

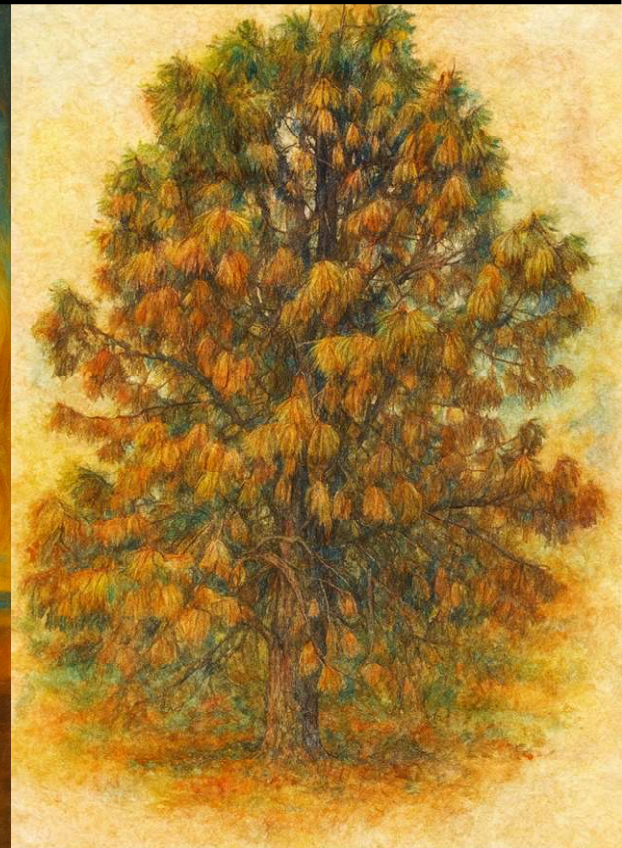


IUFRO

7.02.03 and 7.02.10

Athens, Greece • May 18-21, 2026

Will it wilt? From bark to xylem an invasion away



BOOK OF ABSTRACTS

of the Joint Meeting of the IUFRO working parties

"Vascular Wilt Diseases" and "Pine Wilt Disease" (7.02.03 and 7.02.10)



Institute of Mediterranean and Forest Ecosystems
Athens, 2026



IUFRO

7.02.03 and 7.02.10

Athens, Greece • May 18-21, 2026

The current book collects the abstracts of the presentations, oral and digital posters, presented at the Joint Meeting ‘Will it wilt? From bark to xylem an invasion away’ of the IUFRO working parties "Vascular Wilt Diseases" and "Pine Wilt Disease" (7.02.03 and 7.02.10) from May 18th to May 21st 2026, in Athens, Greece

Organizing and Scientific Committee

Barnes Irene, Professor BGM, University of Pretoria – FABI, South Africa [WP 7.02.03 Deputy Co-ordinator]
Bernier Louis, Researcher – Associate Professor, Centre for Forest Research, Canada [WP 7.02.03 Deputy Co-ordinator]
Bonifácio Luís, Senior Researcher, INIAV, Portugal [WP 7.02.10 Deputy Co-ordinator]
Han Hyerim, Researcher, National Institute of Forest Science, Republic of Korea [WP 7.02.10 Co-ordinator]
Robinet Christelle, Research Director, Deputy Director URZF – INRAE, France [WP 7.02.10 Deputy Co-ordinator]
Santini Alberto, Research Director, CNR-IPSP, Italy [WP 7.02.03 Co-ordinator]
Shinya Ryoji, Associate Professor, School of Agriculture, Meiji University, Japan [WP 7.02.10 Deputy Co-ordinator]
Soulioti Nikoleta, Scientist, IMFE, ELGO-DIMITRA, Greece [Local Organizer]
Sun Jianghua, Professor of Entomology, Institute of Zoology, Chinese Academy of Sciences/Distinguished Professor, Hebei University, P.R. China [WP 7.02.10 Deputy Co-ordinator]
Tzima Alik, Assistant Professor, Agricultural University of Athens, Greece [Local Organizer]

To be cited as:

Barnes I., Bernier L., Bonifácio L., Han H., Robinet C., Santini A., Shinya R., Soulioti N., Sun J., Tzima A. (eds), 2026. Will it wilt? From bark to xylem an invasion away: BOOK OF ABSTRACTS of the Joint Meeting of the IUFRO working parties "Vascular Wilt Diseases" and "Pine Wilt Disease" (7.02.03 and 7.02.10), Athens: ELGO DIMITRA. Institute of Mediterranean Forest Ecosystems, 77p., ISBN: 978-960-9619-08-0

https://willitwilt.pages.dev/files/abstracts_willitwilt.pdf



Institute of Mediterranean and Forest Ecosystems
Athens, 2026

Table of Contents

Bark Beetle Symbiosis / Chemical Ecology	5
From Pheromone Discovery to Neurobiology: A New Framework for Understanding Sensory-driven Behavior in <i>Bursaphelenchus xylophilus</i>	5
<i>Xylotrechus stebbingi</i> a Non-Native Occasional Vector of <i>Ceratocystis platani</i> in Europe	6
Population Genetic Assignment to Characterize Long-distance Dispersal of <i>Monochamus galloprovincialis</i> , Vector of the Pine Wood Nematode	7
The Potential Role of Bark, Ambrosia and Nitidulid Beetles in the Dispersal of the Wilt Pathogen, <i>Ceratocystis manginecans</i> in Indonesian Forestry Plantations	8
Cryo-SEM Analysis of the Spiracular Microstructure of <i>Monochamus alternatus</i> , a Vector of Pinewood Nematodes	9
Microbial Volatile Attractants from Beetle Surfaces Guide Pinewood Nematode Tracheal Invasion	10
<i>Geosmithia</i> Species, Including Several New Species, Recovered from South African Bark Beetles	11
Chemical Ecology of Ambrosia Beetles: Knowledge and Perspectives to Manage Exotic Species	12
Identification and Taxonomy	13
The Tree Wilt Pathogen <i>Ceratocystis albifundus</i> : Three Decades of Intriguing Discovery	13
Current Status of Dutch Elm Disease Caused by <i>Ophiostoma novo-ulmi</i> in Korea	14
Hidden Diversity in <i>Ophiostoma novo-ulmi</i> : Evidence from Northern Europe	15
Integrating Phylogenetic, Ecological, and Pathogenicity Evidence to Resolve Taxonomic Boundaries in the <i>Ceratocystis manginecans</i> Complex	16
Unseen Communities: Wood- and Soil-Inhabiting Nematodes in Greek Pine Forests	17
Fungi Associated with <i>Hylurgus ligniperda</i> and <i>Orthotomicus erosus</i> Infesting Pines in Croatia and South Africa	18
Host-Pathogen Interactions	19
A Climate-Dependent Vector–Pathogen–Host Transmission Model for the Pine Wilt Nematode	19
Vascular Fungal Endophytes: a Means to Breed Resistance to Dutch Elm Disease?	20
Pathogen Survival on Pruning Tools: <i>Ceratocystis platani</i> , a Case of Study	21
Is Root Disease a Factor in Mediterranean Oak Borer (<i>Xyleborus monographus</i>) Host Choice in Oregon White Oak (<i>Quercus garryana</i>)?	22
Sixteen Years of Transdisciplinary Research on Thousand Cankers Disease in Walnuts	23
A Global Call to Understand White Pine Blister Rust	24
Recent Birch Decline in Sweden	25
Pathways of Invasion / Disease Management and Control	26
<i>Ceratocystis</i> Rising in Africa: Future Threats to Forestry and Agriculture	26
Sharing the Japanese Experiences of Struggle for Controlling Pine Wilt Disease	27
Paradigm Shift in the Management of Pine Wilt Disease in Korea	28
<i>Ceratocystis</i> Invasion in Greece	29

Overcoming Polymorphism Limitations: Novel SSR Markers for Populations Genetic Analysis in <i>Bursaphelenchus xylophilus</i> and <i>Bursaphelenchus mucronatus</i>	30
How Vaccination Reshapes the <i>Ulmus glabra</i> Mycobiome under Dutch Elm Disease	31
Key Details for the Effective Use of Semiochemicals to Monitor or Control Pest Populations in the Field	32
An Integrated, Innovative Framework for Monitoring <i>Fraxinus angustifolia</i> Dieback and Resilience in Riparian Forests	33
Population Biology / Breeding	34
Pine Wilt Disease in Spain: Current Epidemiological Status and Genetic Resistance in <i>Pinus pinaster</i>	34
Metabolic Interaction between <i>Ophiostoma novo-ulmi</i> and <i>Geosmithia</i> spp.	35
From Genetic Architecture to Environmental Effects: Insights for Breeding Dutch Elm Disease-Resistant <i>Ulmus minor</i>	36
Breeding of Pine Varieties Resistant to Pine Wilt Disease and Molecular Detection of Early Host Responses	37
Vertical Distribution, Fungal Communities, and Biotic Interactions: Deciphering the Spread of <i>Bursaphelenchus xylophilus</i> in European Pine Forests	38
Establishing Pre-breeding Lines for Avocado Tolerance to Laurel Wilt	39
Genomes and Bioinformatics	40
Diversity of Mating Systems in Wilt pathogens: Insights from the Ceratocystidaceae	40
Genome-wide Evidence for Cryptic Multi-generational Introgression between Invasive <i>Bursaphelenchus xylophilus</i> and Native <i>Bursaphelenchus mucronatus</i>	41
From Transcriptomics to Management: New Insights into Oak Wilt	42
Population Genomics and Transcriptomics Uncover Adaptive Evolution and Virulence in <i>Ophiostoma</i> Species Causing Dutch Elm Disease	43
Pangenome Analysis of <i>Ophiostoma novo-ulmi</i> , the Causal Agent of Dutch Elm Disease	44
One Clone to Rule Them All? Genomics of the North American VSD Pathogen, <i>Ceratobasidium</i> spp.	45
First DIGITAL POSTERS Session	46
Histological Changes and Distribution of Secondary Metabolites in Japanese Black Pine Seedlings Inoculated with Pine Wood Nematode	46
Emergence of <i>Ceratocystis eucalypticola</i> as a Devastating Wilt Pathogen of Eucalyptus in China	47
How to Eradicate an Invasive Forest Pest without Clear-cutting	48
From Wilt to Hope: Exploring Fungal Partners in Swedish Elms	49
Development of a Field-Ready Colorimetric LAMP Assay for Rapid Detection of <i>Bursaphelenchus xylophilus</i>	50
Fungi Associated with Ambrosia Beetle <i>Xylosandrus germanus</i> in Slovakia	51
Identification, Pathogenicity and Fungicide Sensitivity of <i>Diplodia sapinea</i> , the Causal Agent of Pine Shoot Blight in China	52
Rhizosphere Bacterial Strains Showing Protection Efficacy against Fire Blight on Apple	53
Risk Assessment and Surveillance	54

Chinese Plan for the Prevention and Control of Pine Wilt Disease	54
Assessing the Dispersal of <i>Monochamus galloprovincialis</i> , the Vector of the Pine Wood Nematode, in Heterogeneous Landscapes	55
EFSA assessment of control measures for PWN in the EU	56
Automating Pine Wood Nematode Counting with AI: a Tool to Optimize Laboratory Work	57
Host Tree Distribution and Climatic Suitability for Pine Wilt Disease Expression in Austria	58
Trap-Mounted Automated Imaging for Monitoring Pest Insects	59
Testing Novel Generic Lures in France and China for Early Detection of Non-native Cerambycid Species	60
Sudden Emergence of Beech Bark Disease under Drought Stress Revealed through a Multidisciplinary Monitoring Framework Combining Forest Pathology, IoT-based Sensors and Remote Sensing	61
New Methods of Biosurveillance	62
Detecting DED and Phenotyping Elms for DED Resistance Using Near-infrared Spectroscopy	62
ICT technology-based scientific monitoring and digital history management system for pine wilt disease in Korea	63
An Initial Field Study on the Early Detection of Oak Wilt Caused by <i>Bretziella fagacearum</i> in Mature <i>Quercus rubra</i> Using Volatile Organic Compounds	64
Preliminary Exploration in Early Detection of <i>Ceratocystis platani</i> Infection on Plane Trees Using Remote Sensed Data	65
Building Resilience against Laurel Wilt Through Diagnostics and International Partnerships	66
Sudden <i>Quercus petraea</i> Decline on Fruška Gora Mt.: Interacting Climatic Stress and Biotic Agents	67
Second DIGITAL POSTERS Session	68
Modelling Spread Trends and Short-Term Prediction of Pine Wilt Disease Using Spatiotemporal Pattern Mining ...	68
Dissecting the Genetic Architecture of <i>Ulmus minor</i> 's Resistance to Dutch Elm Disease	69
The Temporal Pattern and Biological Prerequisites of PWN (<i>Bursaphelenchus xylophilus</i>) Departure from the Japanese Pine Sawyer Vector	70
Analysis of Vegetation Structure after Control of Pine Wilt Disease in South Korea	71
Evaluating Chemical Cues and Attraction of <i>Bursaphelenchus xylophilus</i> to UK Beetles in the Absence of <i>Monochamus</i>	72
A Spatial Risk Assessment Model for Pine Wilt Disease Based on Outbreak Patterns	74
Spatial Distribution Characteristics of Pine Wilt Disease: Evidence from Wildfire-Affected Areas	75

Bark Beetle Symbiosis / Chemical Ecology

Chair: Hyerim Han and Jianghua Sun

From Pheromone Discovery to Neurobiology: A New Framework for Understanding Sensory-driven Behavior in *Bursaphelenchus xylophilus*

Ryoji Shinya

School of Agriculture, Meiji University, Japan

E-mail: shinya@meiji.ac.jp

Pine wilt disease remains one of the most devastating forest threats worldwide. While the pine wood nematode, *Bursaphelenchus xylophilus*, has been extensively studied from pathological and ecological perspectives, the neural and molecular mechanisms underlying its sensory-driven behaviors have remained largely elusive. Here, we present an integrative neurobiological framework that extends existing knowledge of *B. xylophilus*, using volatile sex pheromones as a model system for understanding sensory perception and behavior. We demonstrate that *B. xylophilus* uses a previously unrecognized class of volatile pheromones to coordinate reproductive behavior. By combining chemical identification, behavioral assays, targeted neuronal ablation, and ultrastructural reconstruction of sensory organs, we identify these pheromone molecules and characterize the sensory basis of their perception by identifying the key amphid neurons responsible for detection. Furthermore, we have established the hermaphroditic species *Bursaphelenchus okinawaensis* as a genetically tractable experimental platform for the molecular dissection of pheromone receptors and downstream signaling pathways. By integrating chemical analysis, neurobiology, and genetics, this work provides a new mechanistic foundation for understanding sensory-driven behavior, reproduction, and population dynamics in the pine wood nematode, and offers new perspectives for the development of innovative management strategies for pine wilt disease.

Key Words: Volatile sex pheromone; Chemical communication; Neurobiology; Genetics; Reproductive behavior

Xylotrechus stebbingi a Non-Native Occasional Vector of *Ceratocystis platani* in Europe

Hari Berto¹, Francesco Pecori¹, Alain Roques², Marie-Anne Auger-Rozenberg², Alessia L. Pepori¹ & Alberto Santini¹

¹CNR Institute for Sustainable Plant Protection, Via Madonna del Piano, 10 - 50019 Sesto fiorentino, Italy

²INRAE- Zoologie Forestiere - Centre de recherche d'Orléans 2163 Avenue de la Pomme de Pin CS 40001 Ardon 45075 Orleans Cedex 2, France

E-mail: alberto.santini@cnr.it

In August 2025, during monitoring operations for management of Canker stain disease (CSD) of plane tree, a quarantine lethal disease caused by *Ceratocystis platani*, larvae of *Xylotrechus stebbingi* were found in the infected tissues of a plane tree along a road in Tuscany (Italy). Larval galleries were filled with frass. Both larvae and frass were collected and immediately brought to CNR-IPSP lab for DNA extraction. Analysis of Cytochrome C Oxidase subunit 1 (COI) region allowed identifying larvae as *Xylotrechus stebbingi*, an insect introduced in Europe in the last decades of 1900s. The presence of *C. platani* DNA was confirmed by a specific qPCR assay (Luchi et al., 2013) from both larvae and frass samples. Lifestyle of *X. stebbingi* is to be clarified: it is frequently reported to be associated with stressed or dying broadleaves on which adults lay eggs on the external bark. This is the first time that *X. stebbingi* was found associated to a CSD-infected *Platanus x acerifolia* tree. The frequency of association of *C. platani* with *X. stebbingi* was further studied by analyzing individuals captured by the network of multilures traps set in several Mediterranean ports and airports by INRAE. Several individuals captured in the outbreak areas of the disease resulted positive to the qPCR assay, showing that the association is frequent, even if not strict and it can favor the inoculum spread. Further studies on insect behavior and lifestyle will contribute to understanding the risk of spread of the disease by this vector.

Key Words: Canker stain disease; Disease spread; Alien insect; Alien pathogen; New association

Population Genetic Assignment to Characterize Long-distance Dispersal of *Monochamus galloprovincialis*, Vector of the Pine Wood Nematode

Varrault Mathilde¹, Desaphy Emma¹, Guichoux Erwan², Chancerel Emilie², Bankhead Stéphanie¹ & Roux Géraldine¹

¹P2E laboratory, University of Orleans, France

²PGTB, Université de Bordeaux - INRAE, France

E-mail: mathilde.varrault@univ-orleans.fr

The pinewood nematode, *Bursaphelenchus xylophilus*, (PWN) is the causal agent of the Pine Wilt Disease, which blocks sap circulation and leads to the death of pine trees in less than two months. Native to North America, this species has caused considerable damage to pine forests in Asia, since its introduction to Japan in the early 20th century, and more recently in southern Europe, on maritime pine in Portugal, Spain and France. *Monochamus galloprovincialis* (Coleoptera; Cerambycidae) is the main insect vector involved in the natural spread of the nematode in Europe, monitoring is based in part on a system for trapping adult insects in risk areas. These insects originate from local population, or could be immigrants from elsewhere, either by natural flight or by transport on contaminated wood. Being able to accurately identify dispersers and individuals' population of origin is therefore important. This study aimed to improve current knowledge about the dispersive risk of the pinewood nematode, with a focus on the dynamics of insect vector propagation at large scale. By using genetic assignment methods, individuals with unknown genetic origin can be assigned to source populations. To provide tools for molecular assignment, Single Sequence Repeats (SSRseq) microsatellite markers, which have the advantages of codominant inheritance and of being hypervariable, are good candidates to characterize polymorphism among populations. Genotyping of individuals sampled within the natural range of *Monochamus galloprovincialis* were used as reference populations for assignment. These newly defined genetic clusters would help to identify the most likely source for trapped individuals, which provide significant help in assessing the potential pathways of PWN expansion across Europe.

Key Words: PWN vector; Molecular assignment; Dispersal

The Potential Role of Bark, Ambrosia and Nitidulid Beetles in the Dispersal of the Wilt Pathogen, *Ceratocystis manginecans* in Indonesian Forestry Plantations

Kira M. T. Lynn^{1,2}, Michael J. Wingfield², Alvaro Duran¹, Samuel A. Santos¹, Marthin Tarigan¹, Deviana Tan¹, Jaliaman Sipayung¹, Wilma J. Nel³ & Irene Barnes²

¹Plant Health Program, Research and Development, Asia Pacific Resources International Holdings Ltd., Pangkalan Kerinci 28300, Riau, Indonesia

²Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Private Bag X20, Pretoria, 0028, South Africa

³Forestry and Agricultural Biotechnology Institute, University of Pretoria, Private Bag X20, Pretoria, 0028, South Africa

E-mail: kira.lynn@up.ac.za

Ceratocystis canker and wilt disease (CCWD), caused by *Ceratocystis manginecans*, poses a significant threat to *Acacia* and *Eucalyptus* plantations in Indonesia. This vascular pathogen colonizes the xylem of infected trees, which frequently become infested with insects, particularly xylem-colonizing ambrosia beetles. The role of these insects in the dispersal of *C. manginecans* in Indonesia has not been investigated. The aim of this study was to identify beetle species associated with *Ceratocystis*-infected trees and to assess their potential role as vectors. Beetles were collected from infected *Acacia* and *Eucalyptus* trees in plantations in Riau, Indonesia, using modified Bambara traps. In addition, beetles and frass were collected from symptomatic *Acacia* trees. Samples were screened for the presence and viability of *Ceratocystis* propagules using quantitative PCR–high-resolution melting analysis (qPCR-HRMA) and carrot baiting. Because beetle infestation was less frequent in *Eucalyptus* trees, bolts were cut from infected trees and placed in emergence chambers to monitor beetle emergence from infected wood. Fourteen beetle species representing nine genera within the Scolytinae and Nitidulidae were identified. qPCR-HRMA detected *Ceratocystis* DNA on 13 of the 14 species, at concentrations as low as 0.0019–0.015 ng. Viable isolates were not recovered directly from beetles. Of 105 frass samples collected from *Acacia* trees, 67 tested positive for *Ceratocystis* DNA; however, only a single isolate was recovered. This limited recovery is likely influenced by methodological constraints, such as reduced viability following environmental exposure. In contrast, emergence chamber assays yielded viable *C. manginecans* from 21% of beetles and 73% of associated frass samples. These results indicated that beetles emerging from infected trees, and particularly their frass, can carry viable *C. manginecans* and likely contribute to inoculum persistence and pathogen dispersal within plantation environments. Further studies are required to quantify transmission efficiency and evaluate epidemiological relevance under field conditions.

Key Words: *Ceratocystis*; Wood associated beetles; Forest disease epidemiology; Vector-mediated dispersal; qPCR

Cryo-SEM Analysis of the Spiracular Microstructure of *Monochamus alternatus*, a Vector of Pinewood Nematodes
Changhyun Lee¹, Junhyung Park², Jin Woo Kim³ & Ki Woo Kim^{1,4*}

¹Department of Ecology and Environmental System, Kyungpook National University, Sangju 37224, Korea

²Human Resources Development Center for Big Data-based Glocal Forest Science 4.0 Professionals, Kyungpook National University, Daegu 41566, Korea

³Department of Forest Environment, Gyeongsangbuk-do Forest Environment Research Institute, Gyeongju 38174, Korea

⁴Tree Diagnostic Center, Kyungpook National University, Sangju 37224, Korea

E-mail: reycool167@naver.com

This study employed cryo-scanning electron microscopy to investigate the spiracular microstructure of *Monochamus alternatus*, the primary vector of pinewood nematodes. Adults were sampled from regions afflicted by pine wilt disease in South Korea. To expose the spiracles, the elytra were carefully removed. The specimens were then mounted on aluminum stubs, cooled to -80°C , sputter-coated with platinum, and examined. The elliptical spiracles (8–10 per individual) measured $60\text{ }\mu\text{m}$ in mean width and $300\text{ }\mu\text{m}$ in mean length. Numerous setae (25–45 per spiracle) were distributed along the aperture, protruding centripetally to form a filter-like array. These setae, coated with mucilage-like material, had lengths of approximately $3\text{--}8\text{ }\mu\text{m}$. Fracturing with a cold knife revealed the intricate branching of tracheae and tracheoles underlying the spiracular apertures. The tracheal openings exhibited circular to oval shapes, with diameters ranging from 30 to $100\text{ }\mu\text{m}$. Consistent with the spiracular setae, the setae within the tracheal system extended centripetally to create a filtering apparatus. These findings provide morphological data on the spiracular microstructure of *M. alternatus*, facilitating interspecific comparisons of vector competency within the genus *Monochamus*.

Acknowledgements: This study was supported by the R&D Program for Forest Science Technology (RS-2024-00404388) funded by the Korea Forest Service (Korea Forestry Promotion Institute).

Key Words: Cryo-scanning electron microscopy (Cryo-SEM); Spiracular microstructure; *Monochamus alternatus*; Tracheal system; Pine wilt disease vector

Microbial Volatile Attractants from Beetle Surfaces Guide Pinewood Nematode Tracheal Invasion

Bin Zhang, Jiahui Duan & Jianghua Sun

College of Life Sciences, Hebei University, Baoding 071002, China

E-mail: binzhang@hbu.edu.cn

The transmission of pine wilt disease (PWD), a global threat to conifers caused by the pinewood nematode (PWN, *Bursaphelenchus xylophilus*), relies on its insect vector, beetles of the genus *Monochamus*. A critical step in this process is the nematode's active invasion of the beetle's tracheal system, yet the chemical cues that guide this targeted entry have remained unknown. Here, we show that the vector's own surface microbiome mediates this interaction. We identified the bacterium *Serratia marcescens* as a dominant cuticular symbiont of *M. alternatus* and found that it emits the volatile methyl ketones, including acetone and 2-butanone. The PWN displayed concentration-dependent chemotaxis toward both the bacteria and these specific ketones. In vivo augmentation of beetle cuticles with *S. marcescens* significantly increased nematode occupancy within the tracheal system. Intriguingly, these ketones play a dual ecological role: they attract nematodes at lower concentrations but suppress their reproduction at higher doses. Our findings establish a novel "vector–microbe–pathogen" chemical communication model, revealing how insect-associated bacteria can facilitate pathogen transmission through volatile signaling. This work may also uncover a new target for disrupting the PWD cycle by interfering with microbial chemical cues.

Key Words: Pinewood nematode; *Monochamus* beetle; Methyl ketones; *Serratia marcescens*

***Geosmithia* Species, Including Several New Species, Recovered from South African Bark Beetles**
Wilma J. Nel¹, Kira M.T. Lynn², Michael J. Wingfield¹, Jiri Hulcr³, Francois Roets⁴ & Irene Barnes¹

¹Department of Biochemistry, Genetics and Microbiology; Forest and Agricultural Biotechnology Institute, University of Pretoria, Pretoria, South Africa

²Plant Health Program, Research and Development, Asia Pacific Resources International Holdings Ltd., Pangkalan Kerinci 28300, Riau, Indonesia

³School of Forest, Fisheries and Geomatic Sciences, University of Florida, Gainesville, FL, USA

⁴Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa

E-mail: wilma.nel@up.ac.za

Bark beetles (Coleoptera: Scolytinae) are small wood-boring insects that contribute to the natural decay of trees by excavating galleries beneath the bark. Many bark beetle species live in association with fungi, including mutualists, as well as others that may be contaminants or have yet-to-be-described roles. The best-known of these fungi are sticky-spored species of the Ophiostomatales and Microascales (Ascomycota), which are commonly attributed as agents of vascular wilt diseases. More recently, *Geosmithia* species (Ascomycota: Hypocreales), which have dry spores, have been documented as another important fungal group associated with bark beetles. New *Geosmithia* species and their vector bark beetles are being increasingly discovered as research surveys expand to consider native environments and hosts. During a broader study of associations between bark beetles, their fungal symbionts, and native tree hosts in the Knysna forests of South Africa's Western Cape, a large collection of *Geosmithia* strains was obtained. In this study, we identified the collection of more than 150 *Geosmithia* cultures obtained from 68 beetles, from at least eight bark beetle genera, although some beetle IDs still need to be verified. Using DNA sequencing and phylogenetic analyses of four molecular markers, 11 *Geosmithia* species were recovered, six of which represent previously undescribed taxa. Formal descriptions of the novel species are currently underway.

Key Words: New species; Beetle-fungus interactions; Native species

Chemical Ecology of Ambrosia Beetles: Knowledge and Perspectives to Manage Exotic Species

Jorge E. Macías Sámano & Robert R. Setter

Synergy Semiochemicals Corp., Delta V4G 1E9, Canada

E-mail: jorge@semiochemical.com

Ambrosia beetles are known to be invasive species that vector a range of pathogenic fungi destructive to agriculture, commercial forestry and urban forest management. Traps baited with attractive semiochemicals are one of the main tools used to monitor the presence and movement of ambrosia beetle invaders globally. Semiochemicals are volatile compounds that could be an insect produced pheromone, the odor of host plants (or close related species) or even the smell of their symbiotic fungi.

Understanding the chemical ecology of the insect and its hosts becomes key to developing an effective monitoring tool. Over the past decade several species of ambrosia beetle have become repeat invaders around the globe including, *Xyleborus glabratus*, *X. germanus*, *Platypus quercivorus* and *Megaplatypus mutatus*. These insects have proven capable of establishing in new regions and impacting new hosts. Tools for monitoring and perhaps mass trapping these insects are crucial to growers and phytosanitary teams as these beetles expand their ranges. Here, we summarize the development of sociochemical tools for these insect vectors of fungal pathogens.

Key words: Chemical ecology, Ambrosia beetles, Monitoring, Management, Exotic species

Identification and Taxonomy

Chair: Irene Barnes and Christelle Robinet

The Tree Wilt Pathogen *Ceratocystis albifundus*: Three Decades of Intriguing Discovery

Michael J. Wingfield¹, Jolanda Roux², Irene Barnes¹ & Brenda D. Wingfield¹

¹Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

²Sappi Forests Pty. Ltd., Research Planning and Nurseries, Grootgeluk, Ngodwana, South Africa

E-mail: mike.wingfield@fabi.up.ac.za

Ceratocystis albifundus was first described (as *C. albofundus*) in 1996 after the fungus was discovered in 1993, causing a vascular wilt disease of non-native *Acacia mearnsii* in South Africa. When the disease was first discovered, the causal agent was thought to be the well-known wilt pathogen *Ceratocystis fimbriata*. While similar to that fungus, the newly discovered pathogen differed in having light-coloured ascomatal bases and convergent ostiolar hyphae. Phylogenetic inference based on DNA sequence data, while only very rudimentary at that time, provided the motivation to describe it as a new species. At that time, the origin of *C. albifundus* was unknown, but its occurrence on a non-native host and its similarity to *C. fimbriata* suggested that it might have been introduced into South Africa. The subsequent discovery of the fungus on native Proteaceae and on numerous other native South African trees provided the first evidence that *C. albifundus* is a native African pathogen. Over the last three decades, the pathogen has been the subject of many studies, including those considering its origin, vector relations, and genetics. Similar to other species in the Ceratocystidaceae, *C. albifundus* is an aggressive pathogen of various trees families, and it could be introduced into other parts of the world where it has the potential to cause serious disease.

Key Words: Fungal pathogen; Tree wilt diseases; *Ceratocystis*

Current Status of Dutch Elm Disease Caused by *Ophiostoma novo-ulmi* in Korea

Ki Hyeong Park¹, Sang-Tae Seo¹ & Dong-Hyeon Lee²

¹Forest Entomology and Pathology Division, National Institute of Forest Science, Seoul 02455, South Korea

²Department of Environment and Forest Resources, Chungnam National University, Daejeon 34134, Republic of Korea"

E-mail: bergpkh0@korea.kr

In 2021, the occurrence of Dutch elm disease (DED) caused by *Ophiostoma novo-ulmi* was first reported in Korea. Although no additional outbreaks have been detected outside the initial outbreak area due to rapid response and containment efforts, the disease has continued to occur within the initial outbreak area. In this study, we evaluated the pathogenicity of *O. novo-ulmi* isolates on tree species in the Family Ulmaceae and investigated the genetic diversity of *O. novo-ulmi* in Korea. Previously, *Ulmus macrocarpa* had been confirmed as a susceptible host in the first report. However, susceptibility of other native *Ulmus* and Ulmaceae species in Korea remained unclear. Field monitoring showed no disease symptoms in Ulmaceae species other than *U. macrocarpa*. Furthermore, no disease development was observed following inoculation of *O. novo-ulmi* onto common Ulmaceae tree species, including *U. parvifolia*, *U. davidiana* var. *japonica*, *Celtis sinensis*, and *Zelkova serrata*. To assess intraspecific genetic variation, we developed microsatellite markers for Korean *O. novo-ulmi* isolates and conducted amplification and polymorphism tests. The genetic diversity analysis showed low genetic diversity and high genetic similarity among the Korean isolates, suggesting a common origin or recent spread from a single population. However, relatively high diversity was detected at several loci, indicating the possible presence of partial genetic differentiation within the population.

Key Words: Dutch elm disease; *Ophiostoma novo-ulmi*; Genetic Diversity; *Ulmus macrocarpa*; Ulmaceae

Hidden Diversity in *Ophiostoma novo-ulmi*: Evidence from Northern Europe

Liina Jürisoo^{1,2}, Caroline Sunnerstam², Annika Soomelt¹, Isabella Børja^{3,4}, Rein Drenkhan¹ & Johanna Witzell²

¹Institute of Forestry and Engineering, Estonian University of Life Sciences, Estonia

²Department of Forestry and Food Technology, Faculty of Technology, Linnaeus University, Sweden

³Division of Biotechnology and Plant Health, Norwegian Institute of Bioeconomy Research (NIBIO), Norway

⁴Forestry and Renewable Energy Section, Norwegian University of Life Sciences, Norway

E-mail: liina.jyrisoo@emu.ee

Dutch elm disease (DED), caused by *Ophiostoma novo-ulmi*, continues to threaten *Ulmus* populations across northern Europe. The pathogen consists of two subspecies – subsp. *novo-ulmi* and subsp. *americana* – with evidence of hybridization where their ranges overlap. In the Nordic countries, contrasting levels of disease establishment offer a valuable context for understanding how pathogen diversity relates to disease dynamics at northern latitudes. Recent surveys from Norway and Sweden indicate the presence of both subspecies and suggest potential hybridization, although the wider population structure remains unresolved. In Finland, where DED is still emerging, available information is insufficient to determine subspecies composition or the presence of hybrids. In Estonia, updated monitoring shows notable changes in DED distribution between 2020 and 2025, revealing shifts in outbreak extent and regional patterns. New data indicates the presence of both recognized subspecies of *O. novo-ulmi* and genetic markers suggesting ongoing hybridization, reflecting dynamic pathogen population processes along the northeastern edge of its range. These findings provide an essential foundation for understanding current disease trajectories and highlight the importance of coordinated regional monitoring for future management strategies.

Key Words: Dutch elm disease; Subspecies composition; Hybridization; Regional monitoring; Disease spread

Integrating Phylogenetic, Ecological, and Pathogenicity Evidence to Resolve Taxonomic Boundaries in the *Ceratocystis manginecans* Complex

Kira M. T. Lynn^{1,2}, Michael J. Wingfield², Leonardo S.S. Oliveira³, Acelino C. Alfenas⁴, Rafael Ferreira Alfenas⁴, Seonju Marincowitz² & Irene Barnes²

¹Plant Health Program, Research and Development, Asia Pacific Resources International Holdings Ltd., Pangkalan Kerinci 28300, Riau, Indonesia

²Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Private Bag X20, Pretoria, 0028, South Africa

³Pesquisa e Desenvolvimento, Bracell Florestal, Alagoinhas, Bahia, Brazil

⁴Departamento de Fitopatologia, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil

E-mail: kira.lynn@up.ac.za

Isolates in the *Ceratocystis manginecans* complex encompass a group of aggressive wilt and canker pathogens of trees. The taxonomic boundaries in this complex have been contentious due to limited morphological differences, interfertility observed in laboratory mating studies, and the application of different species concepts. However, recent studies indicate consistent biological and ecological differences among isolates, with important implications for disease epidemiology and management. We examined phylogenetic relationships, genetic diversity, and population structure in a large collection of isolates treated broadly within the *C. manginecans* complex, including those previously referred to as *C. eucalypticola* and *C. manginecans*. A comprehensive dataset comprising isolates from eight hosts and eleven geographic regions was analysed. Phylogenetic inference based on seven gene regions, and multilocus genotyping of isolates at sixteen microsatellite loci, consistently resolved two genetically distinct groups: Lineage 1 (previously treated as *C. eucalypticola*) and Lineage 2 (previously treated as *C. manginecans*) with some individuals showing evidence of admixture between the two lineages. Morphological comparisons of representative isolates provided additional, albeit subtle, support for lineage differentiation. Field pathogenicity trials across multiple Eucalyptus clones, using representative isolates from each lineage and admixed isolates, revealed significant differences in aggressiveness, with Lineage 2 isolates inducing more severe disease symptoms. Complementary pilot greenhouse trials using a spiked soil inoculation approach further demonstrated lineage-specific differences in infection biology. Admixed isolates showed the highest infection success (30%), followed by Lineage 1 isolates, while Lineage 2 isolates failed to establish infection via soil inoculation. Soil persistence assays indicated that Lineage 1 isolates persisted for up to 12 weeks, whereas Lineage 2 showed markedly lower persistence. Although evidence of admixture indicates incomplete reproductive isolation, the concordance among phylogenetic, population genetic, morphological, and pathogenicity data supports recognition of two divergent evolutionary lineages within the *C. manginecans* complex, providing a biologically meaningful basis for diagnostics, surveillance, and disease management.

Key Words: *Ceratocystis manginecans* complex; Phylogenetic divergence; Species concepts; Infection biology; Species delimitation

Unseen Communities: Wood- and Soil-Inhabiting Nematodes in Greek Pine Forests
Neilan Chotzar¹, Dimitris Avtzis², Maria Argyropoulou³ & Nikolaos Monokrousos¹

¹University Center of International Programmes of Studies, International Hellenic University, Greece

²Forest Research Institute, ELGO-DIMITRA, Greece

³School of Biology, University Aristotle Thessaloniki, Greece

E-mail: nchotzar@ihu.edu.gr

Despite their ecological importance, nematode communities in Greek pine forests remain poorly characterized, and information regarding indigenous pine wood and soil nematode species is largely absent. This study aims to identify, describe, and compare soil and wood-inhabiting nematode communities in Black Pine and Scots Pine forests in Greece and to explore biogeographical patterns across different latitudinal gradients. We shall further investigate potential associations between nematodes and the co-occurring microbial communities. The methodological approach involves systematic seasonal sampling (summer and winter) from both healthy and weakened/dead pine trees. Nematodes will be extracted using a modified Baermann funnel technique and will be assigned to trophic groups, with taxonomic identification to species level for *Bursaphelenchus*, and to genus or family level for other taxa. Alpha and beta diversity indices and two-factor statistical analyses will be applied to assess the impact of seasonality and tree health on nematode community structure. Bacterial and fungal communities will be characterized using markers such as 16S rDNA and ITS respectively. Network analysis will be used to identify taxa and keystone nematode species. This work represents the first comprehensive documentation of indigenous soil and wood-inhabiting nematodes in Greek pine forests. Preliminary data on diversity and microbial-nematode associations will be presented.

Key Words: *Bursaphelenchus*; Pine forests; Latitude; Species richness; Nematode communities

Fungi Associated with *Hylurgus ligniperda* and *Orthotomicus erosus* Infesting Pines in Croatia and South Africa
Marta Kovač¹, Nam Q. Pham² & Mike Wingfield²

¹Croatian Forest Research Institute, Jastrebarsko, Croatia

²Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa

E-mail: martam@sumins.hr & marta.kovac1804@gmail.com

The pine bark beetles, *Orthotomicus erosus* and *Hylurgus ligniperda* are native to Croatia and generally considered minor pests, infesting recently dead or felled trees. In these situations, the fungi are best known as the causal agents of sap stain. Still, it is also possible that they contribute to the establishment and aggressiveness of the beetles under certain environmental conditions. These beetles are well-known to live in close association with fungi, particularly species in the Ophiostomatales. Both *H. ligniperda* and *O. erosus* have been accidentally introduced into countries of the southern hemisphere, where non-native *Pinus* spp. have been established in plantations for the production of timber products. Interestingly, *O. erosus* has become established in South Africa and neighboring countries, whereas *H. ligniperda* is found in *Pinus* plantations in many southern hemisphere countries. In all cases, these insects are found in their introduced environments together with various species of Ophiostomatoid fungi. However, detailed comparisons have not been made between the fungal associates of these beetles in their native and introduced ranges. Consequently, we have established a project to compare the fungi associated with *H. ligniperda* and *O. erosus* in Croatia and South Africa, for which preliminary results will be presented. Utilizing various molecular genetic approaches, including phylogenetics, phylogenomics, and population genetic comparisons, we aim to better understand the biology and pathways of invasion of the two bark beetle species.

Key Words: Blue-stain fungi; Ophiostomatales; Pine bark beetles; *Pinus* spp.

Host-Pathogen Interactions

Chair: Ryoji Shinya and Juan Antonio Martin Garcia

A Climate-Dependent Vector–Pathogen–Host Transmission Model for the Pine Wilt Nematode
Daesol Kim & Junwon Kang

School of Forest Sciences and Landscape Architecture, Kyungpook National University, Korea

E-mail: skyds4499@naver.com

Since pine wilt nematode was first reported in Busan in 1977, it has spread across Korea. Because transmission is mediated by the *M. alternatus*, integrating vector life-cycle dynamics into a transmission model is essential for accurately capturing actual patterns of nematode spread. First, time-dependent demographic parameters were derived from an established population model of *M. alternatus*, followed by construction of a temperature-dependent susceptible–infected (S-I) model parameterized with region-specific climate data. Building on this baseline, both deterministic and stochastic transmission models were implemented to compare regional estimates of the basic reproduction number (R_0) and to evaluate the potential for large-scale (“superspreading”) events. Sensitivity analysis revealed that the vector’s daily mortality rate exerted the greatest influence on R_0 , highlighting the critical role of targeted vector control. Overall, temperature-dependent transmission model—by explicitly reflecting local climatic variability—provides a robust tool for forecasting pine wilt spread and for informing effective management strategies.

Acknowledgments: This study was carried out with the support of ‘R&D Program for Forest Science Technology (RS-2024-00404388)’ provided by Korea Forest Service (Korea Forestry Promotion Institute).

Key Words: Pine wilt disease; Pine wilt nematode; Modelling; Climate Change

Vascular Fungal Endophytes: a Means to Breed Resistance to Dutch Elm Disease?

David Macaya-Sanz¹, Juan Antonio Martin² & Adrian Miguel-Pizarro¹

¹Dpto. Ecología y Genética Forestal, Instituto de Ciencias Forestales (ICIFOR-INIA), CSIC, Madrid, Spain

²Grupo de Investigación FORESCENT, ETSI Montes, Forestal y del Medio Natural, Universidad Politécnica de Madrid, Madrid, Spain

E-mail: macaya.sanz@inia.csic.es

Dutch elm disease (DED) ravaged European elm populations during the 20th century. Since then, efforts have been made to identify and breed resistant trees. These efforts have been paralleled by research aimed at inferring the mechanisms underlying resistance. As the causal agents of DED, fungi of the genus *Ophiostoma*, are vascular pathogens, fungal endophytes inhabiting the xylem represent a plausible, yet still underexplored, component of host resistance. In line with this hypothesis, we recently found that the incidence of certain taxa of vascular fungal endophytes is associated with DED resistance. To explore this topic further, we phenotyped the vascular endophytic community of five controlled crosses of *Ulmus minor*, comprising more than 500 trees, using metabarcoding based on Internal Transcribed Spacer high-throughput sequencing. First, we assessed the extent to which the composition and incidence of endophytes are genetically controlled and thus amenable to breeding. Subsequently, we investigated the genetic architecture underlying the incidence of the most promising taxa. Our results indicate that the incidence of several taxa shows moderate heritability and a non-random genetic architecture, supporting their potential use in resistance-oriented breeding. Using this information as priors, we implemented genomic selection models and evaluated the improvement in predictive accuracy relative to benchmark models based solely on genetic relationship information.

Key Words: Breeding; Heritability; Genomic prediction; Selection; Resistance

Pathogen Survival on Pruning Tools: *Ceratocystis platani*, a Case of Study

Hari Berto^{1,2}, Alessandro Puca², Alessandra Gionni², Alessia Lucia Pepori², Francesco Pecori², Nicola Luchi² & Alberto Santini²

¹University of Florence, Department of Agriculture, Food, Environment and Forestry (DAGRI), Firenze, Italy

²National Research Council, Institute for Sustainable Plant Protection (CNR-IPSP), Sesto Fiorentino, Firenze, Italy

E-mail: hariberto@cnr.it

Pruning and cutting tools as well as terracing machines are the main pathways of canker stain disease spreads. Indeed, different studies have focused on the pathogen's ability to infect healthy plants when infected pruning tools are used without being sanitized. It has also been demonstrated that spores remain viable on pruning tools for up to one month. The objective of this study is to test the viability of the pathogen on simulated pruning tools testing different methods of isolation for a long period. In addition, we want to examine the persistence of the nucleic acids (DNA and RNA) along the timeline to compare with the isolation rate. No research has been conducted so far on RNA-based detection on *C. platani*. As simulated pruning tools we used screws that were contaminated through drilling the infected tissue of a plane tree. Each screw was placed in a sterile tube and stored at 4 C°. The pathogen was then isolated using different techniques and the nucleic acids were extracted. Subsequently, a LAMP assay was performed to verify the presence of the pathogen. At least three screws were used for each test. The baiting test was effectively used to isolate the pathogen. After four months we were able to isolate the pathogen using the baiting test and the DNA and RNA were successfully extracted from the contaminated screws. This study could provide fundamental information for the disease management. Furthermore, exploring the relationship between the vital status of the pathogen and the presence of the nucleic acids is preparatory for other studies finalized to early detect *C. platani*. In the next months the permanence of the pathogen will be monitored.

Key Words: Canker stain disease; Molecular detection; Early detection; Phytopathology; Viability testing

Is Root Disease a Factor in Mediterranean Oak Borer (*Xyleborus monographus*) Host Choice in Oregon White Oak (*Quercus garryana*)?

Kellee Boyer, Jared LeBoldus, Ebba Peterson & Josh Wingfield

Oregon State University, USA

E-mail: kellee.boyer@oregonstate.edu

Xyleborus monographus, also known as Mediterranean oak borer (MOB), is an ambrosia beetle native to Europe, western Asia, and northern Africa. The beetle has recently been identified as invasive in the western United States, specifically the states of Oregon and California. In California and in its native range, *X. monographus* is associated with *Raffaelea montetyi*. *Raffaelea montetyi* is primarily known as a symbiont of the ambrosia beetle *Platypus cylindrus*; this pathogen-vector pair is associated with wilt and decline of cork oaks (*Quercus suber*) in southern Europe. In Oregon, *X. monographus* is attacking Oregon white oak (*Quercus garryana*), an ecologically important keystone species in the region. Although the fungal symbiont(s) associated with *X. monographus* are not yet identified in Oregon, there is interest in understanding the conditions that influence beetle host choice. This study seeks to determine whether preexisting root disease in *Q. garryana* increases likelihood of attack by *X. monographus*. We hypothesize that *Q. garryana* with preexisting root disease are more likely to attract *X. monographus* than are disease-free *Q. garryana*. In the summer and fall of 2025 we evaluated twenty-one trees known to be infested with MOB and twenty-one trees with no evidence of MOB. The trees were located in the city of Wilsonville, where *X. monographus* was first detected in 2023. Wood samples were collected by drilling into the base of each tree to a depth of approximately 25 cm. Fungal DNA present in the wood samples was sequenced using next generation sequencing to determine microbial community composition and presence or absence of pathogenic species. Additionally, we used sonic tomography to evaluate the extent of stem decay for each tree. Presented here are our preliminary results, exploring the relationships between microbial communities, decay percentage, various oak health factors, and *X. monographus* presence.

Key Words: Ambrosia beetle; Oak health

Sixteen Years of Transdisciplinary Research on Thousand Cankers Disease in Walnuts

Denita Hadziabdic

University of Tennessee, Department of Entomology and Plant Pathology, Knoxville, Tennessee, USA

E-mail: dhadziab@utk.edu

Thousand Cankers Disease (TCD), caused by the fungal pathogen *Geosmithia morbida* and the insect vector, walnut twig beetle, *Pityophthorus juglandis*, represents a persistent and complex threat to *Juglans* (walnut) species across North America and Europe. For 16 years, our laboratory has conducted integrated research to elucidate the biological, ecological, evolutionary, and epidemiological drivers of TCD and to advance practical tools for detection and management. We revealed high genetic diversity in both the fungus and insect vector, suggesting that components of the TCD pathosystem were present for extended periods in parts of the affected range prior to disease emergence with widespread impacts. We identified significant intraspecific variation in virulence among *G. morbida* isolates collected across the U.S., indicating that pathogen population structure contributes to observed differences in regional disease severity. *Juglans nigra* phytobiome studies have revealed that both fungal and bacterial community compositions vary geographically and are strongly associated with TCD severity, underscoring the role of host-associated microbial communities in disease development and host responses. To support early detection and surveillance, we developed, optimized, and validated rapid molecular diagnostic tools that enable reliable diagnostic confirmation of TCD in plant samples. These tools, which improve disease detection efficiency and inform optimal management decisions across affected regions, have led to the development of diagnostic tools for other vascular diseases threatening our forests. More recently, we have identified biological control agents that suppress *G. morbida*. Several fungal antagonists restrict *G. morbida* growth through mycoparasitism and antibiosis, highlighting their potential as environmentally sustainable biological control options for disease management. Collectively, this body of work demonstrates the value of transdisciplinary research to address complex forest disease systems. As TCD continues to spread under changing climatic and ecological conditions, these findings provide a foundation for predicting disease dynamics and developing resilient, science-based mitigation approaches.

Key Words: Thousand Cankers Disease; *Geosmithia morbida*; *Pityophthorus juglandis*; *Juglans* spp.; Biological control

A Global Call to Understand White Pine Blister Rust

Nadir Erbilgin

Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada

E-mail: erbilgin@ualberta.ca

High-elevation white pines (*Pinus strobus*) are ecologically important components of mountainous ecosystems across North America, Europe, and Asia, yet many species are experiencing severe declines due to the combined pressures of the invasive pathogen, *Cronartium ribicola* (white pine blister rust; WPBR) and anthropogenic climate change. White pines provide critical ecosystem services, including snowpack retention, hydrological regulation, wildlife habitat, and food resources, and several species function as keystone or foundation taxa. The introduction of *C. ribicola* has resulted in widespread infection, reduced reproductive capacity, increased susceptibility to secondary stressors, and high mortality in susceptible hosts. *Cronartium ribicola* is a macrocyclic, heteroecious rust fungus requiring both telial hosts (*Ribes* and *Castilleja* spp.) and aecial hosts (*Pinus* spp.) to complete its life cycle. Disease impacts vary substantially among white pine species and regions, reflecting differences in host resistance, pathogen lineages, and environmental conditions. North American species such as *Pinus albicaulis* and *P. flexilis* have experienced extensive mortality, whereas several Asian and European species exhibit variable tolerance or resistance, suggesting historical coevolution. Climate change is expected to intensify WPBR impacts by increasing host stress, altering wildfire regimes, and creating climatic conditions more favorable for spore production and infection, thereby disrupting regeneration, range shifts, and ecosystem function. To advance a global understanding of WPBR, I seek international collaboration focused on coordinated collection of infected white pine tissues from naturally infested stands across North America, Europe, and Asia for DNA-based analyses. Collaborators will collect standardized samples of cankered pine tissue and associated *C. ribicola* material, accompanied by site-level metadata (host species, elevation, climate variables, and disease severity). Extracted DNA will be used to characterize pathogen population structure, genetic diversity, and phylogeographic relationships among regions, as well as host genetic variation associated with resistance. Comparative genomic analyses will allow inference of historical introductions, regional differentiation, and potential signatures of local adaptation, providing a foundation for predicting disease spread and informing conservation and resistance-breeding strategies under ongoing climate change.

Key Words: Disease ecology; Genetic structure; Mountain ecosystems; Environmental stressors; Adaptive variation

Recent Birch Decline in Sweden

Iryna Matsiakh¹, Åke Olson², Audrius Menkis³

¹Southern Swedish Forest Research Centre, Swedish University of Agricultural Sciences, Sweden

²Forest management, Forestry Research Institute of Sweden, Sweden

³Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Sweden

E-mail: iryna.matsiakh@slu.se

Between 2023 and 2024, birch decline was investigated in several regions of Sweden, including Uråsa, Hudiksvall, Smöramåla, and Urshult, in both naturally regenerated forest stands and birch plants originating from plantations and seed orchards. The research focused on fungal infections and their potential links to abiotic stress factors, particularly drought. Field observations revealed that many trees exhibited symptoms such as dead branches, sparse crowns, and dead buds. Laboratory analyses and fungal isolations identified several fungal species; however, *Godronia* sp. was by far the most frequently detected species, particularly in dead buds and in the underlying woody tissues. Symptom development suggests that infections may occur in autumn, when buds are physiologically active, with visible damage appearing the following spring. Several other fungal species, including *Cytospora populina*, *Fusarium avenaceum*, *Cryptosporrella betulae*, *Melanconis stilbostoma*, *Diaporthe eres*, and others, were also associated with dead buds, branches, or stem tissues. Greenhouse inoculation experiments were conducted by inoculating birch buds with multiple fungal species to investigate symptom development. In these experiments, *Godronia* sp. also caused dieback of buds and young twigs. Overall, birch decline in Sweden appears to result from a combination of pathogenic fungal infections and environmental stress, particularly drought.

Key Words: Birch; Fungal infection; *Godronia*; Inoculation experiment

Pathways of Invasion / Disease Management and Control

Chair: Alberto Santini and Romina Gazis

Ceratocystis Rising in Africa: Future Threats to Forestry and Agriculture

Irene Barnes¹, Jolanda Roux^{2,3}, Lina del Mar Angel³ & Michael J. Wingfield¹

¹Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

²Department of Plant and Soil Science, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

³Sappi Forests Pty. Ltd., Research Planning and Nurseries, Grootgeluk, Ngodwana, South Africa

E-mail: irene.barnes@fabi.up.ac.za

Ceratocystis species cause serious diseases of plants important to both agriculture and forestry; the best known of which cause tuber rots and vascular wilt diseases of trees. Of the more than 40 phylogenetically recognized species in the genus, nine have been reported from Africa. Based on ecological associations, host range, and population genetic analyses, five of these species are considered indigenous and reside in the “African Clade” of *Ceratocystis*. Of these native species, only *Ceratocystis albifundus* has been associated with significant disease outbreaks. In contrast, several other *Ceratocystis* species have been accidentally introduced into Africa, most likely through the international plant trade. These include *C. manginecans* Lineage 1 (syn. *C. eucalypticola*) and *C. pirilliformis*. *Ceratocystis manginecans*, which resides in the Latin American Clade, is an aggressive pathogen of various tree crops and has been responsible for the large-scale death of *Acacia mangium* plantations in Southeast Asia. This pathogen has also recently been found causing a serious canker and wilt disease on a susceptible *Eucalyptus* variety in South Africa, and is now also known in several other African countries. In addition, a new Lineage of *C. manginecans* has recently been discovered in Central Africa, causing a severe root rot disease of cassava. This has serious implications for food security, particularly in regions where cassava is a staple crop for smallholder farmers. *Ceratocystis* species are becoming increasingly important plant pathogens globally, including in Africa. Dealing with this growing threat will require improved surveillance to reduce new introductions and implement effective disease management.

Key Words: Wilt pathogens; Biosecurity; Invasive species; Africa

Sharing the Japanese Experiences of Struggle for Controlling Pine Wilt Disease

Katsunori Nakamura-Matori

Forestry and Forest Products Research Institute, Japan

E-mail: nakamura_katsunori980@ffpri.go.jp

Japan has a vast experience in research and practice for controlling pine wilt disease (PWD), including both successes and failures that would serve for lessons to the countries suffering from the disease. Basically, the controlling system consisted of the eradication of the vector immatures harboring in dead pine trees and infection prevention of the pathogenic nematodes by insecticide spray to pine trees or trunk injection of the nematocide has already been consolidated. However, most of the control implementations in Japan have failed. Though there are some technical flaws in fact, the primary cause of unsuccessful control is incomplete implementation led by financial or social factors. Budgetary constraints hamper sufficient implementation of PWD control in many cases. Fragmentary ownership of land makes it difficult to develop an appropriate control plan in the region. Prevention spray is a powerful tool to curb the epidemic spread, but its use is becoming restricted because of growing attention to the environment. Consequently, PWD-control is only expected to be successful in the area where we can put full-scale control effort in or the newly emerging places of the disease with a small number of infected trees. In the other area, reduction or elimination of pine trees is desired in terms of isolation of the designated pine stand to be preserved from the source of infection. In such cases, we recommend the replacement of pines by other tree species, though it still cannot achieve widespread agreement among the people. We are often requested to protect a valuable old pine tree and adopt trunk injection and multiple times of prevention spray. The attempt, however, sometimes meets failure probably because of the morphological or physiological conditions of the tree. After all, elimination of the infection source is the most important and effective measure to protect such a pine tree.

Key Words: Eradication; Prevention spray; Trunk injection; Tree species conversion; Priority in control

Paradigm Shift in the Management of Pine Wilt Disease in Korea

Hyerim Han, Jouna Son, Youngwoo Nam, Ki Hyeong Park, Yeon-Jeong Lim & Won Il Choi

Forest Entomology and Pathology Division, National Institute of Forest Science, Seoul 02455, South Korea

E-mail: hrhan123@korea.kr

As of April 2025, Pine Wilt Disease (PWD) in Korea has entered a critical phase, with approximately 1.49 million pine trees affected, marking the start of a third major outbreak. Since its first introduction in 1988, Korea has experienced two large-scale epidemics: the first in 2007, which affected 1.37 million trees, and the second in 2014, which resulted in 2.18 million damaged trees. The recent surge in PWD is attributed to multiple factors, including increased plant stress caused by unusually warm winters and dry springs, earlier emergence and extended activity periods of vector insects, disruption of field-based control capacity during the COVID-19 pandemic, and reductions in government control budgets. Furthermore, the growing volume of fire-damaged trees resulting from large-scale wildfires has provided breeding and overwintering habitats for vector insects, further accelerating the spread of the disease. PWD incidence in Korea shows strong spatial clustering, with approximately 60% of all damaged trees concentrated in the southeastern region, particularly in Gyeongsangbuk-do Province. Cumulative damage has led to large-scale stand-level tree mortality, which in turn increases the risks of secondary disasters such as landslides and wildfires. As PWD increasingly manifests as regionally concentrated and large-scale mortality events, a fundamental shift in the national management paradigm is underway. The new PWD management paradigm is characterized by three key components. First, a national control belt is being established to enable proactive surveillance and intensive containment, thereby reducing the overall affected area. Second, damaged trees are being utilized as forest biomass resources and linked to regional timber and bioenergy industries. Third, long-term protection of forest ecosystems is being pursued through ecological restoration and conservation to ensure sustainability. This paradigm shift is closely associated with the establishment of integrated governance linking the central government, local governments, and the public from a long-term strategic perspective.

Key Words: Pine Wilt Disease (PWD); Major Outbreak; Paradigm Shift; Integrated Management

Ceratocystis Invasion in Greece

Nikoleta Soulioti^{1,2}, Asimina Smarlamaki², Georgios Patsis², Zacharoula Gonou Zagou³ & Aliko Tzima²

¹ELGO-DIMITRA, Institute of Mediterranean Forest Ecosystems, Nikolaou Chlorou 1, 115 28 Ilissia, Greece

²Agricultural University of Athens, Laboratory of Plant Pathology, Iera Odos 75, 118 55 Athens, Greece

³National and Kapodistrian University of Athens, Faculty of Biology, Department of Ecology & Systematics, 157 84 Athens, Greece

E-mail: nsoulioti@elgo.gr

ABSTRACT

In Greece, there has been the invasion and establishment of two plant destructing fungal pathogens, *Ceratocystis platani* in early 2000s and *Ceratocystis ficiicola* in late 2010s. *Ceratocystis platani* has been found to invade Greece in two distinct events, a first one in Peloponnese (South Greece) and a second one in Epirus (North Greece) and it has already caused the mass loss of the abundant native *Platanus orientalis*, creating an ecological and ecosystemic disaster. *Ceratocystis ficiicola* has also been found to invade in two distant areas of mainland Greece and causing the rapid decline and death of fig orchards, resulting in ecological and economic disaster in affected areas. Preliminary population studies suggest that in both invading *Ceratocystis* pathogens, there has been more than one events of invasion, while at the same time differentiation of *Ceratocystis platani* has been observed to occur, overcoming the clonal behavior of this pathogen found in Europe. A new species of *Ceratocystis* is also found to occur. Human transmission as the main disease pathway for both pathogens is highlighted. The role of insects in pathogen transmission is investigated. In the case of *Ceratocystis platani*, the water transmission is further investigated and it is found to be in agreement with previous findings from France, robust proof is provided that it acts as an important natural pathway of transmission downstream. A new colorimetric LAMP protocol is under development, designed in genus level to allow the fast detection of the different pathogens of *Ceratocystis* in different hosts in the field.

Key Words: *Ceratocystis*; Wilt disease; Pathways of Invasion, Population studies, LAMP

Overcoming Polymorphism Limitations: Novel SSR Markers for Populations Genetic Analysis in *Bursaphelenchus xylophilus* and *Bursaphelenchus mucronatus*

Méline Saubin¹, Émilie Chancerel¹, Soizic Rossetti¹, Yannis Clavier², Maria de Lurdes Inacio³, Olivier Lepais¹ & Laure Villate²

¹Univ. Bordeaux, INRAE, BIOGECO, F-33610, Cestas, France

²Univ. Bordeaux, INRAE, BIOGECO, F-33615, Pessac, France

³INIAV, Oeiras, Portugal

E-mail: meline.saubin@inrae.fr

Conventional microsatellite markers development, based on size polymorphism, often yields poorly polymorphic loci in nematodes. This limitation likely explains the low polymorphism of existing markers for *Bursaphelenchus xylophilus* (Mallez et al., 2013) particularly in invasive populations. These markers are nearly monomorphic in populations from Japan, China and Portugal (Mallez et al. 2015, 2020), restricting their utility for fine-scale genetic diversity analysis and hindering efforts to trace invasion routes. To overcome this challenge, we developed highly polymorphic microsatellite markers using allele sequencing (Lepais et al., 2020). This method captures both size and nucleotide substitutions, generating multiallelic haplotypes that provide a rich dataset for genetic analysis. Our objective was to create robust tools for *B. xylophilus* and its European sister species, *B. mucronatus*, while ensuring cross-species transferability and retaining species-specific loci for hybridization studies. We successfully developed around forty SSR markers amplifiable in both species, along with two primer pairs specific to each species. We will present the genetic diversity of these SSR sequences in *B. xylophilus* populations from Canada, Japan and Portugal, as well as in *B. mucronatus* from Europe. These new markers offer promising potential for studying demographic and evolutionary processes across spatial scales, from fine to broad, and for detecting potential hybridization between the two species.

Key Words: *Bursaphelenchus*; Microsatellites; Population genetics; Genetic diversity

How Vaccination Reshapes the *Ulmus glabra* Mycobiome under Dutch Elm Disease

Liina Jürisoo^{1,2}, Ahto Agan¹, Rein Drenkhan¹ & Johanna Witzell²

¹Institute of Forestry and Engineering, Estonian University of Life Sciences, Estonia

²Department of Forestry and Wood Technology, Department of Forestry and Wood Technology, Linnaeus University, Sweden

E-mail: liina.jyrisoo@emu.ee

Dutch Elm Disease (DED), caused by *Ophiostoma novo-ulmi*, continues to cause extensive mortality of *Ulmus glabra* in northern Europe. In Stockholm, preventive vaccination using the biological control agent Dutch Trig[®] has been implemented as a management strategy to mitigate disease spread and preserve remaining elm populations. This study investigates differences in fungal assemblages associated with vaccinated and non-vaccinated *U. glabra*, with particular emphasis on implications for disease management and tree survival. Using next-generation sequencing, fungal communities were assessed in the bark and xylem of symptomless vaccinated and in non-vaccinated trees. Our results indicate distinct differences in fungal assemblage composition between the two groups, suggesting that vaccination not only reduces susceptibility to *O. novo-ulmi* but is also associated with altered fungal community structures within surviving hosts. These findings highlight the importance of integrating pathogen control strategies with an understanding of host-associated fungal communities, supporting a holobiont-based perspective in long-term DED management and urban forest conservation.

Key Words: *Ophiostoma novo-ulmi*; Dutch Trig[®]; Biological control; Fungal community composition; Urban tree health

Key Details for the Effective Use of Semiochemicals to Monitor or Control Pest Populations in the Field

Robert R. Setter¹, Jorge Macias Samano¹, Alain Roques² & Marie-Anne Auger-Rozenberg²

¹Synergy Semiochemicals Corp., Delta V4G 1E9 Canada

²INRAE, Unité de Recherches Zoologie Forestière, Orléans, France

E-mail: bob@semiochemical.com

When releasing semiochemicals in the field for use against insect populations it is crucial to understand the biology of the insect, local environment, and characteristics of the release device. Purity of the pheromone load and accurate stable release rates over time are crucial for the devices to provide a consistent pheromone plume and attract their target population. In most cases, a single compound is used in a single device. The compound being released can be paired with plastics appropriate for controlled release over longer periods extending from 60-120 days, depending upon the chemical moiety and temperature. However, when 5 or 10 compounds are required single release devices for each compound can quickly become unaffordable. In these circumstances, researchers commonly make a cocktail of compounds and release it from a single device. While a pooled approach can be cost effective, control over release rates of each compound is compromised. The relative ratio between compounds in the pool will also change over time if the compounds have different chemical properties, dependant upon how they react with each other in the mix and the interface of the controlled release membrane or substrate. Releasing a mixture of compounds can result in a constantly changing ratio of compounds in the blend that are released over time. This can compromise efficacy in attraction of target species. Here we describe the laboratory development of a single lure containing an 8-compound blend of pheromones attractive to a wide range of species in the family Cerambycidae.

Key words: Pheromones, Kairomones, Release devices, Release rates, Cost/benefit analysis

An Integrated, Innovative Framework for Monitoring *Fraxinus angustifolia* Dieback and Resilience in Riparian Forests

Zlatković Milica¹, Cvjetković Branislav³, Čarter Matjaž², Diminić Danko⁴, Dvorak Milan⁵, Haupman Tine², Karaklić Velisav¹, Kesić Lazar¹, Levanič Tom², Mataruga Milan³, Orlović Saša¹, Perendija Nikola¹, Schwanda Katharina⁶, Stojanović B. Dejan¹, Stojnić Srđan¹, Svetlik Jan⁵, Temunović Martina⁴, Visački Vladimir¹ & Libor Jankovsky⁵

¹University of Novi Sad, Institute of Lowland Forestry and Environment (ILFE), Novi Sad, Serbia

²Slovenian Forestry Institute, Ljubljana, Slovenia

³University of Banja Luka, Faculty of Forestry, Banja Luka, Bosnia and Herzegovina

⁴University of Zagreb, Faculty of Forestry and Wood Technology, Zagreb, Croatia

⁵Mendel University in Brno, Faculty of Forestry and Wood Technology, Brno, Czech Republic

⁶Austrian Research Centre for Forests (BFW), Vienna, Austria

E-mail: milica.zlatkovic@uns.ac.rs

The ongoing dieback of narrow-leaved ash (*Fraxinus angustifolia*) in riparian forests of the Danube region is driven by a combination of abiotic stressors, impaired natural regeneration, and *Hymenoscyphus fraxineus* invasion. Addressing this complex challenge requires innovative, integrated forest protection strategies that combine pathogen surveillance, tree vitality assessment, genetic characterization and spatial analyses. Within the Interreg Danube project SCAN-DANUBE (Strategies for conservation of narrow-leaved ash populations in the Danube basin), a multidisciplinary, technology-driven framework is applied to support conservation, restoration and sustainable management of *F. angustifolia* forests. We monitor tree-level responses to disease using automatic dendrometers and dendrochronological analyses, which together enable early detection of growth reductions and alterations in sensitivity to environmental factors linked to ash dieback. High resolution monitoring of airborne pathogen pressure is achieved through novel spore trap designs combined with qPCR, allowing estimation of infection risk under different silvicultural practices. To support disease informed restoration efforts, advanced SPET targeted genotyping is applied to characterize genetic diversity and hybridization among *F. angustifolia* (including *F. angustifolia* subsp. *oxycarpa* and possibly *F. angustifolia* subsp. *angustifolia*), *F. excelsior*, and *F. pennsylvanica*, providing a solid foundation for identifying appropriate seed sources and guiding seed and seedling transfer. Trees showing reduced symptom severity or maintaining growth under high pathogen pressure will be genetically characterized to confirm their suitability for conservation and restoration programmes. In addition, we performed remote sensing-based analyses of current and historical spatial distribution of *F. angustifolia* using satellite imagery to assess changes in host availability and landscape-level exposure to disease. Integrating innovative monitoring technologies across pathogen, host and landscape scales enhances understanding of ash dieback processes and supports the development of proactive forest protection measures. The SCAN-DANUBE approach provides state-of-the-art, transferable tools for managing disease-driven forest dieback in riparian ecosystems.

Acknowledgements: This study is part of the SCAN-DANUBE project (Strategies for conservation of narrow-leaved ash populations in the Danube basin), supported by the Interreg Danube Region Programme and co-funded by the European Union.

Key Words: Innovative forest protection; Remote sensing; Automatic dendrometers; Spore traps and qPCR; Targeted genotyping (SPET)

Population Biology / Breeding

Chair: Marcin Nowicki and Brenda Wingfield

Pine Wilt Disease in Spain: Current Epidemiological Status and Genetic Resistance in *Pinus pinaster*
Raquel Díaz, Lucía Villar, María Menéndez, Esteban Torres & Eva Prada

Lourizán Forest Research Centre - CIF Lourizán

E-mail: raquel.diaz.vazquez@xunta.gal

Pine wilt disease (PWD), caused by the nematode *Bursaphelenchus xylophilus*, remains a major phytosanitary threat in Spain, with several areas currently demarcated. Despite sustained surveillance and control measures, the disease continues to pose a significant risk of spread, highlighting the need for long-term sustainable solutions based on host resistance. In the absence of effective containment measures, projected economic impacts for 2028 in Galicia (NW Spain) are estimated to exceed €250 million annually. Since 2013, the Lourizán Forest Research Center (CIF Lourizán) has been conducting a research program focused on genetic improvement to develop PWD-resistant reproductive material of *Pinus pinaster*. The program integrates controlled inoculation trials to assess inter- and intraspecific variation in susceptibility and the heritability of resistance, as well as long-term field trials to evaluate growth and form data. Considerable variation in susceptibility was observed among provenances and families of *P. pinaster*, which confirms that resistance to PWD is a heritable trait and shows no evidence of negative correlations with growth performance. By combining seedling survival and symptom development following inoculation with adult tree growth data, the program enabled the selection of the first resistant *P. pinaster* families. Families displaying both resistance and superior growth were officially registered in the Spanish National Catalogue of Base Materials in 2020 and are currently being deployed in Galicia in high risk areas of PWD expansion. The program is now progressing toward a second generation of selection, incorporating PWD resistance alongside growth and wood quality traits as selection criteria for the next cohort of improved families. These results demonstrate that genetic resistance can be effectively integrated into national PWD management strategies for *P. pinaster*, providing a framework for mitigating the impact of the disease in affected and at-risk areas, while supporting the sustained improvement of *P. pinaster* populations and the production of high-quality wood in the long term.

Key Words: *Bursaphelenchus xylophilus*; Genetic breeding program; Resistance; Multi-trait selection; Maritime pine

Metabolic Interaction between *Ophiostoma novo-ulmi* and *Geosmithia* spp.

Alessia Lucia Pepori¹, Hari Berto^{1,2}, Alessandra Gionni¹, Nicola Luchi¹, Francesco Pecori¹ & Alberto Santini¹

¹National Research Council – Institute for Sustainable Plant Protection, Via Madonna del Piano 10, I-50019 Sesto Fiorentino, Italy

²University of Florence, Department of Agriculture, Food, Environment and Forestry (DAGRI), Firenze, Italy

E-mail: alessia.pepori@cnr.it

Dutch elm disease (DED), caused by the invasive vascular pathogen *Ophiostoma novo-ulmi*, one of the most devastating pandemics affecting elms. Within beetle galleries and on elm bark beetle vectors, *O. novo-ulmi* co-occurs with fungi of the genus *Geosmithia*, yet the functional significance of this association remains poorly understood. This study investigates metabolic interactions between *O. novo-ulmi* and *Geosmithia* spp. using in vitro dual-culture experiments and phenotype microarray analysis to elucidate ecological mechanisms potentially influencing disease development and vector ecology. Dual-culture assays on dH₂O agar revealed that *O. novo-ulmi* exhibited significantly enhanced radial growth rates when cultured in proximity to *Geosmithia* isolates. Phenotypic microarray analysis revealed distinct metabolic strategies: *O. novo-ulmi* utilized substrates within 12-24 hours and preferred polyols and simple carbohydrates, while *G. pumila* adopted a progressive colonization strategy, ultimately utilizing 92 substrates in 90 hours and demonstrating greater utilization of nitrogen-enriched substrates, nucleosides and complex organic acids. Fungal competitiveness analysis indicated *G. pumila* superiority, yet *O. novo-ulmi* showed greater growth facilitation in co-culture, suggesting asymmetric mutualism through non-nutritional mechanisms. These results also suggest that physical proximity between *O. novo-ulmi* and *Geosmithia* spp. establishes a localized metabolic interface enabling chemical signaling and nutrient exchange. This mutualistic interaction, demonstrated by the increased growth of *O. novo-ulmi* in co-culture without suppressing *Geosmithia* spp., likely confers selective advantages that explain the evolutionary success of their ecological partnership. Within naturally colonized host tissues, such metabolic interaction may enhance pathogen establishment and persistence, with implications for disease epidemiology, beetle vector ecology, and potential disease management strategies.

Key Words: Metabolic interactions; Dutch elm disease; Biolog FF Plates; Carbon substrate utilization; Dual growth rate

From Genetic Architecture to Environmental Effects: Insights for Breeding Dutch Elm Disease-Resistant *Ulmus minor*
Jorge Domínguez¹, David Macaya-Sanz² & Juan Antonio Martín³

¹Centro Nacional de Recursos Genéticos Forestales Puerta de Hierro, TRAGSA, Madrid, Spain

²Department of Forest Ecology & Genetics, Institute of Forest Sciences (ICIFOR-INIA), Madrid, Spain

³ETSI Montes, Forestal y del Medio Natural. Universidad Politécnica de Madrid, Madrid, Spain

E-mail: juan.martin.garcia@upm.es

Dutch elm disease (DED), caused by *Ophiostoma novo-ulmi*, remains the major threat to the persistence of *Ulmus minor*. This study investigates the genetic basis and environmental modulation of resistance to DED, with the aim of supporting breeding strategies for improved resistant material. Progenies derived from resistant × susceptible (R×S) and resistant × resistant (R×R) crosses, as well as multiple genotypes under contrasting continental and coastal environments, were evaluated. Transgressive segregation was detected in R×S progenies, with a subset of genotypes outperforming their parents, indicating new opportunities for breeding. Moderate to high heritability estimates confirmed a strong genetic control of resistance, although substantial variation among crosses suggests differing underlying genetic architectures. While additive genetic effects predominated, non-additive patterns were also detected, with higher-than-expected resistance in R×S progenies and reduced resistance in R×R progenies. Evidence consistent with maternal effects was also identified. Resistance was highly plastic and strongly shaped by genotype × environment interactions. Coastal conditions favored greater starch reserves and smoother earlywood-latewood transitions, traits associated with enhanced resistance. In contrast, the continental environment promoted wider earlywood vessels and sharper earlywood-latewood transitions, potentially increasing xylem vulnerability. These results underscore the importance of integrating genetic architecture, phenotypic plasticity, and environmental context into breeding programs for DED resistance.

Key Words: Resistance; Breeding; *Ulmus*; *Ophiostoma*; Phenotypic plasticity

Breeding of Pine Varieties Resistant to Pine Wilt Disease and Molecular Detection of Early Host Responses

Limei Song & Jianghua Sun

Hebei Basic Science Center for Biotic Interactions/College of Life Science, Institute of Life Science and Green Development, Hebei University, Baoding, China

E-mail: songlimei@hbu.edu.cn

Pine wilt disease (PWD), often referred to as “pine cancer,” is characterized by rapid spread, a wide damage range, and high mortality, posing a major biological threat to global forest ecological security. Current management strategies still rely primarily on emergency measures such as chemical control and the removal of infected trees, representing a largely passive control mode that makes long-term effective suppression difficult to achieve. Therefore, breeding disease-resistant pine varieties and promoting tree species replacement are key approaches to shift PWD management from “passive removal” to “active prevention.” In our study, through resistance germplasm screening and systematic breeding strategies, we successfully developed a pine variety, “Yaqing,” with strong resistance to pine wilt disease. Under high-intensity artificial inoculation, the disease incidence of “Yaqing” was only 15%, while no disease symptoms were observed under natural infection conditions. This resistant variety provides valuable germplasm resources and a solid foundation for PWD resistance breeding and the large-scale deployment of resistant pines. Meanwhile, we identified a leucine-rich repeat receptor-like protein kinase, PtTHESUES1, localized on the plasma membrane of *Pinus tabulaeformis*. PtTHESUES1 is able to recognize the pine wood nematode (PWN)-secreted protein EF1 at the early stage of infection and rapidly activate host defense responses, thereby revealing an early immune perception mechanism in pine against PWN invasion. PtTHESUES1 not only represents a key molecular target for elucidating the molecular basis of PWD resistance, but also provides an important theoretical basis and practical support for establishing early-response molecular detection systems and early-warning technologies for pine wilt disease.

Key Words: Pine wilt disease; Pine wood nematode; Pine breeding; Molecular detection

Vertical Distribution, Fungal Communities, and Biotic Interactions: Deciphering the Spread of *Bursaphelenchus xylophilus* in European Pine Forests

Yannis Clavier¹, Marjorie Lucas², Estelle Ducourtioux¹, Aure Coudreau¹, Benjamin Dencausse², Aurélien Kohler², Agnès Aubert², Emilie Chancerel², Zoé Compagnie², Priscillia Alves Gomes², Clément Delmas³, Nicolas Papadakis³, Maria de Lurdes Inácio⁴, Luís Bonifácio⁴, Méline Saubin^{2*} & Laure Villate^{1*}

¹Univ. Bordeaux, INRAE, BIOGECO, F-33615, Pessac, France

²Univ. Bordeaux, INRAE, BIOGECO, F-33610, Cestas, France

³Univ. Bordeaux, CNRS, INRIA, Bordeaux INP, IMB, France

⁴INIAV, Oeiras, Portugal

* These authors contributed equally to supervising this study

E-mail: yannis.clavier@u-bordeaux.fr

The pinewood nematode, *Bursaphelenchus xylophilus* (*Bx*), the causal agent of pine wilt disease, is a quarantine organism in Europe. Native to North America and introduced into Asia (~1905), it later spread to Portugal (1999) and Spain (2008). Most recently, *Bx* was detected in the Landes forest, France (November 2025). *Bx* feeds on xylem cells, migrates within the tree, and ultimately causes host death. As the tree declines, fungi colonize the wood, providing an additional food source and potentially influencing nematode population dynamics. Given the recent outbreak in France and the severe damage caused by *Bx*, understanding its interactions with co-occurring organisms in newly invaded ecosystems is of prime importance. Exploring relationships between *Bx*, the native non-pathogenic *B. mucronatus* (*Bm*), and associated fungal communities may help identify ecological factors driving establishment and spread. Among these fungi, *Diplodia sapinea* is of particular interest: it can act both as a potential nutritional partner for the nematode and as an emerging pathogen of stressed *Pinus*. Its dual role suggest that co-occurrence with *Bx* could exacerbate pine susceptibility to one or both organisms. To address these questions, wood samples were collected from *Pinus pinaster* trees at three heights across four French and three Portuguese pine stands. *Bx* and *Bm* were extracted from the wood, quantified, and fungal communities were characterized using metabarcoding. We thus tackle 3 objectives : (i) assess the vertical distribution of *Bx* and *Bm* within trees, (ii) compare associated fungal communities across regions, nematode species, and nematode densities, and (iii) investigate interactions between *Bx*, *Bm* and *D. sapinea* *in vitro*, including the effect of temperature. A nested spatiotemporal sampling will further explore the genetic diversity and joint evolutionary trajectories of these three species. This integrative, multi-risk approach aims to improve our understanding of pathogen dynamics, pine resilience, and forest management strategies.

Key Words: *Bursaphelenchus*; *Diplodia sapinea*; Biotic interactions; Distribution; Biological invasion

Establishing Pre-breeding Lines for Avocado Tolerance to Laurel Wilt

Romina Gazis^{1*}, Jugpreet Singh² & Patricia Manosalva³

¹Tropical Research and Education Center, Department of Plant Pathology, Institute of Food and Agricultural Sciences, University of Florida, USA

²Tropical Research and Education Center, Department of Horticultural Sciences, Institute of Food and Agricultural Sciences, University of Florida, USA

³Department of Microbiology and Plant Pathology, University of California, Riverside, California, USA

E-mail: r.gazisseregina@ufl.edu

Laurel wilt (LW), a lethal vascular disease caused by *Harringtonia lauricola*, has spread across the United States since its introduction in 2002 and now poses a serious threat to global avocado production. The disease has caused the death of more than 500 million trees, including over 300,000 avocado trees in Florida. *H. lauricola* is a nutritional symbiont of several ambrosia beetle species and is now present in thirteen U.S. states. LW continues to spread through beetle-mediated transmission, root grafting, and the movement of infested wood. Current management relies on tree removal, vector suppression, and prophylactic fungicide injections; however, these practices are not fully effective or widely adopted. Consequently, all commercially evaluated cultivars, including ‘Hass’, remain highly susceptible, underscoring the need for genetic resistance or tolerance. We conducted two complementary screening studies using genetically diverse avocado germplasm from Mexico, Florida, and California. The first evaluated open-pollinated progenies from 25 accessions in the Fundación Salvador Sánchez Colín collection, including Mexican and Mexican–Guatemalan types and two Guatemalan–West Indian accessions identified by growers as potentially tolerant. The second assessed 25 accessions representing surviving trees in LW-affected areas, Mexican and Mexican-hybrid ecotypes, and rootstock selections from the University of California improvement program. Disease responses varied widely within and among families, indicating that LW tolerance is likely multigenic. Several accessions produced seedlings with mild or no visible symptoms. The Mexican–Guatemalan family ‘Colín V-33’ consistently exhibited the highest proportion of tolerant seedlings, and additional moderately tolerant accessions, including unique Mexican material and California breeding selections, were also identified. Surviving seedlings are being clonally propagated for validation, and genotyping is underway to identify genomic regions associated with resistance. These findings provide the first formal evidence of heritable LW tolerance in avocado and establish essential pre-breeding germplasm for developing LW-resistant cultivars.

Key Words: Germplasm Screening; Disease Resistance; Breeding Efforts

Genomes and Bioinformatics

Chair: Laure Villate and Limei Song

Diversity of Mating Systems in Wilt pathogens: Insights from the Ceratocystidaceae

Frances Lane, Brenda D. Wingfield, Michael J. Wingfield & P. Markus Wilken

Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

E-mail: Brenda.Wingfield@fab.i.up.ac.za

The Ceratocystidaceae include many important vascular wilt pathogens, including the causal agents of Oak Wilt, *Ceratocystis* Canker and Wilt Disease on numerous angiosperm trees, and Sap streak of sugar maple. While many species in the Family have well-characterized reproductive strategies, this is not true across the group as a whole. Two classical mating systems are recognized in the fungi: heterothallism, where a compatible partner is required, and primary homothallism, in which individuals are self-fertile. There are, however, increasing numbers of reports of Ceratocystidaceae species that display mating behaviors that fall outside these traditional categories. The expanding availability of whole-genome sequences has enabled detailed investigations of the mating-type (MAT) locus in this Family, revealing extensive diversity in its organization, gene content, and evolutionary history. Multiple distinct mating strategies are now recognized, including unisexual reproduction in the genus *Huntia*, unidirectional mating-type switching in *Ceratocystis*, and structural rearrangements of the MAT locus that blur the boundaries between traditionally recognized systems. These unusual configurations suggest the presence of cryptic or flexible reproductive modes that may enhance genetic diversity and adaptability in pathogen populations. Understanding this diversity is essential when seeking to understand population structure, disease spread, and the evolutionary potential of the wilt pathogens in the Ceratocystidaceae.

Key Words: *Ceratocystis* Wilt; Mating types; Unisexual mating

Genome-wide Evidence for Cryptic Multi-generational Introgression between Invasive *Bursaphelenchus xylophilus* and Native *Bursaphelenchus mucronatus*

Yuzuki Ikeda¹, Naoko Ishikawa², Kenichi Yanagisawa³, Yoshihisa Suyama^{2, 4} & Ryoji Shinya¹

¹School of Agriculture, Meiji University, Japan

²Graduate School of Agricultural Science, Tohoku University, Japan

³Nagano Prefecture Forestry Research Center, Japan

⁴WPI-AIMEC, Tohoku University, Japan

E-mail: yuzuyuzu.ikeda1130@gmail.com

Since the first case of pine wilt disease was confirmed in Japan at the beginning of the 20th century, *Bursaphelenchus xylophilus*, the causal agent of pine wilt disease, has spread not only in Japan but also across Asia and Europe. In Eurasian countries, *B. mucronatus*, a native species closely related to *B. xylophilus* and with little or no pathogenicity to pine trees, occurs as two subspecies: Asian type (*B. m. mucronatus*) and European type (*B. m. kolymensis*). Here, we investigate ongoing hybridization between *B. xylophilus* and *B. m. mucronatus* in Japan. Using multiplexed ISSR genotyping by sequencing (MIG-seq), we genotyped 301 field-collected nematodes at 46 genome-wide SNPs. We detected nine hybrids (3.0%), including not only F1 individuals but also advanced-generation backcrosses (B1 and beyond) in both sampling years (2023–2024). Notably, single-locus species identification markers failed to detect 33.3% of hybrids, underscoring the necessity of genome-wide approaches. Controlled crossing experiments revealed a complete absence of pre-mating barriers, with males and females showing equivalent attraction to conspecific and heterospecific partners. Post-mating isolation was asymmetric and subspecies-dependent: crosses between *B. xylophilus* and *B. m. mucronatus* exhibited severely reduced egg viability, whereas laboratory crosses with *B. m. kolymensis* showed near-normal fecundity and only moderate reductions in hatchability. The consistent detection of multi-generational *B. xylophilus* - *B. m. mucronatus* hybrids across years demonstrates that gene flow is not a historical artifact but an active evolutionary process. Results showing that *B. xylophilus* exhibits substantially higher laboratory compatibility with *B. m. kolymensis* indicate that natural hybridization may occur more readily if the pathogen establishes, especially in Europe. Our results highlight the potential impact of hybridization on the spread and dynamics of pine wilt disease.

Key Words: Gene flow; Hybridization; MIG-seq; Reproductive isolation; Speciation

From Transcriptomics to Management: New Insights into Oak Wilt

Sarah L. Boggess¹, Meher Ony¹, Grace M. Pietsch², Margaret E. Staton¹, Beant Kapoor^{1,3}, Kendhl Seabright⁴, Adam Taylor⁴, William E. Klingeman² & Denita Hadziabdic¹

¹Entomology and Plant Pathology Department, University of Tennessee, Knoxville, TN, USA

²Plant Science Department, University of Tennessee, Knoxville, TN, USA

³Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA

⁴School of Natural Resources, University of Tennessee, Knoxville, TN, USA

E-mail: sbogges1@utk.edu

Economically important oak (*Quercus* spp.) trees are used for lumber and artisanal products, like valuable red oak (*Q. rubra*) timber and impermeable white oak (*Q. alba*) staves used for cooperage that benefit from extensive tylose formation. Our published haplotype-resolved, chromosome-scale *Q. alba* and *Q. rubra* genomes provide a foundation for new comparative analyses. Oak wilt is caused by *Bretziella fagacearum* fungus, which may spread by sap-feeding beetles (Coleoptera: Nitidulidae), via root-to-root contact between hosts, and anthropogenically. Symptoms of this destructive vascular disease include leaf wilt and drop, host-plant defense induction that in some species includes vascular discoloration and tyloses formation, and mortality of highly susceptible host trees. *Castanea* spp. (chestnuts) and all oak trees are susceptible to oak wilt disease, with *Q. rubra* considered more susceptible than *Q. alba*. Four research objectives were undertaken to provide new insights used to address oak wilt from mechanisms to IPM-based management. To begin, we conducted comparative RNA-seq analyses of *Q. alba* and *Q. rubra* across four post-inoculation time points and identified molecular drivers of susceptibility between these host species. Next, we linked gene expression patterns to functional host defenses by using confocal microscopy to quantify pathogen-induced vascular occlusion via tyloses formation in these and two other oak species, plus one chestnut species. Meantime, to support early detection and surveillance, we developed a species-specific microsatellite-based TaqMan probe using blue-light fluorescence to detect *B. fagacearum* in environmental host tissue samples and on associated sap beetles. Lastly, we used a controlled laboratory fumigation assay with infected wood bolts to evaluate management with ethanedinitrile as an alternative to highly effective but environmentally hazardous methyl bromide fumigant. Although methyl bromide remained the most effective treatment, ethanedinitrile significantly reduced pathogen recovery, providing an alternative and perhaps more sustainable management option for oak wilt.

Key Words: *Bretziella fagacearum*; *Castanea* spp.; *Quercus* spp.; Vascular Wilt Disease

Population Genomics and Transcriptomics Uncover Adaptive Evolution and Virulence in *Ophiostoma* Species Causing Dutch Elm Disease

Jorge Pallarés^{1,2}, Pauline Hessenauer^{3,4}, Louis Bernier^{3,4}, Angel Baron¹, David Macaya Sanz² & Juan Antonio Martín¹

¹Departamento de Sistemas y Recursos Naturales, Research Group FORESCENT, Universidad Politécnica de Madrid, Madrid, Spain

²Department of Forest Ecology & Genetics, Institute of Forest Sciences (ICIFOR-INIA), CSIC, Madrid, Spain

³Département des Sciences du Bois et de la Forêt, Faculté de Foresterie, de Géographie et de Géomatique, Université Laval, Québec, Québec, Canada

⁴Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, Québec, Canada

E-mail: jorge.pallares@upm.es

Species of the genus *Ophiostoma* causing Dutch elm disease (DED) continue to pose a critical threat to elm populations. Previous transcriptomic studies of the DED pathogens have proposed key virulence functions involved in host colonization. By integrating these well-supported virulence functions with a recent pathogen transcriptomic study, a set of functionally relevant genes was defined. In parallel, 58 new *Ophiostoma* isolates from the Iberian Peninsula were sequenced and combined with publicly available genomes (NCBI), resulting in a dataset of 156 isolates, mainly distributed across Europe and North America, the regions most affected by DED. These isolates span a broad temporal range, from the 1970s to 2025. The identification and filtering of nucleotide variants generated a high-quality SNP dataset, which was used for population structure analyses, clustering, and classification of isolates into subspecies and lineages, as well as for their characterization based on reproductive traits, including MAT type and vegetative incompatibility (VIC) genes. Genomic diversity was analyzed using temporal and geographic approaches, allowing the identification of genomic regions under positive selection as well as regions consistent with neutral diversity. By integrating these selected regions with genes identified through transcriptomic analyses, candidate genes preferentially located within regions under selection were identified. These genes likely represent key components of pathogen adaptation, providing insight into the evolutionary processes underlying virulence, specialization, and spread of the DED pathogens.

Key Words: Dutch elm disease; Population genomics; Transcriptomic; Adaptive evolution

Pangenome Analysis of *Ophiostoma novo-ulmi*, the Causal Agent of Dutch Elm Disease

Concetta De Quattro, Hari Berto, Sara Torre, Alessia L. Pepori, Francesco Pecori, Federico Sebastiani & Alberto Santini

National Research Council, Institute for Sustainable Plant Protection (CNR-IPSP), Sesto Fiorentino Firenze, Italy

E-mail: concetta.dequattro@cnr.it

A major threat to trees of the genus *Ulmus*, including *U. glabra*, comes from the introduction in Europe in the last century of the pathogenic fungi *Ophiostoma ulmi* and *Ophiostoma novo-ulmi* (ONU), which caused two successive epidemic waves of Dutch elm disease (DED), a destructive tracheomycosis that devastated elm populations throughout Europe. ONU includes two subspecies, *novo-ulmi* and *americana*, which during the second wave rapidly replaced *O. ulmi* by overlapping in distribution and forming hybrids. Understanding the contribution of each subspecies to the recent epidemic wave is supported by the availability of historical isolate collections. We performed the genomic characterization of an Italian collection of 63 isolates belonging to the two ONU subspecies, collected ten years apart across different geographic locations in Italy. The first sampling was performed during the pre-epidemic phase (2001) and the second during the epidemic phase (2013). To characterize ONU isolates at genomic level, short-read whole-genome sequencing was generated for all isolates, and de-novo genome assembly was performed for each genome. The quality of the assembled genomes was assessed, resulting in a high percentage of BUSCO completeness. The ONU pangenome was built using our de novo-assembled genomes and publicly available ONU genomes. We examined genomic diversity and pangenome structure to analyze the intraspecific patterns of conservation and variability. Gene prediction was then performed to identify core and accessory genes across the isolates. The integration of the two historical sampling datasets enables robust analysis of the spatial and temporal dynamics of fungal populations, providing new insights into the evolutionary processes underlying the recent DED epidemic.

Key Words: *Ophiostoma novo-ulmi*; Dutch elm disease; Whole-genome sequencing; Pangenome

One Clone to Rule Them All? Genomics of the North American VSD Pathogen, *Ceratobasidium* spp.

Marcin Nowicki¹, Sarah L. Boggess¹, Farhat A. Avin², Fulya Baysal-Gurel², John C. Bonkowski³, Marc A. Cubeta³, Matthew L. Huff^{3,4}, Muhammad Junaid⁵, Katherine Kilbourne⁶, Colton D. Meinecke⁷, Dewayne D. Shoemaker¹, Margaret E. Staton¹, Robert N. Trigiano¹, Jackson H. Turner¹, Caterina Villari⁷, Jean Williams-Woodward⁸ & Denita Hadziabdic¹

¹University of Tennessee, United States of America

²Tennessee State University, United States of America

³Purdue University, United States of America

⁴Medical University of South Carolina, Charleston, South Carolina, United States of America

⁵Universitas Hasanuddin, Makassar, Indonesia

⁶Tennessee Department of Agriculture, Nashville, Tennessee, United States of America

⁷University of Georgia, United States of America

⁸University of Wyoming, United States of America

E-mail: mnowicki@utk.edu

Vascular streak dieback (VSD) has emerged as a multi host vascular disease of ornamental trees and shrubs in North America (US), yet the identity, population structure, and reproductive biology of the associated Ceratobasidiaceae pathogen remain poorly resolved. Building on short read whole genome data from three representative isolates (two from *Cercis canadensis* and one from *Acer* spp.), we used an in house phylogenomic pipeline to place the putative VSD agent within the *Rhizoctonia/Thanatephorus* clade, sister to but distinct from named *Ceratobasidium* taxa, and to identify hundreds of single copy orthologs suitable for downstream marker development. We used these genome resources to design and validate a panel of 25 microsatellite loci. Genotyping of these 25 loci revealed low allelic diversity across sampled VSD populations with no clear host specific clustering, consistent with a recently introduced or clonally expanding lineage. Finally, phylogenomic and population genetic data were integrated into a genomics guided diagnostics pipeline to develop simple-sequence repeat, TaqMan qPCR, and LAMP assays to discriminate the VSD agent(s) from *C. theobromae* and other members of the Ceratobasidiaceae. The sensitivity and specificity of these assays approached or was equal to 1.0 across multiple laboratory-based experiments. These data suggest that US VSD is represented by a genetically depauperate, largely selfing Ceratobasidiaceae lineage with limited genetic diversity and a broad host range. Our experimental approach couples phylogenomic and molecular diagnostics to better refine risk assessments and management strategies for newly emergent wilt and dieback causing fungi.

Key Words: *Ceratobasidium*; Molecular diagnostics; Phylogenomics; Vascular streak dieback; Wilt and dieback diseases

First DIGITAL POSTERS Session

Chair: Francesco Pecori and Nikoleta Soulioti

Histological Changes and Distribution of Secondary Metabolites in Japanese Black Pine Seedlings Inoculated with Pine Wood Nematode

Huang Wenqian¹, Hirakawa Masafumi¹, Umebayashi Toshihiro², Kusumoto Dai¹, Shimizu Bun-ichi³, Taneda Haruhiko⁴, Yamagishi Shohei⁵, Watanabe Atsushi⁶ & Fukuda Kenji¹

¹Graduate School of Agriculture and Life Sciences, The University of Tokyo, Japan

²Graduate School of Life Sciences, Tohoku University, Japan

³Faculty of Life Sciences, Toyo University, Japan

⁴School of Science, The University of Tokyo, Japan

⁵Forestry and Forest Products Research Institute, Japan

⁶Faculty of Agriculture, Kyushu University, Japan

E-mail: wenqian1998@g.ecc.u-tokyo.ac.jp

Pine wilt disease (PWD) caused by the pinewood nematode (PWN) *Bursaphelenchus xylophilus* lead to wilting and death in susceptible pine species. Previous studies suggested that terpenoids diffused within the xylem under negative pressure play an important role in (embolism occurrence during) PWD progression. However, identifying the in-situ dynamics of terpenoids is extremely difficult and requires comprehensive analytical techniques. In this study, 3-year-old Japanese black pine seedlings were inoculated with 5,000 PWN under different light conditions (light condition with negative pressure and full dark condition with minimal negative pressure), and the stems were monitored for two weeks using MRI. Subsequently, frozen samples were collected from the monitored position, and the resin components in the xylem were observed using fluorescence microscopy and mass spectrometry imaging (MSI). Control seedlings showed no embolism. In the inoculated seedlings, embolism gradually expanded under the natural light condition, whereas it was confined near the inoculation site under the dark condition. Interestingly, when some seedlings inoculated under dark condition were moved into the natural light environment, embolism occurred within a day. Strong negative pressure generated by transpiration is necessary for embolism occurrence in PWD. From the anatomical observations, resin canals in the inoculated seedlings showed denaturation and destruction around the inoculation site, regardless of the embolism occurrence. Deposition of substances exhibiting autofluorescence was widely observed on the bordered pits around the inoculation site of the seedlings inoculated under the dark condition. MSI revealed that abietic acid and its related compounds were localized in resin canals in control seedlings. But in the inoculated seedlings, these substances were widely distributed throughout the xylem on the inoculated side, and their abundance was higher than in control seedlings. These results suggest that nematode movement in resin canals stimulates terpenoid synthesis, and the spread of terpenoids induces xylem embolism under negative pressure.

Key Words: Pine wilt disease; MRI; Histology; Mass spectrometry imaging

Emergence of *Ceratocystis eucalypticola* as a Devastating Wilt Pathogen of Eucalyptus in China

FeiFei Liu, YuHua Liang, QuanChao Wang & GuoQing Li

Research Institute of Fast-growing Trees (RIFT), Chinese Academy of Forestry (CAF), Zhanjiang, Guangdong, China

E-mail: shelleyfei@163.com

A severe canker and wilt disease has recently emerged in *Eucalyptus* plantations in Guangxi, southern China, causing significant tree mortality and threatening the regional forestry industry. Unmanned aerial vehicle (UAV) surveys conducted in 2024 revealed severe disease outbreaks, with tree mortality exceeding 30% in affected six-month-old stands. Field symptoms included rapid wilting, leaf chlorosis, bark cankers, and characteristic dark vascular discoloration extending from roots into the stem. The causal agent was consistently isolated from symptomatic tissues and identified as the fungal pathogen *Ceratocystis eucalypticola* using morphological characters and multigene DNA phylogenies based on the β -tubulin (BT1), translation elongation factor 1-alpha (TEF-1 α), and guanine nucleotide-binding protein subunit beta-like protein (MS204) regions. Pathogenicity was confirmed on both seedlings and young trees under controlled conditions, fulfilling Koch's postulates. This emergence of *C. eucalypticola* represents a significant new phytosanitary threat to China's commercially crucial Eucalyptus forestry sector. The aggressive nature of the disease, evidenced by rapid symptom development and high mortality, underscores an urgent need for heightened disease surveillance, awareness, and the development of management strategies to mitigate its impact on plantation sustainability and the regional economy.

Key Words: Eucalyptus; *Ceratocystis* wilt; Plant disease; Disease management; Fungal pathogen

How to Eradicate an Invasive Forest Pest without Clear-cutting

Hongyu Sun^{1,2}, Christelle Robinet², Hervé Jactel³, Monique Mourits⁴, Manuela Branco⁵, Wopke van der Werf¹ & Jacob C. Douma¹

¹Wageningen University and Research, Department of Plant Sciences, Crop Systems Analysis Group, P.O. Box 430, 6700 AK Wageningen, The Netherlands

²INRAE, URZF, 45075, Orléans, France

³INRAE, Univ. Bordeaux, Biogeco, 33610, Cestas, France

⁴Wageningen University and Research, Department of Social Sciences, Business Economics Group, 6700 EW, Wageningen, The Netherlands

⁵Centro de Estudos Florestais, Laboratório Associado TERRA, Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, 1349-017 Lisbon, Portugal

E-mail: christelle.robinet@inrae.fr

The pine wood nematode (PWN), *Bursaphelenchus xylophilus*, is an invasive species causing high pine mortality in invaded areas outside its native range. European Union (EU) regulations stipulate a 500-m-radius clear-cutting around infested trees to prevent the spread of PWN by the vector beetle *Monochamus galloprovincialis*, yet this measure is costly and not fully effective. We used an individual-based model describing the dispersal of the insect vector and its transmission of PWN, to compare the cost-effectiveness of clear-cutting and selective cutting of only the PWN-infested trees for three different methods for surveillance: visual ground surveys, aerial surveys, and insect trap networks. Both strategies eradicated PWN if intensive aerial surveillance was conducted at a time that all infested trees showed symptoms. Selective cutting reduced costs by up to a factor 200 compared to clear-cutting, mainly due to the preservation of healthy trees. Additionally, selective cutting reduces environmental and societal costs. However, eradication is unlikely if symptom expression of infectious trees is incomplete at the time of survey. The results show that selective cutting applied together with modern remote sensing surveillance methods is an environmentally friendly alternative to the mandatory clear-cutting for PWN control in the EU.

Key Words: Bioeconomic analysis; Containment; *Monochamus galloprovincialis*; Pine wilt disease; Surveillance

From Wilt to Hope: Exploring Fungal Partners in Swedish Elms

Caroline Sunnerstam, Dániel G. Knapp, Liina Jürisoo & Johanna Witzell

Department of Forestry and Wood Technology, Faculty of Technology, Linnaeus University, Sweden

E-mail: caroline.sunnerstam@lnu.se

Dutch elm disease (DED) continues to threaten elm populations worldwide, and Sweden's native elms (*Ulmus* spp.) are no exception. This wilt disease is caused by aggressive invasive fungi in the genus *Ophiostoma*. Although the disease is rapidly spreading, some elms show tolerance or possible resistance to the disease. Previous research has shown that certain microbial communities have a positive effect on their host, for example, they may support disease resistance by stimulating defensive mechanisms of the trees. Exploring these communities in potentially tolerant Swedish elms could provide new tools for breeding and conservation, supporting climate-resilient forests. The aim of our studies is to provide new knowledge about elm symbiotic microbial communities and their possible effects on the resistance and tolerance to DED, with the goal of identifying new tools to support breeding and conservation of native elm populations. Using a crowdsourcing approach, we located elms that show tolerance to DED. Sampling efforts and inventories targeted *U. glabra* population in Southern Sweden where the disease has been active for decades. The endophyte communities were studied using metabarcoding and isolation techniques. Approximately 80 isolates were recovered from visually healthy trees, including several *Fusarium* species. The results of biotests showing the activity of selected isolates against DED pathogens are discussed.

Key Words: Dutch elm disease; *Ulmus* spp.; *Ophiostoma*; Microbial communities; Fungi

Development of a Field-Ready Colorimetric LAMP Assay for Rapid Detection of *Bursaphelenchus xylophilus*
Michael McKee¹, Noah Lindeman¹, T. Seth Davis² & Jane E. Stewart¹

¹Colorado State University, Dept. Of Agricultural Biology, Fort Collins, CO, USA

²Colorado State University, Dept. of Forest and Rangeland Stewardship, Warner College of Natural Resources, Fort Collins, CO, USA

E-mail: michael.mckee@colostate.edu

Pine wilt disease (PWD), caused by the pine wood nematode, *Bursaphelenchus xylophilus*, is a lethal vascular wilt that poses serious economic and ecological threats to pine forests worldwide. Rapid and accurate detection of *B. xylophilus* is critical for containment and mitigation of PWD, particularly in regions with emerging outbreaks or heightened invasion risk, such as Asia and Europe. Many molecular diagnostic methods are available for use today, but many are costly, difficult to obtain, and laboratory-based. In this study, we developed a field-ready, colorimetric loop-mediated isothermal amplification (LAMP) assay for the rapid detection of *B. xylophilus* directly from wood samples or shavings. Using the same primer set that is commercially available in the Bx Detection Kit (Nippon Gene Co. Ltd., Tokyo, Japan), this assay uses a colorimetric readout, eliminating the need for specialized equipment. A simple, low-cost DNA extraction method based on Chelex 100 and polyvinylpyrrolidone (PVP) was optimized for use and evaluated alongside the extraction protocol of the Bx Detection Kit. The colorimetric LAMP assay consistently detected *B. xylophilus* DNA from wood samples and demonstrated equivalent sensitivity to the commercial kit, with a detection limit of approximately 19pg of target DNA. Results were obtained in under 40 minutes and were easily interpreted by a visible colour change. This assay provides a rapid, portable, and cost-effective diagnostic tool for forest health professionals, enabling on-site detection of *B. xylophilus* and supporting improved surveillance and management of pine wilt disease.

Key Words: Pine wilt disease; *Bursaphelenchus xylophilus*; Colorimetric LAMP; Field diagnostics; Forest health Surveillance

Fungi Associated with Ambrosia Beetle *Xylosandrus germanus* in Slovakia

Michal Lalík¹, Katarína Pastirčáková², Katarína Adamčíková², Marek Barta², Juraj Galko¹ & Martin Pastirčák³

¹National Forest Centre, Science and Research Section, T. G. Masaryka 2175/22, 960 01 Zvolen, Slovakia

²Institute of Forest Ecology, Department of Plant Pathology and Mycology, Slovak Academy of Sciences, Akademická 2, SK-94901 Nitra, Slovakia

³Division of Applied Biology and Genetics, Department of Plant Production, National Agricultural and Food Centre, Bratislavská 122, 921 68 Piešťany, Slovakia

E-mail: michal.lalik@nlcsk.org

The black timber bark beetle (*Xylosandrus germanus*) is a strongly invasive ambrosia beetle and an important forest pest in Slovakia. This pest is closely associated with symbiotic fungi used as its food source. We investigated the fungi associated with *X. germanus* adults in Slovakia. In this study, *Beauveria bassiana*, *B. pseudobassiana*, *Clonostachys rosea*, *Fusarium oxysporum*, *Ophiostoma quercus*, *Phaeoacremonium scolyti*, and *Talaromyces amestolkiae* were isolated and identified by morphological and molecular analyses. The fungus *Ophiostoma quercus* was most frequently isolated from living beetles, while the entomopathogenic *Beauveria bassiana* was the most commonly isolated from dead beetles. The morphological descriptions of fungi based on isolates from the surface of *X. germanus* adults are provided.

Keywords: Black timber bark beetle; *Fagus sylvatica*; Mycobiota; Scolytinae; Symbiosis

Identification, Pathogenicity and Fungicide Sensitivity of *Diplodia sapinea*, the Causal Agent of Pine Shoot Blight in China

Quanchao Wang, Huachao Xu & Xudong Zhou

College of Forestry and Biotechnology, Zhejiang A & F University, China

E-mail: xudong.zhou@zafu.edu.cn

Pinus species are dominant and economically significant for Chinese forestry. Pine shoot blight, often associated with *Diplodia* species, is a devastating disease that impacts pine health worldwide. Recently, severe symptoms including shoot dieback, needle necrosis and resinous cankers were observed in both mature and young pine stands across various climatic zones in Shandong, Zhejiang and Guangdong provinces. A comprehensive disease survey conducted between 2023 to 2024 led to collection of 377 fungal isolates, which were initially classified as Botryosphaeriaceae-like fungi based on morphological characteristics. Among these, 61% were assigned to the genus *Diplodia* based on ITS sequence analysis. Further molecular identification of 62 representative isolates, using sequences of the translation elongation factor 1- α (*tef1*- α) and β -tubulin (*tub2*) gene regions, confirmed that all tested isolates represented single species, *Diplodia sapinea*. Multi-gene phylogenetic analysis classified these isolates into seven distinct genotypes, indicating that the genetic diversity of *D. sapinea* collected in this study is relatively high. Growth study demonstrated that *D. sapinea* is a thermotolerant species with an optimal growth temperature at 30°C. Pathogenicity assays confirmed that all tested isolates were capable of infecting three major pine species—*P. elliotii*, *P. massoniana* and *P. thunbergii*—with *P. elliotii* being the most susceptible. Significant differences in host resistance were observed among the three species. Fungicide efficacy assays in vitro revealed that among seven fungicides tested, ergosterol biosynthesis inhibitors (EBIs) exhibited the strongest inhibitory activity, whereas quinone outside inhibitors (QoIs) and succinate dehydrogenase inhibitors (SDHIs) were less effective. This study provides the first comprehensive report on the national-scale genetic diversity and host susceptibility of *D. sapinea* in China, identifies highly effective fungicides and provides a scientific foundation for the integrated management of this destructive pine shoot blight.

Key Words: Pine shoot blight; Blue-stain; Disease management

Rhizosphere Bacterial Strains Showing Protection Efficacy against Fire Blight on Apple

Sujeong Kim¹, Stefan Kunz², Youngchan Kim¹ & Yongchull Jeun¹

¹Sustainable Agriculture Research Institute, Jeju National University, Jeju, Korea

²The Bio-Protect GmbH, Konstanz, Germany

E-mail: ycjeun@jejunu.ac.kr

The fire blight caused by pathogenic bacterium *Erwinia amylovora* is one of the most important diseases in Rosaceae species in the world. Management of this disease involves spraying antibiotics before infection or removing infected tissues at an early stage. However, once the disease has progressed, complete control becomes very difficult. This study aimed to identify effective antibacterial agents for controlling fire blight in apple plants by investigating four bacterial strains isolated from Jeju Island in Korea. Among these, *Bacillus circulans* BRH433-2 demonstrated notable antibacterial activity against *E. amylovora*, forming clear inhibition zones on artificial media. Other strains, including *Pseudomonas fluorescens* THJ609-3, *Micrococcus luteus* TRK2-2, and *P. fluorescens* TRH415-2, showed direct antibacterial effects by significantly reducing the cell population of *E. amylovora*. Bioassays revealed that treatments with all four bacterial strains strongly suppressed bacterial ooze formation, effectively reducing fire blight severity. These effects were comparable to those achieved with streptomycin-sulfate treatment. Additionally, real-time PCR analysis showed a slower increase in the *E. amylovora* population on treated apple blossoms compared to untreated controls. These findings suggest that the bacterial strains tested in this study could serve as effective alternatives for managing fire blight.

Acknowledgements: This study was carried out with the support of ‘R&D Program for Forest Science Technology (RS-2024-00404388)’ provided by Korea Forest Service(Korea Forestry Promotion Institute).

Key Words: Biofesticide; Biological control; PGPR

Risk Assessment and Surveillance

Chair: Pierluigi Bonello and Hari Berto

Chinese Plan for the Prevention and Control of Pine Wilt Disease

Fang Guofei^{1,2}, Zhou Yantao^{1,2}, Sun Hong^{1,2} & Wang Yue^{1,2}

¹Center for Biological Disaster Prevention and Control, National Forestry and Grassland Administration, China

²Key Laboratory of National Forestry and Grassland Administration on Invasive Alien Species Prevention and Control, National Forestry and Grassland Administration, China

E-mail: fgfly@163.com

The Chinese government has consistently prioritized biological security, successively enacting the Biosecurity Law and the Measures for the Administration of Alien Invasive Species, among other regulations. Since 2020, facing the northward and westward expansion of the Pine Wilt Disease epidemic and its progression from localized outbreaks to regional spread in endemic areas, the National Forestry and Grassland Administration has adhered to a philosophy of "problem-oriented approach, emancipating the mind, upholding fundamentals while pioneering innovation, and consulting the public", then established a trinity framework integrating strategic, campaign, and tactical levels for epidemic prevention and control during the 14th Five-Year Plan period, and implemented a five-year intensive campaign for the epidemic. This campaign encompasses six key strategies: precise epidemic monitoring, epidemic source blockade and control, enhancement of eradication quality, forest health protection, strengthening of organizational management, and support and guarantee. Through the five-year intensive campaign, have yielded remarkable successes in epidemic prevention and control. Specifically, the strategy achieved the "four reductions": the number of county-level epidemic zones, township-level epidemic points, the total affected area, and the number of dead pine trees. It effectively reversed the trend of rapid epidemic spread. We have established an accountability framework anchored in the Forest Chief System, developed a smart monitoring network powered by remote sensing and digital sensing platforms, and forged an integrated technical system centering on epidemic source removal with complementary measures. Currently, the epidemic prevention and control of pine wilt disease still faces critical challenges. We will maintain the overarching principle of strict prevention and rigorous management, develop more scientific, economical, and streamlined mechanisms for routine epidemic control. Then, implement precise and tiered management strategies based on zoning and classification, strengthen international cooperation, share control experiences, and offer China's approach to global epidemic governance.

Key Words: Pine wilt disease; Systematic management; Targeted measures; Technology empowerment; Chinese approach

Assessing the Dispersal of *Monochamus galloprovincialis*, the Vector of the Pine Wood Nematode, in Heterogeneous Landscapes

Hongyu Sun ¹, Hervé Jactel ², Inge van Halder ², Manuela Branco ³, Luís F Bonifácio ⁴, Jean-Baptiste Rivoal ² & Christelle Robinet ¹

¹INRAE, URZF, 45075, Orléans, France

²INRAE, Univ. Bordeaux, Biogeco, 33610, Cestas, France

³Centro de Estudos Florestais, Laboratório Associado TERRA, Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, 1349-017 Lisbon, Portugal

⁴Instituto Nacional de Investigação Agrária e Veterinária, Oeiras, Portugal

E-mail: christelle.robinet@inrae.fr

The pine wood nematode (PWN), *Bursaphelenchus xylophilus*, is an invasive plant pest responsible for pine wilt disease. Native to North America, it has spread to Asia and several European countries, including Portugal and Spain, and was detected for the first time in France in November 2025. In Europe, the longhorn beetle *Monochamus galloprovincialis* is the only known vector of PWN. Although previous studies have estimated the dispersal capacity of *M. galloprovincialis* in homogeneous landscapes composed of pine stands, little is known about its movement in heterogeneous landscapes that include multiple forest and non-forest land covers. We developed an individual-based model calibrated with mark–release–recapture datasets collected in France and Portugal to estimate key parameters of beetle dispersal behaviour, including flight difficulty and habitat preferences for different land-cover types, and the detection distance governing its response to adjacent land covers. Model predictions were evaluated using independent datasets from France and Portugal, in landscapes with different landcover types, proportions and spatial arrangements. Simulation results indicate contrasting movement responses depending on the different types of land-cover. They suggest that the heterogeneity of the forest landscape can alter the dispersal trajectories of the insect vector and thus slow down the rate of disease spread. This modelling framework provides a basis for predicting the potential spread trajectory of PWN vector beetles following its introduction into a new area and can support early-stage management and surveillance planning.

Key Words: Dispersal; Heterogeneous landscape; Individual-based model; *Monochamus galloprovincialis*; Pine wilt disease

EFSA assessment of control measures for PWN in the EU

Agata Kaczmarek¹, Matteo Crotta¹, Dora Mijic¹, Anna Filipiak², Hervé Jactel³, Nik Cuniffe⁴, Gregor Urek⁵, Luis Bonifacio⁶ & Hans-Hermann Thulke⁷

¹European Food Safety Authority, Italy

²The Institute of Plant Protection – National Research Institute, Poland

³UMR BIOGECO - INRAE, France

⁴University of Cambridge, United Kingdom

⁵Agricultural Institute of Slovenia, Slovenia

⁶National Institute for Agrarian and Veterinary Research, Portugal

⁷Helmholtz Centre for Environmental Research - UFZ, Germany

E-mail: agata.kaczmarek@efsa.europa.eu

The Pine Wood Nematode (*Bursaphelenchus xylophilus*, PWN) remains one of the most significant threats to conifer forests in the European Union. Since the publication of the EPPO Pest Risk Analysis in 2009 and the adoption of EU emergency measures in 2012, subsequently revised in 2018, PWN is currently being managed under a containment strategy in Portugal, while eradication measures are being applied in Spain. The outbreak reported in France in November 2025, together with the evolving epidemiological situation, underscore the need to reassess current EU measures, particularly those related to the scale of clear-cut preventive felling and the width of buffer zones established to prevent pest spread. In response to Member States' requests, EFSA has been mandated under Articles 29(1) and 31(1) of Regulation (EC) No 178/2002 to provide updated scientific support for evaluating the effectiveness of these measures. The mandate comprises two interconnected tasks. Under Task A, EFSA is requested to conduct a literature review of control measures and existing models to assess how variations in clear-cut widths and buffer-zone sizes influence eradication and containment outcomes. Under task B, EFSA will develop modelling scenarios incorporating recent scientific findings and outbreak data from affected EU regions to evaluate the performance of different clear-cutting strategies and buffer-zone configurations. The modelling will consider both eradication and containment objectives, exploring a range of feasible widths and assessing how complementary measures, such as enhanced surveillance, can strengthen control efforts. This presentation will summarize the purpose, structure, and expected outcomes of the mandate, highlighting how updated evidence and modelling will support the future refinement of EU phytosanitary measures against PWN.

Key Words: Pest risk assessment; Modelling; PWN

Automating Pine Wood Nematode Counting with AI: a Tool to Optimize Laboratory Work

Clément Delmas^{1,2}, Yannis Clavier¹, Estelle Ducourtieux¹, Aure Coudreau¹, Méline Saubin³, Nicolas Papadakis^{2*} & Laure Villate^{1*}

¹Univ. Bordeaux, INRAE, BIOGECO, F-33615, Pessac, France

²Univ. Bordeaux, CNRS, INRIA, Bordeaux INP, IMB, France

³Univ. Bordeaux, INRAE, BIOGECO, F-33610, Cestas, France

*Equal contribution

E-mail: laure.villate@u-bordeaux.fr

Nematode counting is an unavoidable step in pinewood nematode research. However, manual counting of nematodes from microscope images is time-consuming, prone to human error, and challenging when worms overlap, are translucent, or obscured by debris. To address these challenges, we developed a user-friendly AI-powered application that automatically detects and counts nematodes in microscope images, while also estimating developmental stages. Due to the initial lack of annotated data, we generated synthetic training images by integrating nematodes into real microscope backgrounds using Poisson blending, a technique that preserves local gradients and lighting conditions. This approach enabled training of an initial model using YOLOv8, a state-of-the-art real-time object detection architecture optimized for speed and accuracy. Its lightweight design and ability to handle small objects and complex backgrounds made it particularly suitable for this task. The model was first trained on synthetic data and then progressively refined using annotations provided by biologists through the application. This iterative process, where real data continuously improved the model, ensured high accuracy while accelerating laboratory workflow. The final model was trained on 285 real annotated images. The final model achieves a 90% F1-score, indicating a strong balance between precision (minimizing false positives) and recall (minimizing false negatives). Additionally, the application provides a first-pass classification of developmental stages based on worm size, supporting population dynamics studies. This project paves the way for standardized and reproducible nematode counts and can be adapted to other nematode species or experimental conditions. The use of YOLOv8-nano, the most lightweight model in the YOLO family, provides strong performance while minimizing processing time and energy consumption. Already adopted by INRAE and University of Bordeaux teams, this tool demonstrates how AI can optimize laboratory workflows while enhancing scientific rigor. It provides a significant time-saving advantage for studying *Bursaphelenchus xylophilus*, a major invasive threat to European forests.

Key Words: *Bursaphelenchus xylophilus*; Automated counting; YOLOv8; AI in microscopy; Object detection

Host Tree Distribution and Climatic Suitability for Pine Wilt Disease Expression in Austria

Eva Papek¹, Tobias Schadauer², Werner Hinterstoisser¹, Jasmin Wilhelm³, Benjamin Schumacher² & Gernot Hoch¹

¹Unit of Forest Damage Diagnostics & Research, Department of Forest Protection, BFW - Austrian Research Centre for Forests, Austria

²Unit of Remote Sensing, Department of Forest Inventory, BFW - Austrian Research Centre for Forests, Austria

³Department of Agriculture and Forestry, Styrian Provincial Government, Austria

E-mail: eva.papek@bfw.gv.at

ABSTRACT

The pine wood nematode *Bursaphelenchus xylophilus*, the causal agent of pine wilt disease (PWD), is currently absent in Austria. Its introduction and establishment depend on human activities, climatic conditions, and the presence and distribution of vectors and host trees. To optimize risk surveillance and monitoring in Austria, we examined potential risk areas for an establishment of *B. xylophilus* by analysing host tree distribution and modelling potential PWD symptom expression. In Austria, *Pinus sylvestris* and *Pinus nigra* are the species most at risk of being affected by PWD. We mapped their nationwide spatial distribution using phenology time series derived from Sentinel-2 satellite imagery. The two species are widely distributed across the country, accounting for approximately 5% of the Austrian tree species composition. Although climatic conditions are not a limiting factor for the survival of *B. xylophilus* in Austria, not all areas are suitable for the development of PWD symptoms. Depending on temperature, three zones of symptom expression have been described: asymptomatic, symptomatic with delayed symptom expression, and symptomatic. Recent climate data was used to model the potential symptom expression of PWD, by employing mean annual and mean summer temperatures. To gain insight into the potential expression of PWD symptoms under a changing climate, we modelled symptom expression using RCP scenarios. All three symptom expression zones are present in Austria and asymptomatic areas are expected to decrease with global warming. Combining knowledge regarding host tree distribution with potential PWD symptom expression can be used to optimize survey assays for different parts of the country. In symptomatic regions, monitoring should include visual inspections and sampling of symptomatic trees and vector beetles. In areas where PWD symptom expression is absent or delayed, sampling of vector beetles is of great relevance, and surveys are more difficult and costly.

Key Words: *Bursaphelenchus xylophilus*; Symptom expression; Host tree distribution; Climate change

Trap-Mounted Automated Imaging for Monitoring Pest Insects

Markus Kramer, Felix Dehon & Christian Pylatiuk

Karlsruhe Institute of Technology, Germany

E-mail: markus.kramer@kit.edu

Early detection of invasive and economically important pest insects is essential for effective plant health protection and biosecurity. However, most surveillance programs rely on manual trap inspections, resulting in delayed detection and limited temporal resolution. In addition, automated imaging approaches are often constrained by unreliable triggering, inconsistent image quality, and high energy demands that limit autonomous field deployment. We present a trap-mounted automated imaging system that can be installed on existing interception traps without altering their capture performance. The system images insects as they fall through the trap, using a laser-based detection plane to reliably trigger image acquisition. A global-shutter camera combined with controlled, diffused LED illumination captures sharp, distortion-free images independent of ambient light conditions, generating standardized image data suitable for morphological assessment and automated identification. The system is designed for minimal energy consumption and operates in an event-driven manner with low idle power demand and short energy peaks during image acquisition. Although the current prototype is powered externally, the system architecture is explicitly designed to support future autonomous operation using a solar panel and battery. Laboratory validation with representative pest insect species demonstrated reliable detection, consistent image quality, and robust system performance. The modular design supports live release, dry catch, and wet-preserved collection, ensuring compatibility with diverse monitoring objectives and regulatory requirements. By enhancing existing traps with standardized, low-power imaging at the point of capture, this approach addresses key limitations in current pest insect surveillance and provides a practical foundation for next-generation automated and AI-assisted monitoring systems.

Key Words: Camera Trap; Monitoring; Image Acquisition

Testing Novel Generic Lures in France and China for Early Detection of Non-native Cerambycid Species

Alain Roques¹, Lili Ren² & Marie-Anne Auger-Rozenberg¹

¹INRAE, Unité de Recherches Zoologie Forestière, Orléans, France

²Beijing Forestry University, Beijing, China

E-mail: alain.roques@inrae.fr

Due to globalization, non-native cerambycids are increasingly transported in areas other than their native ones. Pheromone blends expected to provide a generic attractiveness at insect-genus or -family level have been developed in order to enhance the possibilities of trapping unpredicted species at arrival. Until now, the attractive designs consisted of cotton wicks impregnated with a blend solution including eight different sex- and sex-aggregative pheromones corresponding to those of the most important cerambycid genera. These cotton wicks placed on multifunnel traps were replaced every 3 weeks. Although such designs proved to be very efficient for cerambycid detection, further GC analyses showed that the most volatile pheromones quickly evaporated from the cotton wicks, and the composition of the blend emissions was thus largely changed after 10 days. Synergy Semiochemicals®, Canada, provided us novel designs consisting of pouches including the same 8-pheromone blend but expected to ensure stable emissions for 90 days at least. Tests were developed during 2025 in forests of France and China in order to compare the attractiveness of traps baited with these pouches with regard to those of traps baited with impregnated cotton sticks changed every 10 days or 20 days. Black and green traps were used. In both countries, the attractiveness of the pouches for cerambycid individuals as well as for cerambycid species appeared equal, and sometimes higher, than the one of impregnated cotton wicks even changed every 10 days. However, large differences were observed between black and green traps baited with pouches. The combined use of traps of both colours is suggested to enhance detection of non-native species at arrival in ports of entry.

Key words: Cerambycid, Pheromones, Attractants, Traps, Release devices, Non-native

Sudden Emergence of Beech Bark Disease under Drought Stress Revealed through a Multidisciplinary Monitoring Framework Combining Forest Pathology, IoT-based Sensors and Remote Sensing

Milica Zlatković, Srđan Stojnić, Vladimir Visački, Lazar Kesić & Saša Orlović

University of Novi Sad, Institute of Lowland Forestry and Environment (ILFE), Serbia

E-mail: milica.zlatkovic@uns.ac.rs

European beech (*Fagus sylvatica* L.) forests have long been considered resilient in Serbia, including those on Fruška Gora Mountain. However, in 2025 a sudden and previously unrecorded outbreak of beech bark disease was detected across several forest stands during field activities of the Climate Smart *Fagus sylvatica* Forests (CSFagus4EST) project, supported by the European Forest Institute. Symptoms included bark necroses, crown dieback, and rapid tree mortality, recorded in managed, coppice, and unmanaged stands, including trees located at an ICP Forests Level II bioindication plot. By the end of the vegetation season, some affected trees had completely died, while others exhibited wound closure and callus formation, indicating markedly different disease trajectories under comparable site conditions. The outbreak followed several consecutive years of reduced winter precipitation and prolonged drought, suggesting that climate-induced physiological stress played a key predisposing role. Bark samples collected from symptomatic trees yielded *Nectria* spp. and Botryosphaeriaceae spp., with species-level molecular phylogenetic identification currently ongoing. Within CSFagus4EST, classical forest pathology is integrated with cutting-edge monitoring approaches, including automatic dendrometers and IoT-based sensors that continuously track stem radial growth and microclimatic conditions, alongside remote sensing analyses capturing canopy-level stress responses. This multidisciplinary monitoring framework enables near real-time detection of physiological stress, supports interpretation of disease development across spatial scales, and allows linking tree growth dynamics with pathogen impact. This study represents the first occurrence of beech bark disease on Fruška Gora Mt. and demonstrates the value of integrating ground-based observations, continuous sensor data, and remote sensing as an early warning system for climate-driven forest decline. By combining these complementary data streams, the project aims not only to track disease progression and recovery dynamics, but also to identify potentially tolerant or resilient beech individuals, thereby supporting the development of climate-smart forest management strategies at the southern margin of the *F. sylvatica* distribution.

Acknowledgements: This research was supported by the project: “Climate Smart *Fagus sylvatica* Forests (CSFagus4EST)”, funded by the European Union through FORWARDS (Horizon Europe Project No. 101084481) grants to third parties managed by European Forest Institute (EFI)."

Key Words: Beech bark disease; Climate-induced stress; IoT-based forest monitoring; Remote sensing; Innovative Forest protection

New Methods of Biosurveillance

Chair: Agata Kaczmarek and Kellee Boyer

Detecting DED and Phenotyping Elms for DED Resistance Using Near-infrared Spectroscopy

Pierluigi (Enrico) Bonello¹, Anna O. Conrad² & Alberto Santini³

¹Department of Plant Pathology, The Ohio State University, Columbus, Ohio, U.S.A.

²USDA Forest Service, Northern Research Station, Delaware, Ohio, U.S.A.

³National Research Council, Institute for Sustainable Plant Protection, Sesto Fiorentino, Italy

E-mail: bonello.2@osu.edu

Currently, screening for DED resistant elm is based on very time-consuming, and expensive, destructive approaches. It requires specialized training and extensive use of always scarce human capital to scout large areas, collect specimens, and plant them in common gardens for subsequent inoculation assays to test for resistance, which often requires waiting for several years for trees to reach a suitable size. Here, we describe a project based on near infrared (NIR) reflectance spectroscopy, coupled with either multivariate statistical modeling or machine learning (a type of artificial intelligence – AI), for the classification of individual trees resistant to specific pathogens. While much of the IR work on screening for resistance to date has been based on analysis of plant extracts, the detection of the infected state of pre-symptomatic plants has also been developed based on leaf NIR reflectance, a much more user-friendly approach. Clearly, these data-driven and data-intensive approaches hold tremendous promise for the surveillance/monitoring and host resistance development components of invasive pathogen management. This project will help develop a set of modern tools for Italy and Europe to address the ongoing challenges provided by DED.

Key Words: Dutch elm disease; European elms; Early detection; Resistance phenotyping; Advanced tools

ICT technology-based scientific monitoring and digital history management system for pine wilt disease in Korea
Choi Jaewon, Bae Seong-hyun, Jeong Sung-cheol, Kim Yong-hun, Hwang Jin-hyeong, Lee Changjoon & Yoo Seok-bong

Korea Institute for Forest Disaster Safety, Korea

E-mail: jwchoi74kofpi@gmail.com

The present study examines the 'ICT-convergence smart management system' that has been introduced to Korean forest sites in response to the accelerating spread of pine wilt disease due to climate change. The prevailing management system is predicated on the principles of scientific monitoring and comprehensive digital history management, with these elements constituting its fundamental strategies. Firstly, the physical limitations of existing human resource monitoring were overcome by means of a combination of drones (UAVs) and Artificial intelligence (AI) deep learning technology. The acquisition of Image data with high-resolution RGB sensors is subject to analysis, with the objective of precisely extracting the location of dead trees with GPS coordinates. This process is synchronized in real-time with field personnel's mobile devices, with the aim of maximising monitoring precision and minimizing blind spots. Secondly, the transparency of the control process was ensured through the implementation of a QR code-based full-lifecycle management system. The entire process, from the discovery of suspected infected trees to diagnosis, felling, and product treatment (e.g. rushing, fumigation), was integrated with the smart monitoring and control system and digitized in real-time. This GIS-based integrated control system has been demonstrated to be effective in preventing control omissions and has been shown to significantly enhance the reliability of post-management. In conclusion, the digital transformation in the forestry sector has innovated administrative processes from manual methods to data-centric ones, and the accumulated big data is expected to be utilized as a core resource for predicting future occurrences of pine wilt disease and establishing optimal control strategies.

Key Words: Pine wilt disease; ICT; QR code; AI deep learning; Big data

An Initial Field Study on the Early Detection of Oak Wilt Caused by *Bretziella fagacearum* in Mature *Quercus rubra* Using Volatile Organic Compounds

Léa Lebert¹, Mathieu Gosselin¹, Philippe Tanguay², Louis Bernier¹ & Ilga Porth¹

¹Institute of Integrative Biology and Systems, Laval University, Québec Canada

²Laurentides Forestry Centre, Canada

E-mail: lea.lebert.1@ulaval.ca

Oak wilt, caused by the fungus *Bretziella fagacearum*, is a disease that already causes extensive damage to oak populations. In northern red oak (*Quercus rubra*, section Lobatae), mortality is systematic and can occur within only a few weeks. Once a tree is infected, it is too late, and it must be cut down to prevent further spread. Because visual symptoms are commonly used for disease detection, an alternative detection method is needed, as the disease may already have spread to other trees by the time symptoms become visible, making intervention too late for them as well. Volatile organic compounds (VOCs) were used to attempt early detection of infection. It has been demonstrated many times that VOCs produced by plants change in response to different types of stress, both abiotic and biotic. A first field experiment was conducted to test whether a simple VOC collection technique could be used under field conditions to detect oak wilt before the appearance of visual symptoms. A push-pull sampling method combined with thermal desorption followed by gas chromatography and mass spectrometry (TD-GC-MS) was developed for analysis. The results of this initial field trial appear promising. Four groups were defined: healthy trees, asymptomatic trees, asymptomatic tissue from symptomatic trees, and symptomatic tissue from symptomatic trees. Seven compounds (including three alcohols and two aldehydes) were detected exclusively in symptomatic tissues. Four additional compounds were found to effectively discriminate among the groups, ranked by decreasing contribution: (Z)-3-hexen-1-ol acetate (39.8%), 3-hexenal (22.5%), (Z)-3-hexen-1-ol (15.6%), and isoprene (14.3%). However, additional experiments will be required to assess differences among sites, as this study was conducted at a single location. Ultimately, these results could be used in later stages to develop a portable field tool capable of providing real-time responses, enabling forest managers to easily detect oak wilt at an early stage.

Key Words: Oak wilt; *Bretziella fagacearum*; Early detection; Volatile organic compounds; Field experiment

Preliminary Exploration in Early Detection of *Ceratocystis platani* Infection on Plane Trees Using Remote Sensed Data

Hari Berto^{1,2}, Giovanni Marino², André P.M. Fabbri², Alessandra Gionni², Alessia Lucia Pepori², Francesco Pecori², Nicola Luchi² & Alberto Santini²

¹University of Florence, Department of Agriculture, Food, Environment and Forestry (DAGRI), Firenze, Italy

²National Research Council, Institute for Sustainable Plant Protection (CNR-IPSP), Sesto Fiorentino, Firenze, Italy

E-mail: hariberto@cnr.it

Early detection of pest and pathogen infection based on unmanned aerial vehicles (UAVs) surveys has been developing rapidly during the last decade. This technique can be a huge opportunity for the management of plant diseases in forests and urban areas. This study explores some of the most relevant techniques to process remote sensed data to early classify canker stain disease infection. Sensors carried on drones can provide essential information for early identification of *C. platani*. However, the main issue is to define the right approach for establishing semiautomatic identification based on machine learning and deep learning models. A UAV survey was carried out in a highly infected area in the province of Pisa (Italy). The investigation used a Dji Matrice 300 RTK drone equipped with thermal, multispectral, and hyperspectral sensors. During the survey the trees were classified based on the degree of symptoms shown: healthy, asymptomatic and symptomatic. Symptomatic trees may be easily identified through visual inspection and simple vegetation indices values whereas asymptomatic trees differentiate slightly from healthy trees only for some more complex vegetation indices. In this work data were elaborated using different techniques and the results were compared to list advantages and disadvantages of the different methodologies used. These results are vital to avoid misinterpretation of future outputs: they proved fundamental insights on the potential of remote sensing in disease identification, even though they show many limitations as well. For that reason we can consider UAV survey an ally tool for health tree monitoring, but not a substitute of the field phytosanitary inspection. Finally, all the information retrieved is essential for establishing a proper early identification study for *C. platani* based on remote sensed data.

Key Words: Canker stain disease; Phytosanitary survey; Pathogen control; Remote sensing; Artificial intelligence

Building Resilience against Laurel Wilt Through Diagnostics and International Partnerships

Romina Gazis¹ & Jorge R. Díaz-Valderrama^{1,2}

¹Tropical Research and Education Center, Department of Plant Pathology, Institute of Food and Agricultural Sciences, University of Florida, USA

²Facultad de Ingeniería y Ciencias Agrarias, Universidad Nacional Toribio Rodríguez de Mendoza de Amazonas, Perú

E-mail: r.gazisseregina@ufl.edu

Laurel wilt, caused by *Harringtonia lauricola* and vectored by multiple species of ambrosia beetles, poses a persistent threat to avocado orchards and lauraceous forests across the Americas. Early infections are challenging to detect due to low pathogen titers, heterogeneous pathogen distribution within trees, and interference from various fungal co-inhabitants. Therefore, effective management relies on sensitive, field-deployable diagnostic tools integrated into coordinated surveillance efforts. This talk highlights recent advances in developing portable molecular assays for the rapid detection of *H. lauricola* in both avocado tissues and beetle vectors. Building on genomic analyses of diverse *H. lauricola* isolates, we designed and validated the HL-0354 LAMP assay, which offers high specificity and a detection limit of 0.5 pg of pathogen DNA, outperforming earlier detection assays. When paired with an optimized Chelex-based crude extraction method, the assay achieved 98% accuracy in symptomatic tissue and reliably detected *H. lauricola* across multiple beetle species common in orchards. Its simplicity, speed, and minimal equipment requirements make it well-suited for use in orchard surveys, sentinel plant networks, and trap-based vector monitoring. These diagnostic innovations directly support regulatory agencies and state departments of agriculture, which require rapid, robust results to guide containment actions, enforce quarantine measures, and conduct regional monitoring. By enabling on-site confirmation of infections, this approach shortens response times and enhances early-detection capacity. The program further strengthens international collaborations, with partners in Taiwan, Peru, Mexico, Australia, and other regions adapting the diagnostic tools to local hosts and vector communities. These partnerships promote harmonized detection standards, expand surveillance coverage, and support coordinated responses to the cross-regional spread of laurel wilt. Together, these advancements provide a scalable, diagnostics-centered framework for improving surveillance, regulatory readiness, and global resilience against laurel wilt.

Key Words: Loop-mediated isothermal amplification (LAMP); Field-deployable diagnostics; Ambrosia beetle surveillance; Phytosanitary regulation; Early detection systems

Sudden *Quercus petraea* Decline on Fruška Gora Mt.: Interacting Climatic Stress and Biotic Agents
Milica Zlatković, Dejan B. Stojanović, Srđan Stojnić, Vladimir Visački, Dejan V. Stojanović & Saša Orlović

University of Novi Sad, Institute of Lowland Forestry and Environment (ILFE), Serbia

E-mail: milica.zlatkovic@uns.ac.rs

In 2025, a rapid decline of sessile oak (*Quercus petraea*) has been observed on Fruška Gora Mountain (Serbia), raising serious concerns for the stability and future persistence of these forests. The decline has intensified abruptly and appears closely linked to recent climatic anomalies, particularly the prolonged absence of winter snow cover and reduced soil moisture availability, which have significantly altered tree water balance and resilience. This study applies a multidisciplinary approach to identify the interacting climatic, ecological, physiological, and biotic drivers of *Q. petraea* vitality loss. We analyze tree growth responses in relation to climatic and site-specific environmental factors, with special emphasis on drought and extreme weather events. Physiological assessments of mature trees and seedlings are combined with analyses of previous silvicultural measures to evaluate their long-term effects on current tree condition. Interestingly, field surveys conducted at selected sites revealed symptoms consistent with stripe canker disease on declining trees. Associated *Fusarium* spp. and ophiostomatoid species were isolated, and their molecular phylogenetic identification to species level is currently in progress, indicating a potential pathogenic component contributing to oak decline under stress conditions. Additionally, changes in the rhizosphere microbiome of healthy versus declining trees will be investigated using metabarcoding techniques. Remote sensing methods are employed to differentiate severely affected stands from those maintaining vitality, while the role of major defoliators is assessed as an additional stress factor. Finally, the effectiveness of *Q. petraea* regeneration methods will be evaluated and refined. By integrating classical forest monitoring with advanced molecular, physiological, and remote sensing tools, this study contributes to innovative strategies for forest protection and adaptive management under accelerating climate change.

Acknowledgments: This study is part of the project “Investigation of sessile oak (*Quercus petraea*) decline on Fruška Gora Mountain”, funded by the Provincial Secretary for Higher Education and Scientific Research.

Key Words: Oak decline; Integrated forest health monitoring; Emerging fungal pathogens; Rhizosphere microbiome; Adaptive forest protection

Second DIGITAL POSTERS Session

Chair: Denita Hadziabdic and Nadir Erbilgin

Modelling Spread Trends and Short-Term Prediction of Pine Wilt Disease Using Spatiotemporal Pattern Mining
Geonhwi Jung, Mooyoung Im, Nahyun Park, Bomok Choi, Kay Zin Lin Min, Hanmin Kim, Myeongjun Kim, Daesung Kim, Kyeongsoo Lee & Joowon Park

Department of Forestry, Kyungpook National University, Republic of Korea

E-mail: alzaki3040@knu.ac.kr

Pine wilt disease (PWD) is a major coniferous forest disease that has become a global concern across Asia, Europe, and North America. In South Korea, despite ongoing control programs, the cumulative number of affected trees reached approximately 1.49 million as of 2025, indicating a continued increase in damage. Because PWD tends to expand into areas adjacent to previously affected regions, predictions based solely on single-year occurrence distributions are limited in representing diffusion and temporal trends. To address this limitation, this study analysed spatiotemporal patterns of PWD over a five-year period (2021–2025) and developed a short-term predictive model for future damage occurrence. Nationwide locations of PWD-infected trees collected between 2021 and 2025 were analysed. Spatial clustering and interannual changes in disease occurrence were examined using hotspot analysis on 1km grid. Temporal trends in affected areas were further analysed using a space–time cube, and future PWD occurrence was predicted using a forest-based forecasting approach incorporating spatiotemporal information. Hotspot analysis showed that in 2021, PWD occurrences were primarily concentrated in Gyeongsang region along coastal areas. Over time, hotspot locations shifted westward, and by 2025, relatively strong hotspots emerged in Jeollabuk-do, northern Gyeonggi, and northwestern Gyeongsangbuk-do. These spatial patterns were consistent with temporal trend analysis, which indicated decreasing trends in initial high-occurrence areas of Gyeongsang region and increasing trends in western regions and northern Gyeonggi. Space-time cube-based forecasting suggested that areas with upward trends are likely to maintain relatively high occurrence levels in the future, with additional potential risk areas emerging adjacent to existing affected regions. These results demonstrate that integrating spatiotemporal trend analysis with forecasting supports priority monitoring and management of PWD.

Key Words: Pine wilt disease; Spatiotemporal; Hotspot analysis; Prediction model; Pattern mining

Dissecting the Genetic Architecture of *Ulmus minor*'s Resistance to Dutch Elm Disease

Adrián Miguel-Pizarro^{1,2}, Juan José Robledo-Arnuncio¹ & David Macaya-Sanz¹

¹Instituto de Ciencias Forestales (ICIFOR, INIA-CSIC), Madrid, Spain

²Universidad Complutense de Madrid (UCM), Madrid, Spain

E-mail: adrian.miguel@inia.csic.es

Dutch elm disease (DED), caused by the fungal pathogen *Ophiostoma novo-ulmi*, has devastated European populations of field elm (*Ulmus minor*). Despite sustained breeding and conservation efforts, the genomic basis of resistance remains only partially resolved, limiting the deployment of molecular tools in selection programs. Here, we performed quantitative trait loci (QTL) mapping in *U. minor* using controlled crosses to identify genomic regions associated with DED resistance. Phenotypic and genotypic data were collected from 435 progeny individuals derived from three crosses involving three parental genotypes that are resistant to the disease. Resistance-related traits were assessed through artificial inoculation during the fourth growth season. High-density SNP genotyping was obtained via restriction site-associated DNA sequencing (RAD-seq), and high-resolution genetic linkage maps were constructed to support genome-wide QTL scans. Building on these results, we analyze QTL profiles and phenotypic variation across crosses to compare effect directions, assess cross-family consistency, and prioritize regions showing stable associations with resistance-related traits. As a next step towards applied breeding, we have developed an initial genomic prediction benchmark based on weighted linear mixed models using genome wide SNP and QTL information to estimate genomic breeding values and evaluate predictive ability through cross-validation, both within and across families. Together, this initial approach links trait architecture with predictive performance, providing a practical basis for marker-assisted strategies, genomic selection, and the pyramiding of resistance alleles and haplotypes to support breeding and ecological restoration under ongoing disease pressure.

Key Words: QTL; Genomic Selection; Genetic Mapping; DED; Breeding

The Temporal Pattern and Biological Prerequisites of PWN (*Bursaphelenchus xylophilus*) Departure from the Japanese Pine Sawyer Vector

Hyeon Suk Jo¹, Jin Woo Heo¹, Je-Heon Lim¹, Su Bin Kim² & Dong-Soon Kim¹

¹Department of Plant Resources & Environment, Jeju National University, Jejudaehak-ro 102, Jeju 63243, Korea

²Horticultural and Herbal Crop Environment Division, The National Institute of Horticultural and Herbal Science, RDA, Korea

E-mail: dongsoonkim@jejunu.ac.kr

The transmission of pine wilt disease (PWD) critically depends on the departure of pine wood nematodes (*Bursaphelenchus xylophilus*, PWN) from their insect vectors, yet the conditions governing nematode departure remain incompletely understood. In this study, we investigated the temporal pattern and biological prerequisites of PWN departure from the Japanese pine sawyer beetle (*Monochamus alternatus*), with the aim of clarifying its epidemiological significance. Experimental assays demonstrated that PWN departure occurred exclusively when beetles were alive and actively interacting with host tissues. No nematode departure was observed from dead beetles, even after prolonged exposure periods exceeding 20 days, regardless of the presence of host material. In contrast, living beetles feeding on pine tissues released substantial numbers of nematodes, indicating that departure is an active, beetle-mediated process rather than a passive consequence of nematode persistence within the vector. Field-collected beetles captured using pheromone traps showed a general seasonal decline in average nematode load; however, some individuals retained high numbers of PWN until late in the flight season. This suggests that transmission potential may persist longer than commonly assumed and that late-season beetles can still contribute to the formation of new infections. These findings highlight that the risk of PWD transmission is tightly coupled to live-beetle activity and nematode departure dynamics, rather than simply to vector presence. Incorporating nematode departure models into epidemiological frameworks may improve predictions of outbreak timing and support the development of more effective early-warning and management strategies, particularly in areas where vectors are present but visible disease symptoms are absent.

Acknowledgments: This work was conducted with the support of R&D Program for Forest Science Technology (RS-2024-00404388) provided by Korea Forest Service (Korea Forestry Promotion Institute).

Key Words: Pine wilt disease; Nematode release; PWN transmission; PWN release model

Analysis of Vegetation Structure after Control of Pine Wilt Disease in South Korea

Seong-Rok Lee¹, Seung-Jae Lee¹, Dong-Bin Shin¹, Ah-Rim Lee¹, Yeong-Eun Kim¹, Hee-Ji Kang¹, Tae-Chul Hur², Joon-Hyung Park² & Seung-Hwan Oh³

¹Department of Forestry, Kyungpook National University, South Korea

²Forest Ecology & Restoration Center, Korea Forest Conservation, South Korea

³School of Forest Sciences and Landscape Architecture, Kyungpook National University, South Korea

E-mail: dltjdfhr0008@naver.com

With climate change, damage caused by forest pests and diseases is expanding, and among them, pine wilt disease (PWD) has been reported not only in NE Asia but also in various regions continuously. In the case of South Korea, damage caused by PWD has become severe over wide areas, and various studies have been conducted. However, most studies have focused on spatial information-based approaches, such as remote sensing, while field survey-based studies remain insufficient. Therefore, this study aimed to analyze the current status of vegetation structure through field surveys after PWD control in Pohang, which is the region most severely damaged by PWD in South Korea. Field surveys were conducted in 43 forest stands in the Pohang area where control treatments were implemented following the occurrence of PWD. Vegetation and tree surveys were carried out according to the phytosociological methods of the Zürich–Montpellier(Z–M) school. Vegetation survey data were analyzed using Two-Way Indicator Species Analysis (TWINSpan) to objectively classify vegetation types based on indicator species, and Canonical Correspondence Analysis (CCA) was used to identify relationships between vegetation patterns and environmental factors. As a result of the study, vegetation types were classified into four types: the *Ligustrum obtusifolium* – *Juniperus rigida* community, the *L. obtusifolium* typical community, the *Pinus thunbergii*–*P. densiflora* community, and the *P. thunbergii*–*Rhus trichocarpa* community, and these reflected differences according to species composition and topographic characteristics. In addition, DBH class distributions were analyzed for each vegetation type. As a result, *P. densiflora* and *P. thunbergii* were mainly dominant in the upperstory across all vegetation types. Meanwhile, in the understory, although regeneration of Pinaceae species was prominent after pine wilt disease damage, various species such as *Quercus variabilis*, *Styrax japonicus*, and *Robinia pseudoacacia* entered at relatively high densities and constituted the understory vegetation. CCA was conducted only for understory species with a frequency of five or more. As a result, major dominant understory species such as *Q. variabilis*, *R. pseudoacacia*, and *Castanea crenata* showed low correlations with species richness (S) and also low correlations with slope, indicating that they were located in relatively low-slope areas. The PWD-damaged sites were observed to maintain a structure in which *P. densiflora* and *P. thunbergii* dominate the upperstory even after control treatments, whereas establishment of various species was progressing in the understory. These results can be used as important baseline data for establishing future management and restoration strategies for damaged sites; however, in order to obtain more precise data, follow-up studies are required from various perspectives, such as analyzing successional patterns in PWD-damaged sites over time, or investigating non-damaged stands and untreated stands and comparing them with treated stands to evaluate the effects of PWD and control measures on vegetation structure.

Acknowledgments: This study was carried out with the support of 'R&D Program for Forest Science Technology (RS-2024-00404388)' provided by Korea Forest Service (Korea Forestry Promotion Institute).

Key Words: Pine wilt disease; Vegetation structure; Vegetation survey; Two-Way Indicator Species Analysis (TWINSpan); Canonical Correspondence Analysis (CCA)

Evaluating Chemical Cues and Attraction of *Bursaphelenchus xylophilus* to UK Beetles in the Absence of *Monochamus*

Talor Whitham^{*1,2}, James Ryalls², Luke Bell², Maria L. Inácio^{3,4}, Robbie Girling², Thomas Prior⁵, Margarida Correia⁵, Anna Platoni¹, Max Blake¹, Luís Bonifácio^{3,4} & Sarah Facey¹

¹Forest Research, Alice Holt Lodge, Farnham, Surrey, GU10 4LH, United Kingdom

²School of Agriculture, Policy and Development, University of Reading, Earley Gate, Reading, RG6 6EU, United Kingdom

³INIAV, Av. da República, Quinta do Marquês, 2780-157, Oeiras, Portugal

⁴GREEN-IT Bioresources for Sustainability, ITQB NOVA, Av. da República, 2780-157 Oeiras, Portugal

⁵Fera Science Ltd., Sand Hutton, York, YO41 1LZ, United Kingdom

E-mail: t.c.whitham@pgr.reading.ac.uk

Pine wilt disease (PWD) is one of the most serious threats to conifer forestry worldwide. Pine wood nematode *Bursaphelenchus xylophilus*, (PWN), the causative agent behind the disease establishes novel phoretic associations with local *Monochamus* species in every region it successfully establishes in. PWN aggregates towards its *Monochamus* vector in response to the beetle's cuticular compound profile. Although PWN has not yet established in the UK, repeated interceptions, increasing climatic suitability and recent findings in neighbouring countries highlight the need to understand whether native UK beetles could act as alternative vectors in the absence of *Monochamus*. Several UK Curculionidae and Cerambycidae species share similar feeding ecologies and are known to carry related *Bursaphelenchus* species, suggesting potential but untested compatibility with PWN. This research integrates chemical characterisation and behavioural assays to assess the threat to the UK posed by an establishment of PWN without any accompanying *Monochamus*. Cuticular compound profiles of *Monochamus galloprovincialis* were characterised using both immersive and headspace 2D gas chromatography–mass spectrometry (GC×GC MS), alongside solvent extraction GC-MS; and compared with profiles from UK-native beetles selected for ecological similarity and historical nematode associations. These comparisons aim to distinguish any unique and shared compounds between UK beetles and a known vector of PWN. Characterisation will also differentiate genuine beetle derived compounds from plant volatiles present in the extracts. Complementary bioassays evaluate PWN movement towards pentane extracts of beetle cuticles. Mixed life stage nematodes were inoculated onto agar arenas and their distribution across attraction, neutral and outer zones were quantified over 24–48 hours. Preliminary observations indicate that some UK beetle extracts may elicit unexpected attraction responses. However, behavioural attraction alone cannot confirm vector suitability. Integrating chemical profiles with attraction assays will allow us to determine whether nematode responses are driven by genuine beetle derived cues, plant volatiles, or shared compound classes across taxa.

Key Words: Pinewood nematode; Cuticular compound; Attraction

Assessing the Early Detection of Asymptomatic Pine Wilt Disease Using UAV Multispectral Imagery
Wontaek Lim & Youngwoo Nam

Forest Entomology and Pathology Division, National Institute of Forest Science, South Korea

E-mail: orangmania99@korea.kr

Pine wilt disease (PWD), caused by the pine wood nematode (*Bursaphelenchus xylophilus*, PWN), poses a severe threat to pine forests. Effective management depends on early detection, yet operational surveillance still largely relies on visible symptoms, which limits the identification of asymptomatic infections. Here, we evaluated whether asymptomatic PWN infection can be detected across the progression of asymptomatic PWD using multi-temporal multispectral imagery. Multispectral data were acquired at approximately weekly intervals over a PWD-affected area for nearly two years using an unmanned aerial vehicle (UAV), while experimental PWN inoculation was conducted in parallel. Spectral reflectance, greenness indices, and vegetation indices were compared across four asymptomatic stages, temporally aligned by the timing of subsequent symptom onset. Detectability of asymptomatic infected trees was assessed using a Random Forest–based balanced subsampling ensemble model. Distinct spectral differences and high classification performance (>90%) indicated that asymptomatic PWN-infected trees can be detected as early as 7–8 weeks before visible symptom onset, with spectral separability increasing as disease progression advanced. Among spectral variables, the normalized difference red-edge (NDRE), associated with plant water stress, consistently emerged as the most informative indicator across asymptomatic stages, likely reflecting PWN-induced reductions in host water potential. Stage-dependent shifts in contributing spectral variables further suggest that time-varying physiological changes in infected trees are spectrally expressed over time. These results provide a scientific basis for developing early-warning, multi-scale surveillance frameworks integrating satellite, manned aircraft, and UAV platforms, and for improving proactive PWD management strategies.

Key Words: Early detection; Asymptomatic infection; Invasive forest pest; Pine wood nematode; Multi-temporal spectral data; Stage-dependent shift

A Spatial Risk Assessment Model for Pine Wilt Disease Based on Outbreak Patterns

Wontaek Lim, Min-Jung Kim & Youngwoo Nam

Forest Entomology and Pathology Division, National Institute of Forest Science, South Korea

E-mail: orangmania99@korea.kr

Pine wilt disease (PWD), caused by the pine wood nematode (*Bursaphelenchus xylophilus*) native to North America, has spread across East Asia and Europe, resulting in severe damage to the native pine species. To support effective management of PWD, numerous studies have assessed outbreak potential using species distribution models based on machine learning techniques; however, most have been limited to evaluating the outbreak potential under climatically suitable conditions. To overcome these limitations, this study assessed PWD outbreak risk by explicitly incorporating previous-year spatial patterns of PWD outbreaks as explanatory variables, using 30 Random Forest-based subsampling ensemble models. The models predicted infection probability across South Korea at a spatial resolution of 100 m grid cells, using variables related to PWD outbreak patterns, host distribution (host species-specific coverage area), climatic conditions (MB index and drought), and social factors (population). In particular, PWD outbreak patterns were quantified by spatially aggregating infected tree counts for each grid cell, across nine distance classes ranging from 0 to 10 km, to account for the dispersal distance distribution of vector insects, based on infected tree location data managed by the Korea Forestry Promotion Institute. The models were trained using PWD outbreak data surveyed in 2022 and 2023, and their performance was evaluated using data surveyed in 2024. As a result, 90% of the infected sites identified in 2024 were captured within the top 16.7% of predicted probabilities, and 99% were captured within the top 35.8%. Future studies should focus on improving the precision of predicted probabilities through the additional collection of PWD outbreak information and further refinement of explanatory variables. The results of this study are expected to provide more accurate PWD outbreak risk information through continued refinement and to support surveillance and control decision-making processes.

Key Words: Forest pest management; Invasive forest pest; Pine wood nematode; Machine learning; Species distribution model

Spatial Distribution Characteristics of Pine Wilt Disease: Evidence from Wildfire-Affected Areas

Heeji Kang, Heewon Kwon, Youngjin Kim & Dong Shiqi

Department of Forestry, Graduate School, Kyungpook National University, Republic of Korea

E-mail: khj05025@naver.com

Pine Wilt Disease (PWD), caused by the pine wood nematode, is a major forest disease that poses substantial damage to pine forest ecosystems and forest management. With recent advances in remote sensing and spatial analysis, research on early detection and spread patterns of PWD has expanded. However, quantitative evidence on how large-scale disturbances such as wildfires influence the spatial distribution of PWD remains limited. This study investigates the association between wildfire disturbance and PWD incidence using distribution data collected before and after a major wildfire event in South Korea. We first assessed spatial clustering of PWD using Global Moran's I and Local Indicators of Spatial Association (LISA). We then applied a Generalized Additive Model (GAM) to estimate the effects of proximity to wildfire-affected areas and topographic factors on PWD incidence. The results reveal significant spatial clustering around wildfire-affected areas, with clustering tending to intensify over time following the wildfire. The GAM results indicate a nonlinear relationship in which PWD incidence increases closer to wildfire-affected areas, and incidence also tends to increase with elevation and slope. These findings highlight the need for strengthened monitoring and control of PWD in and around wildfire-affected areas and suggest the importance of intensive management during the post-fire period.

Acknowledgements: This study was carried out with the support of 'R&D Program for Forest Science Technology (RS-2024-00404388)' provided by Korea Forest Service (Korea Forestry Promotion Institute).

Key Words: Pine wilt disease; PWD; Moran's I; LISA; GAM

Organized by



Institute for Sustainable Plant Protection
National Research Council of Italy



National Institute of
Forest Science
Republic of Korea



In collaboration with



Sponsors



Synergy Semiochemicals

PROTECTING TREES NATURALLY

ISBN: 978-960-9619-08-0