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PHYTOPHTHORA

12th Meeting of the IUFRO Working Party 7.02.09:
Phytophthora in Forests and Natural Ecosystems

13 – 18 SEPTEMBER 2026 | GRABOUW, WESTERN CAPE
SOUTH AFRICA



PROGRAMME

Welcome Message



It is a great pleasure to welcome you to the 12th Meeting of the IUFRO Working Party 7.02.09, *Phytophthora* in Forests and Natural Ecosystems, in South Africa.

Climate change and human activities are intensifying pressures on forests and natural ecosystems, while *Phytophthora* species pose significant threats to native vegetation, forestry and agriculture. In South Africa, *Phytophthora cinnamomi* threatens endemic plants and the avocado industry, while species such as P. *alticola* and P. *frigida* affect the commercial forestry sector.

As global climate change continues to heighten these threats, addressing research gaps and developing innovative solutions are more important than ever.

This meeting brings together researchers, practitioners and policymakers from around the world to exchange knowledge, share new discoveries, forge collaborations and advance our understanding of *Phytophthora* and its impacts on forests and natural ecosystems. Together, we aim to foster sustainable strategies that protect these ecosystems and strengthen their resilience for future generations.

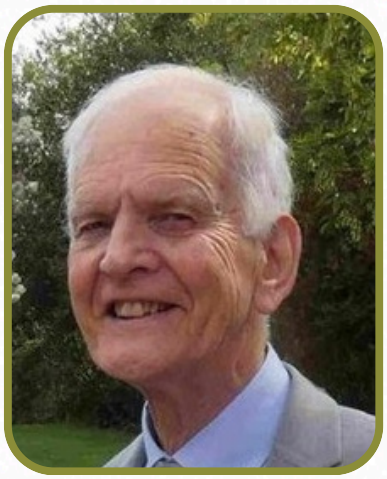
As we gather in Grabouw, Western Cape, and explore the remarkable Cape Floristic Region, I encourage you to embrace this opportunity to learn from one another, share ideas and strengthen our collaborative efforts to better understand and manage *Phytophthora* diseases.

We warmly welcome you to South Africa and hope that this meeting provides an inspiring, productive and enjoyable experience for everyone.

Tanay Bose
Conference Chairperson

Prof. Clive Brasier

United Kingdom



As an undergraduate at Hull University, Clive became fascinated by ecology, mycology, genetics and evolution. After joining Forest Research UK, he combined these interests to investigate the behaviour and the scale of the threats posed to forests and natural ecosystems by introduced pathogens, especially *Phytophthora* and Dutch elm disease. In the 1990s, with Everett Hansen (Oregon State University) and later Ken Old (CSIRO, Canberra), he co-founded the IUFRO *Phytophthora* Working Party. He is currently Emeritus Mycologist at Forest Research, UK.

Abstract

A sideways look at concepts and terminology in *Phytophthora*

In recent decades the rapid accumulation of information around the behaviour and diversity of *Phytophthora* pathogens is leading to a paradigm shift in understanding the evolutionary history and adaptation of the genus. It may also be leading to, and in some instances may now require, a rethink of some long-embedded concepts and terminology. These range from what constitutes a species and the validity of having a taxonomic 'type' to defining host range and breeding systems and distinguishing what is a *Phytophthora*'s natural or endemic behaviour versus what is an artifact resulting from its introduction. These issues will be discussed.

Dr. Michael Seidl

The Netherlands

Michael is Associate Professor at Utrecht University, the Netherlands, where he leads the Microbial Genome Evolution team (https://www.uu.nl/staff/MFSeidl). They use computational methods as well as data from large-scale genomics experiments to investigate processes that impact genome organization, functioning and evolution in fungal and plant pathogens, ultimately to explain their remarkable successes in agriculture.



Abstract

Evolutionary Genomics of Peronosporaceae towards understanding pathogenic success.

Plant pathogens pose a major threat not only to global food security but also to forests and natural ecosystems. While much current research focuses on filamentous fungal pathogens, many of the key conceptual advances that underpin our understanding of pathogenic success have emerged from studies of oomycetes, particularly within the Peronosporaceae and the genus *Phytophthora*. In this talk, I will highlight seminal discoveries from oomycete research that have shaped contemporary thinking on the evolutionary and molecular basis of plant–microbe interactions. I will then draw on our recent work on spinach downy mildews to illustrate how insights and advances from across fields can be leveraged to drive discovery, even in comparatively understudied pathosystems. Together, these examples outline a forward-looking framework for accelerating research into the evolutionary success of Peronosporaceae.

Conference Committee

Conference Chair
1. Dr. Tanay Bose – FABI, University of Pretoria

Management Committee
1. Prof. Almuth Hammerbacher – FABI, University of Pretoria
2. Prof. Irene Barnes – FABI, University of Pretoria
3. Prof. Bernard Slippers – FABI, University of Pretoria

Scientific Committee
1. Prof. Michael Wingfield – University of Pretoria
2. Prof. Niklaus Grünwald – Oregon State University & USDA Agricultural Research Service
3. Prof. Treena Burgess – Harry Butler Institute, Murdoch University
4. Dr. Trudy Paap – FABI, University of Pretoria
5. Dr. Wilma Nel – FABI, University of Pretoria
6. Dr. Tyler Bourret – PhytoWorld LLC, Seattle, Washington, USA
7. Dr. Thomas Jung – Mendel University
8. Dr. Bruno Scanu – University of Sassari

Field trip Committee
1. Prof. Michael Wingfield – FABI, University of Pretoria
2. Dr. Wilma Nel – FABI, University of Pretoria
3. Dr. Felipe Balocchi – FABI, University of Pretoria
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Sunday, 13 September 2026	
Time	**Programme**
14:00 – 17:00	Conference Registration at City Lodge V&A Waterfront
17:00	Transport to Cabo Beach Club, Evening function

Monday, 14 September 2026	
Time	**Programme**
08:00 – 09:00	Check-out and departure to Kirstenbosch
09:30 – 14:00	Kirstenbosch visit and lunch at Moyo Restaurant, Kirstenbosch National Gardens
14:00	Departure to Houwhoek Hotel via Stony Point Penguin Colony
18:30	Dinner at Houwhoek Hotel

Tuesday, 15 September 2026		
Time	**Speaker**	**Presentation title**
08:00 - 08:05	Tanay Bose	Welcome
08:05 - 08:15	Nari Williams	Introduction to the IUFRO Working Party 7.02.09
08:15 - 08:45	Clive Brasier	**Plenary lecture:** A sideways look at concepts and terminology in *Phytophthora*
Session 1: Oral Presentations Chair: Hazel Daniels		
08:45 - 09:00	Amy Eacock	Development of a rapid, field-based method and a real-time multiplex PCR for simultaneous detection of multiple forestry *Phytophthora* species
09:00 - 09:15	María Rodríguez-Solís	Climate and soil as environmental filters of *Phytophthora* soil communities in Australia
09:15 - 09:30	Richard O'Hanlon	Insights into the spread of *Phytophthora ramorum* in Ireland
09:30 - 09:45	Nari Williams	Drivers of barrier permeability and their role in determining phosphite treatment efficacy for kauri dieback: an epidemiological analysis
09:45 - 10:00	Treena Burgess	*Phytophthora cinnamomi* interacts with fire and drought to shape soil carbon and fungal functional guilds across a Mediterranean forest
10:00 - 10:30	**Refreshment Break**	
Session 2: Oral Presentations Chair: Anna Harris		
10:30 - 10:45	Thomas Jung	The evolution and biogeography of *Phytophthora* Clade 7a including 11 new species
10:45 - 11:00	Felipe Balocchi	Unrecognized risks: *Phytophthora* species and biosecurity gaps in South Africa
11:00 - 11:15	Joan Webber	Impacts of *Phytophthora pluvialis* and likely risk to conifer forestry in Britain
11:15 - 11:30	Viola Papini	Detecting *Phytophthora × cambivora*: A qPCR approach implementing an LNA-modified probe
11:30 - 11:45	Andrè Drenth	Anton de Bary and *Phytophthora* in the 21st Century
11:45 - 12:00	Bruno Scanu	From nursery pathways to wild olive decline: monitoring emerging *Phytophthora* spp. across Mediterranean olive ecosystems through field surveys and spatial risk assessment
12:00 - 13:30	**Lunch Break**	

Tuesday, 15 September 2026		
Time	**Speaker**	**Title**
Session 3: Oral Presentations **Chair: Duccio Migliorini**		
13:30 - 13:45	Sophie Eccersall	Towards the development of high-throughput screening protocols for red needle cast disease
13:45 - 14:00	Alejandro Solla	Breeding *Quercus suber* and *Quercus ilex* trees for *Phytophthora* disease resistance in Spain
14:00 - 14:15	Hazel Daniels	Impacts of cuprous oxide treatment on red needle cast-infected pine plantations of Aotearoa New Zealand
14:15 - 14:30	Ian Horner	Integrated *Phytophthora agathidicida* Management Based on Research to Drive Kauri Protection
14:30 - 14:45	Dang Nhu Quynh	The first report of *Phytophthora cactorum* causing disease in Vietnamese Lai Chau ginseng (*Panax vietnamensis* var. *fuscidiscus*) and preliminary results on biological control using endophytic microorganisms under *in vitro* conditions
14:45 - 15:15	**Refreshment Break**	
Session 4: Poster Flash Presentations **Chair: Islem Yangui**		
15:15 - 15:20	Belén Mendoza-Chamizo	Intraspecific variability in *Phytophthora cinnamomi* isolates from *Quercus suber*, *Quercus ilex* and *Castanea sativa* in south-western Spain
15:20 - 15:25	Richard O'Hanlon	Searching for *Phytophthora pluvialis* in Ireland
15:25 - 15:30	Joan Webber	What species of magnolia are likely transmissive hosts of *Phytophthora ramorum*?
15:30 - 15:35	Joan Webber	Can recreational mountain bike activity forests contribute to the spread of *Phytophthora*?
15:35 - 15:40	Felipe Balocchi	New records of *Phytophthora* on native trees in South Africa
15:40 - 15:45	Jonàs Oliva	Litter decomposition by *Phytophthora lacustris* and *Ph. gonapodyides* species along an Alpine–Mediterranean stream gradient
15:45 - 15:50	Irene Barnes	First report of oomycetes in kiwifruit orchards in South Africa
16:00 - 17:00	General discussion of the Day 1 oral presentations and poster session	
Post Dinner Panel Discussion		
Co-Facilitators: Clive Brasier, Thomas Jung & Michael Seidl		Broad subject area: taxonomy, evolution, biosecurity, host-pathogen genetics
18:30	**Dinner**	

Wednesday, 16 September 2026		
Time	**Speaker**	**Presentation title**
08:00 - 08:30	Michael Seidl	**Plenary lecture:** Evolutionary genomics of Peronosporaceae: Towards understanding pathogenic successes
Session 5: Oral Presentations **Chair: Felipe Balocchi**		
08:30 - 8:45	Agnes Simamora	Landscape-level dynamics of *Phytophthora* spp. in Indonesia
08:45 - 09:00	Sanzida Hoque	Biotic suppression of *Phytophthora cinnamomi* across contrasting soil environments
09:00 - 09:15	Carmen Morales-Rodríguez	Illumina mRNA-seq analysis of defence-inducing treatments in Mediterranean woody hosts of *Phytophthora cinnamomi*.
09:15 - 09:30	Tanay Bose	IDphy *Phytophthora*: the online resource for molecular and morphological identification based on the types
09:30 - 09:45	Andrea Vannini	A three-year assessment of the efficacy of K-phosphonate trunk injection to mitigate the impact of *Phytophthora* cinnamomi in a cork oak forest in Italy
09:45 - 10:15	**Refreshment Break**	
Session 6: Oral Presentations **Chair: Michelle Thompson**		
10:15 - 10:30	Anna Harris	Emergence of *Phytophthora pseudosyringae* associated with larch decline in Britain
10:30 - 10:45	Zhi Xu	Dissecting the genetic control of antagonistic microbial bioactive compounds in *Pinus radiata* pathogen suppression
10:45 - 11:00	Sarah Green	Genomic insights into the evolution and virulence of *Phytophthora austrocedri*
11:00 - 11:15	Nari Williams	Population structure of *Phytophthora* cinnamomi in New Zealand
11:15 - 11:30	Bruno Scanu	A survey of oomycete diversity in West African mangrove river forests reveals three novel *Phytophthora* taxa
11:30 – 11:45	Stephanie Tomscha	Where is the Pathogen? Building the evidence base for Kauri Dieback management in New Zealand
11:45 - 13:00	**Lunch**	
Session 7: Oral Presentations **Chair: Carmen Morales-Rodríguez**		
13:00 - 13:15	Sarah Green	Metabarcoding sheds light on Phytophthora pluvialis outbreaks and co-existing *Phytophthora* spp. in commercial forests across Britain
13:15 - 13:30	Jonàs Oliva	The effect of nitrogen fertilization on the symbiosis between *Frankia* and *Alnus glutinosa* and its susceptibility to *Phytophthora × alni*
13:30 - 13:45	Kylie Ireland	Dieback detector dogs
13:45 - 14:00	Mnqobi Zuma	Interacting effects of fire, drought and *Phytophthora cinnamomi* on plant-soil relationships
14:00 - 14:15	Simone Prospero	Testing the potential of *Pseudomonas* bacteria for the biocontrol of ink disease of chestnut
14:15 - 14:30	Marília Horta Jung	Diversity of oomycete species in marine and brackish-water ecosystems in Europe and their potential involvement in widespread seagrass declines
14:30 - 15:00	**Refreshment Break**	
15:00 - 15:30	Mike Wingfield	Tree diseases in South Africa: A broad perspective

Wednesday, 16 September 2026		
Time	**Speaker**	**Presentation title**
Session 8: Poster Flash Presentations **Chair: Sophie Eccersall**		
15:30 - 15:35	Tanay Bose	Urban green spaces are critical nodes in global *Phytophthora* biosecurity
15:35 - 15:40	Anna Harris	Sporulation and pathogenicity of *Phytophthora pseudosyringae* on conifers
15:40 - 15:45	Richard O'Hanlon	Evolutionary relationships and a tree-based alignment selector interactive phylogeny of the emerging lineages of the plant pathogen *Phytophthora ramorum*
15:45 - 15:50	Thomas Jung	Modelling disease expression of *Phytophthora ramorum* to estimate potential economic impacts in European forests
15:50 - 15:55	Anna Harris	Monitoring impact of *Phytophthora ramorum* on an avenue of mature beech (*Fagus sylvatica*) in England from 2021 to 2024
15:55 - 16:00	Anna Harris	*Phytophthora ramorum* and *Phytophthora pseudosyringae* in larch (*Larix*): Associations with *P. ramorum*-infected bilberry (*Vaccinium myrtillus*) and evaluation of spore-based sampling methods in England
16:00 - 17:00	General discussion of the Day 2 oral presentations and poster session	
Post-Dinner Panel Discussion		
Co-Facilitators: Treena Burgess, Nari Williams and Alejandro Solla		Broad subject area: risk assessment, influences on pathogen introduction and spread, detection methods, pathogenicity and host range testing, management and control via various processes including site conditions, biocontrol and resistance breeding
18:30	**Dinner**	

Thursday, 17 September 2026		
Time	**Speaker**	**Presentation title**
08:00 - 08:30	Ronald Heath	Plantation forestry in South Africa Success and Challenges
Session 9: Oral Presentations **Chair: Maria Vivas**		
08:30 - 08:45	Monica Gerth	Detecting *Phytophthora* in forest soils: A simple, sensitive PCR workflow
08:45 - 09:00	Almuth Hammerbacher	Tolerance to *Phytophthora* root rot is associated with increased sesquiterpene and reduced flavonoid contents in *Eucalyptus benthamii*
09:00 - 09:15	Tanay Bose	A non-invasive approach for early detection of *Phytophthora* root rot in *Eucalyptus* using hyperspectral leaf reflectance and machine learning
09:15 - 09:30	Ian Horner	Testing efficacy of sterilants for *Phytophthora agathidicida* elimination
09:30 - 10:00	**Refreshment Break**	
Session 10: Oral Presentations **Chair: Viola Papini**		
10:00 - 10:15	Joan Webber	Changing distribution of *Phytophthora ramorum* lineages in Britain
10:15 - 10:30	Max Hayhurst	Decoding infection of European beech by *Phytophthora*
10:30 - 10:45	Anna Harris	Host specific sporulation and seasonal dynamics of *Phytophthora pluvialis* on key conifers in the UK
10:45 - 11:00	Matthew Arnet	Monitoring *Agathis australis* (kauri) health using sap flow and trunk dendrometer sensors following natural infection by *Phytophthora agathidicida* and phosphite treatment
11:00 - 11:15	María Vivas	Modelling *Phytophthora* cinnamomi spread to enhance Dehesa resilience in Extremadura (Spain)
11:15 - 11:30	Islem Yangui	Distribution of *Phytophthora* species associated with *Quercus suber* and *Q. canariensis* decline in Tunisian Forest
11:30 - 13:00	**Lunch**	

Thursday, 17 September 2026		
Time	**Speaker**	**Presentation title**
Session 11: Oral Presentations **Chair: Dang Nhu Quynh**		
13:00 - 13:15	Michelle Thompson	Developing HTS surveillance methods for *Phytophthora* detection in plant nurseries
13:15 - 13:30	Treena Burgess	Managing *Phytophthora* invasions: linking pathogen functional traits, invasiveness, and stage-specific management
13:30 - 13:45	Duccio Migliorini	Community composition of root-associated oomycetes in the south-western Australian hyper-diverse chronosequence ecosystems
13:45 – 14:00	Carmen Morales-Rodríguez	Holistic management of chestnut ink disease in Castanea sativa: field results from the LIFE FAGESOS project
14:00 - 14:15	Alessandra Benigno	Phytopathogenic oomycetes affecting oak trees in Tuscany, central Italy
14:15 - 14:45	**Refreshment Break**	
14:45 - 15:45	Panel discussion on *Phytophthora* research	
15:45 - 16:15	IUFRO Business Meeting	
16:15 - 17:30	IUFRO *Phytophthora* Football Game	
19:00 - 22:00	**Gala Dinner & Award Ceremony**	

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Day 1: 15 September 2026

PLENARY LECTURE: Clive Brasier

A sideways look at concepts and terminology in *Phytophthora*

Clive Brasier
Forest Research, Farnham, United Kingdom

In recent decades, the rapid accumulation of information around the behaviour and diversity of *Phytophthora* pathogens is leading to a paradigm shift in understanding the evolutionary history and adaptation of the genus. It may also be leading to, and in some instances may now require, a rethink of some long-embedded concepts and terminology. These range from what constitutes a species and the validity of having a taxonomic 'type' to defining host range and breeding systems and distinguishing what is a Phytophthora's natural or endemic behaviour versus what is an artifact resulting from its introduction. These issues will be discussed.

ORAL PRESENTATIONS

Session 1 | Chair: Hazel Daniels

OP01: Development of a rapid, field-based method and a real-time multiplex PCR for simultaneous detection of multiple forestry *Phytophthora* species

Amy Eacock[1*], Anna Harris[1], Ashleigh J Elliot[2], Christopher Field[2], Elżbieta Krzywińska[1], Ana Pérez-Sierra[1,3]
[1] Forest Research, Alice Holt Lodge, Farnham, Surrey, United Kingdom; [2] Fera Science Ltd, York Biotech Campus, Sand Hutton, York, United Kingdom; [3] Institut Valencià d'Investigacions Agràries (IVIA)

There are currently several *Phytophthora* species that are of major concern for forestry. Three of these species: *P. pluvialis*, *P. pseudosyringae* and *P. ramorum,* share a similar host range across the British Isles and display similar symptoms and disease progression. As *P. pluvialis* and *P. ramorum* are regulated pathogens in Great Britain, early and accurate detection is fundamental for appropriate management of these potentially invasive and highly destructive pathogens. We developed two diagnostic tests, both targeting the mitochondrial gene Cytochrome c oxidase subunit 2 (cox2): a multiplex real-time polymerase chain (RT-PCR) reaction, which enables simultaneous detection of these three *Phytophthora* species, and an isothermal recombinase polymerase amplification (RPA) assay for detection of *P ramorum* and *P. pluvialis*. The RT-PCR is highly specific and sensitive, with a limit of detection (LOD) ranging from 7.4 - 36 fg of mycelial DNA and is suitable for detection from infected plant material, with >90% diagnostic accuracy. The RPA can be used at the point of sampling and provides results within 20 minutes. This assay showed high specificity at LODs between 1-10 pg of mycelial DNA, depending on species and lineage. Although less sensitive than the RT-PCR assay, this rapid, frontline test is suitable for plant matrices, with positive detections from samples with a RT-PCR positive of <30 cycles. These new diagnostic tools improve accuracy and speed of detection, reducing cost without compromising sensitivity. The RPA assays provide rapid

results in the field, borders, and ports, and enable effective triage of samples for laboratory analysis.

OP02: Climate and soil as environmental filters of *Phytophthora* soil communities in Australia

María Rodríguez-Solís[1,2], Maria Caballol[2,3], Treena Burgess[4], Jonàs Oliva[1,2]
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Environmental factors like climate and soil can act as filters that influence the diversity and composition of plant pathogen communities. Climate has been shown to play a key role in the assembly of *Phytophthora* communities in water bodies. However, whether the same environmental factors influence the assembly of soil communities is unknown. In this study, we examined how climate and soil contribute to the assembly of *Phytophthora* soil communities in >320 sites in Australia. Soil communities were identified through 454 metabarcoding. We analyzed the presence and distribution of environmental filtering and competitive exclusion processes. At sites where environmental filtering showed a climatic signal, we studied the functional diversity of communities within a 50 km buffer around the area. We found evidence of environmental filtering, but signs of competitive exclusion were not detected. Environmental filtering mainly occurred in dry, warm locations with more acidic soils, lower organic carbon levels, and higher bulk density. In sites with environmental filtering, communities were dominated by species with thicker oospore walls, higher temperature tolerance, and the capacity to produce survival structures such as chlamydospores and hyphal swellings. Furthermore, the species present at sites where environmental filtering occurred are not able to produce stem cankers. These results show that climate also influences the composition of *Phytophthora* soil communities and seem to evidence the importance of functional traits for predicting *Phytophthora* distribution.

OP03: Insights into the spread of *Phytophthora ramorum* in Ireland

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Phytophthora ramorum is a fungus-like pathogen of a wide range of plants. It is a regulated organism in the EU and was first found in Ireland in 2002 on rhododendron and viburnum. In 2010, it was first found on *Larix kaempferi* in Ireland. The EU1 lineage was the only lineage found in Ireland until 2021, when the EU2 lineage was also found in a forest. The EU2 lineage has been the most frequently detected lineage in Northern Ireland, UK. One hundred and twenty-four samples from Ireland and Northern Ireland collected between 2005 and 2022 were used in this research to understand the population diversity of *P. ramorum* in Ireland and Northern Ireland. Multilocus genotyping of these isolates, from a range of different hosts and years, allowed us to understand the patterns of spread and make hypotheses on how the pathogen moved in Ireland. Twenty-nine EU1 multilocus genotypes (MLGs) and six EU2 MLGs were observed. The EU1MG1, the most prevalent MLG in both countries (64% IE, 57% NI), was first observed in nurseries on rhododendron and later spread into forests on larch. We found that the EU2 lineage was already present in Ireland by 2018, 3 years earlier than our earliest reported detection. We created a T-BAS SSR interactive tool that placed the genotypes from

Ireland within the wider European diversity of *P. ramorum*. However, we identified 13 novel EU1 and 5 novel EU2 genotypes. The work has helped us identify migration patterns and temporal spread of the pathogen into Ireland

OP04: Drivers of barrier permeability and their role in determining phosphite treatment efficacy for kauri dieback: an epidemiological analysis

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Emergent forest *Phytophthora* pathogens are often managed under significant uncertainty, requiring epidemiological understanding to be developed alongside disease management strategies. *Phytophthora agathidicida*, the causal agent of kauri dieback, threatens kauri (*Agathis australis*), a southern hemisphere conifer that includes some of the world's largest trees. A common management approach uses phosphite injections to reduce host susceptibility and limit disease spread between infected and uninfected stands. We adapted the spatially explicit, multi-host forest epidemiological model SODDr to investigate how poorly understood epidemiological and treatment mechanisms may enable disease emergence across phosphite-treated host barriers. Using published data, we examined three major uncertainties: (1) transmission from secondary hosts, (2) the epidemiological effects of phosphite treatment at the individual host level, and (3) the width of phosphite treatment barriers. Model experiments consistently showed that unknown secondary hosts can negate the benefits of phosphite treatment, even when they support relatively low levels of sporulation. Although it remains unclear whether phosphite cures infected trees and eliminates transmission, model results indicated that barriers are rapidly breached when treated trees remain infected. Increasing barrier width consistently slowed disease spread, regardless of other factors. These findings were robust across both uniform host-density landscapes and simulations of 2,250 randomly distributed host landscapes. The results highlight the importance of understanding both the effects of phosphite treatment on individual trees and the transmission potential of secondary hosts for effective kauri dieback management.

OP05: *Phytophthora cinnamomi* interacts with fire and drought to shape soil carbon and fungal functional guilds across a Mediterranean forest

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Forest soils are increasingly exposed to multiple interacting disturbances, including drought, fire, and pathogen invasion, yet their combined effects on soil carbon and fungal communities are poorly understood. In a landscape-scale study of 202 sites spanning gradients of drought severity, fire frequency and time since fire, and *Phytophthora* presence, I quantified soil carbon pools alongside fungal community composition, including arbuscular mycorrhizal (AMF), ectomycorrhizal (EMF), and saprotrophs. The study aimed to identify how fungal functional diversity and abundance respond to single and combined disturbances, and how

these responses relate to soil carbon dynamics and ecosystem resilience. Preliminary analyses indicate that the interaction of fire frequency and *Phytophthora cinnamomi* presence causes a decline in total soil carbon levels. Ongoing fungal sequencing will enable us to link functional guild responses to changes in carbon storage and interacting disturbances. This work will provide new insights into the role of diverse soil fungi in mediating forest resilience under interacting environmental stressors, including the presence of *Phytophthora cinnamomi*.

Session 2 | Chair: Anna Harris

OP06: The evolution and biogeography of *Phytophthora* Clade 7a including 11 new species

Thomas Jung[1,2], Zoltan Árpad Nagy[1], Ivan Milenković[1,3], Tomas Kudláček[1,4], Bourret Tyler[5], Kageyama Koji[6], Ayaka Hieno[6], Hayato Masuya[7], Seiji Uematsu[8], Nguyen Minh Chi[9], Pham Quang Thu[9], Tamara Corcobado[1,10], Josef Janoušek[1], Tomas Májek[1], Martin Mullet[1], Michal Tomšovský[1], Monique Ferreira[11], Raghuwinder Singh[11], Cristiana Maia[12], Zoran Stanivuković[13], Zeljko Tomić[14], Jozsef Bakonyi[15], Joan Webber[16], Clive Brasier[16], Marília Horta Jung[1,2]

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During recent surveys in natural forests of Japan, Vietnam, Europe and the US, >400 *Phytophthora* isolates from Clade 7a were obtained which, based on multigene phylogenies of eight nuclear and three mitochondrial gene regions, were assigned to five known species, eight new species and one new taxon with a self-fertile (homothallic) and three new species with a self-sterile (heterothallic) A1/A2 breeding system. Although Clade 7a predominantly comprises species with a soil-/waterborne lifestyle, six taxa show convergent tendencies towards a partially aerial lifestyle by producing low proportions of sporangia that can easily be detached at sporangiophore constrictions. Clade 7a shows a disjunct natural distribution with a hotspot of diversity in Southeast and East Asia, and secondary centres in Europe and North America. This suggests an evolutionary history involving a Laurasian distribution and post-Laurasian radiations of their common ancestors. Circumstantial evidence suggests both allopatric non-adaptive and sympatric adaptive radiations contributed to the high diversity of species in Clade 7a. High nuclear heterozygosity levels, relatively high numbers of triallelic sites and partly shared maternal lines with other Clade 7a taxa suggest ten of the 34 taxa (30%) originate from interspecific hybridisations. Five of the hybrid taxa have a self-fertile and a self-sterile breeding system, respectively. The finding of 11 previously unknown species from a single *Phytophthora* subclade emphasizes a critical knowledge gap on the scale of unknown pathogen threats to forests, natural ecosystems and crops, advocating for plant biosecurity protocols be based on pathway risk analyses rather than lists of named organisms.

OP07: Unrecognized Risks: *Phytophthora* species and biosecurity gaps in South Africa

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Several *Phytophthora* species are regarded as highly damaging invasive pathogens across a range of ecosystems. These include well-documented cases such as *P. cinnamomi* in southwestern Australia, *P. agathidicida* in New Zealand and *P. ramorum* in the United States. Consequently, this group of pathogens has received considerable attention as biosecurity threats and the focus of numerous environmental impact studies. In South Africa, a wide diversity of *Phytophthora* species has been detected, including both invasive alien species and taxa considered to be native. The country is among the global leaders in the study and regulation of invasive alien species; however, microbes remain significantly underrepresented in such studies and regulations. Currently, three *Phytophthora* species are listed under South Africa's Alien and Invasive Species regulations. Two of these species, *Phytophthora pinifolia* and *P. kernoviae*, have not been detected in the country. The third species, *P. cinnamomi,* has been known in the country since the 1930s and is listed for regulation but currently no control measures are being applied for its management. This situation is particularly concerning given the significant risk posed by the pathogen to sensitive ecosystems, such as the Cape Floristic Region. Importantly, other plant-pathogenic *Phytophthora* species present in South Africa have not yet been formally recognized as threats, and their impacts are probably being overlooked. The aim of this study was to clarify and highlight the current *Phytophthora* species in South Africa, to outline actions that need to be undertaken and to propose management frameworks based on recent research.

OP08: Impacts of *Phytophthora pluvialis* and likely risk to conifer forestry in Britain

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Unexpectedly, in September 2021, *Phytophthora pluvialis* was detected on western hemlock (*Tsuga heterophylla*) at a forest site in Cornwall, England, that had previously been affected by *P. ramorum*. Symptoms on western hemlock infected with *P. pluvialis* consisted of multiple resinous cankers on branches and trunks, and also occasionally on exposed roots; Douglas fir (*Pseudotsuga menziesii*) growing in mixture with the hemlock was similarly affected. The symptoms differed markedly to those caused by *P. pluvialis* on various conifer hosts in New Zealand and the USA. To benchmark damage caused by *P. pluvialis* at the Cornwall outbreak, assessments were made of lesion size, age, and the frequency with which trunk lesions extended into the underlying sapwood and affected the timber. Since then, between 2021 and 2025, *P. pluvialis* has been detected at about 50 more locations across England, Scotland and Wales, but symptoms are rarely as significant as those seen at the first outbreak in Cornwall, suggesting limited impact. This, coupled with other evidence, has led to a reassessment of the risk *P. pluvialis* poses to conifer forestry in Britain, and contrasts with the continuing major impacts of *P. ramorum.* Possible reasons for the different outcomes following *P. ramorum* and *P. pluvialis* introductions are explored.

OP09: Detecting *Phytophthora ×cambivora*: A qPCR approach implementing an LNA-modified probe

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Phytophthora x cambivora is a long- established, highly destructive hybrid oomycete with an expansive host range in European forests and agroforestry systems. It is the main cause of ink disease in chestnut groves and contributes to the decline of beech and oak trees. The persistence of this oomycete in soil, waterways and nurseries, coupled with international trade, poses an increased risk of its spread and potential serious impact on ecosystems. Conventional diagnostic techniques, based on visual assessment, baiting, and selective cultivation, often suffer from deficiencies in rapidity, sensitivity, and specificity, in addition to requiring personnel with extensive specialized experience. Few methods are currently available for detecting and quantifying the pathogen using real-time PCR. To overcome these limitations, we developed a novel real-time quantitative PCR (qPCR) assay employing a locked nucleic acid (LNA) probe. This assay specifically targets a mitochondrial intergenic region flanked by the NAD7 and COX3 genes, with primers and probe designed using the OligoArchitect™ software. Assay specificity was rigorously evaluated against a comprehensive panel of oomycete and fungal taxa, achieving unambiguous discrimination of the target pathogen. Full validation adhered to ISO 16140 and EPPO PM7/98 standards. The protocol successfully detected *P. x cambivora* in small amounts of infected chestnut tissue, demonstrating a level of sensitivity comparable to that achieved using purified genomic DNA. This qPCR-LNA assay is therefore a robust and reliable tool for rapidly and specifically detecting *P. x cambivora* in a variety of applications and settings, including routine diagnostics, nursery surveillance, and epidemiological surveys.

OP10: Anton de Bary and *Phytophthora* in the 21st Century

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Anton de Bary established the genus Phytophthora in 1876 to classify *Phytophthora infestans*. In addition to proving through rigorous experimentation that *P. infestans* was the cause of late blight in potato he also documented the life cycle of *P. infestans,* including the emergence of motile zoospores and how they penetrated potato leaves and discovered that mycelium survives the winter within infected potato tubers. During his career, he established the science of plant pathology and placed it on a solid foundation through the introduction of rigorous controlled experimentation, the use of controls and a focus on understanding the life cycle of plant pathogens. After 150 years, the genus name Phytophthora survives and while our understanding of the biology and pathology of this genus has expanded a lot, there are still many things we do not understand well. At the same time, the genus Phytophthora is continuing to expand its global impact on plants. Anton de Bary would be very familiar with the challenges we face today, as he worked on a major plant disease problem after a novel Phytophthora species invaded Europe from the Americas. The global geographic expansion of the distribution of Phytophthora species, their aggressiveness, unpredictable host ranges and limited disease control options still pose major challenges today. During this presentation, an overview will be given of Anton de Bary's contributions and enduring legacy to plant

pathology, major developments in our understanding of Phytophthora over the last 150 years and some of the major challenges remaining for current research.

OP11: From nursery pathways to wild olive decline: monitoring emerging *Phytophthora* spp. across Mediterranean olive ecosystems through field surveys and spatial risk assessment

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Mediterranean forest ecosystems are increasingly threatened by emerging *Phytophthora* species associated with decline in both cultivated olive (*Olea europaea* L.) and wild olive (*O. europaea* var. *sylvestris*). In Sardinia, recent outbreaks in olive orchards and natural stands have been linked to multiple *Phytophthora* taxa, raising concerns about pathogen spread across agricultural and forest ecosystems. This study integrates field surveys and spatial risk assessment to investigate the emergence, potential introduction pathways, and environmental drivers of *Phytophthora*-associated decline in wild olive populations. Field surveys conducted in young olive orchards, nursery plants, and declining wild olive stands identified ten *Phytophthora* species. Most of them were detected in both symptomatic plants and propagation material, suggesting that nursery stock as an important pathway for pathogen introduction into new plantations and a potential risk for spread into natural ecosystems. To assess the risk of pathogen establishment in wild olive forests, the severe decline observed in central Sardinia was investigated through a local-scale Species Distribution Modelling (MaxEnt) approach. Fifty-five *Phytophthora*-positive sites were analysed using environmental predictors describing topography, vegetation, hydrology, and landscape features. Spatial risk patterns were mainly driven by moisture-related variables, terrain characteristics, tree cover, and proximity to watercourses, allowing the identification of areas with favourable conditions for pathogen establishment. These findings together indicate that nursery-associated introduction pathways and environmental conditions jointly contribute to the emergence and spread of *Phytophthora* in Mediterranean olive ecosystems. Integrating field observations with spatial risk assessment provides a framework for targeted monitoring, early detection, and biosecurity strategies to protect Mediterranean wild olive forests.

Session 3 | Chair: Duccio Migliorini

OP12: Towards the development of high-throughput screening protocols for red needle cast disease

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Phytophthora pluvialis, the causal agent of red needle cast (RNC), represents an ongoing threat to *Pinus radiata* plantations in New Zealand. The commercial forestry estate in New Zealand covers an estimated 1.7 million ha, of which 90% is represented by radiata pine. Despite the importance of this species and the increasing impact of RNC, the ability to phenotype breeding trials is limited due to the sporadic nature of the disease. This limits the breeder's ability to make genetic improvement towards RNC within the breeding programme. Furthermore, the underpinning host susceptibility and resistance remain poorly understood, limiting the development of effective marker-assisted selection strategies. This research aims to dissect *P. pluvialis–P. radiata* interactions through an integrated approach combining molecular plant pathology, genomics, and controlled artificial inoculations. High-throughput phenotyping assays are being developed, using artificial inoculations under controlled environments to screen a range of radiata families for RNC susceptibility and resistance. These assays are supported by improved pathogen culturing techniques and optimised spore production methods, allowing for reproducible and scalable phenotyping. By integrating artificial inoculation-based screening approaches with genomic analyses, this work will establish a framework for understanding host-pathogen interactions and provide a foundation for the development of durable resistance breeding strategies. Ultimately, this research will contribute to broader efforts that improve forest health and resilience in the radiata pine forestry sector.

OP13: Breeding *Quercus suber* and *Quercus ilex* trees for *Phytophthora* disease resistance in Spain

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Phytophthora-induced diseases in oak species are the main forest health problem in the Mediterranean basin. This is why, in 2019, a programme was launched in Spain to improve the resistance of the holm oak (*Quercus ilex*) and the cork oak (*Q. suber*) to water stress and *P. cinnamomi*. It is funded by MITECO, Junta de Extremadura (GR24154) and European Funds, coordinated by the TRAGSA company, and involves 13 R&D institutions. The aim is to obtain genotypes tolerant to water stress and *P. cinnamomi* that can be used in reforestation projects

in infested areas. Following an analysis of genetic variability, 250 mature trees were selected and their offspring (approximately 24,000 seedlings) were assessed for tolerance to individual and combined stress. Significant heritabilities for resistance and stable tolerance across sites were obtained, and a breeding population was defined. Two seed orchards and a clonal bank are currently being established, and synthetic varieties comprising six *P. cinnamomi*-tolerant cork oak genotypes are being registered. Efforts have been dedicated to the clonal propagation of tolerant material through *in vitro* and micro-cutting techniques, cryopreservation, unambiguous identification of tolerant genotypes (via SNPs), and the identification of molecular markers (EST-SSR and omics) related to tolerance to *P. cinnamomi* and water stress. Preliminary results will be presented regarding the adaptation of tolerant material, the grafting of scions from large acorn-bearing trees onto resistant rootstocks, mycorrhization to increase stress tolerance, and biotization.

OP14: Impacts of cuprous oxide treatment on red needle cast-infected pine plantations of Aotearoa New Zealand

Hazel Daniels[1], Kwasi Adusei-Fosu[2], Catherine Banham[1], Nicolò Camarretta[1], Kiryn Dobbie[1], Damien Sellier[1], Benjamin S.C. Steer[3], Katherine Wardhaugh[1], Emily R. McLay[1], Stuart Fraser[1]
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Red needle cast (RNC), caused primarily by *Phytophthora pluvialis*, is a significant foliar disease of *Pinus radiata* in Aotearoa New Zealand (AoNZ). There are currently no chemical control programmes in place for RNC in AoNZ. A previous trial (2017-2019) found preventative aerial applications of cuprous oxide (current Dothistroma needle blight control method) effective against RNC. Two separate spray trials were established in Central and Eastern plantations in Te Ika-A-Māui, North Island AoNZ. The Central trial (2019-2024) focused on disease impacts and treatment benefits; the Eastern trial (2022-2024) focused on sites with a history of high *P. pluvialis* inoculum pressure. Disease expression was greatest in 2019 (Central) and 2023 (both), reflecting the climate-driven nature of RNC outbreaks. Treatments reduced disease severity in Central plots by 8.8% compared to unsprayed plots, and trees with higher severity scores exhibited reduced growth increments; further work is required to fully quantify impacts. Significant treatment effects were observed in the Eastern trial in 2023; disease severity in sprayed trees (18%) was less than half that of unsprayed trees (45%). Disease severity was lower on trees with greater levels of defoliation at the point of assessment, indicating complex canopy-pathogen interactions. Copper-based fungicides remain a potentially cost-effective tool for RNC control. However, variability in treatment efficacy highlights the need for adaptive management strategies that integrate risk forecasting to optimally time interventions. It also reinforces the need for decision-support tools foresters can use to create integrated pest management strategies that balance productivity, resilience, and sustainability in radiata pine forestry.

OP15: Integrated *Phytophthora agathidicida* management based on research to drive kauri protection

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Phytophthora agathidicida (PA), causal agent of kauri dieback, is devastating kauri forests in parts of northern Aotearoa-New Zealand. Knowledge of disease biology has improved substantially over the past 20 years. Many aspects of the biology and distribution of PA point to possibilities for effective management and containment of kauri dieback. We have evidence that kauri dieback disease is predominantly driven by a single pathogen, PA, which is discretely distributed within forest stands. Many forests and many areas within infected forests, remain apparently pathogen free. Current detection methods are accurate and sensitive, and new methods are being developed. The host range of PA is narrow, and although other species might be very minor hosts, kauri appears to be the predominant driver of pathogen inoculum in the forest. Natural spread appears slow and localised, and the major vectors over larger distances are known (e.g. pigs, people) and potentially controllable. Phosphite has proven a very effective treatment, improving tree health, providing long-lasting protection, suppressing pathogen inoculum, with no known detrimental environmental effects. Phosphite barriers provide the possibility of effective containment of infections. Management of PA and kauri dieback will only be fully effective if a robust integrated approach is taken, combining surveillance and detection, hygiene stations, vector control, track improvements or closures, community engagement and education, ongoing research, training of personnel, phosphite treatment and barriers, informed leadership and coordination, and ongoing commitment and resourcing/funding. These opportunities and challenges will be discussed referencing supporting research showing PA can be managed within kauri forests.

OP16: The first report of *Phytophthora cactorum* causing disease in Vietnamese Lai Chau ginseng (*Panax vietnamensis* var. fuscidiscus) and preliminary results on biological control using endophytic microorganisms under in vitro conditions

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We present the first report of *Phytophthora cactorum* being a damaging pathogen of Vietnamese ginseng and the potential for applying endophytic microorganisms as biological control agents in the integrated management of this disease. Vietnamese Lai Chau ginseng (*Panax vietnamensis* var. fuscidiscus) is an endemic variant of Ngoc Linh ginseng and is commonly found in the high mountainous regions of northern Vietnam. Root and stem rot in intensively cultivated Vietnamese ginseng have become increasingly common, causing significant economic losses and directly threatening the sustainable development of this valuable crop. Samples from ginseng-growing areas in Lai Chau were collected by the Vietnam Academy of Forest Sciences and revealed that typical symptoms of diseased plants included waterlogged wounds, root necrosis, and collar rot. In severely affected plants, rot could spread to the stem and leaves, causing the entire plant to die. The causative agent was isolated on selective NARH and V8 juice agar media and, based on morphological and molecular biological characteristics, identified as *P. cactorum.* Koch's

postulates were confirmed by artificial inoculation of healthy ginseng plants, resulting in similar disease symptoms within 7–10 days. This is the first recorded instance of *P. cactorum* causing disease in *Panax vietnamensis* anywhere in the world. To develop a biocontrol for this pathogen, endophytic microorganisms, including bacteria and fungi, were isolated from the roots, stems and leaves of healthy tissues of Vietnamese ginseng. Isolates were evaluated for their antagonistic activity against *P. cactorum* in vitro. Twelve of the 35 isolates tested significantly inhibited mycelial growth, with inhibition rates ranging from 45% to 85%.

POSTER PRESENTATIONS

Session 4 | Chair: Islem Yangui

PP01: Intraspecific variability in *Phytophthora cinnamomi* isolates from *Quercus suber*, *Quercus ilex* and *Castanea sativa* in south-western Spain

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Phytophthora cinnamomi (Rands) causes significant economic losses in southern Europe and threatens the environmental balance of Mediterranean ecosystems. The pathogen infects important tree species such as cork oak (*Quercus suber*), holm oak (*Quercus ilex*) and chestnut (*Castanea sativa*). Historical records of ink disease symptoms in *C. sativa* suggest that the pathogen has been present in the Iberian Peninsula since 1726. Despite its current worldwide distribution, its invasion history and population biology remain poorly understood. We employed a set of five previously described microsatellite markers, which proved useful for characterising *P. cinnamomi* populations from avocado in South Africa, to analyse a total of 67 isolates of *P. cinnamomi* collected from roots of *Q. suber*, *Q. ilex* and *C. sativa* in three geographically separated regions of southern Spain. Sequence analysis showed that all microsatellite markers were polymorphic, although no clear differentiation was observed among regions or host species. Significant linkage disequilibrium was detected among *loci*, indicating a predominantly clonal population structure and supporting asexual reproduction in *P. cinnamomi* in Spain, consistent with patterns reported elsewhere in Europe. Shannon index values (~0.5) indicated low genetic diversity and a relatively uniform distribution of clonal lineages across the sampled regions. These values are lower than those reported for populations from South Africa, where genetic diversity is also considered low. Further sampling across a wider geographical range would help to confirm these patterns and improve our understanding of the population structure of the pathogen in the Iberian Peninsula.

PP02: Searching for *Phytophthora pluvialis* in Ireland

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Phytophthora pluvilais is a pathogen of *Pseudotsuga menziesii* and *Tsuga heterophylla* in Britain and *P. menziesii* in Belgium. It has also been found causing disease of Pinus in New Zealand and in streams in the USA. It is not regulated in the EU but is on the EPPO alert list. In Ireland, visual surveys and testing have been carried out since 2022. One 60-year-old *Tsuga heterophylla* forest site in the southwest of the country has shown symptoms of branch and top dieback for several years, as well as resinous lesions on lower branches. 61 samples have been tested since 2022, of which 1 in 2023 was positive for *P. pluvialis* by real-time PCR. In line with best practice, attempts have been made to isolate the pathogen from symptomatic *T. heterophylla* samples and from water sources on site by leaf baiting with *T. heterophylla* and *rhododendron* baits and plating onto selective PARP agar. Phytophthora-like cultures isolated from *T. heterophylla* leaf baits in February 2026 were morphologically similar to *P. pluvialis*, and the identity was confirmed by ITS sequencing. A number of other oomycetes have been isolated from this site, namely *Phytophthora ramorum*, *Phytophthora chlamydospora*, *P. gonapodyides*, *Nothophytophthora lirii* and a Lagenidium sp. This is the first detection of *P. pluvialis* in Ireland. Koch's postulates experiments are ongoing.

PP03: What species of *Magnolia* are likely transmissive hosts of *Phytophthora ramorum*?

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Although the impacts of *Phytophthora ramorum* are most visible in larch plantations in the UK, the pathogen is also regularly detected in other environments such as arboreta and spring gardens, which include ornamental plant collections such as *Magnolia* and *Rhododendron.* These gardens are often located in western Britain where the climate tends to be very favourable to *P. ramorum*. In a small study, we focussed on two gardens where *P. ramorum* was already known to be present and which also showcased various *Magnolia* species. Individual trees of different species were assessed for symptoms and isolations made from symptomatic leaves. Additionally, rainwater traps were placed under trees to test the hypothesis that *P. ramorum* was likely infecting and sporulating on *Magnolia* foliage, which would result in detection of the pathogen in the rainwater collected underneath the tree canopies. We found *P. ramorum* tended to be detected in the *Magnolia*-associated water traps late in the year (October and November) when foliar symptoms were usually most visible. Detections were also frequent with some *Magnolia* species but much less so with others, suggesting that only some species are likely to be effective transmissive hosts.

PP04: Can recreational mountain bike activity in forests contribute to the spread of *Phytophthora?*

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Mountain biking emerged in the 1970s and is a popular sport in Britain with an estimated 4 million people riding off-road. In England alone, there are more than 2,500 km of formal mountain bike trails in the public forest estate plus many 'unofficial' trails in the form of off-piste tracks that typically are built by users, most frequently in coniferous plantations. Trees shape the sport, marking turns and creating a sense of speed and connection with nature. Many mountain bikers are also familiar with major forest tree diseases such as sudden larch death (*Phytophthora ramorum*) and ash dieback (*Hymenoscyphus fraxineus*), because of the negative impacts they can have on the sport. In some instances, they have resulted in closure of mountain bike parks and put jobs at risk, with knock-on implications for local economies. However, creation of unofficial trails by bikers may also increase the vulnerability of trees to disease, through earth-moving activities, root and root collar damage from tyre friction, and propagule dispersal. We review a recent outbreak of *P. lateralis* in south-east England in a commercial compartment of mixed-age *Chamaecyparis lawsoniana* used for off-piste mountain bike activity. Disease development was significant and eventually led to the felling of all the trees in the compartment. Exploring levels of awareness and attitudes of bikers and forest managers to tree disease is needed to indicate what biosecurity interventions are most socially acceptable and therefore likely to be adopted, and to identify mechanisms likely to increase biosecure behaviour.

PP05: New records of *Phytophthora* on native trees in South Africa

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Phytophthora is a relatively large genus comprising more than 260 species, many of which are important plant pathogens affecting crops, ornamentals and native ecosystems. Although several *Phytophthora* species are known to occur in South Africa, little attention has been given to the diseases they cause on native flora. Recent tree health monitoring activities in botanical gardens have led to the first detection of several *Phytophthora* species in the country. These include known and likely non-native species as well as novel taxa. The role of many of these species as causal agents of disease remains unclear. This study focused on *Phytophthora* species isolated from symptomatic native trees and aimed to clarify their role in the observed symptoms. Isolates included *P. cinnamomi* from *Podocarpus latifolius* and *Myrsine melanophloeos, P. niederhauserii* from *Harpephyllum afrum* and *Searsia lancea,* and *P. citrophthora* and *P. pseudocryptogea* from *Celtis africana*. All host-pathogen combinations represent new records for South Africa. Pathogenicity tests showed that most isolates were able to infect their respective hosts and reproduce field symptoms. However, only *P. niederhauserii* on *H. afrum* caused severe symptoms and plant death. Isolates from *C. africana* and *M. melanophloeos* produced lesions similar to those observed in the field. However, restricted in size. In contrast, isolates from *P. latifolius* and *S. lancea* failed to reproduce symptoms, suggesting a secondary or opportunistic role in disease development. These

results provide valuable insights into the aggressiveness of *Phytophthora* species on their hosts and help prioritize future research and potential regulatory efforts.

PP06: Litter decomposition by *Phytophthora lacustris* and *P. gonapodyides* species along an Alpine–Mediterranean stream gradient

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Understanding the ecological functions of saprotrophic *Phytophthora* species in freshwater environments remains a major knowledge gap, despite their frequent isolation from submerged leaf litter. While traditionally studied as plant pathogens, several clade 6 species—particularly *Phytophthora lacustris* and *P. gonapodyides*—are common in streams and may contribute to leaf litter breakdown. However, their distribution patterns, substrate preferences and potential role in decomposition across contrasting climatic contexts are still poorly understood. We investigated *Phytophthora* colonisation of naturally occurring leaf litter in 26 forest streams spanning an altitudinal gradient from alpine to Mediterranean conditions in the Pyrenees (NE Spain). At 14 sites, we also conducted a three-month decomposition experiment using *Alnus glutinosa*, *Populus nigra* and *Quercus faginea* leaves to assess how climate, leaf traits and *Phytophthora* colonisation interact to influence decomposition under natural stream conditions. Two saprotrophic species dominated: *P. lacustris* and *P. gonapodyides*, occurring in 78% and 75% of streams, respectively. Their distributions reflected clear niche differentiation: *P. lacustris* was associated with warmer, lower-elevation sites, whereas *P. gonapodyides* occurred in colder sites and showed a stronger affinity for nitrogen-poor and less-decomposed leaves. Leaf species was the primary driver of decomposition rates. *Phytophthora* colonisation was associated with mass loss, indicating a potential functional role in decomposition.

PP07: First report of oomycetes in Kiwifruit orchards in South Africa

Irene Barnes, Felipe Balocchi, Cheyenne A. Theron
FABI, University of Pretoria, Pretoria, South Africa

South Africa's kiwifruit industry has expanded rapidly in recent years, driven by increasing plantings of gold kiwifruit (*Actinidia chinensis*), with production and orchard area steadily rising to meet export demand. Despite this growth, little is known regarding the pathogens affecting this crop in South Africa. During plant health monitoring surveys (2024-2026), kiwifruit vines from orchards in KwaZulu-Natal (KZN) and Limpopo were observed displaying symptoms of wilting, dieback, and basal stem and root discolouration, frequently associated with waterlogged soils. This study aimed to determine if any oomycete taxa were associated with these isolated incidences of vine decline in commercial orchards. Oomycetes were isolated from soil and roots via baiting and directly from fine roots. ITS rDNA sequencing revealed several species in four genera. Preliminary identification of taxa included *Phytophthora citrophthora* (KZN and Limpopo) and *P. pseudocryptogea/cryptogea* (Limpopo), *Phytopythium chamaehyphon* and related species (Limpopo), and *Globisporangium irregulare* and *G. heterothallicum* (KZN). Several of these taxa are associated with kiwifruit vine decline syndrome (KVDS) in Italy and New Zealand, where disease development is linked to a complex of soilborne oomycetes. Additionally, *Globisporangium* spp. have been associated with root

and collar rot of kiwifruit in Turkey. These findings represent the first report of oomycete species associated with declining *A. chinensis* in South Africa. However, further work is required to confirm species identities using multilocus sequencing. In addition, pathogenicity assays will be conducted to determine the relative roles of these taxa as primary pathogens or opportunistic colonisers to better inform targeted disease management strategies.

Day 2: 16 September 2026

PLENARY LECTURE: Michael Seidl

Evolutionary genomics of Peronosporaceae: towards understanding pathogen success

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Plant pathogens pose a major threat not only to global food security but also to forests and natural ecosystems. Many of the key conceptual advances underpinning our understanding of pathogen adaptation have emerged from studies of Phytophthora. Yet whether these concepts extend beyond Phytophthora remains largely unknown. Phytophthora represents only a small fraction of the Peronosporaceae, most of whose members are obligate biotrophic downy mildews. This lifestyle appears to have evolved multiple times independently within the family, but has also long limited experimental and genomic investigation. Consequently, it remains unclear to what extent the evolutionary principles established in Phytophthora, including genome compartmentalization and rapid effector turnover, apply across the wider Peronosporaceae and what mechanisms underpin their repeated pathogenic success. Here, I will argue that recent advances in evolutionary genomics are finally allowing us to address this question. Central to this is the first application of pangenome graph representations to oomycetes, providing a powerful framework to capture the full spectrum of genomic diversity beyond the limitations of a single reference genome and enabling evolutionary change to be tracked at unprecedented resolution. Combined with historical isolate collections spanning nearly two centuries of host-resistance breakdown, infection-stage transcriptomics, and functional genomics, these approaches offer new opportunities to dissect the evolution of virulence in previously intractable pathogens. Using the obligate biotrophic spinach downy mildew Peronospora effusa as an example, I will illustrate how these approaches uncover the evolutionary processes driving pathogen adaptation. Despite remarkable conservation of genome architecture, effector repertoires diversify rapidly through sexual recombination and are deployed in tightly coordinated waves during infection. These findings suggest that recombination-driven effector diversification represents a general mechanism underlying pathogen adaptation across the Peronosporaceae. More broadly, they illustrate how emerging genomic approaches can transform our understanding of pathogen evolution, providing a blueprint for uncovering the evolutionary principles that shape pathogenic success across this diverse and economically important family.

ORAL PRESENTATIONS

Session 5 | Chair: Felipe Balocchi

OP17: Landscape-level dynamics of *Phytophthora* spp. in Indonesia: Reservoirs, climate drivers, and disease emergence across agroecosystems and natural ecosystems

Agnes Simamora[1], Mayavira Hahuly[1], Petronella Nenotek[1], Max Kapa[1], Jesayas Londingkene[1], Norman Riwu Kaho[1], Evert Hosang[2]
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Phytophthora spp. are among the most destructive plant pathogens in humid tropical regions, yet their ecology is still largely interpreted within separate agricultural or forestry contexts. This fragmented perspective limits understanding of how these pathogens persist, adapt, and spread across landscapes. In Indonesia, *Phytophthora* spp. cause major losses in key crops, including cocoa (*Phytophthora palmivora*), black pepper (*P. capsici*), potato (*P. infestans*), vanilla, and citrus. In citrus, the pathogen is associated with foot rot, gummosis, and root diseases that can lead to tree decline or death. At the same time, historical evidence of *P. cinnamomi* associated with forest hosts in Sumatra indicates that *Phytophthora* has long been present in ecosystems. This study synthesizes knowledge to reframe *Phytophthora* dynamics in Indonesia from a landscape perspective. Humid tropical conditions, characterized by high rainfall and persistent moisture, influence pathogen reproduction, dispersal, and disease development. In addition, variability in isolate virulence suggests ongoing adaptive processes across host systems and environmental conditions. We propose a conceptual framework in which natural ecosystems function as reservoirs of *Phytophthora* diversity, while agroecosystems act as amplification systems under favourable climatic and management conditions. This connectivity facilitates pathogen movement, adaptation, and disease emergence across landscapes. Although biological control strategies, including *Trichoderma* spp. and rhizosphere-associated bacteria, show promise, their effectiveness remains dependent on local conditions. This illustrates the importance of integrated and climate-responsive disease management approaches. Indonesia provides an important model system for understanding *Phytophthora* ecology in humid tropical landscapes and for developing sustainable disease management strategies under increasing climate pressure.

OP18: Biotic suppression of *Phytophthora cinnamomi* across contrasting soil environments

Sanzida Hoque, Sarah Sapsford, Treena Burgess, Peter Scott
Harry Butler Institute, Murdoch University, Perth, Australia

Soil microbial communities may limit the impact of soil-borne pathogens; however, the mechanisms underlying the suppression of pathogens such as *Phytophthora cinnamomi* remain poorly understood. This study evaluated the suppressive capacity of soils from 20 sites across Southwestern Australia against *P. cinnamomi.* Soils were characterised for physicochemical properties and suppressive capacity using co-cultivation and volatile organic compound (VOC) assays. Soil suspensions were prepared by mixing 10 g of soil in 90 mL sterile water, followed by tenfold serial dilutions (10^{-1}-10^{-6}) for the co-cultivation assay. Direct microbial antagonism was quantified by plating *P. cinnamomi* onto PDA amended with soil

suspensions. VOC-mediated suppression was assessed using an inverted plate assay in which *P. cinnamomi* grown on water agar was exposed to soil-derived volatiles without physical contact. Pathogen responses were measured by radial hyphal growth, integrity and deformation, including lysis. All soils exhibited varying degrees of suppression compared to the control in co-cultivation assays. Results will be described in relation to the ED_{50} observed in different soil types and geographic locations. Soil from one location showed strong suppression in both co-cultivation and volatile assays, but, in general, combining data from two assays gave a more complete picture of the soil's ability to suppress *P. cinnamomi*.

OP19: Illumina mRNA-seq analysis of defence-inducing treatments in Mediterranean woody hosts of *Phytophthora cinnamomi*

Carmen Morales-Rodríguez[1], Romina Caccia[1], Inas Drais[1], Silvia Turco[2], Angelo Mazzaglia[2], Andrea Vannini[1]
[1]Tuscia University-DIBAF, Viterbo, Italy. [2]Tuscia University-DAFNE, Viterbo, Italy

Phytophthora cinnamomi is one of the most destructive oomycete pathogens affecting ecologically and economically important Mediterranean woody species, including *Quercus ilex*, *Q. suber* and *Castanea sativa*. In the current European context, where the use of potassium phosphite is increasingly restricted, the identification of alternative and more sustainable disease management strategies has become a priority. Among these, treatments capable of inducing or priming plant defence responses represent a promising approach to enhance host resilience. In this study, we present Illumina mRNA-seq data to characterize the transcriptional changes triggered by defence-inducing treatments in Mediterranean woody hosts and to identify molecular pathways potentially associated with enhanced preparedness against *P. cinnamomi*. Transcriptomic profiling revealed a consistent modulation of genes and biological processes related to signalling, oxidative stress response, cell wall organisation and secondary metabolism, pointing to the activation of endogenous defence-related mechanisms. Although preliminary, these findings provide relevant molecular insight into the response of key Mediterranean hosts to defence elicitation and highlight the value of RNA-seq for the evaluation of alternative plant protection strategies. This work contributes to the development of more sustainable approaches for the management of *Phytophthora*-associated diseases in Mediterranean forest and agroforestry systems and provides a first transcriptomic framework for the assessment of novel treatments in species of high ecological and economic importance.

OP20: *IDphy Phytophthora*: the online resource for molecular and morphological identification based on the types

Z. Gloria Abad[1], Treena I. Burgess[2] and Tanay Bose[3]
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Phytophthora is an important genus of plant pathogens recognized for causing diseases of economic, environmental, and regulatory importance globally. The exceptional importance of the genus requires the availability of robust and accurate systems for morphological and molecular identification. The *IDphy* online resource, based on the types of *Phytophthora,* was released in IDtools during September 2019 by the USDA - Science & Technology (PPCDL and ITP) in collaboration with Murdoch University (Australia) for the identification of 161 species. The resource was updated in 2023 to include fact sheets for 212 species (Plant Disease – 2023). *IDphy,* in conjunction with the "Revision of the taxonomy and phylogeny of *Phytophthora*" (Studies of Mycology – 2023), constitutes a monographic work for the genus. Twenty-eight species were validated in the revision, and 50 species have been recently described. Information on the 261 valid species published until 2025 is presented in the recent manuscript for the "Timeline of 180 years of *Phytophthora*" (Plant Disease – 2026). This publication contains an innovative in silico BLAST and phylogenetic sequence analysis using NCBI, expandable databases for Sanger sequencing with 7 genes, metabarcoding with ITS for Second Generation High-throughput sequencing (HTS), a database for ITS and COI regions for Third Generation HTS, and a database for Whole Genome sequences. The resource is projected to be updated with the information published in recent years. With this work, we expect to satisfy the expectations of international researchers who consider *IDphy* as an exceptional online resource for the correct and robust identification of species in the important genus.

OP21: A three-year assessment of the efficacy of K-phosphonate trunk injection to mitigate the impact of *Phytophthora cinnamomi* in a cork oak forest in Italy

Andrea Vannini, Wajid Aurangzeb, Leonardo Guidoni, Carmen Morales-Rodríguez
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The present study aimed to evaluate the efficacy of applying K-phosphonate via trunk injection in reducing symptom expression in mature cork oak trees associated with *Phytophthora* infection foci in a natural cork oak forest in Italy. K-phosphonate treatment significantly changed the distribution of trees among disease severity classes one year after application, with a significant proportion of trees showing a reduction of disease severity. Moderately symptomatic trees (defoliation levels up to 50%) were those that benefited most from the treatment, with effects lasting up to 24 months. Trees with defoliation exceeding 50% (classes 3–4) showed a less consistent response to the treatment compared with those in classes 1–2. Although some individual trees improved, these improvements were often balanced by a similar number of deteriorations. In the untreated control plots, an increment of severity was evident during the three-year assessment. These results are of great relevance in the elaboration of Integrated Pest Management protocols for *Phytophthora* in evergreen oak forests, demonstrating the positive effect of K-phosphonate and the need for yearly treatment to reduce the progression of the disease in the infection foci.

Session 6| Chair: Michelle Thompson

OP22: Emergence of *Phytophthora pseudosyringae* associated with larch decline in Britain

Anna Harris[1], Martin Mullett[2], Joan Webber[1]
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Decline of larch (*Larix spp*.) in Britain has been widely associated with the invasive pathogen *Phytophthora ramorum.* However, since 2016, increasing numbers of symptomatic larch samples have tested negative for *P. ramorum*, but instead *P. pseudosyringae* is frequently recovered from necrotic bark tissues. In Wales in particular, *P. pseudosyringae* has been detected in a substantial proportion of larch samples, raising questions about its role in larch dieback. Historically, *P. pseudosyringae* in Britain has been associated primarily with broadleaved hosts such as European beech (*Fagus sylvatica*) and *Nothofagus* species and was not considered a significant pathogen of conifers. To investigate its potential involvement in larch decline, isolates from British forests were examined using multilocus sequencing, morphological and physiological characterisation, and pathogenicity testing on Japanese larch (*Larix kaempferi*). Phylogenetic analyses revealed two well-supported genetic lineages broadly associated with different hosts: a *Fagus–Nothofagus* lineage and a *Vaccinium–Larix* lineage. These lineages differed in colony morphology, sporangial characteristics and temperature–growth responses. In inoculation experiments, *Larix*-associated isolates produced lesions on larch bark comparable in size to those caused by *P. ramorum*, whereas isolates from other hosts produced significantly smaller lesions. The increasing detection of *P. pseudosyringae* in larch forests, together with evidence of host-associated genetic and phenotypic differentiation, suggests that this species is emerging as a pathogen of larch in Britain and highlights the potential for host-associated diversification within Phytophthora populations in forest ecosystems.

OP23: Dissecting the genetic control of antagonistic microbial bioactive compounds in *Pinus radiata* pathogen suppression

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Phytophthora pluvialis is a major fungal pathogen of *Pinus radiata*, causing red needle cast (RNC). Typical symptoms of RNC include khaki or olive-coloured regions usually with dark resinous bands on the infected needles. In the late infection stage, the infected needles quickly senesce and prematurely drop. In New Zealand, *P. radiata* constitutes approximately 90% of all planted forests, making RNC a significant threat to the forestry sector. In this study, we investigated the bioactivity of microbial bioactive compounds (MBCs) produced by *Trichoderma atroviride* against *P. pluvialis* using both direct and indirect exposure assays. Our preliminary work identified one MBC with particularly strong inhibitory effects on *P. pluvialis* during direct and indirect interactions, which we designated MBC1. To understand the molecular responses triggered by this compound, we analysed transcriptomic data from *P. pluvialis* exposed to different MBC1 concentrations across multiple timepoints to identify

differential gene expression patterns associated with MBC1 treatment. Our transcriptome analysis revealed hundreds of differentially expressed genes (DEGs) in MBC1-treated samples compared with untreated controls. The number of DEGs varied with MBC1 concentration and increased with longer exposure duration. Pathway analysis indicated that MBC1 treatment may influence lipid metabolism, biological oxidation, and fatty acid metabolism, suggesting impacts on energy production and stress responses. Overall, this study demonstrates that MBC1 produced by *T. atroviride* has measurable inhibitory effects on *P. pluvialis* and provides new insights into microbe–microbe interactions with potential applications for biocontrol of forest pathogens.

OP24: Genomic insights into the evolution and virulence of *Phytophthora austrocedri*

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Phytophthora austrocedri is a highly destructive pathogen of trees in the cypress family (Cupressaceae), associated with widespread mortality of Chilean cedar in Argentina and juniper in the UK. Here, we use high-coverage whole-genome sequencing to investigate genome structure, ploidy variation, and patterns of genetic diversity within and between lineages of *P. austrocedri*. Our analyses indicate most isolates are tetraploid, but triploidisation and diploidisation appear to be in progress in some isolates. We confirm that *P. austrocedri* is of hybrid origin (allotetraploid), and that the hybridisation event likely occurred before the two geographical lineages diverged. Levels of genome-wide genetic diversity and within-subgenome heterozygosity are very low, suggesting a history of self-fertilisation. However, the hybrid nature of the pathogen means it maintains high levels of between-subgenome heterozygosity. Finally, we conduct an RNAseq inoculation trial to compare transcriptional responses between two pathogen isolates, with the aim of identifying candidate mechanisms underpinning variation in virulence. Together, this work provides new insight into the genomic architecture, evolutionary history, and infection biology of *P. austrocedri*, and illustrates how genome composition and reproductive strategy may contribute to the success of plant pathogens in novel environments.

OP25: Population structure of *Phytophthora cinnamomi* in New Zealand

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Phytophthora cinnamomi is a globally distributed plant pathogen that threatens biodiversity, particularly in Mediterranean-type climates. In New Zealand, *P. cinnamomi* is widespread across both exotic and indigenous ecosystems, with its impact likely to intensify under projected climate change scenarios. The population diversity and structure of *P. cinnamomi* in New Zealand is poorly understood. This study investigates the genetic diversity of 117 *P. cinnamomi* isolates collected from a range of hosts and regions across New Zealand using

short-read whole-genome sequencing. Population structure analyses are used to identify genetic clusters and assess patterns of diversity within the New Zealand population. The New Zealand isolates are compared with global populations to determine genetic relationships, potential origins, and pathways of spread. Virulence of selected isolates is also evaluated to examine potential associations between genetic variation and phenotypic traits. Understanding the genetic structure and diversity of *P. cinnamomi* in New Zealand will provide insights into its distribution and epidemiology and support the development of targeted management strategies and risk assessments to mitigate its impact on horticultural, forestry, and natural ecosystems.

OP26: A survey of oomycete diversity in West African mangrove river forests reveals three novel *Phytophthora* taxa

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Mangrove ecosystems represent unique and understudied environments for oomycete diversity, particularly in West Africa. In this study, a survey was conducted in mangrove forests along the River Gambia to investigate the occurrence and diversity of oomycetes associated with brackish water habitats. Sampling was performed across multiple sites using baiting techniques and direct isolations from naturally fallen leaves. A diverse assemblage of oomycetes was recovered, including taxa belonging to the genera *Halophytophthora, Phytopythium, Phytophthora* and *Salisapilia*. Morphological characterization of *Phytophthora* isolates, combined with multilocus phylogenetic analyses (ITS, β-tubulin, Cox1, NADH and HSP90 regions), revealed the presence of three previously unknown taxa belonging to Clades 6, 8 and 9. These novel taxa are phylogenetically distinct and exhibit unique morphological and ecological traits, suggesting adaptation to saline and periodically inundated environments typical of mangrove systems. Preliminary observations indicate that within mangrove ecosystems these taxa may play an ecological role in nutrient cycling and that the Phytophthoras also have pathogenic potential. This study provides the first comprehensive assessment of oomycete diversity in West African mangroves and highlights these ecosystems as reservoirs of previously unknown *Phytophthora* taxa. Our findings contribute to a better understanding of the oomycete species composition in tropical coastal environments and underscore the importance of further exploration of poorly investigated regions and ecosystems.

OP27: Where is the Pathogen? Building the evidence base for Kauri Dieback management in New Zealand

Stephanie Tomscha
Tiakina Kauri, Wellington, New Zealand

Kauri (Agathis australis) are a taonga species, highly valued both culturally and ecologically. Following the identification of *Phytophthora agathidicida* (PA), the causal agent of kauri dieback disease, coordinated management efforts have been undertaken to limit its spread. However, it was not until the establishment of the National Pest Management Plan, New Zealand's most robust legislative instrument for biosecurity, that a dedicated management

agency was formally mandated to lead this response. Since then, considerable effort has focused on addressing a fundamental question: Where is PA present and absent? To support this, we have developed and implemented a suite of integrated systems and processes, and an overview of our system is provided in this presentation, including:

- Comprehensive mapping of kauri distribution across their natural range
- Standardised diagnostic pathways, including expert panel approval of testing methods and laboratory accreditation
- A secure, centralised GIS platform to integrate and harmonise data collected across multiple agencies and collaborators
- Data governance frameworks to ensure consistency and quality, enabling the integration of over a decade of legacy datasets
- Decision-support tools to assist stakeholders in designing and implementing surveillance programmes within their own forests

Critically, this work is undertaken in partnership with mana whenua and land management agencies. These collaborations strengthen surveillance, improve data quality, and enable more effective and locally informed responses than could be achieved independently.

Session 7| Chair: Carmen Morales-Rodríguez

OP28: Metabarcoding sheds light on *Phytophthora pluvialis* outbreaks and co-existing *Phytophthora* spp. in commercial forests across Britain

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Phytophthora species, most notably *P. ramorum,* are causing severe damage to UK forestry. Since 2021, cryptic outbreaks of an apparently newly invasive pathogen, *P. pluvialis,* have been increasingly detected on western hemlock and Douglas fir in commercial forestry plantations across Britain. Questions were raised as to the distribution of *P. pluvialis* in the wider environment, its routes of introduction and spread, and the diversity of co-existing *Phytophthora* species, including other possible novel taxa. To address these questions, metabarcoding and baiting methodologies aimed at detecting *Phytophthora* were applied to soil, stream water, and rainwater samples collected over a full calendar year from seventeen sites across Britain. Thirty-five *Phytophthora* species were detected across all sites, substrates, and detection methods, with most detections occurring in stream water by metabarcoding. The three most frequently detected species (in order of abundance) were *P. pluvialis*, *P. gonapodyides* and *P. ramorum*. The regulated pathogens *P. austrocedri*, *P. kernoviae* and *P. lateralis* were also detected. A new species record for the UK, *P. ornamentata,* was detected in soil and stream water at two sites, one in Scotland and one in Wales. *Phytophthora pluvialis* was most frequently detected in March, with rainfall trap metabarcoding data suggesting peak aerial dissemination in late winter/early spring. The pathogen was also detected consistently in soil by metabarcoding, indicating high potential for vectoring by humans and animals. The project's success in generating information useful to the forestry sector has led to continued funding for metabarcoding surveillance for *Phytophthora* in forest soils across Scotland.

OP29: The effect of nitrogen fertilization on the symbiosis between *Frankia* and *Alnus glutinosa* and its susceptibility to *Phytophthora* x *alni*

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Chronic nitrogen pollution and invasive pathogens are pressuring riparian forests, yet their interactions remain poorly understood. *Alnus glutinosa*, a keystone and N-fixing species in European river systems, is threatened by the emergent pathogen *Phytophthora × alni*. We studied the possible effects of N inputs on the soil microbiome, and in particular on the symbiosis between *Frankia* bacteria and alder and its consequences for disease expression. To test this, we conducted a greenhouse experiment manipulating N fertilization and *Frankia* nodulation through soil sterilization and amendments with alder soil. We evaluated the combined effects of soil microbiota, nodulation status, and *P. × alni* infection on alder performance. Alder survival after inoculation was dependent on N fertilization and the addition of soil microbiome from alder stands. In sterile soils without alder soil amendments, N fertilization increased mortality caused by *P. × alni*. In soils amended with alder soil, N fertilization did not increase susceptibility, although it consistently reduced *Frankia* nodulation. Nodulation was also lower in plants with the highest pathogen loads, indicating

that *P. × alni* not only affects alder growth directly but also possibly by interfering with their N-fixing capacity. Overall, our results show that both N fertilization and *P. × alni* weaken alder–*Frankia* symbiosis and can jointly reduce alder capacity to contribute N to riparian ecosystems. We found no evidence that soil microbiota or nodulation confer protection against *P. × alni*, highlighting the vulnerability of alder systems to *P. × alni* infection.

OP30: Dieback detector dogs

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Phytophthora dieback, caused by *Phytophthora cinnamomi*, is one of the most devastating plant diseases in Australia. It is a major threat to Australian biodiversity, and the ecological impacts of the disease are permanent and irreversible, impacting numerous threatened and keystone species. Early detection and mapping are the key to managing the disease effectively. Current diagnostic and mapping methods are costly, time-consuming, and require significant manual work. A pilot test conducted by New South Wales National Parks and Wildlife Service and Tate Animal Training Enterprises in 2022 demonstrated the potential to use the detection dogs as a method of detecting *P. cinnamomi*. A Dieback Detector Dogs consortium, led by the Western Australian Department of Biodiversity, Conservation and Attractions, secured grant funding from the Australian Government's Saving Native Species Program to expand this work nationally. The consortium's main aims were to determine the efficacy of dieback detection dogs under laboratory and field conditions and develop national guidelines for the use of dieback detection dogs in Australia. Laboratory and field case studies were conducted in Western Australia, Tasmania, and New South Wales to evaluate the applicability of detection dogs in screening laboratory soil samples, mapping dieback occurrence, assessing threatened species translocation sites, and screening nursery stock. To date, findings indicate that all trained dogs have a promising sensitivity in detecting *P. cinnamomi*. Further work will incorporate the use of detection dogs in on-ground disease detection to complement other methods and improve dieback management.

OP31: Interacting effects of fire, drought and *Phytophthora cinnamomi* on plant-soil relationships

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Global climate change is intensifying wildfires and driving more frequent, severe droughts and pathogen invasions, fundamentally reshaping native plant communities in forest ecosystems. While the effects of these disturbances on aboveground vegetation are well documented, their combined impacts on belowground function, essential for nutrient uptake and survival, remain poorly understood. The Northern Jarrah Forest in southwestern Western Australia has experienced marked declines in rainfall and rises in temperature since the 1970s. Fires now occur more frequently, and the invasive soil pathogen *Phytophthora cinnamomi* is gradually spreading throughout the forest. As some areas remain disease-free, we investigated how drought and fire history influence the invasion and impact of *P. cinnamomi* in these ecosystems. In a glasshouse experiment, we grew three native species with distinct

nutrient acquisition strategies in soils collected from sites with different fire histories: burned 0–3, 4–6, and >10 years ago. *P. cinnamomi* was inoculated into half the pots to assess its effects across disturbance gradients. *P. cinnamomi* and fire history had distinct, species-specific impacts. *Banksia grandis* was highly susceptible to infection, with earlier mortality in recently burned soils. In *Eucalyptus marginata*, recent fire reduced beneficial mycorrhizal symbionts, and pathogen infection compounded this decline. In *Acacia acuminata*, nodulation, critical for nitrogen fixation, declined with fire alone but increased when both disturbances were present. By simulating *P. cinnamomi* invasion across post-fire soils, this study shows how disturbance history and species traits influence plant–soil relationships, revealing key belowground mechanisms that shape ecosystem recovery under compounding threats.

OP32: Testing the potential of *Pseudomonas* bacteria for the biocontrol of ink disease of chestnut

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Ink disease, caused by the two oomycetes *Phytophthora cinnamomi* and *Phytophthora x cambivora*, is one of the most devastating diseases of sweet chestnut (*Castanea sativa*) in Europe. Its control is particularly difficult, with few fungicides showing a satisfactory effect, but being progressively banned in forest ecosystems or in forest-like plantations because of ecological concerns. Therefore, alternative, nature-friendly methods of control are urgently needed. The bacterial genus *Pseudomonas* contains many species with antifungal and antimicrobial properties. In this study, we isolated bacteria of the genus *Pseudomonas* from the rhizosphere of healthy and diseased chestnut trees in southern Switzerland. Of 166 isolated *Pseudomonas* strains, five showed significant growth inhibition of *P. cinnamomi* and/or *P. x cambivora in vitro*. Three isolates that significantly inhibited the growth of both pathogens were tested against a collection of 20 isolates of each species, which showed that the *in vitro* inhibition is independent of the pathogen isolate. The mechanisms underlying this inhibition remain unclear, since none of the three strains harbored biosynthesis genes coding for well-known antimicrobial secondary metabolites. Phylogenetic analysis on whole genome sequences showed that two of the strains belong to the *P. fluorescens* subgroup, while one strain probably belongs to a new species closely related to the *P. putida* subgroup.

OP33: Diversity of oomycete species in marine and brackish-water ecosystems in Europe and their potential involvement in widespread seagrass declines

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Between 2015 and 2025, more than 1800 isolates belonging to 114 taxa from eight known oomycete genera and one new genus, provisionally named Halomyces, were obtained from 59 marine and brackish water sites in Norway, Portugal, Sardinia and Mauritania. While 36 taxa could be assigned to known species, 68 taxa were unknown to science prior to this study. Of these, 22 taxa (32 %) show numerous heterozygous positions in their ITS and/or *Btub* regions, suggesting hybrid origin. 41 taxa from five oomycete genera were isolated from necrotic thalli of kelp and rockweed and leaf necroses of the seagrasses *Zostera marina*, *Z. noltii, Cymodocea nodosa* and *P. oceanica* in all 4 countries. In Portugal and Norway, extensive rotting of *Z. marina* rhizomes and rootlets was observed and five *Phytophthora* species, i.e., *P. chesapeakensis*, *P. gemini*, *P. condilina*, *P. inundata* and the new taxon *Phytophthora* taxon Clade06a new PT, were isolated. In Mauritania, *Halophytophthora lateralis* and two new *Halophytophthora* taxa, *H.* taxon 10 and *H.* taxon 11, were isolated from necrotic rhizomes and rootlets of *C. nodosa*. Pathogenicity of 16 oomycete species to seagrass leaves was tested. Most aggressive to *Z. marina* was *Pythium* taxon Salt 4, followed by *P.* taxon ×chlamydospora-like, *H.* taxon ×thermoambigua-like, *Nothophytophthora* taxon marina and *Py.* taxon Salt 3. Most aggressive to *C. nodosa* were *P. honggalleglyana*, *P. amnicola*, *Py.* taxon Salt 1, *Py.* taxon Salt 2 and *H. frigida.* All isolates were re-isolated. Our results demonstrate the involvement of oomycete pathogens in the widespread seagrass declines.

POSTER PRESENTATIONS

Session 8 | Chair: Sophie Eccersall

PP08: Urban green spaces as critical nodes in global *Phytophthora* biosecurity

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Urban green spaces are increasingly recognised as critical interfaces linking natural ecosystems, horticultural systems, and global plant trade. Still, their role in the ecology and spread of *Phytophthora* species has not been comprehensively synthesised. We conducted a global review of published studies to evaluate patterns of *Phytophthora* diversity, host associations, geographic distribution, and management challenges in urban environments. A total of 166 confirmed *Phytophthora*-host records from 16 studies conducted between 2005 and 2025 were compiled, representing 28 *Phytophthora* taxa and 96 host taxa across 11 countries. The resulting dataset identified 133 unique host-pathogen associations, with *Phytophthora multivora* emerging as the most widespread and polyphagous species, followed by *P. nicotianae*, *P. cinnamomi*, and *P. ramorum*. Most host plants were non-native ornamentals, highlighting the influence of horticultural trade and urban planting practices on pathogen introduction and establishment. Strong geographic biases were evident, with Spain and South Africa accounting for more than two-thirds of all published records. Simultaneously, a median six-year delay between pathogen detection and publication suggests that emerging threats may remain unrecognised for extended periods. Our synthesis demonstrates that urban green spaces function as important reservoirs and potential sources of inoculum for surrounding natural and managed ecosystems. To address these challenges, we propose an adaptive management framework integrating prevention, surveillance, early detection, response, and long-term resilience. Strengthening coordinated surveillance, harmonising reporting, and incorporating emerging technologies into urban biosecurity programmes will be essential for mitigating *Phytophthora* risks and enhancing the resilience of urban forests and connected landscapes worldwide.

PP09: Sporulation and pathogenicity of *Phytophthora pseudosyringae* on conifers

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Phytophthora pseudosyringae (Pps) has recently emerged as a significant pathogen in UK forests, causing dieback in larch (*Larix*). Although considered a native and therefore not a regulated plant health risk, its symptoms and host range resemble those of regulated pathogen *P. ramorum* (Pr), and the two may even co-occur. British Pps populations comprise three host-associated lineages — conifer, broadleaved, and Vaccinium; the conifer lineage appears unique to Britain. To assess the risk Pps poses to forestry, we compared pathogenicity and foliar sporulation of each lineage across key conifer species alongside Pr. For sporulation, Pr produced sporangia on significantly more needles than all Pps lineages on all hosts. Sporulation by broadleaved and conifer Pps lineages was similar, but significantly higher than the Vaccinium lineage. Japanese and European larch supported the highest sporulation on infected needles, followed by Douglas fir and western hemlock, while Sitka spruce supported

the least. Pathogenicity also varied with host; Pr caused larger lesions than all Pps lineages on Douglas fir, yew, and Sitka spruce saplings. However, on western hemlock, larch, and Scots pine, lesions caused by conifer and broadleaved Pps lineages were of similar size to those of Pr; the Vaccinium lineage was consistently least pathogenic. These findings suggest that larch is the most epidemiologically significant host for Pps. Although other conifers may be similarly susceptible to larch when infected by Pps, their lower sporulation potential probably constrains their epidemiological impact, making them less likely to generate enough inoculum to sustain multiple infection cycles.

PP10: Evolutionary relationships and a tree-based alignment selector interactive phylogeny of the emerging lineages of the plant pathogen *Phytophthora ramorum*

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The spread of *Phytophthora ramorum*, the causal agent of sudden oak death and sudden larch death, causes destructive losses of trees, woody shrubs, and ornamentals in nurseries and forests in the US, Canada, and Europe since the late 1990s. Twelve lineages of *P. ramorum* are described that vary in global distribution and virulence. Herein, we present a maximum likelihood phylogeny for *P. ramorum* inferred using IQ-TREE and the Tree-Based Alignment Selector (T-BAS) toolkit. The phylogeny was generated based on six loci (avh120, avh121, btub, gweuk.30.30.1, hsp90, and trp1). This phylogeny of *P. ramorum* improves on previous phylogenies because it is dynamic and interactive and incorporates a diverse set of all known global lineages from the United States and Europe (NA1, NA2, EU1, and EU2) and ancestral lineages from the putative native range in East Asia. The phylogenetic relationships inferred in the T-BAS tree support lineages NP1 and NP2 of *P. ramorum* as ancestral to NA1 and NA2 lineages found in North America. In addition, East Asian IC1, IC2, IC3, and IC4 lineages are ancestral to EU1 and EU2 lineages found in Europe. We used sequence data generated from isolates of *P. ramorum* collected from Ireland and Northern Ireland and placed them accurately in the tree. The *P. ramorum* phylogeny is available within the DeCIFR platform (https://decifr.cifr.ncsu.edu/). A *Phytophthora* T-BAS tool that includes 189 species can also be found on the DiCIFR portal. These “interactive phylogeny” can be used to rapidly update and better reflect the evolutionary relationships of new lineages of *P. ramorum* and *Phytophthora* species.

PP11: Modelling disease expression of *Phytophthora ramorum* to estimate potential economic impacts in European forests

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Phytophthora ramorum is an invasive generalist plant pathogen introduced to North America and Europe in the mid-1990s and is now established in forests and the nursery industry. It causes sudden oak death in the western US and sudden larch death in Western Europe, leading to extensive forest decline and mortality. While well studied in California and Oregon, no quantitative assessment exists for its potential economic impact on European forestry. We assessed the potential direct economic impact of *P. ramorum* on larch and beech in Europe under a "no-control" scenario. Climatically optimal areas for disease expression were derived using the CLIMEX niche model with refined parameter values, updated climate data, and *P. ramorum* occurrence records from symptomatic forest trees. These areas were overlaid with host distribution data to identify assets at risk. We then applied a radial range expansion model and a partial budgeting method to quantify annualized average damage costs. Our results indicate that 10% of the study area is climatically optimal for disease expression. Within that area, 4 223 km² of larch and 2 577 km² of beech are at risk. Under worst-case spread and mortality assumptions, annual direct damage costs could exceed €117 million for larch and €130 million for beech. Countries such as the UK, Italy, Austria, and Germany face the highest risks, while potential impacts in Southern Europe are negligible. This study provides an updated risk assessment of the current post-invasion state of *P. ramorum* in Europe, facilitating informed decision-making and the development of appropriate management strategies.

PP12: Monitoring Impact of *Phytophthora ramorum* on an Avenue of Mature Beech (*Fagus sylvatica*) in England from 2021 to 2024

Anna Harris[3], Brontë Thomas[1], Barnaby Wylder[2], Michael Crampton[3], Alex Lewis[3], Amy Eacock[3], Elzbieta Krzywinska[3]
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Phytophthora ramorum is an aggressive, aerially dispersed phytopathogen and quarantine organism in Great Britain. Since its introduction in 2002, it has caused extensive mortality of larch (*Larix* spp.) and dieback of *Rhododendron ponticum*, which also serve as primary epidemiological drivers of the disease. Its broad host range also includes European beech (*Fagus sylvatica*), on which it causes necrotic bark lesions but does not sporulate. Beech is commonly planted in proximity to larch and *R. ponticum* and is often affected when these neighbouring hosts are infected. Whilst statutory action requires removal of infected larch and *R. ponticum,* infected beech is typically retained on site. Despite this, the long-term impact of *P. ramorum* on beech is not well understood. To understand the long-term effect of *P. ramorum* on beech, an avenue of beech trees, adjacent to a *P. ramorum*-infected larch stand, in England's Peak District National Park was monitored. Lesion development and tree health were observed between 2021 and 2024, following removal of *P. ramorum*-infected larch in spring 2021. Lesions from symptomatic beech were sampled and tested using real-time PCR to confirm *P. ramorum* infection. Isolates derived from lesion tissue were processed for DNA

extraction and further species identification. Preliminary results suggest some trees can compartmentalise *P. ramorum* infection following removal of inoculum pressure. They also suggest initial inoculum pressure may contribute to disease outcomes. These findings inform the long-term management of *P. ramorum* on beech and in the wider environment.

PP13: *Phytophthora ramorum* and *Phytophthora pseudosyringae* in larch (*Larix*): associations with *P. ramorum* infected bilberry (*Vaccinium myrtillus*) and evaluation of spore-based sampling methods in England

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Phytophthora pseudosyringae has increasingly been detected on larch (*Larix* spp.) in the UK, causing symptoms comparable to the quarantine disease, *Phytophthora ramorum.* This complicates the surveillance and management of *P. ramorum* by Plant Health authorities. *P. pseudosyringae* is not regulated in Great Britain (GB) and does not require statutory control, whereas *P. ramorum* does. At some sites both pathogens are detected on larch; at others *P. ramorum* is detected in the understory whilst only *P. pseudosyringae* is detected on symptomatic larch; and at some sites only *P. pseudosyringae* is detected. Neighbouring forests may show contrasting diagnostic outcomes despite similar symptoms, raising the question of whether *P. ramorum* is present but undetected in some stands. This study monitored four larch stands in northern England exhibiting symptoms consistent with *P. ramorum*. Two of the sites had an understory of *P. ramorum*-infected *Vaccinium myrtillus*. At all sites, statutory surveillance had detected only *P. pseudosyringae*. Stands were monitored over autumn 2025 using four spore-based methods to determine: (1) whether *P. ramorum* is present on larch alongside *P. pseudosyringae* where it has been detected on *V. myrtillus.* (2) whether *P. ramorum* is absent where only *P. pseudosyringae* has been detected; (3) the comparative efficacy of these methods; and (4) whether detection varies over autumn. Preliminary results suggest that where *P. ramorum* is detected in *V. myrtillus*, larch is also infected. *P. ramorum* detection favours late autumn prior to needle senescence, whereas *P. pseudosyringae* detection does not favour a specific time.

Day 3: 17 September 2026

ORAL PRESENTATIONS

Session 9| Chair: Maria Vivas

OP34: Detecting *Phytophthora* in forest soils: A simple, sensitive PCR workflow

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Direct detection of soilborne *Phytophthora* species remains challenging due to low pathogen abundance, complex soil matrices, and interference from non-target DNA. These constraints are particularly acute when pathogens persist as thick-walled oospores that resist conventional DNA extraction. In New Zealand, *Phytophthora agathidicida* (PA) causes lethal dieback of kauri, ecologically and culturally significant forest trees. Current diagnostics rely on baiting-based assays that require specialised containment facilities, are slow and relatively insensitive, and do not provide quantitative data. We have developed complementary endpoint and quantitative PCR assays optimised for different settings. The workflows use simple size-based physical separation with mesh "teabags" to concentrate *Phytophthora* propagules from bulk soil, followed by optimised lysis to disrupt thick cell walls and extract amplifiable DNA. Primers targeting a high-copy genomic repeat achieved a detection limit of 1 femtogram of PA genomic DNA with high specificity. Validated using 65 forest soil samples, our endpoint assay detected PA in 69% of samples, compared with 11% for an established hybrid baiting–LAMP assay, demonstrating enhanced detection efficiency and surveillance power. Wider studies using the quantitative assay are revealing insights into pathogen distribution and abundance, and into relationships between pathogen loads and disease severity, providing an evidence-based framework for predicting disease onset and guiding management interventions. We are now working with government agencies and indigenous partners to implement these assays through accreditation and community-run laboratories. These methods, built on a simple but sensitive soil PCR workflow, are readily transferable to other soilborne *Phytophthora* species and environmental pathosystems.

OP35: Tolerance to *Phytophthora* root rot is associated with increased sesquiterpene and reduced flavonoid contents in *Eucalyptus benthamii*

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Cold-tolerant *Eucalyptus* genotypes, including *E. smithii*, *E. grandis x E. nitens*, and *E. benthamii*, are increasingly deployed to expand plantations into marginal environments under climate variability. However, these species are often susceptible to Phytophthora root rot, caused by *P. alticola*, which leads to reduced growth and post-planting mortality. Identifying tolerant genotypes and understanding underlying defence mechanisms is therefore critical. We investigated phytochemical traits associated with tolerance in *E. benthamii*. Nineteen families were inoculated with *P. alticola* in a sand pot trial, and disease impact was assessed

12 weeks post-inoculation as reductions in root dry weight of inoculated plants compared to uninoculated controls. Root collars were collected for metabolite profiling using GC–MS and HPLC–MS. Genotypes ranged from highly susceptible to tolerant. Relative concentrations of volatile sesquiterpenes were positively correlated with tolerance, suggesting a role in anti-oomycete defence, whereas flavonoids were negatively associated, consistent with a stress response. Ongoing bioassays are testing the effects of selected compounds on *P. alticola* growth. These findings identify candidate phytochemical markers to support selection of resilient *Eucalyptus* genotypes for plantation forestry.

OP36: A non-invasive approach for early detection of *Phytophthora* root rot in E*ucalyptus* using hyperspectral leaf reflectance and machine learning

Hendrik Johannes Esterhuizen[1], Bernard Slippers[1], Anna Bosman[2], Jolanda Roux[3,2], Wayne Jones[4], Tanay Bose[1], Almuth Hammerbacher[5]
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Phytophthora species are devastating pathogens that cause root and collar rot in a wide range of tree species, posing a significant threat to both natural ecosystems and commercial forestry. In South African plantation forestry, eucalypts are vulnerable to these pathogens. Early and accurate detection of Phytophthora root rot is critical for implementing effective disease management strategies, yet traditional methods often rely on destructive sampling or visual inspection after symptoms have already appeared. In this study, we investigated whether hyperspectral leaf reflectance data could serve as a rapid, non-destructive tool for early disease detection. Using *Phytophthora alticola* and *Eucalyptus benthamii* as a model pathosystem, we inoculated 19 commercially relevant *E. benthamii* genotypes in a controlled sand-infestation pot trial. Four months post-inoculation, we collected leaf reflectance data from both infected and control plants using a leaf clip attached to an ASD FieldSpec 4 spectroradiometer. The resulting high-dimensional dataset was analysed using a custom-built, multi-step machine learning pipeline that included data normalization, visualization, model optimization, and training. Our approach successfully distinguished between infected and healthy trees with 96% accuracy and identified a specific hyperspectral index associated with *P. alticola* infection. These findings were consistent with reductions in dry root biomass observed in inoculated plants. This study demonstrates that hyperspectral sensing, combined with machine learning, holds great promise as a non-invasive tool for the early detection of Phytophthora root rot in trees. Such technology could enable rapid, large-scale monitoring and facilitate timely interventions to mitigate disease impacts in both planted and natural forests.

OP37: Testing efficacy of sterilants for *Phytophthora agathidicida* elimination

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To minimise spread of *Phytophthora agathidicida* (PA), the cause of kauri dieback, wash-stations are installed at public track entrances in kauri forests, with various systems for brushing footwear and spraying with sanitiser. The field efficacy of the recommended sanitiser (SteriGENE®) is unknown. To gather biologically relevant data, a series of replicated experiments was carried out with test sterilants sprayed onto PA-infected substrates. Subsequent bioassays determined PA survival and the ability of spores to subsequently germinate and produce viable colonies or infective bodies. Potential sterilants assayed were SteriGENE, Dettol® and 80% ethanol. When sterilants were sprayed onto a thin layer of PA-oospore-laden agar smeared on paper, PA was reisolated from 93%, 30%, 27% and 0% of samples sprayed with water, Dettol, SteriGENE and ethanol, respectively. Subsequently, forest soil naturally infested with PA was pressed into 'cakes' of various thickness (0.5, 2, or 5 mm) before spraying the cake surface with the sterilants. Using baiting, *P. agathidicida* was subsequently detected in almost all (97%) soil samples, regardless of sterilant applied or thickness of the treated soil layer, indicating that at least a proportion of propagules was able to survive treatment, even in soil layers just 0.5 mm thick. Where soil was finely crumbled before being spray-saturated with the sterilant, all three sterilants suppressed *P. agathidicida* survival. The substantial survival of *P. agathidicida* even in thin layers of soil shows the importance of thorough cleaning of boots before spraying and not relying on the spray to kill propagules in adhering soil or root fragments.

Session 10| Chair: Viola Papini

OP38: Changing distribution of *Phytophthora ramorum* lineages in Britain

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Since ca 2000, the introduced oomycete *Phytophthora ramorum* has caused devastating epidemics on trees in Europe and North America, spreading as four ancient clonal lineages, each likely from a different geographical source in Asia. The most recently recognised lineage, EU2, was first detected in Europe in 2010 but has only been found in the British Isles, and not in mainland Europe. The quarantine status of *P. ramorum* has required annual plant health surveys across England, Scotland and Wales to identify new outbreaks and put containment measures in place. Over an extensive period of surveillance, thousands of samples have been collected from many different hosts in woodlands and forests and tested for *P. ramorum*. Since 2010, regular testing has also recorded the lineage of *P. ramorum* (EU1 or EU2) and created a dataset that has become an important resource in understanding the impact of *P. ramorum*. In contrast to the EU1 lineage, which had spread throughout much of western Britain by 2010, the EU2 was initially restricted to Northern Ireland and a small area of south-west Scotland. Since then, the EU2 has slowly extended its range, with findings first made in England in 2021; in some forests, EU1 and EU2 now overlap. The extensive dataset has allowed us to track *P. ramorum* spread over time, and understand what hosts are most affected in different treescapes. In addition, the data provides clues to the possible introduction pathways of the EU1 and EU2 lineages into Britain and their subsequent spread.

OP39: Decoding infection of European beech by *Phytophthora*

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Trees provide critical crop and ecosystem services like food and carbon capture, but the long-lived nature of trees makes them uniquely vulnerable to pests and pathogens. *Phytophthora* – literally “plant destroyer” – is among the greatest disease threats to trees. In the UK and Europe, European beech (*Fagus sylvatica*), a keystone forest species, is vulnerable to *Phytophthora* species such as *P. ramorum* and *P. plurivora*. Working with *P. ramorum*, *P. kernoviae*, *P. plurivora* and *P. gonapodyides*, the aim of this project is to characterise the infection mechanisms *Phytophthora* species use to colonise beech trees. Live imaging of infection in beech stems was achieved by confocal microscopy using fluorescently labelled *Phytophthora* lines. It was hypothesised that *Phytophthora* species would secrete large quantities of cellulose and hemicellulose-degrading enzymes, and putative lignin-modifying enzymes such as laccases and peroxidases. Vascular fluid was extracted from infected samples and analysed by mass spectrometry to identify hundreds of proteins secreted by *P. ramorum*, *P. kernoviae*, *P. plurivora,* and *P. gonapodyides*. This work will shed light on common mechanisms used by *Phytophthora* to colonise their woody hosts, and whether this differs from infection in established herbaceous plant models.

OP40: Host-specific sporulation and seasonal dynamics of *Phytophthora pluvialis* on key conifers in the UK

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Phytophthora pluvialis (Ppl) was first detected in the UK in 2021 on Douglas fir (DF; *Pseudotsuga menziesii*) and western hemlock (WH; *Tsuga heterophylla*). While previously associated with foliar infections of DF and tanoak in North America, and radiata pine and DF in New Zealand, in Britain it causes both needle infection and stem cankers, signalling a shift in disease expression under UK conditions. This altered behaviour highlights the need to evaluate host-specific sporulation and its contributions to disease spread and risk to other species. This study assessed sporulation across a range of known, economically and ecologically significant hosts under controlled laboratory conditions, including DF, WH, radiata pine, Scots pine, Japanese larch, Sitka spruce, and Rhododendron. Sporulation occurred on all species, with the highest levels on DF, followed by WH. Lower sporulation was observed on radiata pine and other conifers. Overall sporangial production was modest compared with *P. ramorum*, which can produce thousands of sporangia per needle on Japanese larch, whereas Ppl produced 209 on larch and up to 1,071 on DF. These results suggest DF and WH are the primary hosts driving inoculum production in the UK, whereas in New Zealand it is radiata pine. Seasonal assessments indicated that sporulation can occur year-round, but levels vary between DF and WH, suggesting that environmental conditions play an important role in shaping periods of disease outbreak. By identifying key hosts and periods of elevated inoculum production, these findings are informing targeted surveillance and management strategies of Ppl in British forests.

OP41: Monitoring *Agathis australis* (kauri) health using sap flow and trunk dendrometer sensors following natural infection by *Phytophthora agathidicida* and phosphite treatment

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Phytophthora agathidicida (PA) is a root pathogen that infects the foundation species *Agathis australis* (kauri), often resulting in tree death, likely a result of catastrophic hydraulic failure. Water relations measurements of large field trees infected with *Phytophthora* are rare and often focus on single or repeated discrete measurements over time. Continuous measurements of tree water status enable tree decline and the effects of treatment to be monitored over time. This study presents sap flow and high-precision dendrometer sensor data that were used to quantify water stress in mature kauri trees over a summer period. Twenty-four kauri were included in the experiment, in which PA was detected from the rhizosphere of 12 trees, contrasted with 12 trees where PA was not detected using soil baiting. Six trees from each group were treated with phosphite injection. Sap flux density and tree water deficit showed that mature trees infected with *P. agathidicida* were more water-stressed during the drier periods of summer. Phosphite application in PA-detected and PA not detected trees improved the sap flow and tree water deficit of infected kauri without significant phytotoxicity, although transient stress responses consistent with non-visible phytotoxicity were also detected. These findings demonstrate the potential of sap flow and

dendrometer measurements for monitoring kauri health and optimising programs of re-treatment for the long-term protection of kauri using phosphite.

OP42: Modelling *Phytophthora cinnamomi* spread to enhance Dehesa resilience in Extremadura (Spain)

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The dehesa, the largest silvopastoral system in Europe, is of key ecological and economic relevance for rural areas in southwestern Spain. However, its long-term persistence is endangered by critical threats from climate change, land abandonment, and intensification. On top of that, a primary driver of dehesa decline is the oomycete *Phytophthora cinnamomi*, which causes widespread oak decline. There is currently a significant mismatch between these escalating environmental challenges and the management solutions available to stakeholders. In this work, we test a local spatial modelling approach to predict pathogen spread in a *P. cinnamomi* foci. Utilising the phytorisk R package, we quantify invasion risk by integrating high-resolution spatial data and ecohydrological modelling. Model outputs will be combined with proximal sensing data to infer early warning indicators of tree decay. This framework allows for the anticipation of pathogen progression under increasingly arid conditions. By identifying high-risk zones and tree early response, the model serves as a decision-support tool for stakeholders to implement targeted mitigation strategies. These include adapting land-use practices and optimising tree-planting locations in low-probability areas, ultimately bridging the gap between scientific innovation and the long-term sustainability of the dehesa. Acknowledgements: MV has been co-financed 85% by the European Union, the European Regional Development Fund and the Regional Government of Extremadura. Managing Authority: Ministry of Finance. Grant File Number: IB24162. This work was part of the project "DRYAD" (Grant agreement ID: 101156076) funded by the European Union's "Horizon Europe" research and innovation program.

OP43: Distribution of *Phytophthora* species associated with *Quercus suber* and *Q. canariensis* decline in Tunisian forests

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Mediterranean oak forests are increasingly threatened by soil-borne pathogens that drive complex decline syndromes. This study explores the diversity and host-association of *Phytophthora* species within the Aïn Draham forest in Tunisia, focusing on two key oak species. A comprehensive survey was conducted across five sites, involving rhizosphere soil sampling from *Quercus suber* and *Q. canariensis* stands, as well as stream water. Pathogenicity was assessed via monitoring the maximum quantum yield (Qy) and WinRHIZO-based root architectural parameters. Our findings reveal a distinct partitioning of *Phytophthora* species based on the host and environment. While *Q. suber* harbored a highly diverse community

including *P. cinnamomi, P. multivora, P. melonis, P. gonapodyides*, and the *P. cactorum* complex, *P. multivora* was the sole species detected in association with *Q. canariensis.* In contrast, stream water sampling specifically yielded *P. bilorbang* and *P. gonapodyides*. Pathogenicity trials identified a critical physiological threshold at 40 days post-inoculation. Beyond this point, *P. cinnamomi* emerged as the primary driver of root disintegration and photosynthetic collapse, whereas *P. multivora* exhibited a divergence in strategy, characterized by higher host mortality despite moderate root architectural impact. This study highlights the differential susceptibility and pathogen pressure between *Q. suber* and *Q. canariensis*. The detection of host-specific associations and the presence of distinct species in stream water underscore the complexity of *Phytophthora* movement in Tunisian forests. These results provide essential data for developing targeted, site-specific conservation and biosecurity strategies.

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OP44: Developing HTS surveillance methods for *Phytophthora* detection in plant nurseries

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International movement of plant diseases is a global threat that is increasing with globalization and climate change. Plant biosecurity can be challenging, especially with the international trade of plants that can harbour asymptomatic pathogens. The DETECT-PNP project is developing and validating high-throughput sequencing (HTS) methods for environmental DNA (eDNA) with the aim of detecting plant diseases earlier, to prevent damage to ecosystems and economies. To validate this approach, we conducted a glasshouse experiment utilising *Phytophthora ramorum* inoculated into a susceptible host (Rhododendron 'Cunningham's White'). We designed SOPs for conducting inoculation and pathology experiments with waterborne regulated non-quarantine pathogens; a methodology that can guide similar future pathology experiments. Stem inoculation methods achieved infection in 100% of branches inoculated. Symptoms did not progress as expected; observations that can inform future pathology studies will be presented. A range of samples, including water flow-through samples, growing media, roots, stems, and leaves, were collected to assess *Phytophthora* DNA. Water samples were collected repeatedly over the course of seven months and results will be compared to symptom development over time, with the aim of determining a threshold level of detection. Samples were tested by nested PCR, metabarcoding, and/or qPCR, depending on sample type. This work will improve the database of oomycete genomes by culturing *Phytophthora* spp. in Ireland. This work has developed a methodology to assess the potential use of HTS in horticulture, which can contribute to strengthening future plant health surveillance strategies, while also improving nursery management and mitigating the spread of plant diseases.

OP45: Managing *Phytophthora* invasions: linking pathogen functional traits, invasiveness, and stage-specific management

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Effective management of *Phytophthora* requires strategies that reflect differences in host range, invasion ecology, and dispersal pathways. We present a decision framework that integrates predictive invasiveness modelling with a Bayesian management hierarchy to compare priorities among terrestrial narrow-host-range specialists, terrestrial wide-host-range generalists, and water specialists. Using a global *Phytophthora* database previously applied in invasion-risk studies, we estimate invasiveness from complementary metrics: a reporting-based invasiveness score and host phylogenetic diversity. We then assign management options to invasion stages, including the introduction, establishment, spread, and impact, and evaluate their relevance to each functional group through expert-informed Bayesian decision analysis. The framework shows that specialist, generalist, and water-associated taxa require distinct surveillance and intervention strategies, and that water specialists warrant particular attention as reservoirs and potential sources of hybrid lineages.

This approach provides a transparent basis for prioritising management and strengthening evidence-based plant biosecurity policy under uncertainty.

OP46: Community composition of root-associated oomycetes in the south-western Australian hyper-diverse chronosequence ecosystems

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Is there a link between plant diversity of south-western Australian dune ecosystems and the root adaptation to low soil P? We hypothesize that a trade-off between P-acquisition efficiency and plants' resistance against soil-borne oomycetes plays a primary role in this. South-western Australian dune chronosequences occur in a floristic biodiversity hotspot, with exceptionally high levels of plant species diversity and a diverse array of non-mycorrhizal and mycorrhizal nutrient-acquisition strategies. Importantly, they have some of the strongest soil P-availability gradients globally. While the root uptake process of key nutrients by native plants of this ecosystem has been described, little is known about how the native soil microbiome community influences the growth and diversity of plants with non-mycorrhizal nutrient-acquisition strategies, such as Proteaceae. To investigate the presence of a trade-off between a plant's P-acquisition efficiency and its resistance against soil-borne *Phytophthora* and other oomycetes, we collected soil and root samples of Proteaceae across chronosequence gradients in Jurien Bay and in Pemberton (Western Australia), with contrasting rainfall patterns. Our analysis focused on the taxonomic assessment of oomycetes, a large group with many relevant pathogens of the Kwongan woody flora. Soil and root samples have been processed using both traditional diagnostic techniques and advanced metabarcoding approaches. This work provides a novel description of how the community composition of oomycete main genera across the remarkable soil P gradient of the chronosequence and between two locations with different latitude and rainfall.

OP47: Holistic management of chestnut ink disease in *Castanea sativa*: field results from the LIFE FAGESOS project

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Chestnut ink disease, mainly associated with *Phytophthora cinnamomi*, is a major threat to *Castanea sativa* stands in Mediterranean areas. Under current environmental and regulatory conditions, sustainable management strategies are increasingly needed to reduce disease impact and improve stand resilience. Within the LIFE FAGESOS project, a holistic treatment protocol was developed for chestnut stands, combining hygiene measures, pathogen-suppressive soil interventions, beneficial microorganisms, and defence-inducing products. Here, we present preliminary field results from the large-scale application of this protocol in *C. sativa* coppices under operational conditions. Treatments were implemented in multiple disease foci through a coordinated management framework involving local landowners. Field performance was assessed using indicators related to tree vitality, crown condition, symptom expression, and overall stand health, supported by canopy-based observations. The results

indicate a positive response in treated areas and support the feasibility of applying this holistic approach at field scale. Beyond the effect of individual products, the study highlights the importance of integrating complementary actions within a broader management strategy adapted to local ecological and operational conditions. These findings provide practical support for the development of sustainable protocols for chestnut ink disease management and contribute to ongoing efforts to improve the resilience of Mediterranean chestnut ecosystems affected by *Phytophthora*-associated decline.

OP48: Phytopathogenic oomycetes affecting oak trees in Tuscany, central Italy

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Widespread decline in oak forest ecosystems has been documented in Tuscany in recent years, particularly on *Quercus ilex*, *Q. robur*, *Q. cerris* and *Q. suber*. Affected trees exhibit symptoms such as crown dieback, stunted growth, microphyllia and cortical necroses, often associated with exudation of mucilage from the basal stem and the roots. To investigate the etiology of the phenomenon, a comprehensive survey was conducted across multiple forest areas representative of diverse environmental gradients, ranging from coastal zones characterized by prolonged summer drought and high temperatures, to inland hilly regions with more temperate conditions, and mountainous Apennine areas with cooler climates and higher precipitation. A total of 349 samples were collected from necrotic woody tissues and rhizosphere soils of 154 symptomatic trees. Laboratory analyses revealed a high incidence of phytopathogenic oomycetes, identified through an integrative approach combining colony morphology, micromorphological characterization, and molecular phylogenetic analyses based on taxonomically informative loci (e.g., ITS and CoxI regions). The most frequently isolated species were *Phytophthora cinnamomi*, *P. gonapodyides, P. megasperma*, *P. plurivora*, *P. pseudocryptogea, P. pseudosyringae* and *P. quercina*. *Pythium diclinum* and *Phytopythium nanjingense* were also sometimes detected. Our epidemiological surveys suggest that multiple pathogens, acting in an additive or synergistic manner, may be involved in the development of the disease. Physiological analyses and pathogenicity tests are currently being conducted to evaluate the virulence of the strains and the ecological role of the identified taxa. The aim is to clarify their contribution to the decline of oak trees in the investigated forest ecosystems.

