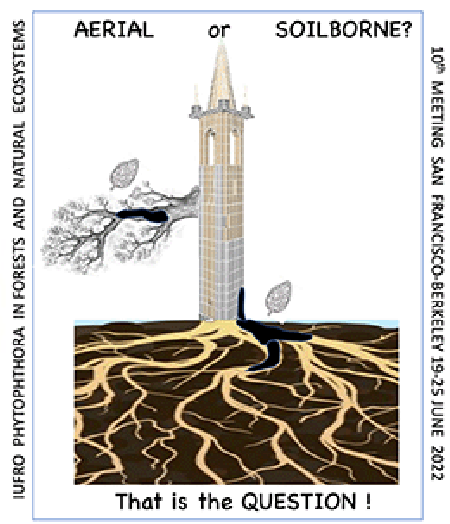
# 10th Meeting of the International Union of Forest Research Organizations (IUFRO)

## Working Party S07.02.09

## *Phytophthora* in Forests and Natural Ecosystems

Sunday June 19 to Saturday June 25, 2022
Berkeley, California



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- Prof. John Taylor
- Fiona Ma

*If you're going to San Francisco*
*Be sure to wear some flowers in your hair…*

(Unless the flowers are infected by *Phytophthora ramorum* or by any other *Phytophthora* for that matter )

Welcome to California!

Your participation at this meeting hopefully marks a new phase of the Covid-19 pandemic, one in which, with care, we will be able to co-exist and co-evolve with this novel threat to humans. Our forests and natural ecosystems, unfortunately, do not have the luxury of receiving vaccines, treatments or to timely modify their social habits and behavior to minimize contagion. Once again, as it has happened nine times before, we gather to share our successes and failures in our quest to improve our understanding of how to predict, prevent, and treat plant diseases that are caused by Phytophthora plant pathogens which have not co-evolved with their newly encountered hosts. The good news is that technology has advanced tremendously and has enriched our toolbox with novelties of unimaginable power: we are here to listen to several such advancements and learn how to best implement them from our colleagues. The bad news is that forests are still incredibly complex, they are increasingly intertwined with industry and are undergoing massive shifts due to climate change. Further, trees keep insisting on not going to see the doctor. In the face of such challenges, in-person meetings may be one of the most effective ways forward to blaze new trails.

We are humbled by the presence of such a group of esteemed colleagues and old friends, and we are truly thankful for your efforts to travel in such difficult times. California needs you: Phytophthoras are causing unprecedented tree mortality in California forests, threatening entire ecosystems at the local but even regional level. By threatening the survival of oaks and tanoaks, *Phytophthora ramorum* alone has cast a shadow on the long-term viability of one of the largest carbon offset programs in the world, which relies on healthy trees as carbon storage. The effects of Phytophthora plant disease on wildfire behavior are beginning to be unveiled in California, and by using infected plant stock in reforestation and restoration projects, we have further endangered California natural ecosystems that were already at risk. The interconnectivity between industry and natural ecosystems is extremely marked in California, where Phytophthora infestations often cross over between nature and agricultural/horticultural settings and vice versa. We will showcase some of these complex situations during the conference and we do long for your input. However, we will also show you the beauty this place has to offer with its unique Western "feeling", rugged coastlines, towering redwood forests, impressive skylines and bridges, Victorian homes, hills and mountains rising up from the bay or the ocean, a vast and most fertile agricultural valley and one of the most diverse human populations in the world. We believe that, by the time you leave, you too will be singing...

*I left my heart in San Francisco*

Matteo Garbelotto and Doug Schmidt

# Conference Program and Schedule

## MONDAY 20 June

8:40-9:10 Opening Ceremony.
Welcome by Matteo Garbelotto
Inaugural address Fiona Ma, California State Treasurer
Opening address by Prof. John Taylor

9:10-9:50 Keynote Address - Meeting the challenges of *Phytophthora* diagnostics in California, a diverse agricultural and natural ecosystem - Suzanne Latham

**Diagnostics (Chair: Carmen Morales-Rodriguez)**
9:50-10:10 Finding the optimal protein set assign to the identification of cork oak plants inoculated with *Phytophthora cinnamomi* using Cover Problem approach - Ana Cristina Coelho

10:10-10:30 Detecting *Phytophthora* infections of trees using volatilomics - Patrick Sherwood

10:30-11:00 BREAK

11:00-11:15 Update on *Phytophthora* diagnostics in Ireland - Richard O'Hanlon

11:15-11:30 DNA metabarcoding complemented by baiting is the best methodological approach to unravel *Phytophthora* diversity in different kinds of ecosystems - Santa Olga Cacciola

11:30-11:40 Cryopreservation of different *Phytophthora* species - Biljana Đorđević

**Diversity and Distribution I (Chair: David Rizzo)**
11:40-12:05 Cataloging *Phytophthora* species of agriculture, forests, horticulture, and restoration outplantings in California - Tyler Bourret

12:05:12:25 Current Status of *Phytophthora* in Australia - Treena Burgess

12:25-12:45 The *P. ramorum* outbreak in western France - Benoit Marçais

LUNCH

**Diversity and Distribution II (Chair: David Rizzo)**
2:15-2:35 Why *Phytophthora* scientists must also be fire scientists - Richard Cobb

2:35-2:55 Emerging ink disease of chestnut in southern Switzerland - Simone Prospero

2:55-3:10 Differential distribution of *Phytophthora* species in a heterogeneous forest landscape - Carmen Morales-Rodriguez

3:10-3:25 Oomycete Detections and Associated Vegetation Decline in California's North Coast - Chris Lee

3:25-3:35 A survey in natural ecosystems of Louisiana revealed a high diversity of previously known and new *Phytophthora* taxa - Tomas Majek

3:35-4:05 BREAK

**Management (Chair: Nari Williams)**

4:05-4:25 The decline of the monumental cork oak forest of San Vito and Valle Marina: adopted mitigation strategies and preliminary results - Andrea Vannini

4:25-4:40 Are oomycetes associated with the dieback of western redcedar? - Joseph Hulbert

4:40-4:55 *Phytophthora agathidicida* oospore deactivation by heat treatment - Matthew Arnet

4:55-5:10 Evidence of phosphonate tolerance in *Phytophthora cinnamomi* from New Zealand avocado orchards - Shannon Hunter

5:10-5:20 Understanding and managing the impact of *Phytophthora* diseases in horticulture - Fryni Drizou

5:20-5:30 Screening for Resistance to *Phytophthora lateralis* in Port-Orford-cedar (*Chamaecyparis lawsoniana*) - Elizabeth Stamm

5:30-5:40 LIFE-FAGESOS- *Phytophthora*-induced decline of *Fagaceae* ecosystems in Southern Europe exacerbated by climate change: preserving ecosystem services through improved integrated pest management - Andrea Vannini

5:40-6:00 Daily Open discussion lead by Carmen Morales - Rodrigues, questions for speaker

6:00 Housekeeping

# TUESDAY 21 June

**Morning ZOOM session.( Chair: Matteo Garbelotto)**

9:00-9:40 Keynote Address - Disturbance effects on pathogens and disease emergence - Lauren Waller

9:40-10:00 Global invasion history of the emerging plant pathogen *Phytophthora multivora* - Tetyana Tsykun

10:00-10:20 Rehabilitation of old *Phytophthora cinnamomi* impacted jarrah (*Eucalyptus marginata)* forest sites using seed enhancement technologies - Shanika Harshani

10:20-10:40 Phosphite spray for the control of oak decline induced by *Phytophthora* in Europe - Alejandro Solla

10:40-11:10 BREAK

11:10-11:30 Dilution of *Phytophthora cinnamomi* inoculum in chestnut stands by non competent host species - Cécile Robin

11:30-11:50 The susceptibility to *Phytophthora* root-rot varies among genotypes of *Eucalyptus nitens* - Tanay Bose

11:50-12:10 Diversity and impact of *Phytophthora* species in Mediterranean ecosystems - Bruno Scanu

12:10-12:30 Updates on *Phytophthora* research: SOD reemergence, Sherlock assays, and rps10 metabarcoding - Niklaus J Grünwald

LUNCH

**Ecology and Epidemiology (Chair: Jared LeBoldus)**

2:00-2:25 Distribution of *Phytophthora* communities along a climatic gradient in Europe - Jonàs Oliva

2:25-2:45 Interactions between fire and *Phytophthora ramorum* - David Rizzo

2:45-3:00 Synergistic effect of a heat wave and *Phytophthora x alni* infection on alder species performance - Inês Gomes Marques

3:00-3:15 *Phytophthora* species surveys of burnt areas of Angeles National Forest reveal species-specific patterns of distribution and variability of pathogenicity towards common native chaparral - Sebastian Fajardo

3:15-3:30 Detection of *Phytophthora* species from *Quercus suber* stands using DNA metabarcoding and baiting isolation - Salvatore Seddaiu

3:30-3:45 Population genetics clarify the epidemiological relationships among the three main California hosts of the pathogen *Phytophthora ramorum*, causal agent of Sudden Oak Death - Matteo Garbelotto

3:45-4:15 BREAK

4:15-4:30 Multivariate Bayesian analysis to identify traits associated with invasiveness of *Phytophthora* pathogens - Treena Burgess

4:30-4:45 *Phytophthora agathidicid*a and kauri dieback – are other hosts and other *Phytophthora* species important? - Ian Horner

4:45-5:00 Improving the understanding of the spatial and temporal dynamics of kauri decline in the Waipoua Forest and its association with *Phytophthora agathidicid*a - Nari Williams

5:00-5:10 *Phytophthora ramorum* Variant Abundance is Driven by Sporulation Capacity and Environmental Optimums - Adam Carson

5:10-5:20 Dynamics of endophytic fungal microbiome in tanoak leaves associated with *Phytophthora ramorum* infections in southwestern Oregon - Yung-Hsiang Lan

5:20-5:30 Modeling a risk map for ink disease in Switzerland - Simone Prospero

5:30-6:00 Daily open discussion led by Ana Cristina Coelho, questions for speakers

6:00 Housekeeping

## WEDNESDAY – June 22 – Field Trip

## Buses Depart promptly at 8:30am

# THURSDAY – June 23

9:00-9:40 Keynote Address - Marianne Elliott - *Phytophthora ramorum* in Washington State, USA: Management successes, failures and challenges.

**Host-pathogen-environment interactions (Chair: Simone Prospero)**
9:40-10:00 Role of host resistance in sustainable management of *Phytophthora* leaf disease in natural rubber (*Hevea brasiliensis*) - Narayanan Chaendaekattu

10:00-10:20 Expanding the host range of *Phytophthora cinnamomi* in the southeastern United States - Linus Schmitz

10:20-10:35 Evidence for natural resistance in larch and juniper to *Phytophthora* - Sarah Green

10:35-10:50 Pathological, physiological and metabolomic effects of co-infections by *Phytophthora cinnamomi* and the A1 and A2 mating types of *P. x cambivora* on *Castanea sativa* - Tamara Corcobado,

10:50-11:15 BREAK

11:15-11:30 *Phytophthora cinnamomi* on "laurel oak" in South Carolina, USA - Steven N. Jeffers

11:30-11:45 Response of two riparian woody plants to *Phytophthora spp*. and drought: the role of plant ecological preferences and pathogenicity - Inês Gomes Marques

11:45-12 Microscopy determination of the host-pathogen interaction between *Alnus glutinosa* and several *Phytophthora species* - Jonas Oliva

**Management II (Chair: Nari Williams)**
12:00-12:20 The USDA Forest Service Support of the Sudden Oak Death Program in California - Philip Cannon

12:20-12:35 Sudden Oak Death in Oregon Forests: New clonal lineage and increased disease management - Sarah Navarro

12:35-12:50 What to do about NA2: A new lineage of *Phytophthora ramorum* in Oregon forests - Kelsey Sondreli

LUNCH

**Evolution, Genetics and Genomics (Chair: Ana Cristina Coelho)**

2:00-2:20 Genomic biosurveillance of *Phytophthora ramorum* detects intralineage variants and interlineage hybrids - Richard Hamelin

2:20-2:35 A wide variety of viruses exists in *Phytophthora* and *Halophytophthora spp.* - Leticia Botella

2:35-2:50 Diversity of viruses in *Phytophthora* Clade 5 - Milica Raco

2:50-3:05 Population dynamics of the sudden oak death pathogen *Phytophthora ramorum* in Oregon after first invasion - Jared LeBoldus

3:05-3:20 A comparative genomics study of *Phytophthora pluvialis* isolated from different conifer host species - Martha Sudermann

3:20-3:30 Six New *Nothophytophthora* Species from natural ecosystems in Europe and Asia - Henrieta Datkova

3:30-3:55 BREAK

3:55-4:10 Phylogeny and morphology of *Phytophthora quercina* isolates from Europe and North Africa - Andrea Brandano

4:10-4:25 Forest Phytophthora: ecology, diversity and management - Noelia López-García

**Public Engagement (Chair: Carmen Morales-Rodriguez)**

4:25-4:45 Citizen Science: the best way forward to collect and publicly share large datasets. - Matteo Garbelotto

4:45-5:00 Forest Health Watch: empowering communities to keep trees healthy - Joseph Hulbert

5:00-5:10 *Phytophthora* knowledge and disease resistant planting preferences among nonindustrial forest landowners in southern Oregon, USA. - Norma Kline

5:10-5:25 Daily open discussion led by Nari Willimas, questions to speakers

5:25 Housekeeping

# FRIDAY – June 24

9:00-9:40 Keynote Address - Understanding drivers of *Phytophthora* emergence through the plant nursery trade in Britain - Sarah Green

***Phytophthora* in nurseries and associated with restorations/disturbance (Chair: Santa Olga Cacciola)**

9:40-10:05 Battling Soilborne *Phytophthoras* in California Restoration Sites and at the Wildland Urban Interface - Janell M. Hillman

10:05-10:25 From problems to solutions: addressing habitat restoration as a source of wildland *Phytophthora* introductions - Tedmund J. Swiecki

10:25-10:35 Use of remote sensing data and GEE for detection and monitoring of cork oak decline caused by *Phytophthora cinnamomi* - Andrea Brandano

10:35-11:00 BREAK

11:00-11:15 Do not let the bad boys out: containment of *Phytophthoras* in a research nursery - Wolfgang Schweigkofler

11:15-11:30 Using Scent Dogs to Detect Pathogenic *Phytophthora* - Lauralea Oliver

11:30-11:45 A standardized method for detecting *Phytophthora* by baiting leachate from batches of container nursery plants - Tedmund Swiecki

11:45-12:00 Improving restoration nurseries best management practices by evaluating the efficacy of *Phytophthora* detection methods - Johanna Del Castillo Múnera

12:00-12:10 Thermotherapy to eliminate *Phytophthora* from root systems of container plants - Elizabeth A. Bernhardt

12:10-12:20 *Phytophthora* root rot: susceptibility of garden plants - Fryni Drizou

12:20-12:30 Testing the pathogenicity of three *Phytophthora* species on California hosts commonly used in restoration - Inês Gomes Marques

12:30-12:45 Discussion led by Susan Frankel

12:45-1 Business Meeting

LUNCH followed by free afternoon
5:45 Cocktails & Social Dinner at the Heyns Hall and Patio, UC Berkeley Faculty Club

# Conference Presentation Details

## MONDAY 20 June

### 8:40-9:10 Opening Ceremony
### 9:10-9:50 Suzanne Latham - Keynote Address

### Meeting the challenges of *Phytophthora* diagnostics in California, a diverse agricultural and natural ecosystem

Suzanne Rooney-Latham and Cheryl L. Blomquist

California Department of Food and Agriculture, Plant Pest Diagnostics Center. Sacramento, CA

California is one of the most geologically and climatically varied states in the United States and one of the most biodiverse regions in the world. The state lies within one of the global hot spots for floristic biodiversity and endemism, with nearly 6,000 native plant species, many found nowhere else in the world. California's massive agricultural systems, large population with its accompanying sprawling suburban growth, and climate change have contributed to nearly a third of the flora species being classified as rare, threatened, or endangered. Invasive plant pathogens, such as *Phytophthora ramorum*, have also caused significant damage to California's ecosystems. While the presence of *Phytophthora* species has been documented in commercial ornamental California nurseries for years and more recently during *P. ramorum* regulatory surveys, the disease problems in native plant nurseries had gone largely unnoticed until 2012. The discovery of an exotic root and crown pathogen, *Phytophthora tentaculata*, on native stock destined for restored and pristine habitats caused serious alarm within the native plant community. Subsequent surveys confirmed that soilborne *Phytophthora* species are common in California's restoration nursery production systems and have been repeatedly introduced into California wildlands (Frankel et al. 2020; Rooney et al. 2019; Sims et al. 2019). The increased awareness of *Phytophthora* has resulted in more refined pathogen detection methods, increased sensitivity of diagnostic assays, and ultimately, the discovery of new *Phytophthora* species and new host-pathogen relationships in native and agricultural systems.

Frankel, S.J., Conforti, C., Hillman, J., Ingolia, M., Shor, A., Benner, D., Alexander, J. M., Bernhardt, E., and Swiecki, T.J. 2020. *Phytophthora* introductions in restoration areas: Responding to protect California native flora from human-assisted pathogen spread. Forests 11: 1291.

Rooney-Latham, S., Blomquist, C.L., Kosta, K.L., Guo, Y.Y., and Woods, P.W. 2019. *Phytophthora* species are common on nursery stock grown for restoration revegetation purposes in California. Plant Disease 103: 448-455.

Sims, L., Tjosvold, S., Chambers, D., and Garbelotto, M. 2019. Control of *Phytophthora* species in plant stock for habitat restoration through best management practices. Plant Pathology 68: 196-204.

## Diagnostics

## 9:50-10:10 Finding the optimal protein set assignment for the identification of cork oak plants inoculated with *Phytophthora cinnamomi* using Cover Problem approach

Ana Cristina Coelho[1] and Gabriela Schütz [1,2]

[1]Center for Electronic, Optoelectronic and Telecommunications (CEOT), Universidade do Algarve, Faro, 8005-139, PORTUGAL, [2]Instituto Superior de Engenharia, Universidade do Algarve, Faro, 8005-139, PORTUGAL

Cork oak decline in the Mediterranean forests is a complex phenomenon, observed with remarkable frequency in the southern part of the Iberian Peninsula, causing the weakening and death of these woody plants. Defoliation of the canopy, dry peripheral branches and exudations on the trunk are visually observable symptoms used for the prognosis of decline, complemented by the identification of *Phytophthora cinnamomi* in the rhizosphere of the trees and adjacent soils. Recently, a large proteomic dataset obtained from leaves of cork oaks inoculated and non-inoculated with *P. cinnamomi* has become available (Coelho et al 2021; identifier PXD021455) and can be exploited to search for an optimal set of proteins, markers of the biological pattern of decline. Combinatorial optimization problems belonging to the large class of Cover Problems have been applied to solve real-world problems in molecular biology and biochemistry. Thus, using published data from the cork oak leaf proteome, we mathematically modeled the problem to select molecular markers. A set of proteins (features) was found that represent dominant effects on host metabolism resulting from oomycete action on roots. These results contribute to an early diagnosis of the biochemical changes associated with *P. cinnamomi* infection of cork oak. We hypothesize that these markers may be decisive for detecting trees that go into decline due to interaction with the pathogen, helping in the management of cork oak forest ecosystems.

Coelho, A.C., Pires, R., Schütz, G., Santa, C., Manadas, B. and Pinto, P., 2021. Disclosing proteins in the leaves of cork oak plants associated with the immune response to *Phytophthora cinnamomi* inoculation in the roots: A long-term proteomics approach. PLoS ONE 2021, 16(1), e0245148. DOI 10.1371/journal.pone.0245148

## 10:10-10:30 Detecting *Phytophthora* infections of trees using volatilomics

Patrick Sherwood[1], Stephen Woodward[2] and Michelle Cleary[1]

[1]Southern Swedish Forest Research Centre, Swedish University of Agricultural Sciences, University of Agricultural Sciences, Sweden; [2]Department of Plant and Soil Science, University of Aberdeen, United Kingdom

*Phytophthora* species are some of the most destructive forest pathogens in places where they have been introduced outside of their native range. New methods are needed for screening plant material to limit the accidental spread of *Phytophthora*. This project investigated whether volatilomics could successfully: (i) distinguish *Phytophthora* species from each other under *in vitro* growth conditions and (ii) detect *Phytophthora cinnamomi* and *Phytophthora plurivora* infections in *Quercus robur* and *Fagus sylvatica* saplings. Nine different *Phytophthora* species *in vitro* volatilomes were analyzed. Few species emitted unique compounds, but blends of volatile organic compounds (VOCs) could largely distinguish species at select time points. Infections of trees were detectable at 9 and 21 days post artificial stem inoculations, based on the accumulation of a few compounds. None of the *in vitro Phytophthora*-produced VOCs were detected in infected trees. Root infection assays are currently being conducted.

10:30-11:00 BREAK

## 11:00-11:15 Update on Phytophthora diagnostics in Ireland

Richard O'Hanlon[1], Amanda Brechon[1], Brian O Loinsigh[1], Kayleigh Waites[1], Louise Cullen[1], Maria Destefanis[1], Manuel Lopez Vernaza[1], Rebecca Ham [1]

[1] Department of Agriculture, Food and the Marine, Ireland

Evolving EU phytosanitary regulations have changed how official laboratories in the EU diagnose *Phytophthora* infections in plants. The changing status of *Phytophthora ramorum*, as well as implications of the official controls regulation of the EU have meant that laboratories have had to put much more emphasis on quality assurance in testing. Ireland continues to have outbreaks of *P. ramorum* (EU1 and EU2) in *Larix* forests and has tested 400 samples for *Phytophthora* in 2021. Up until 2020, only the EU1 lineage of *P. ramorum* was detected in Ireland. However, in mid 2021 an outbreak of the EU2 lineage of *P. ramorum* was detected in a 65ha mixed forest of *Larix kaempferi* and *Abies procera*. Surveillance using methods from O'Hanlon et al. (2018) was set up to indicate the levels of spread of the pathogen at the site. Over the course of 4 months of weekly sampling, *P. ramorum* spread was detected on 13 of 15 sampling occasions. The spread was detected regularly in forest streams, while rainwater traps detected the pathogen on five occasions. Eradication actions were

undertaken by the national plant protection organization in late 2021. Further work was carried out in implementing diagnostic methods for the detection of *Phytophthora pluvialis*, after the detections of this pathogen in Britain (Perez Sierra et al. 2022). Sampling is underway for *P. pluvialis*, with no detections to date.

O'Hanlon, R., Choiseul, J., Brennan, J.M. and Grogan, H., 2018. Assessment of the eradication measures applied to *Phytophthora ramorum* in Irish *Larix kaempferi* forests. Forest Pathology, 48(1), p.e12389.

Pérez-Sierra, A.; Chitty, R; Eacock, A; Jones, B; Biddle, M; et al. (2022) First report of *Phytophthora pluvialis* in Europe causing resinous cankers on western hemlock. New Disease Reports; 45.

## 11:15-11:30 DNA metabarcoding complemented by baiting is the best methodological approach to unravel *Phytophthora* diversity in different kinds of ecosystems

Santa Olga Cacciola, Federico La Spada[1], Francesco Aloi[1], Mario Riolo[1,2,3], Antonella Pane[1], Peter J.A. Cock[4], Eva Randall[4], David E.L. Cooke[4]

[1] Department of Agriculture, Food and Environment, University of Catania, 95123 Catania, Italy;[2] Department of Agriculture, University Mediterranea of Reggio Calabria, 89122 Reggio Calabria, Italy[3] Council for Agricultural Research and Economics, Research Centre for Olive, Fruit and Citrus Crops (CREA-OFA), 87036 Rende, Italy, [4] The James Hutton Institute, Invergowrie, DD2 5DA Dundee, Scotland, United Kingdom

Over the past two decades, molecular diagnostic tools for identification of cultured *Phytophthora* species in combination with conventional isolation techniques have proved robust methods for the surveillance of *Phytophthora* communities from different kinds of ecosystems. More recently, metabarcoding approaches started to emerge as new paradigms for the detection and surveillance of all the species of a target genus present within an environmental sample. In this study, the Illumina metabarcoding and a conventional baiting isolation technique complemented each other to unravel the variability in *Phytophthora* communities from (i) natural, (ii) semi-natural and (iii) horticultural ecosystems of Sicily. Of 39 composite rhizosphere soil samples (17 from a nature reserve, 12 from a botanical garden and 10 from a citrus orchard) processed by both leaf baiting and Illumina metabarcoding 28 (72%) were classified as *Phytophthora*-positive (10 from the nature reserve, 11 from the botanical garden and 7 from the citrus orchard). In total, the 1,406,613 ITS1 sequences obtained by metabarcoding together with the 155 baited isolates enabled the discrimination of 21 *Phytophthora* taxa, five exclusively by baiting (*P. bilorbang*, *P. cryptogea*, *P. gonapodyides*, *P. parvispora* and *P. pseudocryptogea*), 12 exclusively by metabarcoding (*P. asparagi*, *P. occultans*, *P. psycrophila*, *P. syringae*, *P. aleatoria*/*P. cactorum*, *P. castanetorum*/*P. quercina*, *P. iranica*-like, *P.* unknown taxon 1, *P.* unknown taxon 2, *P.* unknown taxon 3, *P.* unknown taxon 4, *P.* unknown taxon 5) and four with both techniques (*P. citrophthora*, *P. multivora*, *P. nicotianae* and *P. plurivora*).

Results from this study suggested that the combined use of an efficient leaf baiting technique and a reliable metabarcoding detection method is the best approach for describing the variability of *Phytophthora* communities from natural and managed ecosystems. This study also revealed new insights about the behavior of some *Phytophthora* species and the presence of rare or undescribed *Phytophthora* taxa.

Burgess, T.I.; White, D.; McDougall, K.M.; Garnas, J.; Dunstan, W.A.; Català, S.; Carnegie, A.J.; Worboys, S.; Cahill, D.; Vettraino, A.M.; et al. Distribution and diversity of *Phytophthora* across Australia. Pac. Conserv. Biol. 2017, 23, 150–162.

Bose, T.; Wingfield, M.J.; Roux, J.; Vivas, M.; Burgess, T.I. Community composition and distribution of *Phytophthora* species across adjacent native and non-native forests of South Africa. Fungal Ecol. 2018, 36, 17–25.

La Spada F, Cock PJA, Randall E, Pane A, Cooke DEL, Cacciola SO. DNA Metabarcoding and Isolation by Baiting Complement Each Other in Revealing *Phytophthora* Diversity in Anthropized and Natural Ecosystems. Journal of Fungi. 2022; 8(4):330. https://doi.org/10.3390/jof8040330

## 11:30-11:40 Cryopreservation of different *Phytophthora* species

Đorđević B, Bačová A, Hýsková A, Jung T.

Phytophthora Research Centre, Faculty of Forestry and Wood Technology, Mendel University in Brno, 61300 Brno, Czech Republic *Corresponding author: biljana.dordevic@mendelu.cz

In the past years, huge demand has been rising for reliable sources of *Phytophthora* cultures with stable characteristics for use as research and reference materials. However, the annual refreshing in agar media is very costly, time consuming and labor intensive with genetic stability implications of conventional serial transfers, including issues regarding potential loss by contamination and failure to regrow (Kapoore et al. 2019). Preservation of valuable genetic material is essential for any biological field with applications in freezing and storage of rare germplasm. Compared to serial sub-culturing on fresh nutritional media, cryopreservation often represents an optimal long-term conservation technique (Houseknecht et al. 2012). Cryopreservation is commonly defined as ultra-low temperature storage - in liquid nitrogen at temperatures ranging from -135 to -196 °C - of living cells, tissues and organs capable of resuming normal functions after return from a cryobank. The crucial factors influencing successful cryopreservation include proper pre-treatment, cryoprotectants, adequate freezing pace and cold-hardening. Finding the appropriate method for cryopreservation of each species is the ultimate goal of research in this field. In this study, we evaluated different cryopreservation treatments to identify proper cryoprotectant solutions, cold-hardening and other conditions appropriate for long-term maintenance. Altogether one hundred *Phytophthora* isolates from different temperature regions were tested (sterile, homothallic and heterothallic). Different cryopreservation conditions tested were appropriate for survival of the majority *Phytophthora* isolates, however, in some cases, preservation conditions were largely isolate specific.

Houseknecht, J.L., Suh, S., Zhou, J.J. (2012) Viability of fastidious *Phytophthora* following different cryopreservation treatments. Fungal Biology 116(10):1081-9.
Kapoore, R.V., Huete-Ortega, M., Day, J.G., Okurowska, K., Slocombe, S.P., Stanley, M.S., Vaidyanathan, S. (2019) Effects of cryopreservation on viability and functional stability of an industrially relevant alga. Scientific Report 9:2093.

## Diversity and Distribution I

## 11:40-12:05 Cataloging *Phytophthora* species of agriculture, forests, horticulture, and restoration outplantings in California

Tyler Bourret[1], Susan Frankel[2], Sebastian Fajardo[1] & David Rizzo[1]

[1]UC Davis,One Shields Ave, Davis CA , [2]Pacific Southwest Research Station, Albany, CA

A meta-analysis of *Phytophthora* detections within the state of California was conducted using publicly available sequences as a primary source of data. Accessions of ITS rDNA were cataloged from 800 Californian *Phytophthora* isolates, analyzed and determined to correspond to 80 taxa. Pathways of introduction and spread were analyzed by categorizing isolates' origins, grouped by land-use: (1) agriculture, (2) forests and other natural ecosystems, (3) horticulture and nurseries, or (4) restoration outplantings. The pooled *Phytophthora* meta-communities of the restoration outplantings and horticulture land-use categories were the most similar, whereas the communities pooled from forests and agriculture were least similar. *Phytophthora cactorum*, *P. pini*, *P. pseudocryptogea* and *P. syringae* were identified in all four land-use categories. *Phytophthora cactorum*, *P. ramorum* and *P. nicotianae* were associated with the greatest number of host genera, with 19, 17, and 13, respectively. The *Phytophthora* species most prevalent in California differ from those compiled from the scientific literature.

## 12:05-12:25 Current Status of *Phytophthora* in Australia

Treena Burgess,

Phytophthora Science and Management, Harry Butler Institute, Murdoch, Perth, Australia

In Australia, production losses in agriculture and forestry result from several well-known cosmopolitan *Phytophthora* species and infestation of natural ecosystems by *Phytophthora cinnamomi* have caused irretrievable loss to biodiversity, especially in proteaceous dominated heathlands (Burgess et al. 2019). For this study, all available records of *Phytophthora* in Australia were collated and curated. Australian databases hold records for 99 species, of which 19 are undescribed. Eight species have no records linked to molecular data, and their presence in Australia is considered doubtful. The 99 species reside in 10 of the 12 (-15) clades recognised within the complete phylogeny of *Phytophthora* (Burgess et al. 2021). The first species reported in Australia in 1900 was *Phytophthora infestans*. By 2000, 27 species were known, predominantly

from agriculture. The significant increase in species reported in the subsequent 20 years has coincided with extensive surveys in natural ecosystems coupled with molecular taxonomy and the recognition of numerous new phylogenetically distinct but morphologically similar species. Routine and targeted surveys within Australian natural ecosystems have resulted in the description of 27 species since 2009 (Burgess et al. 2017). The distribution of records is skewed toward regions with considerable activity in high productivity agriculture, horticulture and forestry, and native vegetation at risk from *P. cinnamomi*. However, for Western Australia, there is a large dataset covering species recovered from urban, rural and natural ecosystems that can be further divided into those from exotic or native hosts. The level of human disturbance in these environments has also been recorded. This data set enables two theories to be explored; the invasiveness of introduced *Phytophthora* species and the role of the urban environment as a bridgehead for these invasions.

Burgess TI, Edwards J, Drenth A, Massenbauer T, Cunnington JH, Mostowfizadeh-Ghalamfarsa R, Dinh Q, Liew ECY, White D, Scott P, Barber PA, O'Gara E, Ciampini JA, McDougall K, Tan Y-P, 2021. Current Status of *Phytophthora* in Australia. Persoonia - Molecular Phylogeny and Evolution of Fungi 47, 151-177.

Burgess TI, McDougall KL, Scott P, Hardy GESJ, Garnas J, 2019. Predictors of *Phytophthora* diversity and distribution in natural areas across diverse Australian ecoregions. Ecography 42, 594-607.

Burgess TI, White D, McDougall KL, Garnas J, Dunstan WA, Català S, Carnegie AJ, Worboys S, Cahill D, Vettraino A-M, Stukely MJC, Liew ECY, Paap T, Bose T, Migliorini D, Williams B, Brigg F, Crane C, Rudman T, Hardy GES, 2017. Distribution and diversity of *Phytophthora* across Australia. Pacific Conservation Biology 23, 150-162.

## 12:25-12:45 The P. ramorum outbreak in western France

Benoit Marçais[1], Simon Laubray, Renaud Ioos

[1]INRAE, France

In 2017, *P. ramorum* was identified in *Larix kaempferi* stands located in the state forest of Saint-Cadou and Hanvec (Finistère, Brittany). It was decided to clearcut 35 ha of affected and healthy neighboring larch stands in 2017-18 winter and 2018 spring in order to limit the epidemic development. A research program was initiated to investigate the possible means of *P. ramorum* survival on the local woody trees and understory species (Desprez-Loustau et al. 2018). Larch stands within a 15 km radius as well as the neighborhood of rhododendron nurseries with former *P. ramorum* report were surveyed. Altogether, very limited presence of *P. ramorum* was detected in 2018-21. Two new stands of infected *L. kaempferi* were found in close vicinity of the Saint-Cadou state forest, with clearcutting achieved in 2019 and 2021. *Phytophthora ramorum* was detected in the vicinity of affected larch stands of Saint-Cadou and also in the vicinity of 2 *Rhododendron* nurseries located at 15 km from the outbreak on *Castanea sativa* and on sub-spontaneous *Rhododendron*. In particular, in the Saint-Cadou forest, a disease focus was found to develop in 2020-21 on chestnuts in absence of any source of inoculum from larch. Altogether, the data confirm the epidemic course observed in Great Britain with establishment of *P. ramorum* on planted *Rhododendron*, spread to sub-spontaneous *Rhododendron*, strong disease development on Japanese Larch and final spread to chestnuts. We also confirm that the major risk in the Brittany context where larch is very scarce.

Desprez-Loustau, ML, Robin C, Ioos R, Marçais B, Pautasso M. 2018. Host species in the context of control of *Phytophthora ramorum*. ANSES opinion, Collective expert appraisal report. Available at: https://www.anses.fr/en/content/anses-opinion-and-report-host-species-context-control-phytophthora-ramorum

LUNCH

## Diversity and Distribution II
## 2:15-2:35 Why *Phytophthora* scientists must also be fire scientists

Richard Cobb

California Polytechnic State University, San Luis Obispo

If you are reading this abstract, I would wager that you're convinced *Phytophthora* is important. I would further wager that you expect *Phytophthora* to respond to environmental variation, including important disturbance events. What may or may not be more prominent in your thinking is whether the important work you do dovetails with the dominant management problem that co-occurs with some of the most impactful *Phytophthora* outbreaks: wildfire (Cobb 2022). Fire ecologists and managers envision and define forest health in very similar ways to forest pathologists but without the biological nuance needed to predict their dynamics. Similarly, forest pathologists are often surprised that the dynamics of wildfire occur at a spatial extent which does not correspond to that of most forest *Phytophthora* outbreaks – that is, *Phytophthora*-wildfire interactions do occur, but the relationship is often less obvious than you may expect (He et al. 2021). I demonstrate this problem for *Phytophthora ramorum* in California (Daniels et al. 2022), with three case studies: 1) fire-disease interactions using three major wildfires, 2) results from combined fuels-disease management experiments, and 3) an illustration of the disconnect between how managers view the risk, constraints, and effectiveness of wildfire vs disease management in this wildfire prone landscape. *Phytophthora*-focused forest health professionals will benefit from asking if *Phytophthora* management can influence the effectiveness of wildfire mitigation treatments and identifying when simple changes to fuels reduction treatments also improve *Phytophthora* management. While this statement is probably self-evident to the reader, understanding how to communicate your work in a fire-science framework will position you and your science to take advantage of management where *Phytophthora* are not the primary concern.

Cobb, R. C. 2022. The intertwined problems of wildfire, forest disease, and climate change interactions. Current Forestry Reports.

Daniels, H. A., S. M. Navarro, and J. M. LeBoldus. 2022. Local Eradication of *Phytophthora ramorum* Is Effective on Both NA1 and EU1 Lineages in Oregon Tanoak Forests. Plant Disease 106:1392–1400.
He, Y., G. Chen, R. C. Cobb, K. Zhao, and R. K. Meentemeyer. 2021. Forest landscape patterns shaped by interactions between wildfire and sudden oak death disease. Forest Ecology and Management 486:118987.

## 2:35-2:55 Emerging ink disease of chestnut in southern Switzerland

Simone Prospero[1], Malve Heinz[1], Juanita Engelbrecht[2], Patrick Fonti[1]

[1]WSL, Switzerland; [2]University of Pretoria, South Africa

In southern Switzerland, European chestnut (*Castanea sativa*) is the dominant tree species up to about 900 m a.s.l., forming a continuous forest belt of 30,000 hectares. Since the 1990s, an increasing mortality of chestnut trees has been observed. The specific symptoms displayed by the declining trees (i.e. thinning of the crown, small chlorotic leaves, necrotic lesions at the root collar) suggested an emergence of ink disease. In this study, we determined: 1) the current distribution and the causal agents of ink disease, 2) the population structure of *Phytophthora cinnamomi*, 3) the dynamic of an infection by both *P. cinnamomi* and *P. ×cambivora*, and 4) which tree species could potentially replace European chestnut in infected sites. Results of these analyses will be presented and discussed.

Prospero S, Conedera M, Heiniger U, Rigling D. 2006. Saprophytic activity and sporulation of *Cryphonectria parasitica* on dead chestnut wood in forests with naturally established hypovirulence. *Phytopathology* 96: 1337–1344.
Prospero S. 2017. Il mal dell'inchiostro del castagno: una malattia in espansione *Forestaviva* 68: 26-27.

## 2:55-3:10 Differential distribution of *Phytophthora* species in a heterogeneous forest landscape

Carmen Morales-Rodriguez; Leonardo Guidoni; Andrea Vannini

Tuscia University; Via San Camillo de Lellis snc 01100 Viterbo Italy

The Castelporziano Presidential Estate is located 25 Km from Rome's center, extending over a surface of 5,892 hectares. Various forest types characterize the lowland forest, including stone pine pure forest, biodiverse Mediterranean maquis, and evergreen and deciduous oak forests mainly composed of holm oak, cork oak, and English oak (Blasi et al 1998). In the last decade decline and mortality associated with *Phytophthora spp*. were recorded affecting single trees or small groups of oaks. A biodiversity study was carried out first to describe the spatial distribution of the different Phytophthora spp. having the oak species as a descriptor; second the biodiversity of the fungal community associated with oak rhizospheres specifically addressing the antagonists and symbionts with a possible role in supporting tree resilience versus oomycetes impact. Totally 22 different species of Phytophthora have been recorded, 18 species associated with cork oak, 16 with holm oak, and 12 with English oak. In all the three groups *P. cinnammomi* is the most abundant species, occupying around a third of the relative abundance in all three oak species considered, followed by *P. psychrophila* (range 8-17%) and *P.syringae* (range 2-11%). *Phytophthora quercina* was detected on English oak only, while *P. multivora* and *P. europea* were associated with holm oak only. The biodiversity of the fungal community confirmed the presence of some taxa, such as the genus *Russula*, associated with resilient trees in previous studies.

Blasi, C., and M. L. Carranza. 1998. Unita` ambientali e sottoinsiemi di paesaggio del Parco Nazionale del Circeo. Pages 13–21, in A. Stanisci and S. Zerunian, editors. Flora e Vegetazione del Parco Nazionale del Circeo. Ministero per le Politiche Agricole, Gestione ex Azienda di Stato Per Le Foreste Demaniali, Sabaudia, Italy

## 3:10-3:25 Oomycete Detections and Associated Vegetation Decline in California's North Coast

Chris Lee[1], Tyler Bourret[2], Kim Corella[1], Suzanne Latham[3], Cheryl Blomquist[3], Susan Marshall[4], Tedmund Swiecki[5], Elizabeth Bernhardt[5] & Yana Valachovic[6]

[1]California Department of Forestry and Fire Protection, [2]University of California, Davis, [3]California Department of Food and Agriculture, [4]California Polytechnic State University, Humboldt, [5]Phytosphere Research; [6]University of California Cooperative Extension

California's northern coast, from Santa Cruz County up to the Oregon border, is a fertile crossroads for native and non-native oomycete diversity. Over the last half-century, and particularly during the last twenty years, numerous non-native oomycete plant pathogens have been detected in this area that features abundant precipitation, mild temperatures, and pervasive anthropogenic landscape alteration. Although the best-known of these are *Phytophthora ramorum* and *Phytophthora lateralis*, others are present and causing damage, some well-characterized (e.g., *Phytophthora cinnamomi*) and others yet to be comprehensively assessed (e.g., *Elongisporangium undulatum*, *Phytophthora pseudocryptogea*). In many cases the vegetation declines associated with these detections are severe and extensive. The diversity and widespread nature of oomycete pathogens in this region presents an acute need for further research into their pathogenicity, host ranges, spread mechanisms, and management. This presentation features a gallery of these detections and declines with descriptions of associated abiotic and biotic factors.

Bourret, T.B., Fajardo, S.N., Engert, C.P., & Rizzo, D.M. (2022). A barcode-based phylogenetic characterization of *Phytophthora cactorum* identifies two cosmopolitan lineages with distinct host affinities and the first report of *Phytophthora pseudotsugae* in California. Journal of Fungi 8, 303.

Garbelotto, M., Frankel, S.J., & Scanu, B.(2018). Soil- and waterborne *Phytophthora* species linked to recent outbreaks in Northern California restoration sites. California Agriculture, 72(4), 208-216.

Lee, C.A., Voelker, S., & Angwin, P.A. (2019). Investigating causes of bishop pine decline on California's north coast. Chapter 8 (pp. 145-153) in Potter, K.M., Conkling, B.L., eds. Forest Health Monitoring: National Status, Trends, and Analysis 2018. Asheville, NC: USDA Forest Service.

## 3:25-3:35 A survey in natural ecosystems of Louisiana revealed a high diversity of previously known and new *Phytophthora* taxa

Tomas Majek[1], Tamara Corcobado Sánchez, Ivan Milenković, Monique Ferreira de Souza, Raghuwinder Singh, Josef Janousek, Marília Horta Jung, Thomas Jung

[1]Phytophthora Research Centre, Faculty of Forestry and Wood Technology, Mendel University in Brno, Zemědělská 3, 61300 Brno, Czech Republic

In 2020 a survey of *Phytophthora* diversity was performed at 14 locations, natural forests, rivers and marshes across the state of Louisiana. Rhizosphere soil samples and naturally fallen leaves floating in forest streams were collected and transported to the laboratory at Louisiana State University where the isolation tests were performed using a standardized baiting method (Jung et al. 1996). Collected leaves from streams and necrotic leaves from baited soils were plotted on sterilized paper towels, and segments with necrotic spots plated onto selective PARPNH-V8 agar (Jung et al. 1996). Emerging *Phytophthora* colonies were immediately subcultured onto fresh V8 agar and subjected to sequencing of the ITS and cox1 gene regions for species identification. Over 500 isolates containing eight known and seven putatively new *Phytophthora* taxa, together with multiple *Pythium* and *Phytopythium* species were obtained. Most isolates belonged to *P. chlamydospora*, *P. ×stagnum* and *P. mississippiae*. In addition, at several sites *P. cinnamomi* and *P. citrophthora* were isolated. Furthermore, seven yet undescribed *Phytophthora* taxa were found, including two taxa each from *Phytophthora* Clades 2 and 7, and three taxa from Clade 10. Morphological studies, temperature-growth tests and multigene phylogenetic analyses are currently underway for the official description of all new *Phytophthora* taxa. Since the pathogenicity and host ranges of the new taxa are still unknown, their occurrence in natural ecosystems could pose a potential risk as does the finding of the aggressive wide-host range pathogen *P. cinnamomi*.

Jung T, Blaschke H, Neumann P, 1996. Isolation, identification and pathogenicity of *Phytophthora* species from declining oak stands. European Journal of Forest Pathology 26, 253-72

3:35-4:05 BREAK

## Management

## 4:05-4:25 The decline of the monumental cork oak forest of San Vito and Valle Marina: adopted mitigation strategies and preliminary results

Andrea Vannini, L. Guidoni, W. Aurangzeb, C. Morales Rodriguez

DIBAF-Università degli Studi della Tuscia, Italy

The Regional Reserve of Monti Ausoni e Lago di Fondi includes the San Vito e Valle Marina forest, the largest cork oak forest in peninsular Italy hosting several centenary-old monumental trees that deserve to be singly protected and preserved. The oomycete population of this forest has been studied by metabarcoding (HTS) and classical biological diagnostics, suggesting *Phytophthora cinnamomi* as the main driver of the decline. *Phytophthora cinnamomi* heavily impacts this area in three large foci covering a surface of 50.7 hectares (45.7% of the total area). The Department of Environmental protection of the Latium Region funded an applied project aiming to mitigate the impact of *P. cinnamomi* in the cork oak forest of San Vito and Valle Marina. Potassium phosphonate has been used to mitigate the impact on trees and increase their resilience and resistance to the pathogen. About 1,800 and 300 trees were treated with K-phosphonate by trunk injection respectively in 2021 and 2022 in the three foci. The persistence of phosphonate at appreciable concentrations 'in planta' was confirmed after one year of the treatment. A possible mechanism of release of phosphonate in soil by treated plants putatively made available for neighboring untreated ones was also hypothesized and discussed. Furthermore, the crown status and recovery/death of treated plants in the different disease classes has been evaluated. A soil drench treatment with Biofence FL© to contrast the inoculum pressure in soil and its dispersal was tested in mesocosm and open field by evaluating the oomycide activity on artificial inoculum buried at different depths. Biofence FL© is a commercial product consisting of a liquid formulary and Brassica flour. *Brassica* spp. contain high concentrations of glucosinolates (GLS) in specific cell types that are part of the natural defense systems of these plants. The efficiency to control oomycetes has been demonstrated in the case of *Phytophthora* spp. and it is comparable with the traditionally used conventional chemical oomycides (Morales-Rodriguez et al., 2016).

Morales-Rodríguez, C., Vettraino, A. M., & Vannini, A. (2016). Efficacy of biofumigation with *Brassica carinata* commercial pellets (BioFence) to control vegetative and reproductive structures of *Phytophthora cinnamomi*. Plant Disease, 100(2), 324-330.

## 4:25-4:40 Are oomycetes associated with the dieback of western redcedar?

Joseph Hulbert, Jennifer Olson, Nicole Vonberckefeldt, Taylor Warnick, Kara Lanning, Marianne Elliott, Gary Chastagner

Washington State University, Washington, United States of America

Western redcedar is a culturally important tree species in the Pacific Northwest. It has provided many resources to indigenous communities in the region since time immemorial, but concern about its availability for future generations has grown since 2015 when the region experienced a notable drought. Increased levels of dieback have been reported and cultural resource managers need confirmation or rejection of a relationship between tree health and oomycete communities. Assessment of these communities will reveal potentially important factors to account for in conjunction with climate adaptation planning. This work will inform future research needs to avoid the planting of maladapted seed-sources, and possibly identify emerging or under-recognized ecosystem impacts from cryptic oomycete species.

## 4:40-4:55 *Phytophthora agathidicida* oospore deactivation by heat treatment

Matthew Arnet, Ian Horner

Plant and Food Research, Private Bag 1401, Havelock North 4157, New Zealand

The thermal tolerance of *Phytophthora agathidicida* (the pathogen responsible for kauri dieback), and the potential for using thermal extremes to eliminate the pathogen from soil or planting material were assessed. A series of experiments were carried out to assess low and high temperature extremes, with each experiment informing the choice of parameters for subsequent analysis. Deactivation of *P. agathidicida* oospores was assessed in vitro on V8 agar, inoculated sterile kauri roots and in inoculated kauri roots in potting mix and three different naturally infested field soils containing colonized kauri roots. Freezing infected material was ineffective at completely deactivating *P. agathidicida* but recovery declined over time at both -15 and -20°C. No isolates survived at temperatures above 45°C for all time periods measured. Two days at 40°C resulted in a complete kill of all *P. agathidicida* inoculum, while it took 14 days to achieve the same result at 35°C. Interestingly, *P. agathidicida* had lower tolerance to heat in naturally colonized soil at 35°C, with only one detection after 4 days. A preliminary study to determine the thermal tolerance kauri (*Agathis australis*) was conducted. Seedlings were exposed to temperatures ranging from 20°C to 45°C for up to 14 days. Seedling survival was found to overlap with temperature x time combinations found to deactivate *P. agathidicida*, providing a possible method for treating kauri seedling potentially infected with *P. agathidicida*.

## 4:55-5:10 Evidence of phosphonate tolerance in *Phytophthora cinnamomi* from New Zealand avocado orchards

Shannon Hunter[1], R. McDougal[2], N. Williams[1] and P. Scott[3]

[1]Plant and Food Research, Private Bag 1401, Havelock North 4157, New Zealand, [2]Forest Protection, Scion, Rotorua 3010, New Zealand, [3]Western Australia Department of Primary Industries and Regional Development, Perth, Australia

There is a limited number of chemical control agents for managing *Phytophthora* root and collar rot diseases of avocado internationally, of these, phosphite is one of the most effective. To determine if prolonged phosphite use in New Zealand avocado orchards has led to decreased sensitivity of *Phytophthora cinnamomi* Rands to phosphite, 57 isolates were collected from phosphite-treated and untreated avocado orchards and screened for tolerance using a mycelial growth inhibition assay. The inhibitory effect of phosphite on mycelial growth was tested in vitro using six concentrations of phosphite. Based on $EC_{50}$ tests three phosphite susceptible ($EC_{50}$ range 17.5 – 25.9 µg/mL) and three tolerant ($EC_{50}$ range 81.8 – 163.2 µg/mL) isolates were selected. The effect of phosphite on the colonization of lupin seedling roots and sporangia and zoospore production of three susceptible and three tolerant isolates were determined. The three tolerant isolates colonized lupin roots more extensively than the three sensitive isolates in the presence of 5 and 10 g/L phosphite. The tolerant isolates were able to asymptomatically colonize further above the lesion margin in the 5 g/L phosphite treated lupins relative to the phosphite sensitive isolates but no isolates were completely resistant to phosphite. The tolerant isolates produced more sporangia and consequently zoospores, in the presence of phosphite than the susceptible isolates.

DOBROWOLSKI, M. P., SHEARER, B. L., COLQUHOUN, I. J., O'BRIEN, P. A. & HARDY, G. E. S. J. 2008. Selection for decreased sensitivity to phosphite in *Phytophthora cinnamomi* with prolonged use of fungicide. Plant Pathology, 57, 928-936.\

KASUGA, T., HAYDEN, K. J., EYRE, C. A., CROUCHER, P. J. P., SCHECHTER, S., WRIGHT, J. W. & GARBELOTTO, M. 2021. Innate resistance and phosphite treatment affect both the pathogen’s and host’s transcriptomes in the tanoak-*Phytophthora ramorum* pathosystem. Journal of Fungi, 7.

MA, J. & MCLEOD, A. 2014. In vitro sensitivity of South African *Phytophthora cinnamomi* to phosphite at different phosphate concentrations. South African Avocado Growers' Association Yearbook, 37.

## 5:10-5:20 Understanding and managing the impact of *Phytophthora* diseases in horticulture

Fryni Drizou[1] Lisa Ward[2], Elizabeth J. Beal[1], Glen Powell[1]

[1]Royal Horticultural Society, Department of Plant Health, RHS Wisley, Woking, Surrey, [2]Forest Research, Foss House, York

*Phytophthora* diseases are consistently one of most commonly found diseases in UK gardens. In the RHS gardens, they cause significant plant losses. The past years we faced outbreaks of *P. ramorum* in RHS Rosemoor, which has raised questions on the efficacy surveillance and management of this pathogen. While a significant amount of literature is available for *Phytophthora* affecting forestry and agriculture, this

pathogen diversity and impact on gardens has not been widely studied. Great number of plants come into gardens via global plant trade. *Phytophthora* diseases are intercepted mainly with visual inspections and plant quarantine. However, considering that some species can be asymptomatic, these interception methods become questionable. Further, the lack of control methods for *Phytophthora* limits our management strategies to cultural practices and plant destruction, both timely and costly to gardeners. Understanding which *Phytophthora* species are most prevalent in gardens, their interaction with horticultural plants as well as the origin and pathways of *Phytophthora* spread in gardens, will enable us to evaluate and improve surveillance and develop sentinel planting recommendations.


Beal L, Waghorn I, Perry J, Clover GRG, Cromey M. Susceptibility of Garden Plants to *Phytophthora* Root Rot. Plant Dis. 2020 Sep 8. doi: 10.1094/PDIS-04-20-0765-RE. Epub ahead of print. PMID: 32897156.

Garbelotto, M, Schmidt, D, Popenuck, T. Pathogenicity and infectivity of *Phytophthora ramorum* vary depending on host species, infected plant part, inoculum potential, pathogen genotype, and temperature. Plant Pathol. 2021; 70: 287– 304. https://doi.org/10.1111/ppa.13297

Green S, Cooke DEL, Dunn M, Barwell L, Purse B, Chapman DS, Valatin G, Schlenzig A, Barbrook J, Pettitt T, Price C, Pérez-Sierra A, Frederickson-Matika D, Pritchard L, Thorpe P, Cock PJA, Randall E, Keillor B, Marzano M. PHYTO-THREATS: Addressing Threats to UK Forests and Woodlands from *Phytophthora*; Identifying Risks of Spread in Trade and Methods for Mitigation. Forests. 2021; 12(12):1617. https://doi.org/10.3390/f12121617

## 5:20-5:30 Screening for Resistance to *Phytophthora lateralis* in Port-Orford-cedar (*Chamaecyparis lawsoniana*)

Elizabeth Stamm[1], David Showalter[1], Evan Heck[2], Richard Sniezko[2], Jared LeBoldus[1]

[1]Department of Botany and Plant Pathology, Oregon State University , [2]Dorena Genetic Resource Center, US Forest Service

Port-Orford-cedar (*Chamaecyparis lawsoniana*) is an integral ecological component of mixed-conifer forests in southwest Oregon and northwest California as well as an economically valuable timber tree and horticultural crop. In the early 1950's, its range was infiltrated by the non-native root-rot pathogen *Phytophthora lateralis*, dealing a devastating blow to native populations. While most naturally-occurring Port-Orford-cedars show high levels of susceptibility to *P. lateralis*, heritable resistance was demonstrated by Hansen et al. in 1989, with subsequent elucidation of the two types of resistance by Sniezko et al. 2000. With the objective of restoring Port-Orford-cedar in stands affected by *P. lateralis*, a breeding and screening program was created through a collaborative effort of USDA Forest Service, USDI BLM, with key research support and inoculation facilities with Oregon State University. Through this initiative, resistance screening trials conducted at Oregon State University are used to inform the breeding program at USDA Forest Service Dorena Genetic Resource Center and produce resistant seed stock. Resistant seed is now being used for reforestation and restoration by numerous groups. Resistance screening is continuing in order to expand the number of resistant parent trees in some containerized orchards and to increase the level of resistance in orchards. Further research on topics such as durability and stability of resistance, along with evaluation of pathogen persistence over time in resistant plantings is needed.

Hansen, E.M., Hamm, P.B. and Roth, L.F. (1989). Testing Port-Orford-Cedar for Resistance to *Phytophthora*. The American Phytopathological Society, 73, pp.791–794.

Schenck, N., Fourrier-Jeandel, C. and Ioos, R. (2016). A robust and specific real-time PCR tool for the detection of *Phytophthora lateralis* in plant tissues. European Journal of Plant Pathology, 146(2), pp.231–244. doi:10.1007/s10658-016-0909-7.

Sniezko, R.A., Johnson, J.S., Reeser, P., Kegley, A., Hansen, E.M., Sutton, W. and Savin, D.P. (2019). Genetic resistance to *Phytophthora lateralis* in Port-Orford-cedar (*Chamaecyparis lawsoniana* ) – Basic building blocks for a resistance program.PLANTS, PEOPLE, PLANET, 2(1), pp.69–83. doi:10.1002/ppp3.10081.

## 5:30-5:40 LIFE-FAGESOS- *Phytophthora*-induced decline of *Fagaceae* ecosystems in Southern Europe exacerbated by climate change: preserving ecosystem services through improved integrated pest management

Andrea Vannini[1], B. Scanu[2], F. Ruiz-Gomez[3], J. Laranjo[4], C. Morales-Rodríguez[1]

[1]DIBAF-Università degli Studi della Tuscia, Italy, [2]Università degli Studi di Sassari, Italy, [3]University of Cordoba, Spain, [4]Tras-os-Montes e Alto Douro, Portugal

This new EU LIFE project aims to address and remediate one of the most severe threats associated with Global Changes, i.e climate and biological invasions: The outbreak of Alien Invasive Plant Pathogens, adversely impacting natural and semi-natural forest ecosystems. *Phytophthora* diseases are increasing their impact and distribution range in evergreen oak and chestnut ecosystems of the Mediterranean basin, boosted by temperature increases and extreme weather events such as flooding and drought (Ruiz Gómez et al., 2019). Scarce public awareness, sensible human impact on forest areas, and the new EU regulation on fertilizers, that limits the use of K-phosphonate in natural and seminatural ecosystems, further increase the risk for *Fagaceae* ecosystems. Challenged Forest Ecosystems need improved tools & strategies to enhance their adaptation to the outlined issue, finally ensuring their preservation as important natural carbon sinks. The project FAGEOS, by joining 13 multi-actor partners, among which the Universities of Tuscia, Sassari (Italy) Cordoba (Spain), Tras-os-Montes e Alto Douro (Portugal), will develop, test, and transfer knowledge and technologies to contrast *Phytophthora* epidemics, specifically addressing: i) The delivery of regional maps for risk- and impact assessment of *Phytophthora* diseases in the Mediterranean basin in diverse current and predicted climatic scenarios, ii) The development, validation, implementation, and dissemination of Integrated Pest Management (IPM) protocols, tailored to the specific target ecosystem and iii) The delivery of fully accessible monitoring protocols, based on validated, innovative models & technologies.

Ruiz Gómez, F. J., Navarro-Cerrillo, R. M., Pérez-de-Luque, A., Oβwald, W., Vannini, A., & Morales-Rodríguez, C. (2019). Assessment of functional and structural changes of soil fungal and oomycete communities in holm oak declined dehesas through metabarcoding analysis. *Scientific reports*, *9* (1), 1-16.

# TUESDAY 21 June

## Morning ZOOM session

## 9:00-9:40 Keynote Address - Disturbance effects on pathogens and disease emergence

Lauren Waller

Tiakina Kauri, Ministry of Primary Industries

Emerging diseases from fungal and fungal-like pathogens are causing more large-scale native plant declines and localized extinctions than ever before. Declines have accelerated due to anthropogenic disturbances, such as invasion by novel plants and pathogens and climatic change (Burgess et al 2022). In this talk, I will discuss past, present and future work aimed at understanding how disturbance influences ecological interactions between plants and pathogens and disease emergence in plant communities (Waller et al. 2020. I will discuss some of the challenges and barriers to understanding and managing the effects of disturbance on plant communities and present methods we can use to measure and understand the impacts of disease on plant communities and ecosystems (Waller et al. In Press).

Burgess, T. I., Oliva, J., Sapsford, S. J., Sakalidis, M. L., Balocchi, F., & Paap, T. (2022). Anthropogenic Disturbances and the Emergence of Native Diseases: a Threat to Forest Health. *Current Forestry Reports*, 1-13.

Waller, L.P., Sapsford, S., Thurston, A. & Black, A. (in press). Is provenance or phylogeny a better predictor of growth and survival of a soil pathogen in leaf litter? Forest Ecology and Management.

Waller, L. P., Allen, W. J., Barratt, B. I. P., Condron, L. M., França, F. M., Hunt, J. E., Koele, N., Orwin, K.H., Steel, G.S., Tylianakis, J.M. and Wakelin, S.A. & Dickie, I. A. (2020). Biotic interactions drive ecosystem responses to exotic plant invaders. *Science*, *368*(6494), 967-972.

## 9:40-10:00 Global invasion history of the emerging plant pathogen Phytophthora multivora

Tetyana Tsykun[1], Simone Prospero[1], Corine N. Schoebel[1], Alexander Rea[2], Treena I. Burgess[3]

1)Swiss Federal Research Institute WSL, Zürcherstrasse 111, CH-8903 Birmensdorf, Switzerland, 2) Department of Diagnostic Genomics, PathWest Laboratory Medicine Western Australia, Australia, 3) Phytophthora Science and Management, Harry Butler Institute, Murdoch, Perth, Australia

Global trade of plants and plant material has significantly increased the geographic distribution of many plant pathogens. *Phytophthora multivora* is one of well-known invasive pathogens of forest ecosystems. Following the description of *P. multivora* from dying native vegetation in Australia in 2009, the species was subsequently found to be common in South Africa where it does not cause any remarkable disease. There are now reports of *P. multivora* from many other countries worldwide. A global collection of 335 isolates from North America, Europe, Africa, Australia, the Canary Islands, and New Zealand was used to unravel the worldwide invasion history of *P. multivora*, using 10 microsatellite markers for all isolates and sequence data from five loci from 94 representative isolates. The *P. multivora* populations in South Africa, Australia, and New Zealand show the most complex genetic structure, suggesting they are well established and evolutionary older than those in Europe, North America and the Canary Islands. According to the conducted analyses, the world invasion of *P. multivora* most likely commenced from South Africa, which can be considered the center of origin of the species (Tsykun et al. 2022). The pathogen was then introduced to Australia, which acted as bridgehead population for Europe and North America. Our study highlights a complex global invasion pattern of *P. multivora*, including both direct introductions from the native population and secondary spread from bridgehead populations.

Tsykun T., Prospero S., Schoebel C. N., Rea A., Burgess T. I. (2022). Global invasion history of the emerging plant pathogen *Phytophthora multivora*. BMC genomics, 23(1), 1-16.

## 10:00-10:20 Rehabilitation of old *Phytophthora cinnamomi* impacted jarrah (*Eucalyptus marginata*) forest sites using seed enhancement technologies.

Shanika Harshani[1], Giles Hardy[1], Treena Burgess[1], Todd Erickson[2]

[1]Phytophthora Science and Management, Centre for Climate Impacted Terrestrial Ecosystems, Harry Butler Institute, Murdoch University, Murdoch 6150, Australia, [2]Department of Biodiversity, Conservation and Attractions, Kings Park Science, Perth, WA, Australia

The jarrah forest in Western Australia has been severely impacted by Phytophthora dieback. Complete eradication of the pathogen from infested sites is not possible. Therefore, attempts to rehabilitate dieback sites with P. cinnamomi tolerant native plant species are being made. To achieve this, seed enhancement techniques are being tested. A vegetation survey and a pathogenicity assessment were carried out to quantify the impact of the pathogen and identify the tolerant native plant species. Seed enhancement technologies improve seed germination and seedling emergence, prevent seed predation and simplify seed distribution. Extruded pellets were selected as the most suitable seed enhancement for the potential species use in rehabilitation. The optimum percentages of dry ingredients required to produce pellets were examined using five different formulations with seeds of four species: Acacia acuminata, Calothamnus sanguineus, Hakea laurina and Melaleuca seriata. Seeds were placed in the middle of the pellet. Seedling emergence in pellets compared to the controls was considerably reduced in all species. Next, two differently produced pellets; premade and field-deployed, were tested using the best pellet formulation and randomly placing the seeds of same species across the pellet. Above 80% emergence in A. acuminata pellets and higher emergence over controls in pellets of M. seriata and C. sanguineus indicate the feasibility of using pelleted seeds to rehabilitate dieback sites.

## 10:20-10:40 Phosphite spray for the control of oak decline induced by *Phytophthora* in Europe

Alejandro Solla[1], Gerardo Moreno [1], Tadeusz Malewski [2], Thomas Jung [3], Marcin Klisz [4], Miłosz Tkaczyk[4], Marta Siebyla[4], Andrea Perez[1], Elena Cubera[1], Heorhiy Hrynyk[5], Wieslaw Szulc [6], Beata Rutkowska [6], Juan Antonio Martín[7], Lassaad Belbahri[8], Tomasz Oszako[9]

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Forest decline induced by *Phytophthora* is a global phenomenon that affects many tree species. Since the 2000s, in central Europe, the health of *Quercus robur* has been declining due to various biotic and abiotic factors. In drought-prone areas of the Mediterranean region, forests of *Q. ilex* have shown tree mortality since the 1980s. The efficacy of potassium phosphite, applied as a foliar or trunk spray at a range of concentrations between 0 and 35%, was investigated over several years in four field trials with mature oaks. Specifically, experiments 1 and 2, conducted on *Q. robur* in Poland indicated that aerial and trunk spray of 35% phosphite improved the crown condition of unhealthy trees. The efficacy of treatments was not dependent on the initial tree health condition, although its effects started earlier in trees that had lower crown transparency. Treatments did not alter the abundance and composition of edaphic and endophytic bacteria of trees. Moreover, aerial spray enhanced the N, P and Mg leaf content and induced the formation of fine roots without compromising the secondary growth of trees. In experiment 3, conducted in Spain on *Q. ilex*, foliar spray did not improve the crown condition of trees. However, foliar spray of 0.56% phosphite induced twig growth in treated south-facing trees. No reduction in *Phytophthora* inoculum was observed with the use of phosphite. Our study provides the basis for the development of a cost-effective management tool for *Phytophthora* in Europe and motivates future research into the optimization of treatments in *Q. ilex* and *Q. robur*.

Solla, A., Moreno, G., Malewski, T. et al. (2021). Phosphite spray for the control of oak decline induced by *Phytophthora* in Europe. Forest Ecology and Management, 485, 118938.

10:40-11:10 BREAK

## 11:10-11:30 Dilution of *Phytophthora cinnamomi* inoculum in chestnut stands by non-competent host species

Cécile Robin, France Marylise Marchand

INRAE, UMR BIOGECO, 33 610 Cestas, France

Host diversity and susceptibility are driving factors of emerging forest diseases caused by *Phytophthora* species (Prospero and Cleary 2017). A high host diversity may decrease the disease risk, an effect that is called the dilution effect (Keesing et al. 2006). Conversely, an amplification effect is observed when less susceptible species are reservoir hosts. Evidence of both models exists for diseases caused by *Phytophthora* in the forest environment. In the case of the chestnut ink disease (CID), caused by *P. cinnamomi* and/or *P. x cambivora*, any strong evidence has been provided for either type of effect. On chestnut trees, true "ink symptoms" caused by *P. cinnamomi* are rarely observed at the collar level. However, root infections result in a generalized tree dieback which is difficult to distinguish from dieback induced by drought or anoxia. Therefore, the detection of *P. cinnamomi* in soil or in roots is necessary to investigate whether forest diversity can limit the dissemination of the pathogen. We adapted a metabarcoding pipeline to assess the quantity of *P. cinnamomi* in the soil. In a chestnut forest mixed with other tree species, the abundance of *P. cinnamomi* was lower in mixed than in pure sub-plots, suggesting the existence of a dilution effect related to community diversity. Host competence is defined as the host ability to transmit inoculum to another plant. Through an experimental approach, we obtained the first evaluation of host competence for *P. cinnamomi* of different forest species. The sessile oak (*Quercus petraea*) and the pedunculate oak (*Q. robur*) were found to have very low competence for *P. cinnamomi*. These results are in good agreement with the dilution effect observed. They could have important implications for the management of chestnut and oak ecosystems threatened by the ink disease.

Prospero, S., & Cleary, M. (2017). Effects of host variability on the spread of invasive forest diseases. Forests, 8(3), 1–21.

Keesing, F., Holt, R. D., & Ostfeld, R. S. (2006). Effects of species diversity on disease risk. Ecology Letters, 9(4), 485–498.

## 11:30-11:50 The susceptibility to *Phytophthora* root-rot varies between the genotypes of *Eucalyptus nitens*

Tanay Bose[1], Almuth Hammerbacher[2], Wayne Jones[3],, Bernard Slippers[1], Michael J Wingfield[1]

[1]Departments of Biochemistry Genetics and Microbiology, and Zoology and Entomology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa, [2]Department of Zoology and Entomology Forestry and Agricultural Biotechnology Institute (FABI) University of Pretoria South Africa,[3] Sappi Forests Pty. Ltd. South Africa, Jolanda Roux, Sappi Forests Pty. Ltd. South Africa

*Eucalyptus nitens* is an important cold-tolerant tree species commercially planted in South Africa. This eucalypt species is threatened by various native and invasive pests and pathogens, including *Phytophthora*. Recently, a previously unknown root-rot disease has been affecting *E. nitens* plants in the first year of planting up to the age of four years. The severity of this disease resulted in a reduction of land planted for this species in South Africa. The causal agent of this disease could not be conclusively identified, but the symptoms observed in the field indicated *Phytophthora* as a plausible candidate. DNA fingerprinting of the affected trees showed that the selfed genotypes of E. nitens were highly susceptible to this root-rot disease. In this study, greenhouse trials were conducted to test the pathogenicity of two *Phytophthora* species (*P. alticola* and *P. cinnamomi*) on three genotypes of *E. nitens* (selfed, outcrossed, and hybrid-*E. nitens* x *E. grandis*). The data from these trials showed that (1) selfed *E. nitens* seedlings were highly susceptible to the *Phytophthora* species tested, followed by the outcrossed genotype, (2) root rot severity was higher among seedlings inoculated with *P. cinnamomi*, and (3) the hybrid genotypes showed tolerance towards both the *Phytophthora* species tested. This study confirmed the deleterious effects of inbreeding, which can substantially reduce fitness among tree species, making them susceptible to an assortment of native and introduced plant pathogens, such as various species of *Phytophthora*.

JONES, W. R. 2019. Survey results of *Eucalyptus nitens* survival plots SES001T. Howick, KwaZulu-Natal: Sappi Forests.

JONES, W. R., STANGER, T. K. & NDWALANE, W. 2004. Final results from *Eucalyptus nitens* trial series EG003T-EG005T. Research Document 09/2004. Howick, KwaZulu-Natal: Sappi Forests.

MARAIS, C., REYNOLDS, M. & MYBURG, A. A. 2017. Pedigree reconstruction of *E. nitens* showing signs of disease stress (SAP1.2.58b). Pretoria, South Africa: Forest Molecular Genetics Programme, University of Pretoria.

## 11:50-12:10 Diversity and impact of *Phytophthora* species in Mediterranean ecosystems

Bruno Scanu

Università degli Studi di Sassari, Italy

The Mediterranean basin is recognized as a global biodiversity hotspot accounting for more than 25,000 plant species that represent almost 10% of the world's vascular flora. However, Mediterranean ecosystems are currently threatened by invasive tree pathogens and climate change, which may act in synergy and potentially lead to significant economic and ecological losses. Species in the genus *Phytophthora* are among the most emerging tree pathogens in Mediterranean areas, in contrast with their need for free water to spread. Over the last decade, several new and previously unrecovered *Phytophthora* species have been detected in ornamental, agricultural and forest plants, in different environments, including agricultural and forest ecosystems, gardens and amenity parks (Jung et al. 2018). Ornamental and forest nurseries have shown to be the main pathway for introduction and spreading of *Phytophthora* species, with an exponential increasing of new arrivals of exotic species. This is the case of *P. heterospora*, a recently newly described species from olive trees in Italy, but most likely introduced from south-east Asia (Scanu et al. 2021). This pathogen is now well-established in agricultural tree crops in areas with Mediterranean and semi-arid climatic conditions, probably favored by the intensive cultivation systems. Mediterranean maquis vegetation and agroforestry systems dominated by evergreen oak or wild olive trees are severely impacted by *P. cinnamomi*, although several other new and unusual species seem to emerge and perhaps be involved in these decline events (Seddaiu et al. 2020). The diversity and impact of *Phytophthora* species on the sustainability of some of the most important Mediterranean-type ecosystems and the possible control strategies of the diseases they cause will be discussed.

Jung, T., Pérez-Sierra, A., Durán, A., Horta Jung, M., Balci, Y., Scanu, B., 2018. Canker and decline diseases caused by soil- and airborne *Phytophthora* species in forests and woodlands. Persoonia, 40, 182–220.

Scanu, B., Jung, T., Masigol, H., Linaldeddu, B.T., Jung, M.H., Brandano, A., Mostowfizadeh-Ghalamfarsa, R., Janoušek, J., Riolo, M., Cacciola, S.O. *Phytophthora heterospora* sp. nov., a new pseudoconidia-producing sister species of *P. palmivora*. Journal of Fungi 2021; 7(10), p.870.

Seddaiu, S., Brandano, A., Ruiu, P.A., Sechi, C., Scanu, B., 2020. An Overview of *Phytophthora* species inhabiting declining *Quercus suber* stands in Sardinia (Italy). Forests 2020, 11, p.971.

## 12:10-12:30 Updates on *Phytophthora* research: SOD reemergence, Sherlock assays, and rps10 metabarcoding

Niklaus J Grünwald

USDA ARS Corvallis, OR

Sudden oak death (SOD) continues to reemerge Oregon (LeBoldus et al., 2022). It was first detected in SW Oregon forests in 2001. The first invasion belonged to the NA1 clonal lineage of the SOD pathogen *Phytophthora ramorum*. We discovered a second invasion in 2015 by the EU1 lineage. In 2021, yet a third invasion was discovered and was characterized as belonging to the NA2 clonal lineage (Peterson et al., 2022). Rapid detection of pathogens is a crucial component of clinical diagnostics. CRISPR-Cas technology has recently been applied to developing diagnostic assays for specific recognition of DNA or RNA sequences. However, discovery of target RNA or DNA sequences that have conserved primers of the ingroup and a variable and diagnostic CRISPR RNA or DNA region for differentiating an ingroup from outgroups requires extensive bioinformatic analyses of genome sequences. We developed the algorithm KRISP that can identify primers and diagnostic CRISPR RNA or DNA regions that differentiate a set of ingroup and outgroup taxa at any taxonomic rank. We provide a proof-of-concept application using *P. ramorum* genomes. Using KRISP we were able to find a crRNA locus that can differentiate *P. ramorum* from other *Phytophthora* spp. We used LwaCas13a with the SHERLOCK technology to validate the assay and were able to get specific amplification of *P. ramorum* without cross amplification of non-target *Phytophthora* spp. The KRISP algorithm provides a novel tool for designing CRISPR-Cas diagnostic assays based on available genome sequences and results in a novel diagnostic assay requiring further validation in planta. Metabarcoding is revolutionizing microbial ecology by circumventing the limits of traditional culture-based techniques. We developed the new metabarcode locus, rps10, that has higher specificity and sensitivity for oomycete community analysis than the prior standard method based on ITS (Foster et al., 2022).

Riddell, C., Voglmayr, H., et al. (2022). A new oomycete metabarcoding method using the rps10 gene. Phytobiomes Journal PBIOMES-02-22-0009-R. https://doi.org/10.1094/PBIOMES-02-22-0009-R.

LeBoldus, J.M., Navarro, S.M., Kline, N., Ritokova, G., and Grünwald, N.J. (2022). Repeated emergence of sudden oak death in Oregon: Chronology, impact, and management. Plant Disease PDIS-02-22-0294-FE. https://doi.org/10.1094/PDIS-02-22-0294-FE.

Peterson, E.K., Sondreli, K.L., Reeser, P.W., Navarro, S., Nichols, C., Wiese, R., Fieland, V.J., Grünwald, N.J., and LeBoldus, J.M. (2022). First report of the NA2 clonal lineage of *Phytophthora ramorum* infecting tanoak in Oregon forests. Plant Disease in press. https://doi.org/10.1094/pdis-10-21-2152-pdn.

LUNCH

## Ecology and Epidemiology

## 2:00-2:25 Distribution of *Phytophthora* communities along a climatic gradient in Europe

Jonàs Oliva[1], Maria Caballol[1], Miguel Angel Redondo[2], Benoit Marcais[3], Thomas Jung[4], Ivan Milenkovic[4], Tamara Corcovado[4], Miguel Nemesio[5]

[1]University of Lleida, JRU-Agrotecnio-CTFC, Spain, [2]Swedish University of Agricultural Sciences, Sweden, [3]INRA-Nancy, France, [4]Mendel University, Czech Republic, [5]TEAGASC

Ireland's climate is one of the main abiotic constraints for species distributions in natural habitats. Little is known about how temperature and precipitation affect *Phytophthora* communities. We correlated climate with diversity and functional diversity of *Phytophthora* communities from 267 rivers and streams in Spain, France, Ireland, Southern (below the Arctic circle and Northern Sweden (above Arctic circle) including both a latitudinal (Spain-Northern Sweden) and an altitudinal gradient (Spain). Samples in Spain were taken both in autumn and spring so seasonal variation could be studied. Preliminary results show an agreement between the climatic signal found in both altitudinal and latitudinal gradients. In both, low temperatures and high rainfall areas constraining factors for diversity, correlate with functional traits such as resistant structures or optimal temperatures. Winter temperatures had the highest correlation with diversity indices revealing the potential effects of climate change if winters become milder in the near future.

## 2:25-2:45 Interactions between fire and *Phytophthora ramorum*

David Rizzo[1], Davis Allison Simler-Williamson[2], Margaret Metz[3], Kerri Frangioso[1],

[1]Department of Plant Pathology, University of California, [2]Department of Biological Sciences, Boise State University, [3]Department of Biology, Lewis & Clark College

Sudden oak death (SOD), associated with the introduced pathogen *Phytophthora ramorum*, causes acute, landscape-scale tree mortality in California's fire-prone coastal forests. Using long-term datasets that describe wildfire occurrence and *P. ramorum* dynamics across the Big Sur region, we examined the influence of recent and historical fires on epidemiological parameters, including pathogen presence, infestation intensity, reinvasion, and host mortality. Past wildfire altered disease dynamics and reduced SOD-related mortality, indicating a negative interaction between these abiotic and biotic disturbances. Frequently burned forests were less likely to be invaded by *P. ramorum*, had lower incidence of host infection, and exhibited decreased disease-related biotic disturbance, which was associated with reduced occurrence and density of epidemiologically significant hosts. Our findings indicate that fire history has contributed to heterogeneous patterns of biotic disturbance and disease-related decline across this landscape, via changes to both the occurrence of available hosts and the demography of epidemiologically important host populations (Simler-Williamson et al. 2021). These results highlight that human-

altered abiotic disturbances may play a foundational role in structuring infectious disease dynamics, contributing to future outbreak emergence and driving biotic disturbance regimes.

Simler-Williamson AB, Metz MR, Frangioso KM, Rizzo DM. 2021. Wildfire alters the disturbance impacts of an emerging forest disease via changes to host occurrence and demographic structure. Journal of Ecology 109 (2), 676-69

## 2:45-3:00 Synergistic effect of a heat wave and *Phytophthora xalni* infection on alder species performance

Inês Gomes Marques[1], Cristina Vieites-Blanco[1], Maria João Barrento[2], Arthur Cupertino[1], Ana Rodrigues[1], Alejandro Solla[3], Teresa Soares David[4], Patricia María Rodríguez-González[1]

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The pathogen *Phytophthora ×alni* compromises the health of riparian ecosystems in Europe. The geographic expansion of the disease in Southern European countries and the foreseen intensification of warmer temperatures calls for research combining biotic and abiotic stresses on alder health. The objective of this study was to assess the morphological and physiological damages caused by a heatwave and infection by *P. ×alni* on European alder species. We subjected two-year-old *Alnus glutinosa* and *Alnus lusitanica* seedlings to 20 days of a simulated heatwave, followed by 20 days of stem-inoculation with *P. xalni*. We applied 4 treatments: control, heatwave (H), *P. xalni* (P), and heatwave + *P. xalni* (H+P). Seedlings' response was assessed through biomass traits, predawn water potential, and chlorophyll fluorescence measurements. Disease symptoms were assessed by the percentage of leaf necrosis. Predawn leaf water potential and chlorophyll fluorescence were lower in P and H+P treatments for both alder species. Higher specific leaf area and lower leaf dry matter content also showed different trends for both alder species in the H+P treatment. The surviving seedlings of the H treatment recovered chlorophyll fluorescence and leaf necrosis values similar to controls, showing that the *P. xalni* infection was the main cause for decline in performance. Overall, the H+P treatment showed a synergistic effect on traits for both alder species, with less severe effects on *A. glutinosa*.

Gomes Marques, I.; Barrento, M. J.; Vieites-Blanco, C., Scotti, P.Semedo, J. N.; Rodrigues, A. P.; Solla, A.; David, T. S.; Rodríguez-González, P. M. (2021) 'Predicting alder decline under multiple stress: combining heatwave and *Phytophthora xalni*'. Poster in SEFS 12 -Symposium for European Freshwater Sciences, 29 th of July, Dublin, Ireland, online.

## 3:00-3:15 *Phytophthora* species surveys of burnt areas of Angeles National Forest reveal species-specific patterns of distribution and variability of pathogenicity towards common native chaparral

Sebastian Fajardo[1]; David Rizzo[1]; Tyler Bourret[1]; Susan Frankel[2]

[1]University of California Davis, [2] US Forest Service, Pacific Southwest Research Station, Albany, CA

In the attempt to renew and restore degraded habitats through the practice of restoration, Phytophthora species could potentially be introduced into natural ecosystems by unintentionally outplanting infested plant stock. Between 2018-2021 Phytophthora surveys were done in areas of the Angeles National Forest, Southern California, to assess Phytophthora distribution in areas adjacent to restored areas from which Phytophthora spp. were previously detected. From these surveys 15 species of Phytophthora were associated with chaparral-grassland and oak woodland areas, many areas with a historical fire past. Common associated host in these areas were Adenostoma fasciculatum, Quercus agrifolia and Salix spp. Detected Phytophthora spp. were found in both upland and riverbed areas, and strongly associated with riparian areas of both chaparral and oak woodland areas. Phytophthora spp. were also encountered in water ways and off-road tracks and trails, indicating a potential natural and anthropogenic-associated routes of dispersal. Pathogenicity tests were performed using the encountered Phytophthora species on common native chaparral plants, which identified A. fasciculatum as a highly susceptible host. These tests have also indicated that P. crassamura, P. cactorum and P. multivora are all capable of infecting Eriodictyon crassifolium, A. fasciculatum, S. mellifera and Eriogonum fasciculatum. Thus, a high risk for disease exists for the plant hosts associated with the presence of Phytophthora species. Phytophthora species can infect common Southern California chaparral plants and potentially disperse to adjacent areas through water ways and soil movement.

## 3:15-3:30 Detection of *Phytophthora* species from Quercus suber stands using DNA metabarcoding and baiting isolation

Seddaiu Salvatore[1*], Riddell Carolyn[2], Sechi Clizia[1], Ruiu Pino Angelo[1], Sarais Luca[1], Mulas Antonio[1], Mello Antonietta[3],Andrea Brandano[5], Cock Peter[4], Green Sarah[2], Scanu Bruno[5]

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In the last several decades, cork oak ecosystems have been increasingly threatened by biotic and abiotic stress factors inducing critical decline phenomena. A three-year survey was conducted to analyze the diversity of *Phytophthora* species in different seasons (January-June/July) across six healthy and declining cork oak stands in Sardinia (Italy). The occurrence of *Phytophthora* species in the soil was tested using both soil baiting method and high throughput illumina sequencing. The results obtained by baiting showed the occurrence of several *Phytophthora* species including *P. cinnamomi*, *P. quercina*, *P. pseudocryptogea*, *P.×cambivora*, P*. tyrrhenica* and *P. psychrophila*. All these species were isolated in winter, probably due to the favorable mild temperatures and wet conditions. In summer, the number of *Phytophthora* species isolated was lower, with *P. cinnamomi*, P*. tyrrhenica* and *P. pseudocryptogea* identified in the first two years of sampling. High throughput illumina sequencing analyses detected a lower diversity of *Phytophthora* species in comparison with those isolated by baiting, although it allowed us to detect an additional species, *P. cactorum*. In this study, only in some cases a correlation between species detected through the baiting isolations and those with genomic analysis was found. This investigation demonstrated both the complementarity of the two diagnostic techniques used and some of their limitations, in relation to species diversity and seasonality conditions.

Seddaiu, S., Brandano, A., Ruiu, P.A., Sechi, C. and Scanu, B., 2020. An Overview of *Phytophthora* Species Inhabiting Declining *Quercus suber* Stands in Sardinia (Italy). Forests*,* 11(9), 971.

Riddell, C.E., Frederickson-Matika, D., Armstrong, A.C., Elliot, M.; Forster, J., Hedley, P.E., Morris, J., Thorpe, P., Cooke, D.E.L., Pritchard, L., Sharp, P.M. and Green, S., 2019. Metabarcoding reveals a high diversity of woody host-associated *Phytophthora* spp. in soils at public gardens and amenity woodlands in Britain. PeerJ, 7, e6931.

## 3:30-3:45 Population genetics clarify the epidemiological relationships among the three main California hosts of the pathogen *Phytophthora ramorum*, causal agent of Sudden Oak Death.

Matteo Garbelotto[1]; Melina Kozanita [1]; Nik Grunwald [2].

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It has been demonstrated that California bay laurel (*Umbellularia californica*) is the major transmissive host of *Phytophthora ramorum*, the causal agent of Sudden Oak Death, in coastal California oak woodlands (Davidson et al. 2005), and is a superspreader of infection both in tanoak (*Notholithocarpus densiflorus*) (Cobb et al. 2012) and coast live oak (*Quercus agrifolia*) populations (Garbelotto et al. 2017). However, little is known about the population structure of the pathogen in each of these three hosts, and no direct evidence has been provided on contagion pathways among these three main hosts. Here we employ a population genetics approach to identify the relationship among *P. ramorum* populations in bay laurels, oaks and tanoaks to clarify the contribution that each host may have on the epidemiology of SOD and on the microevolution of its causal agent. Additionally, we explore differences in population structure in wet vs. dry years and at sites with various levels of disease incidence and prevalence, within a single watershed where the disease is known to be in an endemic phase. We conclude that structure exists between hosts, that bay laurel is the source population for both tanoak and oak epidemics, and that tanoak contributes minimally to oak infection. We also conclude that in spite of their common source of inoculum, oaks and tanoaks are sinks that select for different pathogen genotypes due to the variance in selection pressure in each host type. Finally, we conclude that different sites supported a dominance of different genotypes, more genotypes overall and more persistent genotypes, when compared to other sites, and that these 'hotspots' are likely to play a more significant epidemiological and evolutionary role for the pathogen.

Cobb RC, Filipe JA, Meentemeyer RK, Gilligan CA, Rizzo DM (2012) Ecosystem transformation by emerging infectious disease: loss of large tanoak from California forests. Journal of Ecology, 100(3):712-22.

Davidson JM, Wickland AC, Patterson HA, Falk KR, Rizzo DM (2005) Transmission of *Phytophthora ramorum* in mixed evergreen forest in California. Phytopathology, 95, 587-596.

Garbelotto M, Schmidt D, Swain S, Hayden K and Lione G (2017) The ecology of infection between a transmissive and a dead-end host provides clues for the treatment of a plant disease. Ecosphere, 8(5):e01815.

3:45-4:15 BREAK

## 4:15-4:30 Multivariate Bayesian analysis to identify traits associated with invasiveness of *Phytophthora* pathogens

Treena Burgess, Bruce Marcot[1]and Peter Scott[2]

[1]U.S. Forest Service, Pacific Northwest Research Station, Portland, Oregon, USA, [2]Department of Primary Industries and Regional Development, [3] Baron-Hay Court, Kennsington WA 6151, Australia

The *Phytophthora* genus is associated with significant plant diseases in natural ecosystems, and in production and urban environments globally. *Phytophthora* pathogens pose formidable management and biosecurity challenges as they are increasingly spread globally and often cause major diseases within newly-invaded environments. Many significant new diseases, including Kauri dieback and Sudden Oak death, are caused by species of this pathogen which were only described after the discovery of the disease. Based on the rate of identifying new species, models suggest there may be up to four times more *Phytophthora* species than are currently described formally. These new species may have serious impacts, even if they are not currently associated with serious diseases, as their potential, yet unknown threat, may jeopardize market access. A multivariate Bayesian traits analysis was conducted to identify traits that may be associated with serious impacts and that can be easily assessed in newly-discovered species. The Bayesian approach proved more informative than logistic modeling approaches, as it was more tolerant of incomplete

data, provided risk models and capacity to include management decisions and utility functions, and that proved robust using cross-validation approaches.

Burgess TI, Edwards J, Drenth A, Massenbauer T, Cunnington JH, Mostowfizadeh-Ghalamfarsa R, Dinh Q, Liew ECY, White D, Scott P, Barber PA, O'Gara E, Ciampini JA, McDougall K, Tan Y-P, 2021. Current Status of *Phytophthora* in Australia. Persoonia - Molecular Phylogeny and Evolution of Fungi 47, 151-177.

Burgess TI, McDougall KL, Scott P, Hardy GESJ, Garnas J, 2019. Predictors of *Phytophthora* diversity and distribution in natural areas across diverse Australian ecoregions. Ecography 42, 594-607.

Burgess TI, White D, McDougall KL, Garnas J, Dunstan WA, Català S, Carnegie AJ, Worboys S, Cahill D, Vettraino A-M, Stukely MJC, Liew ECY, Paap T, Bose T, Migliorini D, Williams B, Brigg F, Crane C, Rudman T, Hardy GES, 2017. Distribution and diversity of *Phytophthora* across Australia. Pacific Conservation Biology 23, 150-162.

## 4:30-4:45 *Phytophthora agathidicida* and kauri dieback – are other hosts and other *Phytophthora* species important?

Ian Horner[1], Matthew Arnet[1], Nari Williams[1], Caitlin Donahoe[1], Ellena Carroll[1], Julia Soewarto[2], Vicky Hodder[2]

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*Phytophthora agathidicida* causes decline and death of the giant kauri trees of northern New Zealand forests. To date, kauri is the only species known to be susceptible to *P. agathidicida* in the forest. However, it is expected that other forest species could potentially harbour or help proliferate the pathogen, while not necessarily showing obvious disease symptoms. Trials have been established where 'clean' nursery-grown seedlings of various common species have been planted into infected kauri forests, to determine if roots are colonized by *P. agathidicida*, and whether symptoms are evident. These trials are supported by glasshouse inoculation studies, and targeted sampling of roots from multiple species in infected stands. During soil testing in kauri forests to determine presence of *P. agathidicida*, a number of other *Phytophthora* species have also been detected. The role of these species in kauri dieback is unknown. Preliminary results of these studies and the ecological implications will be presented and discussed.

## 4:45-5:00 Improving the understanding of the spatial and temporal dynamics of kauri decline in the Waipoua Forest and its association with *Phytophthora agathidicida*

Nari Williams[1], Taoho Patuawa[2], Matthew Calder[3], Sapphire Davenport[2], Tom Donovan[2,4], Hone Hohaia[2], Corad Marsh[2], Taoho Tane[2], Andrew McDonald[5], Audrey Lustig[6], Cecelia Arienti[6], Dean Anderson[6], Matt Arnet[1], Caitlin Donahoe[1], Kate Richards[7], Ian Horner[1]

1. New Zealand Institute for Plant and Food Research, 30 Crosses Road, Havelock North 4130, 2. Te Roroa Group, 1 Waipoua River Road, RD6 Dargaville, 3. Department of Conservation, Dargaville, 4. Donovan Ecological Services, 5. Biospatial Limited, New Zealand, 6. Manaaki Whenua – Landcare Research, PO Box 69040, Lincoln 7640, 7. New Zealand Institute for Plant and Food Research, 120 Mt Albert Road Mt Albert, 1025

*Phytophthora agathidicida* is the key plant pathogen associated with root infection and dieback in kauri (*Agathis australis*) a keystone species of the forested areas of northern New Zealand. This observational study drew on historic aerial imagery, oblique aerial photography and LiDar data to identify and assess the crown health of kauri greater than 10 m that were distinguishable above the understory. Ground-surveillance was carried out across representative areas of forest with targeted trees allocated at random. Trees and vegetation health assessments were made, soil samples collected and analyzed for the presence of *P. agathidicida* and other *Phytophthora* pathogens. The patterns of crown decline and infection foci were analyzed spatially and temporally and analyzed against key topographic, hydrological and anthropogenic traits to test current disease dynamic hypotheses. Our study aims to determine if: 1) geomorphology and topographic traits are associated with the epidemiology of *P. agathidicida*; 2) elucidate the rate of crown decline that may be attributed to *P. agathidicida* infection; 3) test if the expansion of established *P. agathidicida* foci is consistent with a combination of root-to-root contacts and water flow; and 4) the intensification of disease impacts results primarily from the multiplication of infested patches and short-distance dispersal events.

## 5:00-5:10 *Phytophthora ramorum* Variant Abundance is Driven by Sporulation Capacity and Environmental Optimums

Adam Carson

Oregon State University

Sudden oak death (SOD) is a plant disease caused by the oomycete pathogen *Phytophthora ramorum*, which was introduced to the mixed conifer forests of coastal California and southwestern Oregon. The production of zoospores borne in sporangia is the primary mode of transmission of this pathogen on the landscape. An experiment was conducted to compare sporulation capacity, aggressiveness, growth rate, and temperature optimums of EU1 and NA1 isolates of *P. ramorum* collected in Oregon forests. Forty fully-sequenced *P. ramorum* isolates, representing common and rare genotypes from the first five years of the SOD outbreaks, were grown on artificial media and used to inoculate tanoak (*Notholithocarpus densiflorus*) leaves in growth chambers set to 6℃, 11℃, and 16℃. For each isolate, rate of growth, lesion area, and sporangia production were measured. The objective was to evaluate potential drivers of variant abundance within both the NA1 and EU1 populations from Oregon forests.

Elliott, M., Sumampong, G., Varga, A., Shamoun, S.F., James, D., Masri, S. and Grünwald, N.J., 2011. Phenotypic differences among three clonal lineages of *Phytophthora ramorum*. Forest Pathology, 41(1), pp.7-14.

Goheen, E.M., Hansen, E.M., Kanaskie, A., McWilliams, M.G., Osterbauer, N. and Sutton, W., 2002. Sudden oak death caused by *Phytophthora ramorum* in Oregon. Plant disease, 86(4), pp.441-441.

## 5:10-5:20 Dynamics of endophytic fungal microbiome in tanoak leaves associated with *Phytophthora ramorum* infections in southwestern Oregon

Yung-Hsiang Lan

Oregon State University

Tanoak (*Notholithocarpus densiflorus*) is a foundation species in Oregon and California mixed conifer forests, where it serves a diversity of ecological functions. However, *Phytophthora ramorum*, the pathogen causing sudden oak death (SOD), kills tanoak trees negatively impacting their survival. To understand the impacts on the foliar microbiome community associated with tanoak trees infected with *P. ramorum*, we climbed 36 trees at different stages of infection near Brookings, Oregon. From each tree we sampled 8 canopy positions. At each position, we estimated the incidence of infection, and sampled leaf discs on: 1) the 3rd -5th leaves from 10 shoots; and 2) 10 fully expanded leaves following their emergence in the spring. The objective of this preliminary study is to characterize the foliar microbiome of tanoak trees, including: 1) endophyte community assembly over the growing season at different canopy positions; and 2) how SOD infection impacts the foliar microbiome community.

Busby, P.E., Peay, K.G. and Newcombe, G. (2015). Common foliar fungi of *Populus trichocarpa* modify *Melampsora* rust disease severity. *New Phytologist*, 209(4), pp.1681–1692. doi:10.1111/nph.13742.

Gervers, K.A., Thomas, D.C., Roy, B.A., Spatafora, J.W. and Busby, P.E. (2022). Crown closure affects endophytic leaf mycobiome compositional dynamics over time in *Pseudotsuga menziesii var. menziesii*. *Fungal Ecology*, 57-58, p.101155. doi:10.1016/j.funeco.2022.101155.

## 5:20-5:30 Modeling a risk map for ink disease in Switzerland

Simone Prospero

Swiss Federal Research Institute WSL, Zürcherstrasse 111, CH-8903 Birmensdorf, Switzerland

Ink disease caused by the two invasive oomycetes *Phytophthora cinnamomi* and P. *xcambivora* is an emerging threat to sweet chestnut (*Castanea sativa*) stands in southern Switzerland. These soilborne pathogens infect the roots and can rapidly kill a tree. As both species are particularly thermophilic, the emergence of ink disease has been linked to climatic change, in particular warmer winters. In this study, we modeled the future distribution of *P. cinnamomi* and *P. xcambivora* in Switzerland under

ongoing climate change to define chestnut stands that may be under high risk of ink disease.

# THURSDAY June 23

## 9-9:40 Keynote Address - Marianne Elliott - *Phytophthora ramorum* in Washington State, USA: Management successes, failures and challenges

Marianne Elliott, Joseph Hulbert, Gary Chastagner

WSU Puyallup Research and Extension Center

*Phytophthora ramorum* has been present in the ornamental nursery trade in western WA since 2003. Initially regulations required extensive surveys at nurseries that shipped host material interstate. It was found that repeat positive nurseries, many of which have stopped interstate shipping, were responsible for most of the *P. ramorum* detections. Federal regulations have changed so that more emphasis is placed on mitigation and monitoring at positive nurseries to reduce the occurrence of repeat positives. In 2019 no symptomatic plants were found at these formerly positive nurseries, but *P. ramorum* went undetected at a previously negative nursery and was shipped nationwide. While *P. ramorum* is still occasionally found in western WA, as indicated by positive streams, landscape sites, and nurseries, it has not moved into forest ecosystems and caused major damage. Unlike California and southern Oregon, western WA forests do not contain a major component of bole hosts for *P. ramorum*. Cooperation between state and federal agencies and WSU has resulted in a large amount of knowledge being gained about the behavior of *P. ramorum* in WA, including the effectiveness of monitoring, mitigation, and educational activities (Elliott et al 2021). Some management successes include diagnostic tools that have increased our ability to detect *P. ramorum* and track its movement in the nursery industry, and determine the effectiveness of mitigation practices. Steaming has emerged as an effective management tool in nurseries and landscape sites. Better use of BMPs have increased understanding of the role of clean plants in limiting spread of *Phytophthora* and other pathogens. Early failures included ineffective mitigation practices, limited understanding of host range, and time delays between disease detection and mitigation. Major challenges associated with the spread and management of SOD include SOD fatigue, lack of economic incentive to produce clean plants, and variability within the ornamental nursery industry. *Phytophthora ramorum* is still a concern in WA State after 18 years due to undetected residual populations and new introductions. The lack of a serious forest outbreak can be attributed to the absence of bole hosts, effective mitigations at positive sites, intensive inspection for P. ramorum at shipping nurseries in the early years, and public awareness of the problem.

Elliott M, Strenge D, Hulbert J M, and Chastagner G. 'Multiagency collaboration strengthens applied research and mitigation of *Phytophthora ramorum* at a botanical garden in Washington State', Plant Health Progress, 22(3):240-249 (2021). https://doi.org/10.1094/PHP-02-21-0045-FI

## Host-pathogen-environment interactions

## 9:40-10:00 Role of host resistance in sustainable management of *Phytophthora* leaf disease in natural rubber (Hevea brasiliensis)

Narayanan Chaendaekattu

Rubber Research Institute of India, Kottayam 686 009, India

Subsequent to successful domestication outside its natural range of distribution, natural rubber (NR; mainly, *Hevea brasiliensis*) has been exposed to a wide range of fungal pathogens. Of various host-pathogen interactions, *Phytophthora* abnormal leaf fall (ALF), or premature leaf fall, is the most devastating disease capable of causing up to 60 percent losses in latex productivity from NR plantations. Until now, prophylactic fungicidal control is the only management strategy. This approach is becoming unsustainable. In view of the very narrow genetic base of the host, identification and use of resistance sources has also been a challenging task. In addition, very little information is available about the genetics of *Phytophthora* leaf diseases in *Hevea* spp. . Recombination breeding for yield carried out over the years at the Rubber Research Institute of India has led to the development of several promising high yielding clones. Studies carried out on ALF disease in these clones led to the identification of clones which exhibit variation in resistance to the pathogen (Serrano et al. 2014). Identification and use of exotic disease resistant germplasm in breeding has also resulted in several promising high-yielding genotypes with putative resistance to *Phytophthora.* This breeding population offers an excellent source for further hot-spot evaluation, upgrading and deployment in large-scale plantings for sustainable NR in the future.

Serrano, M., Coluccia, F., Torres, M., L'Haridon, F. and Métraux, J.P. 2014. The cuticle and plant defense to pathogens. Frontiers in Plant Science 5: 274 10.3389/fpls.2014.00274

## 10:00-10:20 Expanding the host range of *Phytophthora cinnamomi* in the southeastern United States

Linus Schmitz, Steve Jeffers

Clemson University, 105 Collings St. 214 BRC, 29634, Clemson SC

*Phytophthora cinnamomi* is a globally occurring, soilborne Oomycete plant pathogen that can significantly impact trees in landscape settings and natural forest ecosystems. Symptoms include bleeding trunk cankers, stem lesions, root rot, and wilting. While seedlings and younger trees may die as a result of infection, unhealthy and symptomatic mature trees may be cut down as a safety precaution. In recent years, we have observed symptoms on oak species in the red oak group, including root rot on northern red oak seedlings (*Quercus rubra*) and bleeding trunk cankers on water oak (*Q. nigra*). Pathogenicity of *P. cinnamomi* to *Q. rubra* has been documented in Europe, particularly in France. However, to our knowledge, pathogenicity of *P. cinnamomi* to *Q. rubra* and *Q. nigra* has not been demonstrated in the United States. Therefore, we conducted greenhouse experiments to complete Koch's postulates and prove pathogenicity. For each oak species, seedlings were inoculated with two or three isolates of *P. cinnamomi* previously recovered from diseased host plants. Northern red oak seedlings developed symptoms with and without periodic flooding. Water oak seedlings only exhibited aboveground symptoms and mortality when subjected to extended periods of flooding (7 days). However, isolations from roots of inoculated plants of both species confirmed that infection occurred on all seedlings independent of flooding.

Robin, C., Capron, G., and Desprez-Lostau, M. L., 2001. Root infection by *Phytophthora cinnamomi* in seedlings of three oak species. Plant Pathology, 50(6), pp. 708–716.

Marçais B., Dupuis F., and Desprez-Loustau M.L., 1996. Susceptibility of *Quercus rubra* root system to *Phytophthora cinnamomi*; comparison with chestnut and other oak species. Forest Pathology, 26(3), pp. 133-143.

## 10:20-10:35 Evidence for natural resistance in larch and juniper to *Phytophthora*

Green, S[1]., Dun, H.F., MacKay, J.J, Riddell, C., Clark, D., Clarke, T
[1]Forest Research, EH25 9SY, UK

*Phytophthora* pathogens are having increasing impacts on woody hosts in managed and natural landscapes across the UK largely due to human-mediated transmission exacerbated by changing climatic trends. Two recently invasive species, *P. ramorum* and *P. austrocedri,* have established across the country and are causing extensive mortality of their respective hosts; larch, an exotic commercial forestry plantation species, and juniper, a native species with high ecological value as a constituent of woodland ecosystems. Predicting or controlling the impact of an invasive pathogen requires an understanding of both the pathogen and the host, including the capacity of the host to respond to the new threat. If natural resistance occurs in these host populations, larch could be retained as valuable timber species in the UK and long-term decline of juniper could be halted. We will present the results of preliminary clonal trials undertaken to determine whether survivor larch (Dun, 2021) and juniper trees (Green et al. 2020) in otherwise high mortality stands have natural resistance to their respective *Phytophthora* pathogens. We will also discuss the management implications of our initial findings and the next steps being undertaken to determine whether tolerance traits are heritable and could form the basis of resistance breeding programs.

Dun, H. 2021. Sudden larch death – from epidemiology to host resistance. PhD thesis, Department of Plant Sciences, University of Oxford.

Green, S., James, E.R., Clark, D., Clarke, T-K., Riddell, C.E. 2020. Evidence for natural resistance in *Juniperus communis* to *Phytophthora austrocedri.* Journal of Plant Pathology 103, 55-59.

## 10:35-10:50 Pathological, physiological and metabolomic effects of co-infections by *Phytophthora cinnamomi* and the A1 and A2 mating types of *P. xcambivora* on *Castanea sativa*.

Tamara Corcobado[1], Ivan Milenković[1,2], Tomáš Kudláček[1], Iñigo Saiz[1,3], Miloš Trifković[4], Tomáš Májek[1], Henrieta Ďatková[1], Aneta Bačová[1], Dálya László Benedek[4], Thomas Jung[1,5*]

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Sweet chestnut (*Castanea sativa*) orchards make important contributions to the economy of many countries. However, their cultivation has been decreasing due to their susceptibility to several diseases and pests. Among them, ink disease, caused mainly by *Phytophthora cinnamomi* and *P. ×cambivora*, has severely affected the vitality of sweet chestnut. This study aims to assess the impacts of the A2 mating type of *P. cinnamomi* and the A2 and A1 mating types of *P. ×cambivora*, when alone or co-occurring, on sweet chestnuts physiological status and survival. Plants growing from seeds, that originated in Serbia and Portugal, were subjected to seven treatments in the summer of 2021: (i) inoculation with *P. ×cambivora* A2; (ii) inoculation with *P. ×cambivora* A1; (iii) inoculation with *P. cinnamomi* A2; (iv) co-inoculation with *P. ×cambivora* A1-*P. ×cambivora* A2; (v) co-inoculation with *P. ×cambivora* A1-*P. cinnamomi* A2; (vi) co-inoculation with *P. ×cambivora* A2-*P. cinnamomi* A2; and (vii) control. During the experiment, weekly assessment of mortality and disease symptoms, measurements of gas exchange, chlorophyll fluorescence and leaf spectral reflectance, and leaf metabolomic profile were accomplished. Survival of Serbian origin plants inoculated either with *P. cinnamomi* A2 or *P. ×cambivora* A1-*P. ×cambivora* A2 was lower in comparison with the plants of Portuguese origin. Serbian plants responded earlier to the co-inoculation of *P. ×cambivora* A2 and A1 than Portuguese plants. Portuguese plants has a more acute physiological adjustments to *Phytophthora* infection, which were accompanied by a higher concentration of most of the detected metabolites under *P. ×cambivora* A2-*P. cinnamomi* A2 and under *P. ×cambivora* A1-*P. cinnamomi* A2 treatments over their Serbian counterparts. The results suggest that the more pronounced adjustments of Portuguese chestnut plants

led to a slower progression to mortality compared with Serbian plants with the sole exception of the co-inoculation with *P. ×cambivora* and *P. cinnamomi* A2.

European chestnut stands, and their association with Ink Disease and crown decline', *European Journal of Plant Pathology*, 111(2), pp. 169–180. doi: 10.1007/s10658-004-1882-0.

10:50-11:15 BREAK

## 11:15-11:30 *Phytophthora cinnamomi* on "laurel oak" in South Carolina, USA

Steven N. Jeffers, Mastin M. Greene and Linus T. Schmitz

Dept. of Plant and Environmental Sciences, Clemson University, Clemson, SC 29634

*Quercus laurifolia* is native to the coastal plains of the southeastern United States. However, identification of this species has been problematic for years. It often is confused with morphologically similar species (e.g., *Q. hemisphaerica*), and the common name "laurel oak" has been used for both of these oak species. *Phytophthora cinnamomi* was first isolated from bleeding cankers on "laurel oak" in Florida (Wood and Tainter 2002). Since then, we have repeatedly isolated *P. cinnamomi* from "laurel oaks" in South Carolina—usually on trees identified by arborists. The identity of the host came into question based on the location of symptomatic trees, which typically occurred in more upland and drier habitats where *Q. hemisphaerica* naturally occurs. The natural habitat of *Q. laurifolia* is on wetter, lowland sites. Therefore, we evaluated the susceptibility of *Q. laurifolia* and *Q. hemisphaerica* to *P. cinnamomi* in a series of greenhouse experiments because pathogenicity of *P. cinnamomi* to "laurel oak" previously had not been reported. Three isolates of *P. cinnamomi* recovered from diseased "laurel oaks" were used, and the identities of all three isolates were confirmed based on DNA sequencing and morphological characteristics. Pathogenicity was confirmed only after subjecting seedlings growing in infested soilless container mix to periodic flooding—i.e., plants were flooded for 7 days and then drained for 7 days. *Q. hemisphaerica* was significantly more susceptible than *Q. laurifolia*. Therefore, *Phytophthora* cankers on "laurel oaks" in South Carolina was most likely occurring on *Q. hemisphaerica* and not on *Q. laurifolia.*

Wood, A. K., and Tainter, F. H., 2002. First Report of *Phytophthora cinnamomi* on *Quercus laurifolia*. Plant Disease 86(4), 441.

## 11:30-11:45 Response of two riparian woody plants to *Phytophthora* spp. and drought: the role of plant ecological preferences and pathogenicity

Gomes Marques, I.*[1,2]; Solla, A.[3]; David, T. S.[1,4]; Rodríguez-González, P. M. [1]; Garbelotto, M.[2]

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Management of ecosystems based on knowledge of how trees respond to the combination of biotic and abiotic stress can increase their resilience and health. The purpose of this study was to understand how two co-existing riparian woody plants with different ecological preferences would respond to drought conditions when infected previously by *Phytophthora* species. A greenhouse experiment was conducted with saplings of a drought resistant species, *Frangula californica*, and an obligate-riparian species, *Alnus rhombifolia*. We compared the responses of plants to: 1) imposed drought conditions; 2) infection by *Phytophthora cactorum* or *Phytophthora crassamura*,;and (3) the combination of infection and drought conditions. The response of *A. rhombifolia* and *F. californica* saplings was assessed through the observation of disease symptoms, and morphological and physiological parameters. Results evidenced that the decline of *F. californica* saplings was mostly induced by *P. cactorum* while both pathogens were causing decline in *A. rhombifolia*. Drought conditions impacted more *A. rhombifolia* saplings while water availability was a facilitator of *Phytophthora* spp. infection of *F. californica* saplings. The infection of *A. rhombifolia* saplings by *Phytophthora* spp. worked as a predisposing factor for drought decline but also induced lower water losses, which made the effect of the drought-imposed conditions less severe on plants. Our results show that the use of *F. californica* and *A. rhombifolia* for revegetation purposes in sites infested by *Phytophthora* species should integrate knowledge obtained in this study, to increase the success of the restoration strategy.

Gomes Marques, I. et al. (2022) 'Response of two riparian woody plants to *Phytophthora* species and drought', Forest Ecology and Management, 518, p. 120281.doi: 10.1016/J.FORECO.2022.120281.

## 11:45-12:00 Microscopy determination of the host-pathogen interaction between *Alnus glutinosa* and several *Phytophthora* species

Jonas Oliva
University of Lleida, JRU-Agrotecnio-CTFC, Spain

*Phytophthora xalni* is a major pathogen to *Alnus glutinosa* in Europe. Little is known about the underlying susceptibility reasons for susceptibility. We studied the microscopic interaction between alder and *P. xalni* and we compared it with other pathogenic *Phytophthora* species such as *P. cambivora*, *P. plurivora*, *P. cactorum*, *P. castanetorum* and *Halophytophthora* spp. Pathogenicity (lesion size) had the strongest correlation with host defense responses such as reinforced parenchyma cells or tyloses. In contrast, we saw comparably smaller differences in terms of pathogen biomass amongs *Phytophthora* species. Our results suggest that pathogenicity may depend on the host response and that a tolerant interaction may allow alder to survive the attacks of some *Phytophthora* more than others.

## Management II

## 12-12:15 Sudden Oak Death in Oregon Forests: New clonal lineage and increased disease management

Sarah Navarro[1], Gabriela Ritokova [2], Jared Leboldus[3], Ebba Peterson[3], Kelsey SØndreli[3], Paul Reeser[3], Elizabeth Stamm[3], Nicholas Grunwald[4], Valerie Fieland[4], Charles Grell[1], Randall Wiese[2], and Casara Nichols[2]

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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 attempted to eradicate and slow the spread of disease through a program of a state quarantine, early detection, survey and monitoring, and destruction of infected and nearby host plants. Eradication treatments, totaling approximately 3243 ha, eliminated disease from most infested sites, but the disease continued to spread slowly, mostly in a northward direction. In 2021, the Oregon SOD Program found two new infestations of *P. ramorum* outside the state SOD quarantine area. The first, detected in March 2021, was on federal National Forest lands along the north bank of the Rogue River, six miles north of any previously known infestation. Infected trees were identified by interpretation of high-resolution aerial imagery as a part of the annual USFS and ODF Aerial Detection Survey. The second infestation, just outside Port Orford, 21 miles northwest of the Rogue River and 13 miles south of Coos County, was detected in April 2021 (Peterson et al., 2022). Collected samples have tested positive for the NA2 and NA1 clonal lineages of *P. ramorum*. Previously found only in nurseries, this is the first time the NA2 clonal lineage has been found in wildlands. Since April 2021, this infestation has been the program's top priority with ODF, USFS, and OSU surveying over 400 acres of ground transects and collecting over 200 samples, resulting in 154 positive detections. This presentation will review program developments in treatments, funding, and continued stakeholder involvement in Oregon.

Peterson, E.K., Sondreli, K.L., Reeser, P.W., Navarro, S., Nichols, C., Wiese, R., Fieland, V.J., Grünwald, N.J., and LeBoldus, J.M. (2022). First report of the NA2 clonal lineage of *Phytophthora ramorum* infecting tanoak in Oregon forests. Plant Disease in press. https://doi.org/10.1094/pdis-10-21-2152-pdn.

## 12:15-12:30 The USDA Forest Service Support of the Sudden Oak Death Program in California

Philip Cannon

USDA Forest Service

Old timers that own forested landscapes in the Coast Range near Santa Cruz, California remember seeing something like Sudden Oak Death as far back as 1990. However, it was not until 2004 when Matteo Garbelotto, Dave Rizzo and Everett Hansen, working with cambial tissues from dying tanoaks (*Northolithocarpus densiflorus*) and Coast Live Oak (*Quercus agrifolia*) in China Camp, CA, determined that *Phytophthora ramorum* was the organism responsible for the death of those trees. By that time the pathogen had already spread to several locations in a 30 kilometer-wide and 300 km long strip of land that ran along the coast range from Big Sur in the south to Mount Sonoma in the north. Intense studies were begun to learn more about the etiology of the disease. Initial studies suggested that 10 meters was the likely maximum annual spread, so many of the earlier control measures were designed around preventing spreads of this distance. Later, however, additional studies revealed that the pathogen might occasionally be moved as much as 3 kilometers in a single violent storm. Since 2004 the Federal Government has supported Sudden Oak Death Programs in California and Oregon with the intention of limiting the deleterious impacts of this disease in these two states. The basic objective of the SOD Program in California is to work with California institutions towards the realization of three objectives: 1) monitor the spread of the disease in the state; 2) educate the concerned public about what is happening with their SOD-susceptible trees; and 3) limit the spread of the disease. This presentation describes the way in which this program has been run in California since 2004 and gives a frank assessment of how effective it has been. It also discusses the program's future.

Rizzo, DM, M. Garbelotto, E. Hansen. 2005. *Phytophthora ramorum*: integrative research and management of an emerging pathogen in California and Oregon forests. Annual review of Phytopathology, 43: 309-35.

## 12:30-12:45 What to do about NA2: A new lineage of *Phytophthora ramorum* in Oregon forests

Kelsey Sondreli and Jared LeBoldus
Department of Botany and Plant Pathology, Oregon State University

*Phytophthora ramorum* is an invasive pathogen in Oregon and California and in several European countries. In Oregon, this pathogen causes Sudden Oak Death of tanoak (*Notholithocarpus densiflorus*), which is the most susceptible host and main driver of the epidemic. There are four lineages of *P. ramorum* in the US and Europe (NA1, NA2, EU1, EU2). Forest infestations in Oregon were all caused by the NA1 lineage until the EU1 lineage was introduced in 2015. In 2021, the NA2 lineage was found infecting wild tanoak trees in Port Orford, Oregon. This is the first report of the NA2 lineage in wildland forests. Two studies were conducted to determine the differences in aggressiveness among the four lineages of *P. ramorum*. In the first experiment, 12 isolates (3 from each lineage) were used to inoculate 1-year old tanoak seedlings. Lesion lengths were measured one week later. The majority of the variation in lesion length was among isolates rather than among lineages. On average the NA2 inoculated trees had the longest lesions. In the second experiment, 30 isolates from each lineage were used to inoculate 1-year old tanoak seedlings. Isolate explained the majority of the variation for all lineages with the exception of EU2. Overall, 78% of NA2 inoculated plants were girdled after one week compared to 75% of EU2, 56% of EU1, and 33% of NA1. Overall, the NA2 lineage has the potential to cause larger lesions and more severe disease on tanoak with unknown consequences for Oregon forests.

12:45-2 LUNCH

## Evolution, Genetics and Genomics

### 2:00-2:25 Genomic biosurveillance of *Phytophthora ramorum* detects intralineage variants and interlineage hybrids

Richard Hamelin[1], Renate Heinzelmann[1], Nicolas Feau[2], Guillaume Bilodeau[3], Brian Boyle[4] and Isabelle Giguère[4]

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*Phytophthora ramorum*, an emergent pathogen that causes the sudden oak and larch death, spreads as reproductively isolated divergent clonal lineages. We use a genomic biosurveillance approach by sequencing genomes of *P. ramorum* from survey and inspection samples and report the discovery of novel variants of *P. ramorum* that are the result of hybridization via sexual recombination between North American and European lineages. We show that these hybrids are viable, can infect a host and produce spores for long-term survival and propagation. Genome sequencing revealed novel genotypic combinations at 54,515 single nucleotide polymorphism loci. More than 6,000 of the novel genotypes at these loci are predicted to have a functional impact in genes associated with host infection, including effectors, carbohydrate-active enzymes and proteases. We also observed post-meiotic mitotic recombination that could generate additional genotypic and phenotypic variation and contribute to homoploid hybrid speciation. Our study highlights the importance of plant pathogen biosurveillance to detect novel variants and inform management and control.

## 2:20-2:35 A wide variety of viruses exists in *Phytophthora* and *Halophytophthora* spp.

Leticia Botella[1, 2] Marilia Horta Jung[1], Josef Janoušek[1], Milica Raco[1], Cristiana Maia[3], Thomas Jung[1]

(1) *Phytophthora* Research Centre, Department of Forest Protection and Wildlife Management, Faculty of Forestry and Wood Technology, Mendel University in Brno, Zemědělská 1, 613 00 Brno, Czech Republic (2) Department of Genetics and Agrobiotechnology. Faculty of Agriculture and Technology, University of South Bohemia in České Budějovice, Na Sádkách 1780, 370 05 České Budějovice, Czech Republic (3) Centre for Marine Sciences (CCMAR), University of Algarve, Faro, Portugal

The diversity of fungal and oomycete viruses (mycoviruses) is massively expanding thanks to the availability of new technologies. Nevertheless, there is still a big gap in the global virome catalogue of these lower eukaryotes. In order to clearly understand the essential patterns and processes of virus evolution a wider range of organisms, including oomycetes, must be sampled and screened. Over the last few years, we have investigated the virome of different species of *Phytophthora* and *Halophytophthora* collected from estuaries in southern Portugal, and rivers, mangroves and ponds, and natural forests in subtropical and tropical areas in Southeastern Asia (Botella et al. 2020; Botella & Jung 2021; Raco et al. 2022). Based on high-throughput sequencing (RNA-seq) numerous novel species of double stranded (ds), positive (+) and negative (-) single-stranded (ss) RNA viruses have been detected and characterized. The study of the prevalence of these viruses together with their abundance and diversity indicate that they are regular members of their oomycete host populations. Furthermore, multiple viral infections appear to be common, and some oomycete isolates are able to host up to 15 viruses. If these viruses are biological entities and have an effect on their hosts remains unknown but our work represents a step forward understanding the origin, spread and evolution of RNA viruses in oomycete species.

Botella, L. and Jung, T. (2021) Multiple Viral Infections Detected in *Phytophthora condilina* by Total and Small RNA Sequencing. *Viruses* **13**: 620.

Botella, L., Janoušek, J., Maia, C., Jung, M.H., Raco, M., and Jung, T. (2020) Marine Oomycetes of the Genus *Halophytophthora* Harbor Viruses Related to Bunyaviruses. *Front Microbiol* **11**: 1–13.

Raco, M., Vainio, E., Sutela, S., Eichmeier, A., Hakalová, E., Jung, T., and Botella, L. (2022) High Diversity of Novel Viruses in the Tree Pathogen *Phytophthora castaneae* Revealed by High-Throughput Sequencing of Total and Small RNA. *Front Microbiol* **13**: 911474.

## 2:35-2:50 Diversity of viruses in *Phytophthora* Clade 5

Milica Raco 1, Czechia Jung Thomas 1, Mullet Martin 1, Horta Jung Marilia1, Balci Yilmaz 2, Botella Leticia1

1 Phytophthora Research Centre, Department of Forest Protection and Wildlife Management, Faculty of Forestry and Wood Technology, Mendel University in Brno, Brno, Czechia 2 USDA- APHIS / Plant Protection and Quarantine, Maryland, USA

Over the past few years, an increasing number of novel viral species have been discovered in many major taxa of phytopathogenic fungi and in some oomycetes. Novel technologies, such as high-throughput sequencing (HTS), have allowed the detection and description of many previously unknown viral species and revealed their high abundance and taxonomic diversity. Although usually causing latent infections, there has been an increase of reported virus-induced hypovirulence (reduced virulence) in a number of fungal hosts, attracting considerable attention to their use as possible biocontrol agents. In oomycetes, a growing number of viruses with double-stranded (ds) RNA, positive-sense (+) single-stranded (ss) RNA, and negative-sense (−) single-stranded (ss) RNA genomes have been recently reported, yet most species remain neglected. *Phytophthora* phylogenetic Clade 5, an understudied and one of the smallest *Phytophthora* clades, currently includes four species and at least three undescribed taxa. In this study, a combination of traditional and novel virus detection technologies such are dsRNA extraction based on CF-11 cellulose affinity chromatography and high-throughput sequencing (HTS) of total RNA were used to investigate the potential virome of native populations of *P. castaneae*, *P. heveae* and two new species belonging to *Phytophthora* Clade 5 informally designated as *P. sp. castaneae*-like and *P. sp. myristicae-castaneae*-like, isolated from across East, Southeast Asia and from Panama. The investigation revealed high viral prevalence and diversity of novel viruses resembling members of the order *Bunyavirales* (-ssRNA) and virus families *Chrysoviridae* (dsRNA), *Endornaviridae* (+ssRNA), *Megabirnaviridae* (dsRNA), *Narnaviridae* (+ssRNA), *Totiviridae* (dsRNA), the proposed families *Fusagraviridae* (dsRNA), *Fusariviridae* (+ssRNA), and the virus group provisionally named *Ustiviruses* (dsRNA). Further study of these viral communities could potentially lead to designing biological control methods for suppression of their phytopathogenic hosts.

Weir, B.S., Paderes, E.P., Anand, N., Uchida, J.Y., Pennycook, S.R., Bellgard, S.E. and Beever, R.E., 2015. A taxonomic revision of *Phytophthora* Clade 5 including two new species, *Phytophthora agathidicida and P. cocois.* Phytotaxa, 205(1), pp.21-38. doi: 10.11646/phytotaxa.205.1.2

Raco, M., Vainio, E.J., Sutela, S., Eichmeier, A., Hakalová, E., Jung, T. and Botella, L., 2022. High Diversity of Novel Viruses in the Tree Pathogen *Phytophthora castaneae* revealed by High-Throughput Sequencing of Total and Small RNA. Front. in Microbiol. doi: 10.3389/fmicb.2022.911474

Jung, T., Scanu, B., Brasier, C.M., Webber, J., Milenković, I., Corcobado, T., Tomšovský, M., Pánek, M., Bakonyi, J., Maia, C., Bačová, A., Raco, M. …. & Horta Jung, M., 2020. A survey in natural forest ecosystems of Vietnam reveals high diversity of both new and described *Phytophthora* taxa including *P. ramorum*. Forests, 11(1), p.93. 11:93. doi: 10.3390/f11010093

## 2:50-3:05 Population dynamics of the sudden oak death pathogen *Phytophthora ramorum* in Oregon after first invasion

Jared LeBoldus, Hazel A. Daniels, Nicholas C. Carleson[1], Niklaus Grünwald[2]

[1] Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, [2] Horticultural Crops Research Laboratory, United States Department of Agriculture – Agriculture Research Service, Corvallis, OR, USA

Genomes of isolates from the first five years of the NA1 and EU1 epidemics in Oregon were sequenced to determine population genetic dynamics. These years were chosen so that patterns of evolution and mutation in each population could be compared between lineages. Our results suggest that 1) NA1 was present in Oregon much earlier than 2001, and 2) current management (rapid detection, response, and treatment) appears to keep the genetic diversity of the EU1 population low. The NA1 population had much greater genetic diversity—the median pairwise variance within NA1 samples was 0.20 per kbp, compared to 0.05 per kbp for EU1 samples. A Wilcoxon Rank Sum test confirmed that the medians of each lineage population were not equal ($p < 0.001$). There was a significant correlation between genetic relatedness and geographic distance in the NA1 population ($p = 0.042$) which was not present in the EU1 population ($p = 0.402$). Differences in treatment boundaries between NA1 and EU1 and the "head start" NA1 had between infection (researchers speculated ~1998) and discovery in 2001 may explain this contrast between the two epidemics.

## 3:05-3:20 A comparative genomics study of *Phytophthora pluvialis* isolated from different conifer host species

Martha Sudermann[1], Elizabeth Stamm[1], Jeffrey Chang[1], Niklaus Grunwald[2], Jared LeBoldus[1]

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Understanding the origins of plant pathogens is crucial for mitigation strategies. *Phytophthora pluvialis* was first described in Oregon, USA in 2013, after being discovered in streams, soil and rain traps near Douglas-fir trees (*Pseudotsuga menziesii*). To date, only one outbreak was observed on the Oregon coast in 2015. In contrast, *P. pluvialis* is the cause of red needle cast on radiata pine (*Pinus radiata*) in New Zealand, and more recently has caused cankers on western hemlock (*Tsuga heterophylla*) in the United Kingdom. Earlier studies have suggested that the center of origin of the pathogen is the United States. As a first step to understanding why *P. pluvialis* is more commonly associated with disease in conifer trees in the UK and New Zealand, but not United States, we sequenced four isolates that were collected from western hemlock in the UK and five isolates from Oregon that were collected beside Douglas-fir growing in different locations. Analyses of whole genome sequences confirmed that North America is likely the place of origin of the introductions into both New Zealand and the United Kingdom. Using both long and short read sequencing, we are sequencing additional isolates, assembling high quality reference genomes, annotating the assemblies, and examining whether genetic and genomic variation exists between isolates collected from different hosts and from geographic locations.

Pérez-Sierra, A., Chitty, R., Eacock, A., Jones, B., Biddle, M., Crampton, M., Lewis, A., Olivieri, L., Webber, J. f., 2022. First report of *Phytophthora pluvialis* in Europe causing resinous cankers on western hemlock. New Disease Reports 45, e12064. https://doi.org/10.1002/ndr2.12064

Reeser, P., Sutton, W., Hansen, E., 2013. *Phytophthora pluvialis* , a new species from mixed tanoak-Douglas-fir forests of western Oregon, U.S.A. North American Fungi 8, 1–8. https://doi.org/10.2509/naf2013.008.007

Tabima, J.F., Gonen, L., Gómez-Gallego, M., Panda, P., Grünwald, N.J., Hansen, E.M., McDougal, R., LeBoldus, J.M., Williams, N.M., 2020. Molecular Phylogenomics and Population Structure of *Phytophthora pluvialis*. Phytopathology 111, 108–115. https://doi.org/10.1094/PHYTO-06-20-0232-FI

## 3:20-3:30 Six New *Nothophytophthora* Species from natural ecosystems in Europe and Asia

Datkova Henrieta, Milenković Ivan[1], Corcobado Tamara[1], Janoušek Josef[1], Talgø Venche[2], Marthin Tarigan[3], Durán Alvaro[3], Kageyama Koji[4], Hieno Ayaka[4], Masuya Hayato[5], Uematsu Seiji[6], Webber Joan F.[7], Brasier Clive M.[7], Horta Jung Marilia[1], Jung Thomas[1]

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Surveys in natural ecosystems of the Czech Republic, Indonesia, Japan, Montenegro, Norway and Slovakia produced numerous *Nothophytophthora* isolates. A preliminary phylogenetic analysis of the internal transcribed spacer (ITS) distinguished six new *Nothophytophthora* species with the following preliminary names: *N. kysucae* (Slovakia); *N. moravia* (Czech Republic); *N. balcanica* (Montenegro); *N tropicalis* (Sumatra); *N. norvegica* (Norway), and *N. japonica* (Japan). Detailed studies of colony morphologies and growth-temperature relations, morphological and morphometric features of sexual and asexual structures, and multigene phylogenetic analyses are currently underway for their official descriptions. Colony morphologies of all novel *Nothophytophthora* species and the eight described species were examined after 18 days of growth at 20°C on Potato Dextrose Agar (PDA), Vegetable juice Agar (V8A) and Carrot juice Agar (CA). Temperature-growth relations were recorded for all new species together with all described species on clarified V8A. Three copies per isolate were incubated at 20°C for 48 hours and then transferred to 10, 15, 20, 22.5, 25, 27.5 and 30°C. After 24 hours the colony margins were marked. Radial growth was measured after 8 days along two intersecting lines at right angles intersecting the middle of the inoculum. The optimum temperatures for growth were 20°C for *N. japonica* and *N. moravia*, 22.5°C for *N. balcanica* and *N. tropicalis*, and 25°C for *N. kysucae* and *N. norvegica*. Maximum temperatures were 25°C for *N. japonica* and *N. moravia*, and 27.5°C for the other 4 new species. For *N. japonica* and *N. moravia* 27.5°C was lethal. For *N. tropicalis*, *N. balcanica*, *N. kysucae* and *N. norvegica* lethal temperature was 30°C. At their optimum temperatures *N. tropicalis* showed the highest growth rate while *N. moravia* showed the slowest growth of all tested species.

3:30-3:55 BREAK

## 3:55-4:10 Phylogeny and morphology of *Phytophthora quercina* isolates from Europe and North Africa

A. Brandano[1], Z. Tomić[2], M. Mullett[3], T. Kudlacek[3], S. Seddaiu[4], M. Horta-Jung[3], T. Jung[3], B. Scanu[1]

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*Phytophthora quercina* is a fine root pathogen frequently associated with oak decline in Europe (Jung *et al.*, 1999). More recently this pathogen has been isolated in several oak forests throughout the Mediterranean basin, including North African countries (Jung *et al.*, 2013; Smahi et al., 2017). Its limited geographic distribution in Europe and North Africa and the lack of landscape-level mortality of oaks led to the hypothesis that *P. quercina* is native to Europe. To determine the genetic variability among this species, we conducted extensive morphological and phylogenetic analyses of populations sampled in several European and North African countries, using a specific baiting method, and previously identified based on ITS sequences with similarity to the ex-type isolate higher than 99%. Multigene phylogenetic analyses were carried out using three nuclear (ITS, ß-tubulin and HSP90) and three mitochondrial (*cox*1, rps10 and NADH1) gene regions. The six different loci were first analyzed individually, and then a concatenated dataset of all nuclear and mitochondrial sequences was analyzed. For all individual genes and the concatenated datasets, Maximum likelihood and Bayesian Inference analyses were performed. In addition, colony morphology, growth rate at different temperatures and morphological characteristics of the reproductive structures, such as gametangia and sporangia, were assessed. Although a relatively low genetic diversity was observed across the six genes, some isolates showed some variability, apparently not correlated to host or geographic origin, perhaps due to the mainly homothallic breeding strategy of this species. In addition, notable morphological differences in colony growth and morphology were observed between *P. quercina* isolates, suggesting possible emergence of new species in Clade 12. A GBS based population study of *P. quercina* and related species from Clade 12 is currently ongoing, which will give new clues into the origin of this clade.

Jung, T., Cook, D. E. L., Blaschke, H., Duncan, J. M., and Oßwald, W., (1999). *Phytophthora quercina* sp. nov., causing root rot of European oaks. Mycol. Res. 103 (7): 785–798

Jung, T., Vettraino, A. M., Cech, T. L., and Vannini, A. (2013). The impact of invasive *Phytophthora* species on European forests. *Phytophthora: A global perspective*, 146-158.

Smahi, H., Belhoucine-Guezouli, L., Franceschini, A., and Scanu, B. (2017). Phytophthora species associated with cork oak decline in a Mediterranean forest in western Algeria. Integrated Protection in Oak Forests IOBC-WPRS Bulletin, 127, 123-129.

## 4:10-4:25 Forest *Phytophthora*: ecology, diversity and management

Noelia López-García[1], Carmen Romeralo Tapia, Johanna Witzel and Jonas Rönnberg

[1]Sveriges lantbruksuniversitet, SLU / Swedish University of Agricultural Sciences

Damage to trees in forest and urban environments caused by *Phytophthora* species are an increasing threat to the vitality and productivity of these ecosystems in many parts of the world, including Sweden. *Phytophthora*, which seriously damage the fine roots of trees and several other woody plants, is efficiently introduced to new environments through imported plant material (mainly non-native plants through the nursery trade). A study was conducted in collaboration with stakeholders in Southern Sweden investigating potential soil microbiome interactions with *Phytophthoras*. The idea is to develop new biocontrol methods to manage *Phytophthora*-damage in different forest settings. To uncover ecological interactions, the microflora present in soil samples were quantified using a new approach combining high-throughput qPCR Biomark Fluidigm chip technology optimized for oomycete analysis and Next Generation Sequencing. The fungal community included a wide range of pathogens and abundance of ectomycorrhizal taxa. Amongst the most abundant oomycetes, *Phytophthora plurivora*, *Phytophthora cactorum* and *Phytophthora gonapodyides* were identified. Besides, a specific taxon belonging to the genus *Trichoderma* was strongly correlated with the scarcity of pathogenic *Phytophthora* spp. The meta-analysis of the microbiome represents an excellent tool to develop biocontrol strategies for the management of diseases caused by *Phytophthora*.

## Public Engagement
## 4:25-4:45 Citizen Science: the best way forward to collect and publicly share large datasets.

Doug Schmidt; Matteo Garbelotto

Department of ESPM, University of California at Berkeley, CA

Citizen Science (CS) is viewed by many researchers as a way to educate the public while getting communities engaged in a wide range of conservation issues (McKinley et al., 2017). We additionally posit that: a) CS is an invaluable and necessary way to generate scientifically sound and large datasets, b) CS programs should generate datasets that can be used to test scientific hypotheses, and c) CS -generated datasets should be made accessible to the public. The Sudden Oak Death (SOD) blitzes inform and educate the community about Sudden Oak Death, get locals involved in detecting the disease and produce detailed local maps of disease distribution ( Meentemeyer et al. 2015).

The map can then be used to identify those areas where the infestation may be mild enough to justify proactive management. The program has been successful for 15 years in a row, has resulted in the creation of the SODmap (Garbelotto et al., 2017), the largest tree disease distribution database in the world, and produced data used in a significant number of peer-reviewed papers. Furthermore, data in the SODmap has been estimated to have been accessed by over 3 million users, exemplifying how an activity engaging hundreds of volunteers can benefit an entire community of millions. Some of the reasons of the success of the program include: a grassroot bottom-up organization of local events and involvement of communities, a broad and diverse demographic of participants with a high return rate, the "ask" of the program requires significant skill but is simple enough that participants can become skilled in a short well-designed training, the use of pencil and paper in the field rather than using common electronic platforms, providing all necessary collection materials for free, the laboratory testing of all samples collected by volunteers, and the use of high tech on-line platforms to share results in real time with volunteers, agencies and the public.

Garbelotto M, Maddison ER, Schmidt D. SODmap and SODmap mobile: two tools to monitor the spread of sudden oak death (2014). Forest Phytophthoras, 22;4(1).

McKinley DC, Miller-Rushing AJ, Ballard HL et al 2017. Citizen science can improve conservation science, natural resource management, and environmental protection. Biological Conservation, 2208:15-28.

Meentemeyer RK, Dorning MA, Vogler JB, Schmidt D, Garbelotto M (2015). Citizen science helps predict risk of emerging infectious disease. Frontiers in Ecology and the Environment, 3(4):189-94.

## 4:45-5:00 Forest Health Watch: empowering communities to keep trees healthy

Joseph Hulbert

Puyallup Research and Extension Center Washington State University

Biosecurity is a shared responsibility. Our forests face critical threats from the global spread of tree pests and pathogens and the unprecedented rates of climate change. Of particular concern is the urgency for more information and greater capacity to monitor for new disease issues as we plant more trees for climate resiliency and move species for climate adaptation. Community science is one approach to address these pressing issues. Besides the obvious value of community science initiatives for early detection and monitoring, they can also contribute widely to raising awareness, informing decisions regarding control (eradication and containment efforts) to minimize pest and pathogen spread, and even finding resistant plant material for restoration of diseased landscapes. Community scientists can enhance biosecurity.

## 5:00-5:10 *Phytophthora* knowledge and disease resistant planting preferences among nonindustrial forest landowners in southern Oregon, USA.

Norma Kline[1], Tammy Cushing[2] and Lauren Grand[3]

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The non-native pathogens, *Phytophthora lateralis* and *Phytophthora ramorum*, have had serious ecological and economic impacts in southern Oregon forests. Port-Orford-cedar root disease, caused by *Phytophthora* lateralis, has resulted in widespread mortality of Port-Orford-cedar (*Chamaecyparis lawsoniana*) throughout its range since it was first reported in native forestland in 1952. Sudden oak death (SOD), caused by *Phytophthora ramorum*, has killed hundreds of thousands of tanoaks (*Notholithocarpus densiflorus*) in Curry County Oregon since it was first detected in 2001. Landowners can help mitigate the effects of invasive diseases by contributing to early detection efforts provided they have knowledge of disease symptoms. Additionally, landowners can contribute to restoration efforts by planting disease-resistant seedlings. Extension forestry programs are traditional sources of forest health information for nonindustrial forest landowners. Targeting education and outreach approaches based on audience segmentation may be an effective approach to providing landowner education. Understanding ownership objectives can help focus forest health education needs and tailor disease-resistant distribution efforts. Nonindustrial forest landowners in two counties in southern Oregon were surveyed to determine general landowner characteristics and knowledge of the aforementioned diseases. Additionally, landowner knowledge of disease-resistant seedlings, behavior, and preferences regarding planting disease-resistant seedlings were examined. Implications for focusing landowner education and tailoring seedling distribution efforts are discussed.

Kendra, A. and Hull, R. B. (2005). Motivations and Behaviors of New Forest Owners in Virginia. Forest Science, 51(2): 142-154.

Sagor, E.S., Kueper, A.M., Blinn, C.R., Becker, D.R. (2014) Extension Forestry in the United States: A National Review of State-Level Programs. Journal of Forestry, 112(1): 15-22.

# FRIDAY June 24

## 9:00-9:40 Keynote Address - Understanding drivers of *Phytophthora* emergence through the plant nursery trade in Britain

Sarah Green[1], Cooke DEL[2], Barwell, L, Purse, B[3], Frederickson-Matika D[1], Cock PJA[2], Keillor [2], Randall E, Clark M, Pettit T[4,5], Dunn M[1], Schlenzig A[6], Pritchard L[2, 7], Thorpe P[2, 8], Barbrook J[9]

(1) Forest Research, EH25 9SY, UK; (2) The James Hutton Institute, DD2 5DA, UK; (3) The Centre for Ecology & Hydrology, OX10 8BB, UK (4) University of Worcester WR2 6AJ, UK; (5) Eden Project Learning, PL24 2SG, UK; (6) Science and Advice for Scottish Agriculture, EH12 9FJ, UK; (7) University of Strathclyde, G4 0RE, UK; (8) University of St Andrews KY16 9AJ, UK; (9) Animal and Plant Health Agency, YO41 1LZ, UK

Since 2016, a large metabarcoding dataset has been compiled on *Phytophthora* diversity in ~4000 root and water samples collected from 133 plant nurseries located across Britain (Green et al. 2021). An additional metabarcoding dataset has been compiled over the last 5-6 years examining *Phytophthora* diversity in the wider GB environment. All findings are linked to a set of core metadata enabling robust comparative analyses. This study aims to quantify i) how nursery management practices, pathogen traits and biotic interactions influence the diversity and composition of *Phytophthora* communities in UK nurseries and ii) whether the local diversity of *Phytophthora* species in the wider environment is linked to that within nearby nurseries. For example, early results suggest that nurseries using closed water storage facilities have fewer *Phytophthora*-positive samples. Variability among nurseries in *Phytophthora* richness and community composition is found to be related to nursery practices and sampling method using Bayesian phylogenetic mixed effects models. We present the model outputs exploring: which nursery management practices drive species composition; which species commonly co-occur; and whether pathogen functional traits explain which *Phytophthora* species are favored by particular nursery practices (Barwell et al. 2022). We will discuss how environmental drivers and proximity to infected nurseries act as risk factors for *Phytophthora* outbreaks in the wider environment, and whether species traits can mediate these effects.

Barwell, L.J., Purse, B.V., Roy, K., Chalk, M., Cooke, D., Green, S. 2022. Diversity of *Phytophthora* in British nurseries in relation to management practices, pathogen traits and biotic interactions. Final report to Future Proofing Plant Health, Defra, UK (FPPH@Defra.gov.uk)

Green, S., Cooke, D.E.L., Dunn, M., Barwell, L., Purse, B. *et al.* 2021. PHYTO-THREATS: Addressing Threats to UK Forests and Woodlands from *Phytophthora*; Identifying Risks of Spread in Trade and Methods for Mitigation. Forests 12, 1617; https://doi.org/10.3390/f12121617

## *Phytophthora* in nurseries and associated with restorations/disturbance

### 9:40-10:05 Battling Soilborne *Phytophthoras* in California Restoration Sites and at the Wildland Urban Interface

Janell M. Hillman[1], Tedmund J. Swiecki[2], Elizabeth A. Bernhardt[2], Tyler B. Bourret[3], Heather Mehl[3], Susan J. Frankel[4],

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The inadvertent spread of *Phytophthora* species into natural ecosystems in California is a growing threat to environmental, social, and economic resources in restoration areas and adjacent wildlands, including rare and endangered native plant habitats. The Santa Clara Valley Water District (Valley Water) is a wholesale water supplier for over 1.8 million people in Santa Clara County, California with a large suite of capital, water utility, and stream maintenance projects that result in extensive, long-term mitigation commitments in riparian, wetland, and upland habitats throughout the county. In 2014, several of Valley Water's restoration sites on the Santa Clara Valley floor and in the upper watershed were found to be contaminated by soilborne *Phytophthora* spp. Subsequently, an extensive baseline study of nursery stock in historic restoration sites planted by Valley Water revealed a staggering total of approximately 39 *Phytophthora* spp. across 29 sites. In response, Valley Water created a Plant Pathogen Program. The Program has spearheaded development of a comprehensive set of sanitation *Phytophthora* best management practices (BMPs) and contract specifications for work activities; diversification in mitigation site planning to include both clean nursery container stock and direct seeding; a complete reevaluation of restoration practices from seed collection, to growing of stock, to planting out; participation in regional working groups on the emerging pathogen threat; support for an independent native plant nursery accreditation program (Accreditation to Improve Restoration, AIR) in California; education of stakeholders, project planners, regulatory personnel, staff and contractors; and additional testing and site remediation where feasible. Since the implementation of the program, one highly sensitive upper watershed site containing endangered species has been successfully remediated and no *Phytophthora* was detected in 555 tests of 22,085 contract-grown nursery plants from 2017 through 2021. To protect ecological integrity, large scale capital infrastructure projects are incorporating sanitation BMPs to prevent *Phytophthora* introduction and spread at Valley Water facilities and in adjacent watershed areas.

Frankel, S.J., Conforti, C., Hillman, J., Ingolia, M., Shor, A., Benner, D., Alexander, J.M., Bernhardt, E. and Swiecki, T.J., 2020. *Phytophthora* Introductions in Restoration Areas: Responding to Protect California Native Flora from Human-assisted Pathogen Spread. Forests, 11(12), p.1291.

Frankel, S.J., Alexander, J., Benner, D., Hillman, J., Shor, A. 2020. *Phytophthora* Pathogens Threaten Rare Habitats and Conservation Plantings. Sibbaldia: The International Journal of Botanic Garden Horticulture, 18: 53-65. https://doi.org/10.23823/Sibbaldia/2020.288.
Hillman, J., Swiecki, T.J., Bernhardt, E.A., Mehl, H.K., Bourret, T.B., Rizzo, D. 2017. From 31 Flavors to 50 Shades of Grey: Battling *Phytophthoras* in Native Habitats Managed by the Santa Clara Valley Water District. In: Frankel, S.J. & Harrell, K.M. (tech. coords), Proceedings of the Sudden Oak Death Sixth Science Symposium. Gen. Tech. Rep. GTR-PSW-255. Albany, CA: U.S. Department of Agriculture, Forest Service, Pacific Southwest Research Station, p. 57.

## 10:05-10:25 From problems to solutions: addressing habitat restoration as a source of wildland *Phytophthora* introductions

Tedmund J. Swiecki[1]; Elizabeth A. Bernhardt[1], Susan J. Frankel[2], Diana Benner[3], Janell Hillman[4]

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Sampling since 2014 has shown that seedlings from California native plant nurseries for habitat restoration are a continuous source of *Phytophthora* introductions. A wide diversity of soilborne *Phytophthora* species have been detected, including undescribed taxa and first reports of various species in California or the US. Evidence of spread from planting sites into stands of native vegetation has been documented. By definition, habitat restoration cannot include the introduction of *Phytophthora* species that can cause long-term habitat degradation. Nursery *Phytophthora* best management practices (NPBMPs), designed to exclude *Phytophthora* from nursery plants, were developed to address the need for clean seedlings in restoration projects. A pilot program to implement the systematic use of the NPBMPs, Accreditation to Improve Restoration (AIR), was developed and started in 2018. Over 30 California restoration nurseries have been involved in the program to date. Over 5 years, nursery plants grown in full compliance with the NPBMPs recorded no detection of *Phytophthora* in 669 bench leachate tests including 24,588 plants. BMPs and guidelines have also been developed to address other risk pathways involved in habitat restoration practices, including soil movement, import of organic materials, and general phytosanitation. Ongoing efforts are still needed to encourage wider adoption of restoration practices that minimize the risk of *Phytophthora* introduction.

Frankel, S.J., Conforti, C., Hillman, J., Ingolia, M., Shor, A., Benner, D., Alexander, J.M., Bernhardt, E. and Swiecki, T.J., 2020. *Phytophthora* introductions in restoration areas: Responding to protect California native flora from human-assisted pathogen spread. Forests, 11(12), p.1291.
Swiecki, T.J. and Bernhardt, E.A., 2018. Best management practices for preventing *Phytophthora* introduction and spread: trail work, construction, soil import. Prepared for Golden Gate National Parks Conservancy, San Francisco, CA. 73p. viewed 23 May 2022
Swiecki, T.J., Bernhardt, E.A., Frankel, S.J., Benner, D. and Hillman, J., 2021. An accreditation program to produce native plant nursery stock free of *Phytophthora* for use in habitat restoration. Plant Health Progress, 22(3), pp.348-354.

## 10:25-10:35 Use of remote sensing data and GEE for detection and monitoring of cork oak decline caused by *Phytophthora cinnamomi*

A. Brandano[1], L. Arcidiaco[2], B. Scanu[1], G. Matteucci[2], S. Mereu[2]

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Over the last decades the role of pathogens in natural forests has gained increasing attention due to an exponential rise in the number of emergent diseases in worldwide forests. The oomycete *Phytophthora cinnamomi* is one of the most aggressive plant pathogens on earth, which has been identified as the main biotic driver of the severe decline and mortality of evergreen oaks in southern Europe (Brasier, 1996). In the Mediterranean Basin, *P. cinnamomi* is decimating populations of cork oak (*Quercus suber*) stands representing a problem of paramount ecological and socio-economic importance, since cork oak is a major structural element in Mediterranean forests that provides economic and cultural services. Identifying and mapping declining forests is highly relevant for management, however, this is often difficult and costly. The trend of the vegetational index, other environmental conditions being equal, can represent a valid proxy for deriving the state of health and evaluating how external disturbances affect productivity. In this context, the analysis of the time series of the vegetation indices represents a valid tool for evaluating the vegetation dynamics and deriving the various phenological parameters. The objective of the work was to advance in the use of machine learning approaches to the processing of remote sensing data for the detection and monitoring of cork oak forests impacted by *P. cinnamomi*. Two sites, one *P. cinnamomi* infested and one disease-free, were selected in northeastern Sardinia, Italy. Fifteen circular plots were randomly selected. The time series of three vegetation indices (NDVI, SAVI, EVI) were derived from satellite images with high geometric resolution (10m), acquired by the Sentinel2 satellite from January 2016 to December 2020. Whereas the canopy transparency was monitored in two consecutive years using a spherical densiometer. For each plot and for each vegetation index a single continuous trajectory was derived. The analysis of differences in the vegetation intra-annual seasonal cycles in the various sites affected in different ways by the infection, has shown that the phenological phases appear profoundly different, both in terms of temporal shifting and in amplitude.

Brasier, C. M. (1996). *Phytophthora cinnamomi* and oak decline in southern Europe. Environmental constraints including climate change. In *Annales des Sciences Forestieres* (Vol. 53, No. 2-3, pp. 347-358). EDP Sciences.

10:35-11:00 BREAK

## 11:00-11:15 Do not let the bad boys out: containment of *Phytophthoras* in a research nursery

Wolfgang Schweigkofler

Dominican University of California

NORS-DUC, the National Ornamentals Research Site at Dominican University of California, was established in 2009 to study *Phytophthora ramorum* and other quarantine plant pathogens in an open research area, which mimics a commercial nursery. The rationale behind was that many invasive plant pathogens are introduced to new environments through plant trade, and nurseries can play a major role in the initial steps of pathogen establishment, adaptation, and proliferation. Since then, many experiments on the biology, transmission, and control of *Phytophthoras* were conducted at NORS-DUC in collaboration with research partners from other universities and research centers, which lack this kind of infrastructure. In order to fulfill the requirements for the permit, to follow federal and state regulations, and to reduce the risk of escape of pathogens from the research nursery into the surrounding environment, strict containment measures and a rigorous monitoring system were installed. Sentinel plants placed within as well as around the perimeter of the research nursery are used to check for the horizontal movement of air-borne pathogens and for the seasonality of symptom expression. In addition, host plants growing within a quarter of a mile distance to the nursery are monitored for *P. ramorum*. All the water used in the nursery is contained using a pond liner, and treated using a particle filter and an UV filter before being released into the environment. Research plots, tools, and inoculated plants are decontaminated after the end of each experiment using heat treatment by steaming. During 12 years of field experiments, we did not see any sign of pathogen escape into the environment, indicating the success of our containment strategy.

Pastalka, T., Rooney-Latham, S., Kosta, K., Suslow, K., Huffman, V., Ghosh, S. and Schweigkofler, W. 2017. Monitoring using a sentinel plant system reveals very limited aerial spread of *Phytophthora ramorum* from infected ornamental plants in a quarantine research nursery. Plant Health Progress 18, p. 9-16

## 11:15-11:30 Using Scent Dogs to Detect Pathogenic Phytophthora

Lauralea Oliver[1], LLC; Matteo Garbelotto and Tina Popenuck[2]

[1]k9inSCENTive, [2]Department of ESPM, University of California at Berkeley, CA 94720

In searching for more practical methods of screening nursery plants for *Phytophthora*, a study was undertaken at UC Berkeley to determine if it would be possible to train scent detection dogs to discern pathogenic fungus species and discriminate it from other scents in leaves and soil of infected plants. Results from the ongoing scent detection dog study suggest that ecological scent detection dogs may offer an innovative and reliable method to survey for *Phytophthora* in a variety of controlled environments and in a range of substrates including foliage and soil. In recent dilutions testing, the scent dogs have shown an impressive ability to detect the pathogen at very low concentrations in a wide assortment of potted plant soil samples. These results suggest that the dogs may be more sensitive to disease presence than current testing methods.

Garbelotto, M.; Frankel, S.J. and Scanu, B. 2018. Soil- and waterborne *Phytophthora* species linked to recent outbreaks in Northern California restoration sites. California Agriculture. 72(4):208-16. https://doi.org/10.3733/ca.2018a0033.

Swiecki, T.; Quinn, M.; Sims, L.; Bernhardt, E.; Oliver, L.; Popenuck, T. and Garbelotto, M. 2018. Three new *Phytophthora* detection methods, including training dogs to sniff out the pathogen, prove reliable. California Agriculture. 72(4):217-225. https://doi.org/10.3733/ca.2018a0026.

Oliver, Lauralea; Quinn, Matt; Popenuck, Tina; Garbelotto, Matteo. 2020. *Phytophthora* species can be reliably detected by dogs both from infested substrates and infected plants. In: Frankel, Susan J.; Alexander, Janice M., tech. cords. Proceedings of the seventh sudden oak death science and management symposium: healthy plants in a world with Phytophthora. Gen. Tech. Rep. PSW-GTR-268. Albany, CA: U.S. Department of Agriculture, Forest Service, Pacific Southwest Research Station: 28-29.

## 11:30-11:45 A standardized method for detecting *Phytophthora* by baiting leachate from batches of container nursery plants

Tedmund Swiecki[1], Elizabeth A. Bernhardt[1], Sean G. McClanahan[2]

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Well-validated testing procedures play an important role in producing *Phytophthora*-free nursery plants for use in habitat restoration. Although various methods can be used to detect *Phytophthora* in nursery plants, methods vary in sensitivity and few methods have been validated to determine their efficacy under nursery conditions. We developed a standardized method to test container nursery stock by baiting irrigation from leachate multiplant arrays. Plants receive standardized irrigation doses scaled to container size over 90 minutes and leachate is collected and baited in vessels designed to concentrate zoospores around a floating green pear. We tested the sensitivity of the method using arrays of up to 48 non-infected plants and one infected plant. Results of trials were generalized into an estimated probability function which was used with Monte Carlo modeling to examine the influence of factors such as batch infection rate, test array size, and number of arrays per batch for small and large batches. Biasing the test arrays to include suspected infected plants was more efficient than random sampling. In general, 2 to 3 arrays of 40 plants were efficient for *Phytophthora* detection for both large and small batches. The benchtop leachate test uses simple equipment and has been used successfully by several nurseries to detect early contamination resulting from unintentional lapses in nursery cleaning practices.

## 11:45-12:00 Improving restoration nurseries best management practices by evaluating the efficacy of *Phytophthora* detection methods

Johanna Del Castillo Múnera

Plant Pathology Department University of California, Davis

California native nurseries provide plant material for restoration sites. Over the last decade, more than 50 *Phytophthora* spp. have been associated with native plant nurseries in California, creating concern about introducing pathogens into wildlands. To improve *Phytophthora* detection, we evaluated *Phytophthora* testing protocols to support design of an accreditation program for restoration nurseries. The efficacy of three *Phytophthora* detection methods was compared: a leachate baiting method, immunostrips, and direct isolation from root tissue. Experiment 1 was conducted in winter (2021) and replicated in summer (2021). Coffeeberry plants were inoculated with *P. cactorum* and arranged in 3 subsets of inoculated and non-inoculated plants. Every 4-weeks post inoculation (wpi) over 3 months, subsets of inoculated (20%) and non-inoculated plants were tested with the three detection methods. On experiment 1, *P. cactorum* detection success with the leachate baiting method was 66% at 4 wpi, and 100% at 8 and 12 wpi among the 3 subsets. With direct isolation, *P. cactorum* detection success rate increased over time, with 16% at 4 wpi and 50% at 12 wpi. *Phytophthora* detection with the immunostrips was highly variable, ranging from 0 to 33% detection. On experiment 2, detection success rate was lower for all methods, with the leachate method only detecting *P. cactorum* at 12 wpi (66%), direct isolation at 4 wpi (66%) and immunostrips detecting at all sampling points, at a success rate of 83%, 53% and 33%. Results suggest that the current detection methods are variable, and factors like seasonality may influence *Phytophthora* detection rate. These baseline findings are being expanded upon to support monitoring protocols used in a pilot accreditation program for restoration nurseries.

## 12:00-12:10 Thermotherapy to eliminate *Phytophthora* from root systems of container plants

Elizabeth A. Bernhardt; Tedmund Swiecki

Phytosphere Research, Vacaville, CA

We investigated the feasibility of using heat to eradicate *Phytophthora* root infections in live container nursery plants. From existing literature, temperatures between 34 and 51°C for various treatment times appeared to be viable. Direct temperature measurement of heat-treated plants and inoculum showed that timing of exposure to a temperature treatment did not accurately reflect the actual temperature × time treatment. Lag times associated with heat transfer into containers or even test tubes in a water bath were much longer than expected. Some treatments killed plants or caused unacceptable damage, but 47°C for 30 minutes resulted in minimal damage. *Phytophthora cactorum*, *P. sp. kelmania*, and *P. cambivora* in infected pear epidermis or *rhododendron* leaves could be made non-viable when held in 47°C water for 20 minutes or longer. A 30-minute treatment at 47°C appeared to eradicate these 3 species from inoculated *Quercus agrifolia* and *Q. lobata* grown in small (397 ml) containers.

## 12:10-12:20 *Phytophthora* root rot: susceptibility of garden plants

Fryni Drizou[1], Elizabeth J. Beal , Ian A. G. Waghorn[1], Joe N. Perry[2], Gerard R. G. Clover[3], Matthew G. Cromey[1]

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*Phytophthora* root rot (PRR) is a serious disease of horticultural, forest and ornamental plant species. The oomycete genus *Phytophthora* affects a wide host range, making the choice of resistant plants to manage the disease difficult. The Royal Horticultural Society diagnostic dataset of PRR records from U.K. gardens was used to compare susceptibility of different host genera to the disease. This was compared with existing reports of plants recorded as notably resistant or notably susceptible to PRR. An index-based approach separated woody plants and non-woody plants into three categories: low-index (rarely affected), medium-index (sometimes affected) and high-index (frequently affected). Taxus had the highest index. We recorded 30 *Phytophthora* species in our study, of these the wide host range spp., *P. plurivora, P. cryptogea* and *P. cinnamomi* represented 63% of identifications. These results provide confidence in the use of host resistance as part of the integrated management of PRR.

Beal E. J. Waghorn I. A. G. Perry J. N. Clover G.R.G. Cromey M. G. 2021. Susceptibility of Garden Plants to *Phytophthora* Root Rot. Plant Disease 105 (6) pp 1610- 1620

## 12:20-12:30 Testing the pathogenicity of three *Phytophthora* species on California hosts commonly used in restoration

Inês Gomes Marques[1], Matteo Garbelotto[2]

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Plants in restoration nurseries and failing restoration sites in California have been increasingly reported as being infected by *Phytophthora* species. Best management practices that help minimize plant disease depend on a formal confirmation of the pathogenicity of each *Phytophthora* species on its potential plant hosts. Our objective was to assess the pathogenicity of three *Phytophthora* species (*P. crassamura, P. megasperma and P. multivora*) on three plant species commonly used in restoration projects (*Diplacus aurantiacus*, *Ceanothus thyrsiflorus* and *Frangula californica*). In this study, we inoculated plants through root and/or stem techniques and evaluated pathogenicity by tallying mortality and scoring symptoms' severity on stems, foliage and roots. Symptoms developed on all plants inoculated with *Phytophthoras.* Results confirmed that *P. megasperma* and *P. crassamura* are true aggressive pathogens of *D. aurantiacus*, given the high mortality rates they caused shortly after inoculation.

*Phytophthora multivora* was pathogenic to both *F. californica* and *C. thyrsiflorus*, and even though mortality rates were not high, plants still showed significant root damage and leaf necrosis. Overall, root inoculations were more reliable, underlying that stem inoculations may not be an appropriate way to test pathogenicity for all *Phytophthora* species.

Garbelotto, M., Frankel, S. J. and Scanu, B. (2018) 'Soil- and waterborne *Phytophthora* species linked to recent outbreaks in Northern California restoration sites', California Agriculture. University of California, Oakland, 72(4), pp. 208–216. doi: 10.3733/ca.2018a0033.

Rooney-Latham, S. et al. (2019) '*Phytophthora* species are common on nursery stock grown for restoration and revegetation purposes in California', Plant Disease. American Phytopathological Society, 103(3), pp. 448–455. doi: 10.1094/PDIS-01-18-0167-RE.

Sims, L. L. and Garbelotto, M. (2021) '*Phytophthora* species repeatedly introduced in Northern California through restoration projects can spread into adjacent sites', Biological Invasions. Springer Science and Business Media Deutschland GmbH, 23(7), pp. 2173–2190. doi: 10.1007/s10530-021-02496-6.

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