ecosystems for purposes of research and management over the course of more than a decade. Preliminary results suggest in regards to *Phytophthora* clade 3 that California, like Oregon, is a source of great intraspecific diversity.

A Technique for Treating Contaminated Soil with Steam for Eradication of *Phytophthora*

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During a series of large riparian restoration projects in the San Francisco Bay Area, *Phytophthoras* on infected planting stock were inadvertently introduced into a number of sites. There are many planting basins at some of these sites where hosts from a nursery that had a high rate of *Phytophthora* positives were planted. These basins are scheduled for treatment once a potential mitigation approach to kill any introduced *Phytophthoras* is decided upon. Steaming has been shown to be an effective mitigation treatment to eliminate *Phytophthoras* from infested soil. In nursery and landscape sites where *P. ramorum* has been detected, steaming soils to reach a temperature of 50 °C at 30 cm for 30 minutes is an accepted USDA APHIS mitigation treatment. In this project, two steaming techniques were tested. In addition, thermal cover materials for retaining heat in steamed soil were compared. Testing was done at a restoration site in California (CA) and at WSU Puyallup (WSUP).

At the CA site, a 24" diameter steam auger was attached to a hydraulic-powered shaft that passed through a transfer case welded to an excavator bucket. Steam was delivered to the auger via a 2- inch diameter hose that connected a steam generator to the transfer case. Steam was introduced through the auger during soil mixing. In another set of trials the soil was first augered to 24" depth, then a 1.5" diameter injector was used to introduce steam at the bottom of the hole. Temperatures were measured at several depths along the edges of the holes during and after steaming. Testing in a similar soil type at WSUP under several moisture conditions was done using the injector and temperature sensors mounted on a grid inside the hole. The temperature at each point on the grid was measured during and after steaming.

Preliminary results from auger and injector field tests in CA were not conclusive due to saturated soil conditions. Although a steam auger was not tested at Puyallup, the results with the steam injector indicate that the results of at least the steam injector tests at the CA site would have likely been acceptable if they had been done under dryer soil conditions. In the silt loam soil at WSUP, the conditions for killing *P. ramorum* (50 °C for 15 minutes) and *P. pini*, which has a heat resistant spore stage (50 °C for 40 minutes) were reached over most of the soil volume when soil at field capacity was steamed for 5 or 10 minutes.

Data collected during the steaming at both sites indicated that there is little risk of a negative impact to organisms in the bulk soils adjacent to augered and steamed planting basins unless the soil has larger channels for the steam to move outside of the soil in the augered hole.

A thermal cover used after steaming will retain heat in the soil after 10 minutes of steaming when sufficient heat has accumulated. There was little difference between the steamed, uncovered plots and plots with some type of thermal cover after 5 minutes of steaming. After 10

minutes, the differences between thermal cover treatments were significant at all depths. The materials that prevented the most heat loss from the soil were an insulated metal drain pan, rubber floor mats, and denim insulation.

Management of *Phytophthora ramorum* at a Botanical Garden in Washington State, USA

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In March 2015 *Phytophthora ramorum* was detected at The Bloedel Reserve, a 150 acre botanical garden in Kitsap County, WA. Infected plants were destroyed and the soil in an area surrounding these plants was steam-sterilized to a depth of 15 cm during the summer of 2015. An IPM program was developed in an effort to control the spread of *P. ramorum* and other *Phytophthora* species in the garden, reduce the risk of *P. ramorum* spread to the surrounding landscape, and minimize additional destruction of valuable plants and visual impacts to the garden. Several treatments were employed, including the use of *Phytophthora*-specific fungicides, removing host vegetation, soil steaming, replanting affected areas with non-host or host plant species that have shown some resistance to *P. ramorum*, and the use of *Trichoderma* biocontrol agents and mulch to reduce spread of disease from soil to plants. Surveys in the *P. ramorum* positive areas and perimeter were done during 2015-2018. Symptomatic foliage was collected and tested for *Phytophthora* using ELISA. Any ELISA positive samples were tested for *P. ramorum* with PCR. Isolates of *P. ramorum* were genotyped using microsatellite markers.

Many of the *P. ramorum* positives were detected on certain native hosts. In February 2016, the IPM strategy was therefore modified to include the removal of native host vegetation within the positive areas. Fungicides were applied in the positive areas during 2016-2018. The rate of ELISA+ plants was between 37% - 90% during this time period. The rate of ELISA+ samples has decreased in the positive areas since the peak of 90% in October 2016 and has stayed below the initial 72% measured in January 2016.

Seven NA1 microsatellite genotypes of *P. ramorum* were detected at Bloedel between March 2015 – February 2016. The two most commonly found genotypes were identical to the genotypes of *P. ramorum* from two nurseries in Washington State. The remaining five genotypes have only been detected at Bloedel and are very similar to the nursery genotypes. These are probably derived from the nursery genotypes rather than being new introductions.

Fungicide applications and long term continual removal of native host plants in the positive areas, and the reapplication of Plant Helper (*Trichoderma atroviride*) in areas that were identified as higher risk due to slope and proximity of prior positive sites has been continued until the present. The Plant Helper is applied as a soil drench and then covered with a mulch that is made from chipped alder wood and other vegetation, but not containing host plant material, on the Reserve. Expanding the use of *Trichoderma*s in the prior positive areas of the Reserve to include areas further from these known positive sites is being considered. Soil steaming was effective in the immediate areas of the positives that were detected, but there are extensive areas that should be protected from potential infestation, and there may be undetected infestations that could be mitigated by added populations of *Trichoderma* in the soil.

Changes to Sudden Oak Death Affected Redwood Forests in Big Sur after a Short Fire Return Interval

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The forests of Big Sur have been infested with *Phytophthora ramorum*, the pathogen responsible for Sudden Oak Death (SOD), since the mid-1990s or longer. The UC Davis, Rizzo lab, established a plot network of 280 plots in 2006 - 2007 along the central coast of California in Big Sur to monitor the ecological impacts of this non-native invasive pathogen (Meentemeyer et al. 2008, Metz et al. 2012). A lightning caused wildfire in 2008 that burned 1/3 (n=121) of the plots offered researchers the first opportunity to examine the impacts the pathogen would have on forests following a wildfire (Beh et al. 2012; Cobb et al. 2016; Metz et al. 2011, 2013; Simler et al. 2018). After eight years of follow-up surveys, another fire in July 2016, this time human caused, led to another subset of plots being burned (n=114). Much of the 2016 fire re-burned parts of the forest that had burned just 8 short years ago. Here we take a look at how the SOD affected redwood-tanoak forests that burned in 2008 are recovering 10 years post fire, and a preliminary look at what effects two successive, short-interval fires may have on forest resiliency.

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Exploring Interactions among Disease, Fuel Loads, and Fire Intensity in Sonoma County Oak Woodlands

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Understanding the impacts of disease and fire on forested ecosystems is a major challenge facing scientists, land managers, policy makers and landowners. Due to difficulty in predicting wildfire, few studies of ecological effects of fire are based on both pre- and post-fire data. The goal of our research is to use a large scale and long-term plot network with both pre- and post-fire data in eastern Sonoma County to determine the ecological impacts of an exotic pathogen (*Phytophthora ramorum*) and wildfire on oak-woodland forest communities.

We aim to answer the following questions: 1) Do plots with higher inoculum loads and disease prevalence have greater pre-fire fuel loads? 2) Do plots with greater mortality due to disease have greater burn severity? and 3) How do disease and wildfire restructure community composition and vegetation recovery post-fire?

In 2003, 197 15 x 15 plots were established within a 275 km² heterogeneous region in eastern Sonoma County to study *P. ramorum* (Meetenmeyer et al. 2008). Every two years until 2016, measurements of microclimate, disease prevalence, tree growth, mortality and survival of the three most abundant host species, coast live oak (*Quercus agrifolia*), California black oak (*Quercus kelloggii*), and California bay laurel (*Umbellularia californica*) were taken. In 2016, microclimate and fuels loads were quantified using standard forestry protocols (Brown 1974). In 2017, the Central LNU (Lake Napa Unit) Complex fires burned 44,806 ha in Sonoma, Napa and Lake Counties during which approximately half of these study plots burned. In 2018, microclimate data, tree mortality and survival, and fuel loads were quantified across 95 plots (51 burned, 44 unburned). In burned plots, we observed a higher level of root sprouting in *U. californica* post-fire than in oak species. Preliminary results exploring fuel loads and fire indicate that duff depth has a significant effect on fire intensity ($LRX^2 = 4.15$, $p = .0416$). In addition, the interaction between *U. californica* disease prevalence and total downed woody debris is also significant ($LRX^2 = 4.397$, $p = .0360$). Current and future work will continue to explore these relationships and assist with management of oak-woodlands in light of future drought and increased fire risk.

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Rapid Recovery and Detection of *Phytophthora ramorum* Propagules in Nursery Water

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Phytophthora ramorum, causal agent of sudden oak death, continues to threaten U.S. forest ecosystems and the nursery industry. Currently, USDA APHIS's protocol utilizes the Bottle of Bait (BOB) recovery method for *P. ramorum*, which requires collecting water from a source, baiting with healthy rhododendron leaves for a 3-day incubation period, followed by plating on semi-selective media. Rapid methods are needed for recovery and detection of *P. ramorum* propagules from water sources. Working at the National Ornamental Research Site at Dominican University California, we are developing rapid water filtration and flocculation methods for recovery and detection of *P. ramorum* propagules from nursery irrigation water. A mock irrigation pond was established with flow from a *P. ramorum*-infested plot into an adjoining plot. Antibodies raised against *P. ramorum*-specific secreted proteins were applied for detection of zoospores and sporangia from 1 L samples in filter extracts or alum flocculates using standard immunoassay procedures. Results with spiked samples indicate that propagules of *P. ramorum* recovered by filtration or flocculation from spiked nursery water samples can be detected in 24 hours or less.

Genomic and Metagenomic Exploration of Microbial Endophytes and a new Potential *Phytophthora* Species in the Monkey Puzzle Tree *Araucaria araucana* in Chile

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Araucaria araucana (Araucaria or monkey puzzle tree; Class = Pinopsida; Family = Araucariaceae) is an endangered conifer with a fragmented and relict distribution in southern Chile and Argentina. Araucaria is the type species of a genus of relatively old conifers with an ancient distribution that covered the continent of Gondwana, and that now comprises 19 extant species distributed in Oceania and South America.

Araucaria has been historically threatened by logging (banned in 1990), wildfires, overgrazing, invasive trees, and extensive human harvesting of Araucaria seeds. More recently, the Chilean forest authority reported extensive damage spread throughout its geographic distribution in Chile and Argentina, which is characterized by browning of branches and needles following a “bottom-up” pattern and radiating from the trunk to the tip of the branches. While 90% of *A. araucana* population is affected there is only a 2% mortality rate in Chile (CONAF). The disease was dubbed DFA as “foliar damage of the Araucaria tree” for its acronym in Spanish. While there are several hypotheses regarding the cause of DFA including approximately a 10-year drought in the region, the widespread nature of the disease which covers all of its geographic distribution at various intensities, plus gardens, nurseries, and public squares, suggests the influence of a pathogen, opportunistic or otherwise.

Here, we use amplicon sequencing targeting the 16S rRNA and ITS taxonomic marker genes to reveal the structure and composition of Araucaria’s microbial communities throughout its geographic distribution (n > 600). Community analyses suggest that Araucaria’s microbial communities are structured primarily within tree by tissue, and secondarily by sampling site, i.e., Andes or Nahuelbuta mountain ranges and north/south gradient.

To get a more agnostic view of Araucaria’s microbial communities, we complement these analyses with shotgun metagenomic sequencing, which revealed that up to 20% of the endophytic communities are dominated by a *Phytophthora* lineage closely related to subclade VIIIc species that include *P. ramorum*, *P. lateralis*, *P. hibernalis*, and *P. foliorum*. We extracted contigs from this new lineage and were able to reconstruct a preliminary phylogeny. Ongoing efforts include culturing and isolation of this *Phytophthora* member, as well as PCR screening over 300 Araucaria samples (healthy and infected) from its entire geographic distribution. We discuss our results and future experiments in the light of testing whether this lineage of *Phytophthora* is the causal agent of DFA.

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A Survey of *Phytophthora* and *Pythium* spp. in Soil from Upland Prairie Restoration Sites in Western Oregon

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Native upland prairie and oak savanna habitats were once widespread in the Willamette Valley of western Oregon, but have been diminished by conversion to other land uses. These threatened habitats are considered essential for rare and endangered species such as the Fender's blue butterfly (*Icaricia icarioides fenderi*). Restoring native upland prairie habitats is a major goal of wildland restoration in Oregon.

The inadvertent spread of *Phytophthora* species from nurseries into native ecosystems can have long-term environmental and economic impacts, as has been seen with *Phytophthora ramorum*, *P. lateralis*, *P. cinnamomi*, *P. tentaculata*, and other species. The risk may be particularly great when nursery-grown plants infested with *Phytophthora* spp. are planted in restoration sites, introducing pathogens directly into native habitats.

The objective of this study was to estimate the prevalence and species composition of *Phytophthora* and *Pythium* in upland prairie restoration sites in western Oregon. We tested soil from 55 upland prairie/oak savanna sites using two methods: baiting and next generation sequencing. Soils were baited with pears; pure cultures from bait lesions were Sanger sequenced for species identification based on the ITS region. In addition, DNA was extracted from each soil sample, amplified with PCR, sequenced with the Illumina MiSeq platform, and analyzed to assess microbial communities (*Phytophthora* and *Pythium*, fungi, and bacteria). Only the findings of *Phytophthora* and *Pythium* spp. will be reported here.

Pythium species were nearly ubiquitous, detected in 46 of the 55 sites. *Pythium attrantheridium*, reported to be an indigenous plant pathogen, was the most abundant species. Other species included the *Py. glomeratum*-complex, *macrosporum*, *ornacarpum*-complex, *pachycaule*-complex, *paroecadrum*, *parvum*, *pectinolyticum*, *ultimum*, *mamillatum*-complex, *terrestris*-complex and *volutum*. *Phytophthora* species were detected, but in only 7 of 55 sites, and included *P. cambivora*, *megasperma*, *fragariae*-complex, *cactorum*-complex and an unknown species. There was no clear association between planting history or management practices and the presence of *Phytophthora* or *Pythium* species. Results of this study provide a snapshot of the current distribution of *Phytophthora* and *Pythium* species in restoration sites in western Oregon and can serve as a baseline for recognizing future introductions.

Comparative Epidemiology of NA1 and EU1 *Phytophthora ramorum* Populations in Curry County, OR

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The 2015 detection of the *Phytophthora ramorum* EU1 lineage in Oregon forests represents a new threat to sudden oak death management in Curry County. Effective control of EU1 requires knowledge of how its regional epidemiology compares to that of the NA1 lineage. EU1 may be more aggressive and spread at a faster rate than has been observed over the 17 years NA1 has been managed in Oregon forests. EU1 may also infect some hosts, notably conifers, at a greater frequency.

To assess any differences between the two lineages, we compared disease trajectories in forest sites recently infested with either the EU1 or NA1 lineages. Seven sites for each lineage were sampled in the spring and summer of 2017 and 2018. We established 20 x 10 meter transects in four directions upslope, downslope, and laterally along the slope, centered on the presumed source of inoculum contributing to secondary spread. In 5 m² plots (representing distance intervals 0-5, 5-10, 10-15, and 15-20 m from the center of the site), we noted which plant species were present and collected symptomatic, understory foliage of all known hosts. Lesions were plated in selective media to confirm infection by *P. ramorum*. If the EU1 lineage were more aggressive than the NA1 lineage, we predicted the pathogen would be recovered more frequently at any single distance, and be recovered at a further distance in EU1 sites than in NA1 sites.

Phytophthora ramorum was not significantly more widespread at EU1 sites than at NA1 sites. Disease incidence was greatest close to the center of the site for both lineages; recovery declined for both lineages with increasing distance at identical rates. Infection frequencies were either similar for both lineages or greater at NA1 sites at all distance intervals. Tanoak (*Notholithocarpus densiflorus*) and evergreen huckleberry (*Vaccinium ovatum*) were the two most commonly infected hosts, and were found infected in near- equal frequencies for both lineages. Of the 19 other hosts collected, *P. ramorum* was only recovered rarely from bay laurel (*Umbellularia californica*), sword fern (*Polystichum munitum*), and salal (*Gaultheria shallon*). Neither lineage was isolated from understory conifer branches or seedlings.

Despite documented differences in virulence and sporulation capacity between the two lineages in laboratory trials, both appear identical in their capacity to cause disease during early infestation stages. Further investigation should be considered should epidemic trajectory diverge between the two lineages as sites are left untreated.

Distribution of *Phytophthora quercina* in the Midpeninsula Regional Open Space District

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Detections of *Phytophthora* spp. in native habitats have precipitated the need to understand *Phytophthora* diversity in restoration sites and surrounding wildlands. Typically, *Phytophthora* diversity is assessed by collecting and baiting soil or stream water. While baiting successfully recovers several different species, it strongly selects for those adapted to the assay conditions. As a result, many *Phytophthora* species in the sample may not be detected.

As part of surveys in the Midpeninsula Regional Open Space District (MROSD), we collected soil from restoration sites and adjacent non-planted areas in December 2017. In addition to soil baiting using pears, 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 and metabarcoding analyses in an attempt to identify the oomycete species present. Numerous species were detected in the metabarcoding analyses which were not detected by baiting, including the oak root pathogen, *Phytophthora quercina*.

Phytophthora quercina may contribute to oak decline in Europe (Jung et al. 1999) and was not known to be in the United States until its recovery from outplanted valley oak (*Quercus lobata*) in neighboring Santa Clara County in 2016 (Bourret 2018). We detected this species via metabarcoding in 13 soil samples across 4 different MROSD preserves. Of these, 11 samples were from unplanted, minimally disturbed areas. The distribution and results from our attempts to bait *P. quercina* from soils collected in 2018 using different methodology will additionally be presented.

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***Phytophthora* Diversity in Lake Mathews, the Irrigation Water Source for a Southern California Nursery**

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Phytophthora can survive, propagate and disseminate through water bodies, gaining access to plant nurseries which rely on surface sources of water for irrigation purposes. Lake Mathews, a reservoir at the western terminus of the Colorado River Aqueduct, serves as the main source of irrigation water for several nurseries in southern California. Some of the nurseries do not disinfect Lake Mathews water before using it for irrigation. We examined the diversity of *Phytophthora* species detected in this water over the span of 30 months.

We periodically collected two 1-L water samples from Lake Mathews as supplied by the Western Municipal Water District to a large container nursery in southern California. One set of samples was filtered and DNA from filters was used to detect all *Phytophthora* species present. Duplicate samples were baited with rhododendron leaves, and DNA from leaf baits with lesions was used to determine which pathogenic *Phytophthora* species were present in water. In both cases, the ITS1 region was first amplified from the filter and leaf bait DNA, and then sequenced with high-throughput Illumina MiSeq sequencing for metabarcoding.

Twenty-two *Phytophthora* taxa were detected on filters; of these, 12 taxa colonized leaf baits. The ITS1 sequences originating from this study showed over 99% similarity to some of the important *Phytophthora* taxa including: *P. lateralis*, *P. citricola*-complex, *P. capsici*-cluster, *P. cryptogea*-complex, *P. citrophthora*-cluster, *P. tropicalis*, and *P. amaranthi*. We also detected ITS1 sequences that matched *P. kernoviae*. The temporal dynamics of these taxa in water and potential implications for nursery plant health will be presented.

Is Sudden Oak Death becoming a Threat to California's Chaparral Ecosystem?

First Indications for *Phytophthora ramorum* moving into Drier and Warmer Habitats

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Since its introduction into California, *Phytophthora ramorum* was found predominately on a rather narrow band along the coast characterized by mild temperatures and abundant year-long moisture (in the 'fog belt'). The presence of foliar hosts, especially California bay laurel (*Umbellularia californica*), common in this ecosystem, is an essential driver for the spread of the disease to 'dead-end hosts', such as coast live oak (*Quercus agrifolia*). Recently, *P. ramorum* was detected on several plants typical for the chaparral plant community (manzanita, *Arctostaphylos spp.*; chaparral pea, *Pickeringia montana*) on a high, sun-exposed ridge in Marin County (Rooney-Latham et al. 2017). During 2018, a severe outbreak of disease was observed on chaparral plants on Mt. Tamalpais in Marin Co., with symptoms including wilting, branch dieback and occasionally plant death. Leaves and branches of several plants showed a positive reaction for *Phytophthora spp.* using immuno-strips; and *P. ramorum* was detected using PCR from a manzanita stem. In addition, *Neofusicoccum australe* (Botryosphaeriaceae) was isolated from a symptomatic plant. The infested area is on a southern slope with no apparent presence of California bay laurel or tanoak (*Notholithocarpus densiflorus*). Potted rhododendron plants were placed near symptomatic plants on Mt. Tamalpais to monitor the possible spread of airborne inoculum during winter 2018/19 and the effect of environmental parameters such as rainfall on the timing and appearance of disease symptoms. Inoculation experiments using *P. ramorum* on several *Arctostaphylos* species are on-going. While it is still unclear whether the observed symptoms are caused by a disease complex, and which role *P. ramorum* has in it, mounting evidence indicates that *P. ramorum* is expanding its host range and moving into new environments.

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Susceptibility of Canadian Flora to EU2 Lineage of *Phytophthora ramorum* and Pathogen Sporulation Potential

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To assess the risk posed by an invasive alien pathogen such as *Phytophthora ramorum*, it is often a good strategy to evaluate its capacity to infect plants prevalent in the area of interest. This approach has been used successfully where potential hosts were identified by artificial infections before being found naturally infected by *P. ramorum*. Establishment of *P. ramorum* in Canadian nurseries and landscapes could result in large economic losses and limitations to trade in ornamental plants and threats to biodiversity and sustainability of forest ecosystems. To date, we have investigated the susceptibility of selected eastern and western Canadian host plants to three lineages (NA1, NA2 and EU1) (Elliott et al. 2011, Jinek et al. 2011). However, there is an urgent need to determine the susceptibility and risk assessment of the newly emerged lineage EU2 in the UK and its potential threat to Canadian flora and impact on nursery and forestry.

A total of 33 host species commonly found in western and eastern Canadian landscapes were selected in this study. Detached leaves/needles were inoculated with *P. ramorum* EU2 mycelia which was isolated from a stream bait near an infected larch plantation in Scotland. Inoculation methods, assessment of lesion area and sporulation potential were conducted using the methods of Shamoun et al. 2017, and Harris and Webber 2016, respectively.

There was a large variation in aggressiveness and sporulation potential among the evaluated hosts. Among the non-conifer species, the EU2 isolate produced the largest lesions on Pacific dogwood (*Cornus nuttallii*), manzanita (*Arctostaphylos spp.*), *Camellia*, *Rhododendron caucasicum x ponticum*, and salal (*Gaultheria shallon*) in the west; sumac (*Rhus typhina*), yellow birch (*Betula alleghaniensis*), wintergreen (*Gaultheria procumbens*), and white ash (*Fraxinus americana*) in the east. For conifer hosts, we found that the EU2 isolate was most aggressive on both balsam fir (*Abies balsamea*) and white spruce (*Picea glauca*) in the east and grand fir (*Abies grandis*), sitka spruce (*Picea sitchensis*), Douglas-fir (*Pseudotsuga menziesii*), and western larch (*Larix occidentalis*) in the west. As for sporulation potential, Garry oak (*Quercus garryana*), red alder (*Alnus rubra*) and bigleaf maple (*Acer macrophyllum*) in the west; sugar maple (*Acer saccharum*) in the east, were potential spore producers but not significantly different from bay laurel. For the sporangia per unit lesion area, Himalayan blackberry (*Rubus discolor*), raspberry (*Rubus idaeus*), and grape (*Vitis vinifera*) were significantly higher than California bay laurel (*Umbellularia californica*). These results confirm the potential threat of EU2 lineage to Canadian flora.

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Variation in Susceptibility to the EU1 and NA1 Lineages of *Phytophthora ramorum* among Southern Oregon Tanoak Families

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Phytophthora ramorum, the cause of Sudden Oak Death (SOD), is an oomycete pathogen that has invaded coastal California and southern Oregon mixed-hardwood forests. In southern Oregon forests, tanoak (*Notholithocarpus densiflorus*) is the most susceptible species developing lethal stem cankers and sporulating from infected leaves and branches. Two lineages (NA1 and EU1) of *P. ramorum* occur in Oregon forests. The first step in a successful tanoak breeding program is to determine if variation in resistance to these two lineages exists. The objectives of this study are to: (i) characterize the variability in resistance of *N. densiflorus* among families using lesion length; and (ii) determine whether lineage, isolate, family, or their interactions significantly affect variation in lesion length. In a growth chamber experiment approximately 1,000 seedlings from 14 tanoak families were inoculated with 3 isolates of the NA1 lineage and 3 isolates of the EU1 lineage. Stem lesions were measured seven days after inoculation.

Averaged across all tanoak families, there were no significant differences in lesion length between the EU1 and NA1 lineages; however, there were significant differences among the six isolates tested. The averages for each family by isolate combination show an overall pattern of increased average lesion length for EU1 isolates. The majority (89%) of the variation in lesion length is explained by isolate (lineage). The family by isolate (lineage) interaction suggests that more than one isolate may be needed in order to screen for resistance to *P. ramorum*. In addition, for a resistance screening program to be successful, a reliable method to vegetatively propagate tanoak needs to be developed.

Role of Herbivorous Insects on California Bay Laurel in Sudden Oak Death Disease Dynamics

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In California, leaves of California bay laurel (*Umbellularia californica*) are considered the primary naturalized source of inoculum for the devastating forest disease sudden oak death (caused by *Phytophthora ramorum*), and yet this plant and insects associated with its leaves remain understudied. Previous studies have considered the role of insects as synergistic factors on trees that die of *P. ramorum* such as oaks, but none have related disease prevalence to insect presence on bay laurel. Indeed, joint effects of insects and pathogens on bay laurel have been investigated surprisingly rarely. Insect attack may prime bay laurel leaves for *P. ramorum* infection by damaging the leaf surface to allow entry of pathogen hyphae. On the other hand, literature on aphids suggests that plant defenses against aphids are similar to those against pathogens. Thus, aphid attack may activate the plant's immune response and suppress susceptibility to a pathogen. In addition, infestation by plant enemies may occur when a plant's defenses are reduced due to environmental stress.

We studied interactions between insects, *P. ramorum*, and bay laurel in a region that has been a hotbed of Sudden Oak Death infection since the early 2000s. In two observational studies, we documented the abundance of scale insects and aphids on bay laurel trees. The first study showed that abundance of the armored scale insect *Aspidiotus nerii* (oleander scale, family Diaspididae) on bay laurel leaves at Fairfield Osborn Preserve related negatively to disease expression of *P. ramorum*. The second study sampled trees across a broad geographic area in eastern Sonoma County. Here, we found that the most abundant insects belonged to the suborder Sternorrhyncha, which includes aphids, scale, whiteflies, and other sessile insects. Across this region, abundance of the California laurel aphid (*Euthoracaphis umbellulariae*) was negatively related to *P. ramorum* disease expression. These studies suggest that plant defense was primed by the insects and that they may have reduced disease levels in nature.

In spring 2016, we conducted an insect-removal study on trees in multiple localities in Fairfield Osborn Preserve. We compared the progress of insect population change and disease expression for leaves on undisturbed control branches and branches that were subjected to three different removal treatments. The most abundant insects were the same sessile insects that we had discovered in our observational field studies. Both oleander scale and California laurel aphid abundance showed a negative relationship with disease levels at the outset of data collection. Insect abundance peaked early in the season (December/January), and disease expression increased just as insect abundance declined in the third month of the experiment. Throughout the season, control branches showed statistically significantly larger numbers of insects present than branches that underwent insect removal treatments. Data analysis of the season-long relationship between insect abundance and SOD prevalence is still underway. Results suggest that insects play a role in dynamics of disease expression in oak woodlands.

Spread the Word, not the Disease! Sudden Oak Death Outreach and the UC Master Gardener Program of Sonoma County SOD Specialists

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Sonoma County has more Sudden Oak Death (SOD) than any other county in California, and the disease is still spreading. At least 163,000 acres of Sonoma County's forests are affected by SOD based on USDA Forest Service aerial surveys, and tanoak, *Notholithocarpus densiflorus* deaths attributed to the disease in the Northern California Shared Service Area increased almost eight-fold between 2016-2017. SOD Blitz data showed a nine-fold increase in estimated true infection rate of trees in some areas of Sonoma County between 2015-2017, and new outbreaks continued to appear in 2018.

Thanks to funding from the USDA Forest Service, the Sudden Oak Death Outreach Program of Sonoma County provides practical, evidence-based information to a diverse audience. The goal of the program is to understand the impact of SOD in Sonoma County, promote forest health to preserve wildlife habitat and save high value trees, and to prevent spread into disease-free areas via community education and citizen science research. Many homeowners, tree care professionals, and land managers rely upon UCCE Sonoma's SOD Outreach Program for up-to-date information about disease biology, diagnosis, spread, and management options.

Master Gardener SOD Specialists are volunteer educators who receive specialized training in SOD in order to work with homeowners, community groups, college students, and public parks users. They do so through various educational events such as library presentations, displays at farmers' markets and community festivals, an information desk staffed 35 hours/week, and leading six SOD Blitz events throughout the county each year. The program coordinator, Kerry Wininger, works with landowners, tree-care professionals, tribal groups, educators, and natural resource managers on disease detection and management through site visits, phone and email, and educational meetings. She also provides Master Gardener trainings, supervises interns, and creates visibility in the press, media, and online. The Program Advisor, Steven Swain, supplies expertise in adult education, helps develop workshops, and gives scientific direction to the overall program.

By empowering knowledgeable and passionate volunteers to interact with the public, the Sudden Oak Death Outreach Program of Sonoma County helps spread the word about SOD to the wider community at a very low cost, helping to mitigate the many impacts of this disease.

A Healthy World and Plants with *Phytophthora*? Multiple Introductions of Tree Pathogens to a Newly Established Woodland

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Established between 1996 and 2010, a site in Dorset was the largest newly-created mainly broadleaved woodland in England. It covered 202 ha (499 acres) and the planted tree species were mostly native, intermixed with small components of non-native species. Historically the site had been managed as farmland for centuries (predominantly grassland but also arable crops), divided by undisturbed hedgerow systems.

The site came to attention in 2011 when the site manager reported dieback of alder and ash (*Fraxinus excelsior*) trees. In an area of around 1 ha, more than 100 ash trees were observed with aerial stem cankers. *Phytophthora syringae* was identified as the causal agent, of which ash was a previously unknown host (Webber et al. 2014). During further site visits, grey alder (*Alnus incana*) was observed with dieback and bleeding stem cankers, and both the symptoms and on-site diagnostic tests indicated the causal agent was a root-attacking *Phytophthora* sp. In 2013, laboratory testing identified *Phytophthora siskiyouensis* from the alder stem and root cankers, and also from associated soil samples. It was estimated that 10% of ca. 1000 *A. incana* trees planted on the site were affected (Perez-Sierra et al. 2015). Follow-up investigations in 2014 which established the distribution of disease also yielded further isolations of *P. siskiyouensis*. Since then, gradual felling of *A. incana* under biosecurity restrictions has been ongoing. The most recent site investigation in 2018 recorded only a very small number of

A. incana trees remaining, with a few of these still exhibiting symptoms. The decline of affected alder trees has been very gradual, and the site remains the only European record of

P. siskiyouensis. Other findings from the site include the confirmation of *P. plurivora* from the rhizosphere soil of a healthy common alder (*Alnus glutinosa*), and *P. cambivora* causing bleeding stem cankers in small-leaved lime (*Tilia cordata*). Following the first UK identification of ash dieback caused by the fungus *Hymenoscyphus fraxineus* in planted ash trees in Leicestershire in 2012, the Dorset site was also found to have accepted a significant proportion of its ash planting material from the same supplier. Subsequent investigations in 2013 concluded that *H. fraxineus* was likely to have been introduced and causing symptoms on ash trees on the site as early as 2007 - 2008.

Although the site for this new woodland could not be described as pristine undisturbed land, the communities of *Phytophthora* species attacking the recently established trees were varied and even novel. There is a strong likelihood that all were introduced on infected planting stock, which clearly illustrates the importance of careful selection of species, consideration of supply origin and the need for improved biosecurity practices in nurseries supplying planting stock.

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