Conference Program

Invasive Forest Pathogens & Implications for Biology & Policy

IUFRO Working Party 7.02.02

May 7-11, 2017

Niagara Falls, Ontario

(cover photo courtesy of T. Hsiang)

Canadian Institute of Forestry / Institut forestier du Canada — IUFRO — Ontario Ministry of Natural Resources and Forestry — University of Guelph — Natural Resources Canada / Ressources naturelles Canada

Program Overview

Time	Sun, 7 May	Mon, 8 May	Tues, 9 May	Wed, 10 May	Thurs, 11 May
6:30 – 7:00	Participants arrive during the day	Breakfast in hotel			
7:00 – 7:30			Breakfast in hotel	Breakfast in hotel	Breakfast in hotel
7:30 – 8:00					
8:00 – 8:30		Field trip 8:00 – 18:00 Bus to depart at 8:00 from front of hotel.			
8:30 – 8:45			Session 1: Introductions	Session 5: Keynote 2	Session 8: Conifer foliar disease
8:45 – 9:00					
9:00 – 9:15					
9:15 – 9:30			Session 2: Keynote 1		
9:30 – 9:45				Next meeting	
9:45 – 10:00				Coffee	
10:00 – 10:15			Coffee		Coffee
10:15 – 10:30				Session 6: Diplodia, etc.	
10:30 – 10:45			Session 3: Invasive pathogens		Session 9: Stem diseases
10:45 – 11:00					
11:00 – 11:30					
11:15 – 11:30					
11:30 – 11:45					
11:45 – 12:00					Closing remarks
12:00 – 12:30			Lunch	Lunch	Participants depart
12:30 – 13:00					
13:00 – 13:30			Session 4: Pitch canker	Session 6: Cont.	
13:30 – 14:00				Session 7: Ash dieback	
14:00 – 14:30					
14:30 – 14:45					
14:45 – 15:00			Preview poster session 1	Preview poster session 2	
15:00 – 15:30			Coffee	Coffee	
15:30 – 16:00			Poster session 1	Poster session 2	
16:00 – 16:30					
16:30 – 17:00			Free time	Free time	
17:00 – 18:00					
18:00 – 19:00	Registration	Dinner on own	Dinner on own		
19:00 – 20:00				Group dinner: Brasa Brazilian Steakhouse	
20:00 – 21:00					

Table of Contents by titles in sequence (authors listed in Index)

Program: Presenting authors shown, but all coauthors listed in index

SUNDAY, MAY 7

18:00 – 20:00 Registration at Hilton Fallsview Hotel

MONDAY, MAY 8

6:30 – 7:30 Breakfast in hotel

8:00 – 18:00 Field trip, all day, bus to depart at 8:00 from in front of the hotel.

TUESDAY, MAY 9

7:00 – 8:00 Breakfast in hotel

Oral Session 1: Welcome and introduction
Chair: Tod Ramsfield

8:30 Welcome to Niagara Falls
Tom Hsiang, University of Guelph, Canada

8:45 Introduction from IUFRO 7.02.02 coordinator
Julio Diez Casero, University of Valladolid, Spain

9:00 Ontario invasive species act
Richard Wilson, Ontario Ministry of Natural Resources, Canada

Oral Session 2: Keynote presentation
Chair: Tod Ramsfield

9:15 A conceptual framework for solutions to black swan events in forest health
Pierluigi (Enrico) Bonello, Ohio State University, USA

Morning Break

10:00 Coffee available in foyer

Oral Session 3: Invasive forest pathogens
Chair: Richard Wilson

10:30 The epidemic of boxwood blight in Turkey: management challenges
Tuğba Doğmuş Lehtijärvi, Suleyman Demirel University, Turkey

10:45 Biology, survival and mating genes of *Cylindrocladium buxicola*
Tom Hsiang, University of Guelph, Canada

11:00 Implications of the invasion of the fungus *Ceratocystis platani* in Europe

Panaghiotis Tsopelas, Institute of Mediterranean Forest Ecosystems, Greece

11:15 Tree pathogens – presence, persistence and expansion in a domesticated world
Monique Sakalidis, Michigan State University, USA

11:30 Infection biology and genetic variation in *Discula destructiva* in Ontario, Canada
Tom Hsiang, University of Guelph, Canada

11:45 Oak decline phenomenon in Poland, relationships between genetic structure and healthiness
Tomasz Oszako and Justyna Nowakowska, Forest Research Institute, Poland

Lunch

12:00 Lunch provided in the foyer

Oral Session 4: Pitch canker disease and advances in pathogen detection
Chair: Tom Hsiang

13:00 Spore dispersal pattern of *Fusarium circinatum* on and infected Monterey pine forest in north-western Spain
Miloň Dvořák, Mendel University of Brno, Czech Republic

13:15 Pathogenicity in *Fusarium circinatum*: annotating candidate genes
Emigdio Jordán Muñoz-Adalia, University of Valladolid, Spain

13:30 COST Action FP1406: Pine pitch canker – strategies for management of *Gibberella circinata* in greenhouses and forests (PINESTRENGTH)
Julio Diez Casero, University of Valladolid, Spain

13:45 Detection and quantification of the air inoculum of *Caliciopsis pinea* in a plantation of *Pinus radiata* in Italy
Leticia Botella, Mendel University of Brno, Czech Republic

14:00 Transnational plans for the management of forest risks (PLURIFOR)
Jorge Martin, University of Valladolid, Spain

14:15 Predicting resistance to sudden oak death in coast live oak using Fourier transform infrared spectroscopy
Katherine D'Amico, *The Ohio State University, USA*

14:30 Observatree: the use of citizen science as an early warning system
Ana Perez-Sierra, Forest Research, UK

Poster session 1 preview

14:45 Oral presentation of 1-2 PowerPoint slides (1-2 minutes) for each odd numbered poster to plenary group

Afternoon break

15:00 Coffee available in foyer

Poster session 1

15:30 Authors of odd numbered posters to be by their poster

Conclusion of day 2

16:30 End of day 2, dinner on your own

WEDNESDAY, MAY 10

7:00 – 8:00 Breakfast in hotel

Oral Session 5: Keynote presentation

Chair: Gaston Laflamme

8:30 Creating epidemics to kill native forest trees: *Diplodia sapinea* and red pine as a case study of errors and omissions
Glen Stanosz, University of Wisconsin – Madison, USA

Determination of the location of the next meeting

Chair: Julio Diez

9:30 A presentation from the group that would like to organize the next meeting

Morning Break

9:45 Coffee available in foyer

Oral Session 6: Botryosphaeriaceous and other forest pathogens

Chair: Glen Stanosz

10:15 A large outbreak of *Diplodia pinea* on *Pinus sylvestris* in Sweden
Jonàs Oliva, Swedish University of Agricultural Sciences, Sweden

10:30 Climate change triggers the pervasive spread of botryosphaeriaceous fungi in the Mediterranean region
Salvatore Moricca, University of Florence, Italy

10:45 *Diplodia corticola* causing disease in new oak species in northeastern USA
Isabel Munck, USDA Forest Service, USA

11:00 Symptoms associated with decay and *Gremmeniella abietina* infection in Aleppo pine stands in Northern Spain
Julio Diez Casero, University of Valladolid, Spain

11:15 Plantation trials of mixed species, white pine and Norway spruce, to minimize damages caused by white pine blister rust and white pine weevil
Gaston Laflamme, Canadian Forest Service, Canada

11:30 Infection biology of the invasive alder rust pathogen *Melampsoridium hiratsukanum* in the eastern Italian alps
Salvatore Moricca, University of Florence, Italy

11:45 The impact of effective microorganism and organic and mineral fertilisers on the growth and mycorrhizal colonisation of *Fagus sylvatica* and *Quercus robur* seedlings in bare-root nursery experiment
Jacek Olchowik, Warsaw University of Life Sciences, Poland

Lunch

12:00 Lunch provided in the foyer

Oral Session 6 (Continued):
Chair: Glen Stanosz

13:00 Disrupting natural disturbance regimes – creating conditions under which native pests Behave like invasive pests
William Livingston, University of Maine, USA

13:15 Where have all the butternuts gone? Butternut canker in Ontario, Canada
Richard Wilson, Ontario Ministry of Natural Resources, Canada

Oral Session 7: *Hymenoscyphus fraxineus*
Chair: Julio Diez

13:30 Selection and testing of *Fraxinus excelsior* genotypes for resistance against *Hymenoscyphus fraxineus* in Sweden
Michelle Cleary, Swedish University of Agricultural Sciences, Sweden

13:45 Interaction between *Hymenoscyphus fraxineus* and *Phytophthora* species in common pathogenicity test on young ash (*Fraxinus excelsior*) seedlings
Tomasz Oszako, Forest Research Institute, Poland

14:00 Population genetic analysis of a parasitic mycovirus to infer the invasion history of its fungal host, the ash-dieback pathogen *Hymenoscyphus fraxineus* and other HfMV1 related studies
Corine Schoebel, Swiss Federal Institute for Forest, Snow and Landscape Research, Switzerland

14:15 Advanced phenotyping using FT-IR distinguishes disease resistance in *Fraxinus excelsior* against *Hymenoscyphus fraxineus*
Michelle Cleary, Swedish University of Agricultural Sciences, Sweden

14:30 The airborne inoculum of *Hymenoscyphus fraxineus* seems to be an efficient transport means for Hymenoscyphus fraxineus mitovirus 1 in the Czech Repbulic
Leticia Botella, Mendel University in Brno, Czech Republic

Poster session 2 preview

14:45 Oral presentation of 1-2 PowerPoint slides (1-2 minutes) for each even numbered poster to plenary group

Afternoon break

15:00 Coffee available in foyer

Poster session 2

15:30 Authors of even numbered posters to be by their poster

Conclusion of day 3

16:30 End of day 2

Group Dinner

19:00 – 21:00 Group dinner at the Brasa Brazilian Steakhouse in the Hilton Fallsview Hotel.

THURSDAY, MAY 11

7:00 – 8:00 Breakfast

Oral Session 8: Conifer foliar diseases
Chair: Tom Hsiang

8:30 Population structure of *Dothistroma septosporum* in northern Europe and Asia
Kalev Adamson, Estonian University of Life Sciences, Estonia

8:45 Dothistroma needle blight in Alberta, Canada
Tod Ramsfield, Canadian Forest Service, Canada

9:00 New perspectives and questions concerning the Swiss needle cast epidemic on the west coast of North America
David Shaw, Oregon State University, USA

9:15 Foliage diseases affecting the quality of noble fir boughs in the U.S. Pacific Northwest
Gary Chastagner, Washington State University, USA

9:30 The long-term impact of foliar disease on *Pinus sylvestris* L. growth: case study of needle cast
Aris Jansons, Latvian State Forest Research Institute, Latvia

9:45 Gemmamyces bud blight of *Picea pugens*: a sudden disease outbreak in central Europe
Ludmila Havrdová, Silva Tarouca Research Institute for Landscape and Ornamental Gardening, Czech Republic

Morning Break

10:00 Coffee available in foyer

Oral Session 9: Stem diseases
Chair: Julio Diez

10:30 Re-emergence of *Neonectria neomacrospora* on *Abies* spp. in Britain
Ana Perez-Sierra, Forest Research, UK

10:45 How similar are fungal communities invading bark stripping wounds of native *Picea abies* and introduced *Pinus contorta* in Europe?
Astra Zaluma, Latvian State Forest Research Institute, Latvia

11:00 Eutypella canker of maple (*Eutypella parasitica*) in Europe
Dušan Jurc, Slovenian Forestry Institute, Slovenia

11:15 Weather influences the severity of butternut canker in Québec
Kishan Sambaraju, Canadian Forest Service, Canada

11:30 Incidence of slime flux in southern Ontario deciduous trees
Tom Hsiang, University of Guelph, Canada

Session 10: Closing remarks

11:45 Closing comments to summarize the meeting and wish everyone safe travels.

LIST OF POSTERS (Numbers indicate poster board location)

1. Major diseases of tropical plantation forests in Indonesia
Abdul Gafur, AAA Fiber Research and Development, Indonesia

2. Economic impact and fungal communities associated with canker damage on white pine (*Pinus strobus*) in New England, U.S.A.
William Livingston, University of Maine, USA

3. Climatic conditions related to recent outbreaks of *Neonectria neomacrospora* on *Abies* spp. in Europe and USA
Ana Perez-Sierra, Forest Research, UK

4. Diseases on subalpine fir (*Abies lasiocarpa*) in Norway and USA
Gary Chastagner, Washington State University, USA

5. Identification of pathogenic and endophytic fungal populations in west coast Douglas-fir foliage *Dixie Daniels, Oregon State University, USA*

6. Global diversity of foliar fungal communities in native and exotic pine (*Pinus* spp.) from arboreta: implications for invasive species introductions
Michelle Cleary, Swedish University of Agricultural Sciences, Sweden

7. *Phomopsis juniperivora* identified in Greece causing dieback on *Juniperus macrocarpa*
Panaghiotis Tsopelas, Institute of Mediterranean Forest Ecosystems, Greece

8. Etiology and management of Diplodia tip blight outbreak on slash pine (*Pinus elliottii*) in Florida

Claudia Alejandra Páez, University of Florida, USA

9. Responses of Austrian pine to an opportunistic pathogen under drought stress
Pierluigi (Enrico) Bonello, The Ohio State University, USA

10. Host range, distribution and the future threat to *Diplodia sapinea* in Turkey
Tuğba Doğmuş Lehtijärvi, Suleyman Demirel University, Turkey

11. Undetected or rare to ubiquitous and damaging: a nonlethal "fungicide" and nursery seedlings in the proliferation of *Diplodia sapinea*
Glen Stanosz, University of Wisconsin-Madison, USA

12. Effects of copper and silver nanoparticles on growth in selected species of pathogenic and wood - decay fungi *in vitro*
Marta Aleksandrowicz-Trzcińska, Warsaw University of Life Sciences, Poland

13. Giant leach blotch disease (*Pleuroceras pseudoplatani*) identified on new maple hosts (*Acer* spp.)
Michelle Cleary, Swedish University of Agricultural Sciences, Sweden

14. Seasonal development of lesions of young common ash in Latvia
Astra Zaluma, Latvian State Forest Research Institute, Latvia

15. Prediction of *Hymenoscyphus fraxineus* impact in forests of the Czech Republic
Ludmila Havrdová, Silva Tarouca Research Institute for Landscape and Ornamental Gardening, Czech Republic

16. Host susceptibility to ash dieback shapes fungal communities of common ash, *Fraxinus excelsior* (L.)
Marta Agostinelli, Swedish University of Agricultural Sciences, Sweden

17. *Lonsdalea quercina* subsp. *populi* subsp. nov. a new bacteria canker on hybrid poplars in Hungary
András Koltay, NARIC Forest Research Institute, Hungary

18. Occurrence of *Botryosphaeria corticola* on oaks in the northcentral United States
Glen Stanosz, University of Wisconsin-Madison, USA

19. Molecular assessment of the latent endophytic pathogen *Gnomoniopsis smithogilvyi* in chestnuts, rootstocks and grafts of six varieties of chestnut trees
Tomasz Oszako and Justyna Nowakowska, Forest Research Institute, Poland

20. Molecular diagnostics of the chestnut canker agents *Gnomoniopsis smithogilvyi* and *Cryphonectria parasitica* in different tissues of *Castanea sativa*
Justyna Nowakowska, Forest Research Institute, Poland

21. *Pseudomonas putida* and *Trichoderma harzianum* may efficiently control the agent of chestnut brown rot and chestnut canker *Gnomoniopsis smithogilvyi*

Tomasz Oszako, Forest Research Institute, Poland

22. Assessment of defoliation on stem infections of birch seedlings with *Phytophthora plurivora*
Tomasz Oszako and Justyna Nowakowska, Forest Research Institute, Poland

23. Understanding the phenology of *Fusarium circinatum* to predict future outbreaks in a changing climate
Tania Quesada, University of Florida, USA

24. Factors affecting the distribution of pine pitch canker in northern Spain
Julio Diez Casero, University of Valladolid, Spain

May 8 field trip itinerary

6:30-7:30	Breakfast hotel
8:00	Board bus front door of hotel
Site 1	Niagara Glen Nature Centre Butternut site Corry Burant, Forest Health, Niagara Parks Commission Introduction to Niagara Gorge Richard Wilson, Butternut field plot
Site 2	Ball's Falls Conservation Area Beech bark disease site Dan Drennan, Forester, Niagara Peninsula Conservation Authority Richard Wilson, Beech bark disease
Site 3	Ruthven Park National Site (Lunch, indoors if raining) Marilynn (overview of the site)
Site 4	Simcoe Research Station Hazel nut research and disease Toktam Taghavi, Hazel nut researcher
Site 5	Norfolk County Woodlot Heterobasidion root disease site Adam Biddle, Superintendent of Forestry, Norfolk County John McLaughlin, BioForest, Forest Pathologist - Research & Development

Return to hotel by 6:00 pm.

Oral presentations

A conceptual framework for solutions to black swan events in forest health

Pierluigi (Enrico) Bonello

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According to Wikipedia, “the black swan theory or theory of black swan events is a metaphor that describes an event that comes as a surprise, has a major effect, and is often inappropriately rationalized after the fact with the benefit of hindsight.” Many instances of destructive epidemics by tree killing pathogens and insect pest outbreaks, particularly those caused by alien invasive species, fit this definition. The question of the day is: What can we do about this state of affairs? In this talk I will present a few case studies as examples of unexpected widespread tree die-offs and their impacts, and then transition into a theoretical analysis of some of the common underlying biological themes that characterize all of these cases. With this information in hand, I will try to demonstrate that focusing on developing and deploying host resistance is the best approach if we are to successfully manage these modern societal challenges in the future.

The Epidemic of Boxwood Blight in Turkey: Management Challenges

Tuğba Doğmuş Lehtijärvi (1), Asko Lehtijärvi (2), Funda Oskay (3), Ayşe Gülden Aday Kaya (4), and Steve Woodward (5).

(1) Suleyman Demirel University, Faculty of Forestry, Isparta, Turkey.

(2) Bursa Technicial University, Faculty of Forestry, Bursa, Turkey.

(3) Çankırı Karatekin University, Faculty of Forestry, Çankırı, Turkey.

(4) Suleyman Demirel University, Yenişarbademli Vocational School, Isparta, Turkey

(5) University of Aberdeen, Institute of Biological and Environmental Sciences, UK

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Boxwood (*Buxus sempervirens* L.) is a small evergreen tree, widely used in ornamental landscaping as individual specimens or in hedges, parterres and groups in many countries worldwide. It is amongst the most important ornamental plants in the towns and cities of Turkey. Since the outbreak of the boxwood blight epidemic, caused by *Cylindrocladium buxicola* in the Eastern Black Sea region in 2011, approximately 90% of the individual trees in the affected areas have died. In Turkey, boxwood blight was first detected and identified in late 2011, in the Eastern Black Sea region, in Trabzon and Artvin provinces. It is not known how and when the pathogen was introduced to Turkey. Nevertheless, the disease seemed to have arrived from Western and Central Europe to the Eastern Black Sea region and Iran. It is likely that the disease was present in the Eastern Black Sea region for several years before disease outbreaks were reported, as the earliest, unpublished observations of symptoms similar to boxwood blight were from the Caucasus in 2007. In November 2012, the degree of damage in the affected areas indicated that the boxwood blight epidemic threatened the existence of natural boxwood populations in the Eastern Black Sea region. By the end of 2012, one or two years after the outbreak was noticed, even in the most severely affected sites single boxwood plants with variable proportions of green canopy remained. Similar observations made in March 2015, in one of the locations, indicated that some individual plants were either more resistant or had escaped the disease. As most *B. sempervirens* plants are highly susceptible to blight, control of the disease with fungicides would provide the only short-term possibility to save the boxwood populations. Although there are several preparations that are effective against the pathogen, none are certified for usage in forests in Turkey. A combination of silvicultural management of the remaining boxwood and ex situ conservation may be the best long time strategy to save the remaining genetic diversity.

Biology, survival and mating genes of *Cylindrocladium buxicola*

Sarah E. Healy and Tom Hsiang

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A new fungus, *Cylindrocladium buxicola,* which can cause a severe disease on boxwood (*Buxus* spp.), was recently observed in North America. The fungus was positively identified by DNA sequence comparisons as the cause of box blight. Whole boxwood plants required wounding for successful infection. In field studies, survival of *C. buxicola* in Southern Ontario was low after the winter, but inoculum retained viability throughout the fall. Whole genome sequencing of two *C. buxicola* isolates revealed the presence of the MAT1-1 gene in an European isolate and MAT1-2 in a North American isolate, implying the possibility for sexual reproduction. The origin and introduction of this pathogen into North America is not known, but it is suspected of having been introduced by nursery stock.

Implications of the invasion of the fungus *Ceratocystis platani* in Europe

Panaghiotis Tsopelas and Nikoleta Soulioti

Hellenic Agricultural Organization "Demeter"- Institute of Mediterranean Forest Ecosystems, Athens, Greece

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Ceratocystis platani (Walter) Engelbr. & T.C. Harr., is a fungal species of North American origin that was accidently introduced into Europe during World War II. It affects exclusively plants of the genus *Platanus* (plane trees), causing the canker stain disease that is always fatal. Although *C. platani* was present since 1944-1945 in Italy and France it was identified for first time in 1972. This late detection of the fungus and the absence of control measures for a long period of time had as a result the wide spread of the disease into many areas in both countries. It has been spread throughout the Italian peninsula causing extensive tree mortality of London plane (*Platanus* x *hispanica* Mill. ex Münchh.) trees in streets and city parks; in Sicily the disease has affected natural populations of the indigenous Eurasian species *Platanus orientalis* L. (oriental plane), which is considered very susceptible to the disease. In France, *C. platani* has been found in five regions in the southern part of the country, causing huge losses in urban and rural areas. The disease is now spreading along the UNESCO World Heritage site Canal du Midì, killing thousands of plane trees of high aesthetic value. However, the most dramatic impact of the disease is on natural stands of *P. orientalis* in Greece. The pathogen has caused mass tree death along rivers and streams in many areas of the country assuming epidemic proportions. It has also killed centuries old iconic trees of impressive size that had been declared "monuments of nature" in this country. *C. platani* has also been reported in Switzerland and Spain, but its distribution seems to be limited in these countries. In recent years, *C. platani* was recorded in Albania and the European part of Turkey and there are unconfirmed reports of its presence in Armenia and Iran. It seems very likely that the pathogen will spread along the natural range of oriental plane in other parts of Southeastern Europe and in Western Asia having a devastating impact on natural populations of this important tree species. *C. platani* could also spread northward to central Europe, where London plane is one of the most common tree species planted in urban areas.

Tree pathogens- presence, persistence and expansion in a domesticated world

Monique L Sakalidis

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Invasive alien pathogens can have devastating and often irreversible impacts on forest ecosystems. Pathways of introduction may reflect natural, intentional or accidental introduction events. In the case of accidental introductions, the elucidation of pathogen pathways is complicated by the fact that the pathogen itself is generally not directly imported but is often linked to the introduction and dissemination of host material. Additionally, commercial planting practices and strategic breeding for traits that are desirable for commercial production (fast growth, high fiber content) may inadvertently shape the evolution of pathogens that exist on these trees. Domestication of wild pathogens alongside their host can generate new diseases that can have devastating consequences. To contain or eradicate a targeted pathogen, forest pathologists use a variety of strategies to detect, identify and characterize pathogens including an assessment of future infection risk and possible pathogen spread. Molecular tools and next-gen sequencing provide pathologists with an in-depth insight into speciation, population dynamics and adaptation. The Dothideomycete fungus, *Sphaerulina musiva* is an endemic fungus that occurs naturally on wild poplar in north-eastern and north-central North America where it causes innocuous leaf infections. In domesticated poplars this fungus causes a new disease that results in wounds (cankers) on the stem of the trees- in the most extreme cases trees literally snap in half. In order to manage disease spread and prevent further incursions a detailed review of historical records and the genomes of 83 strains of the pathogen were decoded. Regional adaptation generating local geographic populations were found. These geographic populations also displayed significant difference in virulence profiles on different genotypes of *Poplar trichocarpa*. Modeling using genomic profiles shows that the pathogen originated in the US, a center of diversity and has repeatedly spread or been introduced into Canada. The most likely vector enabling these repeated introductions is symptomless poplar material exchanged for commercial plantations or breeding programs. Future research that integrates next-gen tools with field and lab based epidemiology research in order to combat the spread and impact of the invasive pathogen *Ceratocystis fagacearum* that causes the disease Oak Wilt in Michigan will also be discussed.

Infection biology and genetic variation in *Discula destructiva* in Ontario, Canada

Mihaela Stanescu and Tom Hsiang

Environmental Sciences, University of Guelph, Guelph, Ontario, Canada

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The most important fungal disease of dogwoods (*Cornus* spp.) in North America is anthracnose caused by the introduced pathogen, *Discula destructiva*, which was first observed locally in the 1980's. In artificial inoculation studies, we found that wounds and leaf trichomes may provide a point of entry and help the pathogen survive endophytically without producing symptoms on "non-host" plants such as oak, maple and pear. The genome of several isolates of this fungus was sequenced, and we found only one mating type within *D. destructiva* populations (>100 isolates) from eastern and western North America. The lack of sexual reproduction of this fungus in North America, and along with the multi-locus haplotyping results, confirms the low genetic variation within populations on the west and east coasts of North America.

Oak decline phenomenon in Poland, relationships between genetic structure and healthiness

Tomasz Oszako (1), Miłosz Tkaczyk (1), Małgorzata Gorzkowska (2), Anna Tereba (2), Lassaâd Belbahri (3), and Justyna A. Nowakowska (2).

(1) Department of Forest Protection, Forest Research Institute, Braci Leśnej 3, Sękocin Stary 05-090, Poland.

(2) Laboratory of Molecular Biology, Forest Research Institute, Braci Leśnej 3, Sękocin Stary 05-090, Poland.

(3) Laboratory of Soil Biology, University of Neuchâtel, Rue Emile Argand 11, 2009 Neuchâtel, Switzerland

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The main wave of oak decline in Poland was recorded in the early 80. It was considered as a complex disease involving predisposing (e.g. drought), inciting (e.g. insect defoliators) and contributing factors (e.g. secondary pests). Quite recently oomycetes genus Phytophthora (especially *P. quercina*) are charged to be responsible for destruction up to 90% of fine roots in Central European oak stands. Several trials with phosphites as elicitors of plant resistance were performed in order to protect fine roots and recovery of tree crowns. The monitoring of healthiness was conducted aerially as well as from the ground. For 7 of 8 root parameters were improved after phosphite treatments including surface and length of fine roots. The genetic structure of 3 investigated oak stands in central-western Poland were assessed with chloroplast DNA markers in comparison with health status of particular stand.

The findings revealed that healthiness of oaks is growing with the increase of genetic diversity in years 2013 - 2016. Generally, the statistically positive significant correlations was found between synthetic index of damage (SYN), reflecting defoliation and vitality, and the number of alleles (total and observed ones). Moreover, in 2015 such a correlation was found between SYN and biodiversity index of Shannon (I). The number of *Phytophthora* species in soil rhizosphere (evaluated with NGS method) showed a constant decrease within the years 2013 - 2016.

The use of phosphites in oak stands endangered by *Phytophthora* genus is recommended according to our findings.

Spore dispersal pattern of *Fusarium circinatum* on an infected Monterey pine forest in north-western Spain

Miloň Dvořák (1), Patrik Janoš (2), Leticia Botella (1), Gabriela Rotková (3) and Rafael Zas (4).

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(3) Department of Experimental Biology, Masaryk University, Kamenice 735/5, 625 00 Brno, Czech Republic

(4) Department of Forest Genetics and Ecology, Biological Mission of Galicia (MBG-CSIC), Apdo. 28, 36080 Pontevedra, Spain

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The airborne inoculum of *Fusarium circinatum*, the fungal pathogen causing Pine Pitch Canker (PPC), is one of the main means of spread of the disease in forest stands and forest nurseries. Since this world-wide known pathogen was introduced in Europe, its biology in this newly infected area still remains scarcely known. To fulfil this lack of knowledge, we set an experiment on a naturally PPC infected forest of Monterey pine in Galicia (NW Spain) with the following two goals: (i) to describe the seasonal spore dispersal pattern during one year of regular sampling and (ii) to assess the spatial spore dispersal pattern around the infested plot. Portable rotating arm spore traps were used complemented with meteorological measurements. Abundance of *F. circinatum* spores in the samples was evaluated by quantitative PCR (qPCR) with hydrolysis probe. The results give relevant information about (i) the seasonal dynamics of *F. circinatum* inoculum during a whole year and its relation with meteorological conditions, and (ii) the influence of the wind direction and speed on the spatial spreading of inoculum.

Pathogenicity in *Fusarium circinatum*: Annotating candidate genes.

Emigdio Jordán Muñoz-Adalia (1,2), Mercedes Fernández (1,3), and Julio J. Diez (1,2).

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The Pine Pitch Canker Disease caused by the fungus *Fusarium circinatum* Nirenberg & O´Donell is one of the most devastating diseases in pine forests, afforestation and nurseries. This fungus has been widespread in several countries in Europe, America, Africa and Asia becoming an important threat at a global scale. Despite the importance of this forest pathogen, only a little is known about the genes that drive the infection features and the virulence factors implicated when the fungus attacks a healthy host. The genome of *F. circinatum* has been completely sequenced giving the opportunity to annotate candidate genes that take part during fungal infection. Here, we propose the annotation of five candidate genes that keep a high similarity at sequence level (>90%; using Megablast and Blastn algorithms in NCBI database) with genes previously described in other *Fusarium* species and reported as related with fungal virulence.

COST Action FP1406: Pine pitch canker - strategies for management of *Gibberella circinata* in greenhouses and forests (PINESTRENGTH)

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*Fusarium circinatum (*teleomorph: *Gibberella circinata)* was first detected in North America, since when the pathogen has spread into Central and South America, South Africa, Asia and, more recently, Europe. *F. circinatum* is now considered the most important pathogen affecting *Pinus* seedlings and mature trees in many countries globally; asymptomatic seedlings may be planted out, resulting in very serious losses in forests. The main aim of PINESTRENGTH is to establish a European-focused network to increase knowledge of the biology, ecology and pathways of spread of *F. circinatum,* to examine the potential for the development of effective and environmentally-friendly prevention and mitigation strategies and to deliver these outcomes to stakeholders and policy makers. To that end, a multidisciplinary approach is being taken, including researchers, forest managers and policy makers from 35 countries to date. Furthermore, any interested party is encouraged to join this COST Action, participating in some of the six Working Groups (WG1 The pathogen-diagnosis, WG2 Interactions with other forest pests and pathogens, WG3 Pathway of disease spread, WG4 Pest risk analyses, WG5 Management of the disease in forest and nurseries and WG6 Coordination, identifying research gaps and dissemination). For further information, please check http://www.pinestrength.eu/.

Detection and quantification of the air inoculum of *Caliciopsis pinea* in a plantation of *Pinus radiata* in Italy

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Caliciopsis pinea is an ascomycetous fungus that attacks pine trees mainly in sandy and well-drained soils in North America and Europe. Particularly, in Europe *C. pinea* has been observed on exotic pine species, such as *Pinus echinata, P. pungens, P. rigida, P. virginiana* and *P. radiata* and, on native European pines, such as *P. pinaster, P. pinea, P. halepensis.* The main symptoms of its infection include cankerous growths and significant sapping, as well as crown wilting and defoliation. Black-hair-like fruiting structures persist throughout the year and the spores mature in late winter and spring. Spores are disseminated by wind and rain and typically enter through bark lenticels or small insect wounds.

Our study is focused on the description of the seasonal spore dispersal of *Caliciopsis pinea* and its relation to meteorological conditions (temperature, leaf wetness, relative humidity and precipitations), which is needed for a more precise and effective control of the disease. For this experiment one infected *P. radiata* plantation was sampled in the Tuscany (Italy). A rotating arm spore trap together with a weather station were installed to sample the aerospora for 24 h every week from May to November 2016. Air samples were directly analysed after DNA extraction by qPCR using specific primers and Taq-Man MGB probe. The study shows an irregular occurrence of the inoculum of *C. pinea* throughout the entire sampling period with peak levels in mid-June and early August. The statistical analysis of the DNA and climatic data will bring us a clearer idea of the influence of the weather conditions on the spore production of this pathogen. Furthermore, the very low detection limit of the qPCR experiment shows the efficiency and suitability of rotating arm spore traps for early detection of this pathogen.

Transnational plans for the management of forest risks (PLURIFOR)

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The project PLURIFOR (Interreg SUDOE, EU) will focus on the risks posed by storms, fire, soil degradation, pinewood nematode (*Bursaphelenchus xylophilus*), chestnut gall wasp (*Dryocosmus kuriphilus*), eucalyptus weevil (*Gonipterus scutellatus*), the fungus causing pine pitch canker (*Fusarium circinatum*), and emerging pests and pathogens. The aim of PLURIFOR is to help with the development of regional and transnational risk management plans for forest areas susceptible to biotic and abiotic hazards. The focus is on incorporating the latest scientific understanding of hazards to forests in the south-west of Europe into the civil planning mechanisms for dealing with these hazards and their impacts. It involves a direct transfer of knowledge between partner countries and partner institutions working alongside each other to develop evidence-based and up to date risk management plans.

The project comprises 11 partners and 21 associate partners, uniting research institutes, universities, forest related organizations (unions, associations, services) and regional governments and councils from the Interreg SUDOE countries of Portugal, Spain and France.

PLURIFOR kicked off with a meeting in Pierroton, France, on 12th July 2016. After that the participants met in Bilbao, Spain on 24-26th January 2017 to start to organize the activities of the fourth working groups of the project.

In Cantabria (Spain) the project is dealing with the management of *Fusarium circinatum* and *Gonipterus scutellatus*, under the supervision of the University of Valladolid. The development of new diagnostic methods for fungal identification as well as the use of UAVs for identification of the evaluation of the level of damages of the pest in the field, are some of the activities planned for PLURIFOR in this region.

Key-words: *Defoliation, evaluation of damages, biotic and abiotic diseases, management coordination.*

Predicting Resistance to Sudden Oak Death in Coast Live Oak Using Fourier Transform Infrared Spectroscopy

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Invasive pests and pathogens are a serious problem in forests, resulting in severe economic and ecosystem level impacts (1, 8, 10). This is true in coastal California where the invasive pathogen *Phytophthora ramourm*, causal agent of sudden oak death (SOD), is killing millions of native trees, altering forest composition and increasing fire hazards in already high-risk environments (4,9). Coast live oak (*Quercus agrifolia* [CLO]), a tree endemic to California and host to the pathogen, was shown to exhibit variable susceptibility to SOD, suggesting that natural host resistance could be used as a viable management strategy for this disease (5, 6, 7). Recent work showed that Fourier transform infrared (FTIR) spectroscopy, a technique commonly used in food science applications, can also be used to predict resistance in CLO based on phloem phenolic extracts and phenotypes derived from artificial inoculations with *P. ramourm* (2). The goal of this study is to test whether this technique can accurately predict resistance in CLO trees that are naturally infected with the pathogen. To test this, we will utilize pre-infection phloem samples collected in 2010 from trees in areas where the pathogen had not yet been detected. Since sample collection, these trees have been monitored for SOD symptom development, and a subset have been classified as potentially resistant or susceptible based on changes in disease status over time. We will determine if this classification conforms with the predictive FTIR model. If a significant proportion of the CLO population is found to exhibit some level of natural resistance to *P. ramorum*, then the best management strategy may be to let the disease move through the environment and rely on natural selection to maintain resistant CLO. This approach would save resources currently spent on ineffective conventional management strategies. This strategy could be applied to a broad range of forest tree species when they display similar patterns of resistance to pests and pathogens as we have found in the CLO-*P. ramorum* pathosystem.

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Observatree: the use of citizen science as an early warning system

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The number of new pests and diseases arriving to the UK has increased in recent years having a high impact in UK woodlands and the environment. Observatree is a project that started four years ago with the aim of creating a tree health early warning system using citizen science. This project was launched to increase surveillance and to raise awareness of the new threats. To achieve this, a network of 230 volunteers have been fully trained on the recognition of 21 priority pests and diseases using face to face training, webinars, online forum and an information portal. Field guides, posters, pest and disease calendars have been created to support their work. Observatree volunteers have also been trained in biosecurity measures, survey and sampling techniques, planning and health and safety. The online tool TreeAlert was developed to allow the quick reporting of any suspect findings of tree pests and diseases which are of concern in Britain and Observatree volunteers use this tool to report their findings. A team of entomologists and pathologists from the Tree Health Diagnostic and Advisory Service at Forest Research check the reports daily and an operation system involving tree health officers in Britain is in place to take immediate action on reported regulated pests or quarantine organisms. During these four years Observatree volunteers have carried out surveys to detect pests and diseases, to monitor the spread of new findings and also monitor where pests and diseases are not present. They have provided great support on diseases such ash dieback (*Hymenocyphus fraxineus*), sirococcus blight of cedar (*Sirococcus tsugae*), oriental chestnut gall wasp (*Dryocosmus kuriphilus*) and oak procesionary moth (*Thaumetopoea processionea*) amongst others. Best practice and lessons learnt will be discussed.

Creating epidemics to kill native forest trees: *Diplodia sapinea* and red pine as a case study of errors and omissions

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What factors lead to development of disease epidemics on native forest trees? How has a fungus described from Scots pine in France and named *Sphaeria pinea* in 1847 become a pathogen responsible for epidemics in Wisconsin? Shoot blight, canker, and collar rot diseases caused by *Diplodia sapinea* have been particularly damaging to native red pines (*Pinus resinosa*). In just a few decades this pathogen has caused the death of millions of seedlings, saplings, and timber trees. *Diplodia sapinea* has invaded forest tree nurseries, proliferated in young plantations, threatened natural regeneration in stand understories, and caused premature harvest of maturing stands. The history of this fungus, characteristics of its native forest tree host, actions of managers, and studies by researchers provide a case study in errors and omissions leading to epidemics that have killed economically and ecologically important native trees.

A large outbreak of *Diplodia pinea* on *Pinus sylvestris* in Sweden

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In August 2016, a large outbreak of *Diplodia pinea* affecting more than 15 ha of *Pinus sylvestris* forest was observed in Sweden (59.67 N). Never before had this pathogen been observed causing damage on Scots pine in such northern conditions, though in 2013, infected cones were found in several locations nearby. A preliminary inventory in the affected area showed that more than 80% of the trees were attacked, more than half had lost their leader shoot, and on average they had lost 30% of their shoots. In the same stand indications of previous attacks were found, suggesting that inoculum had been already building up. Later surveys showed that the several stands in the surroundings were also affected, though to a lesser extent. The discovery of the pathogen was followed by a large coverage in the media, owing the importance of Scots pine for the forest sector in Sweden. The authorities were faced with the need to advice the owner of the land without a specific legislative framework for pathogen like *Diplodia pinea* which are new in the area, but not included in the quarantine list. In February 2017, the owner was granted permission to cut the affected stand, though how the other less affected stands will be managed is still unclear. Current and future research will focus on understanding the origin of the pathogen, its biology and spreading capacity under northern conditions.

Climate change triggers the pervasive spread of botryosphaeriaceous fungi in the Mediterranean region

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Members of the *Botryosphaeriaceae* family represent a growing threat to agricultural crops, urban greenscapes and natural forest ecosystems in the Mediterranean region. In Italy, in the last few years there has been an exponential increase in the occurrence of diseases caused by species of *Botryosphaeria*, *Diplodia*, *Lasiodiplodia*, *Neofusicoccum and Sardiniella*. These fungi are all involved in the etiology of new or unusual diseases in several typical Mediterranean trees, such as cork oak, holm oak, lentisk, English oak, European ash, narrow-leafed ash, poplar, Phoenician juniper, Turkey oak, and European hackberry, as well as in such exotic tree species as eucalyptus, red oak and Monterey pine. Among the factors that could have favoured this rise in invasive botryosphaeriaceous fungi and their outbreaks, climate change is the most likely. In our studies, comparing isolation frequencies and sporulation curves with climatic parameters revealed a positive correlation between an increase in disease incidence/severity and the higher temperatures/droughts that have recently been occuring during the hottest months of the year. Climate anomalies appeared to inflict stresses and physiological impairment on vegetation, predisposing trees to attack by thermophilic or thermotolerant *Botryosphaeriaceae*, while promoting synergistic interactions among different damaging agents. Ecosystems of small islands, in particular, have proven to be highly vulnerable to attack by these pathogens. This finding raises questions about the origin, introduction and pathway(s) of these fungi and point out the need to develop suitable actions to limit their further spread.

***Diplodia corticola* causing disease in new oak species in Northeastern USA**

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Over the last decade, *Diplodia corticola* (*Dc*) has emerged as an important canker pathogen of oaks (*Quercus* spp.) (Aćimović et al. 2016; Dreaden et al. 2011; Linaldeddu et al. 2013; Lynch et al. 2013) and grapevines (Úrbez-Torres et al. 2010) in the U.S. and Europe. Most recently, *D. corticola* has been reported to be causing cankers and mortality for the first time on northern red oak (*Quercus rubra*) in Maine (Aćimović et al. 2016) and West Virginia (Martin et al. 2017) and black oak (*Q. velutina*) in Massachusetts (Munck et al. 2017). Dead and partially wilted trees of red oak (*Quercus rubra*) were observed on the banks of Saco River in August 2014 near Biddeford, ME. In fall 2014, large overstory *Quercus rubra* with premature leaf browning and drop, bark cankers, and associated mortality were reported from Seneca State Forest (SSF) in Greenbrier Co., WV. In June 2015, bleeding cankers were observed on the main stem of black oaks (*Quercus velutina* Lam.) also damaged by the from gall wasp, *Zapatella davisae* Buffington & Melika (Hymenoptera: Cynipidae) in Barnstable County, MA. For all these trees, the sapwood underneath bleeding cankers was darkly discolored and contrasted sharply with healthy sapwood. Samples were collected, kept cool, and transferred to the laboratory where isolations were performed. The most frequently recovered fungus was a suspect Botryosphaeriaceae species based on colony morphology (Alves et al. 2004). The internal transcribed spacer (ITS1-5.8s-ITS2) region of the rDNA was amplified with ITS1 and ITS4 primers and sequenced in the forward direction. BLASTn searches of the ITS-rDNA sequences resulted in >99% homology with *D. corticola* type culture CBS 112549 (GenBank accession KF766156). In addition to the ITS region, gene portions of nuclear ribosomal small subunit (SSU) or the β-tubulin gene (Bt) were amplified with NS1 and NS4 or Bt2a and Bt2b primers, respectively, and sequenced in the forward direction. BLASTn searches of the SSU and Bt sequences resulted in 100% homology with *D. corticola*. Sequences of all gene regions from representative strains in each State were submitted to GenBank. To complete Koch's postulates, saplings grown in the green house (*Q. rubra*) or naturally established (*Q. velutina*) were inoculated. For each sapling, a bark incision was made before inoculating with mycelial plugs (<4 mm) from <11-day-old cultures. Incisions were wrapped with Parafilm that was removed 1 week post-inoculation. Control saplings were inoculated with sterile agar plugs. After 1 to 5 weeks, the saplings exhibited bleeding cankers. Sapwood discoloration was measured above and below the inoculations. Sapwood discoloration for saplings inoculated with *D. corticola* ranged from 24 to 81 cm for Q. rubra and from 2 to 13 cm for *Q. velutina*. Controls showed normal necrosis associated with wounding but not sapwood discoloration. Strains with the same colony morphology of *D. corticola* were reisolated from inoculated saplings. It is unclear if this disease was present in the U.S., but underreported or if the pathogen was introduced.

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Symptoms associated with decay and *Gremmeniella abietina* infection in Aleppo pine stands in northern Spain

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Gremmeniella abietina (Lagerberg) Morelet is a pathogenic fungus that causes severe damage in coniferous forests, producing the death of the trees, in Central and Northern Europe, North America and Japan. In Spain, where *G. abietina* has only been isolated from symptomatic *Pinus halepensis* trees, the fungal infections have not lead to epidemic outbreaks. In 2001, when the fungus was detected for first time in Spain, forty-one *Pinus halepensis* stands were evaluated in the provinces of Palencia and Valladolid in order to know the distribution and the incidence of the pathogen. *G. abietina* was detected in 5 plots although 25 stands showed the typical symptoms of infection. During August 2012, the same 41 stands were revised for its sanitary condition. In every stand a circular plot of 10 m radius was established and all the trees inside this area were evaluated. The plots were established in areas with symptoms of decline (i.e., defoliation and discoloration of needles) and four trees in each stand were sampled in order to know if *G. abietina* was responsible for this damage. The results showed that after 11 years, the fungus has not spread over the region. *G. abietina* fruiting bodies were observed in 3 of the 41 stands evaluated although most of the stands showed symptoms of decline.

Key-words: *Defoliation, discoloration, decline, pathogenic fungi.*

Plantation trials of mixed species, white pine and Norway spruce, to minimize damages caused by white pine blister rust and white pine weevil

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Two pests of white pine plantations are causing important damage to this valuable tree species. White pine blister rust can infect young trees and cause a high mortality rate. White pine weevil kills the leader of a tree, resulting in stem deformation or in the formation of multiple leaders, reducing its commercial value. We can reduce damage caused by white pine blister rust by pruning lower branches on all white pine saplings. However, previous laboratory experiments have demonstrated the weevil's preference for Norway spruce over white pine. Our hypothesis is that we can reduce pruning labour and damage caused by the rust and the weevil if pines and spruces are mix-planted at a 1:3 ratio. Our objectives are to demonstrate that a cost reduction related to pruning can be achieved if there are less white pine per hectare, while weevil attacks should be found mainly on Norway spruce. In cooperation with local foresters of the former Forêt modèle du Bas-St-Laurent, four sites were selected with the goal of reintroducing white pine in this area. Bare root seedlings (3-0) were planted in 2004. Surveys on the health conditions of the seedlings were conducted in 2008 and 2010, and lower branches were pruned twice during these surveys on white pine. In 2016, a survey of residual white pine was completed. Our results show that there is some variation in yearly tree mortality caused by blister rust and that site preparation was also indirectly responsible for pine mortality. In 2008, rust infection was relatively low on two of the sites (2.5%) and reached 7.5% and 9.5% in the two others. In 2010, white pine blister rust infection reached 43.5% on site 4, while it was lower on the other sites. In 2016, the unaffected 15-year-old trees presented a good height growth on all sites, even if their number was lower than expected. White pine weevil`s preference for Norway spruce was effectively demonstrated under field conditions, as a higher (3 sites) or equal (1 site) proportion of Norway spruce trees were attacked compared to white pines. Details on site management strategies are presented to improve white pine survival.

Infection biology of the invasive alder rust pathogen *Melampsoridium hiratsukanum* in the Eastern Italian Alps

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The hetero-macro-cyclic rust fungus *Melampsoridium hiratsukanum* was accidentally introduced into Northern European countries at the end of the past century, probably from Asia, with infected plant material. In a couple of decades, this rust has spread pervasively southwards, infecting species of *Alnus* in several European countries. In Italian alpine valleys, where the fungus arrived about ten years ago, it colonized aggressively grey alder (*Alnus incana*), inducing yearly a heavy defoliation in early summer. *M. hiratsukanum* was always found, in the countries where it was reported, on its telial hosts (*Alnus* sp.), while it was never observed on its aecial host (*Larix* sp.). This induced some authors to hypothesize that this full-cyclic rust fungus can also survive in alder buds, re-infecting the same broadleaf host in a reduced cycle. Since in alpine valleys the larch grows spontaneously, often intermingled with alder, a study was undertaken to ascertain whether aecia that are found in spring on this conifer also belonged to this rust and not solely to the other rusts (species of *Melampsora*), which occur sympatrically in the same valleys and have also larch as their aecial host. To this purpose, infected alder leaves bearing uredinia and larch needles with aecia were collected for the laboratory analysis. Micro-morphological and molecular (DNA-based) identification proved the rust propagules found on both the conifer and the broadleaf hosts to belong to *M. hiratsukanum*. This demonstrates that the rust fungus has established in the Eastern Italian Alps, where it has found an ideal habitat for its survival and reproduction.

The impact of effective microorganism and organic and mineral fertilisers on the growth and mycorrhizal colonisation of *Fagus sylvatica* and *Quercus robur* seedlings in bare-root nursery experiment

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This study compares the influence of effective microorganisms (EM; EM Research Organization, Inc., Uruma City, Okinawa, Japan) and the organic respectively mineral fertilisers Actifos (Act; manufacturer AGROPAK) and Busz Forte (BF; manufacturer Himal) on the growth and mycorrhizal colonisation of two common forest deciduous tree species: *Fagus sylvatica* and *Quercus robur* after one growing season in a bare-root forest nursery. EM, Act and BF were applied to foliage four times, at concentrations according to the manufacturer's recommendations. The control seedlings were not sprayed. The analysed growth parameters of tested tree species (root collar diameter, shoot and root length and dry mass) showed no significant differences among all treatments. Based on morphological and molecular identification, both, seven ectomycorrhizal fungal taxa each were detected on *F. sylvatica* and *Q. robur* roots, three of them (*Peziza ostracoderma*, *Scleroderma areolatum* and *Cenococum*-like) were shared among both plant species. *Pezizaceae* spec. (51.1%) and *Hebeloma* sp. (38.1%) were the most abundant ECM species on *F. sylvatica* roots aacrossmong all treatments on the *F. sylvatica* roots the most abundant was *Pezizaceae* spec. (51.1%) and *Hebeloma* sp. (38.1%), while *Peziza ostracoderma* (26.8%), *Naucoria salicis* (24.1%), *Scleroderma areolatum* (16.9%) were the most abundant on the *Q. robur* roots. Seedlings treated with EM were characterised by the smallest mycorrhizal species richness: 4 for both *F. sylvatica* and *Q. robur. A*ll treatments (Act, BF and EM) affected species composition. Moreover, EM treatment significantly increased the abundance of non-vital root tips (44.8% and 47.8%, respectively for *F. sylvatica* and *Q. robur*). In the case of beech seedlings BF resulted in an increased proportion (16.6%) of dead mycorrhizas. Our data indicate a negative effect of EM on the degree and species richness of

mycorrhization of tested *F. sylvatica* and *Q. robur* seedlings. None of the tested products had a negative effect on growth parameters of treated seedlings, however, seedlings treated with EM were characterised by a significantly higher abundance of dead mycorrhizas.

Disrupting natural disturbance regimes – creating conditions under which native pests behave like invasive pests

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The forests of Maine are almost all naturally regenerated even though harvesting has been present for over two centuries. The changing of the natural disturbance regimes has created conditions that have favored the intensification of native pests. This situation is particularly true with eastern white pine, Pinus strobus. The southern third of Maine and much of New England were cleared for agriculture in the earl 1800's, and then the fields were abandoned from 1870's to 1940. White pine would naturally regenerate in partial openings due to tree blow-downs, but the open fields with grass favored dense development of white pine stands under open conditions. These stands have become vulnerable to white pine weevil (Pissodes strobi) and Caliciopsis canker (Caliciopsis pinea). The latter has been associated with death of up to 50% of white pine stands growing on old fields. Explanations for the increased severity include competition from dense stands, agricultural practices resulting in soil changes affecting white pine rooting, and a severe, late season drought.

Where have all the butternuts gone? Butternut canker in Ontario, Canada

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Butternut canker disease caused by the invasive fungal pathogen *Sirococcus clavigignenti-juglandacearum* is causing rapid decline and mortality throughout the range of butternut in North America. Butternut canker has historically been overlooked and when discovered in 1991 in Ontario the aging of cankers placed the disease entry into Ontario at least 18 years earlier. In 2005 butternut was listed as an endangered species in Canada but little was known about the rate and extent of damage this disease was causing. In 2008, a network of 60 permanent butternut health plots were established throughout the range of butternut in Ontario to examine butternut health and to determine the rate of butternut canker infection and mortality. Preliminary results of a 6-year re-measurement of these plots will be presented along with findings on hybridization and butternut recruitment.

Selection and testing *Fraxinus excelsior* genotypes for resistance against *Hymenoscyphus fraxineus* in Sweden

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Since 2001, the invasive ascomycete fungus *Hymenoscyphus fraxineus* has caused a serious, steady population decline of common ash (*Fraxinus excelsior*) in Sweden. Ash is an important species among the noble broadleaved trees available to forest management in Sweden. Thus, the newly observed ash dieback is a severe setback for noble tree forestry. Several studies throughout Europe have shown large genotypic variation in the level of disease susceptibility among different individuals, and that a small proportion (1-5%) of the natural population of *F. excelsior* exhibits disease tolerance. Here we report on several activities aimed at selecting and testing *F. excelsior* genotypes including: 1) broad-scale mapping, identifying and selecting more than 500 disease-tolerant *F. excelsior* with respect to ash dieback damage in wild populations for further monitoring and testing, 2) documenting symptom development and screening resistance among *F. excelsior* genotypes propagated as clones in a field trial, and 3) early results of progeny testing from known susceptible and tolerant families. Collectively, these activities will help support the development of a more resistant population of *F. excelsior* for planting in Swedish forests, cities, and landscapes.

Interaction between *Hymenoscyphus fraxineus* and *Phytophthora* species in common pathogenicity test on young ash (*Fraxinus excelsior*) seedlings

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During the studies of ash dieback phenomenon in Wolica Nature reserve in Poland, *Hymenoscyphus fraxineus* was constantly isolated from the symptomatic ash tissues. In addition, trees showed the symptoms that could be indicative for the *Phytophthora* infections, such as increased crown transparency, decay and loss of fine roots, and necrosis and wounds of mother roots. After the sampling and isolations from the soil collected under the symptomatic ash trees, three different *Phytophthora* species were isolated, including *P. plurivora, P. megasperma* and *P. sp. hungarica, and P. plurivora* was the most frequently isolated species. However, beside the high aggressiveness of *Hymenoscyphus fraxineus* to European ash, little is known about the interactions between this pathogen and species from the *Phytophthora* genus that infect the roots and tissues of ash trees. Based on this, common pathogenicity test on ash plants was performed with using the isolates of *Hymenoscyphus fraxineus* and three different *Phytophthora* species isolated under the declining ash trees in Wolica Nature reserve in Poland. After the necrosis lengths analysis, there was no statistically significantly difference among the different treatments, and necrosis lengths averaged 1.67 cm. After the root analyses, infected in the soil infestation test, five out of 10 tested root parameters showed statically significant difference, and after the Duncan test significant difference was recorded only comparing to control group of plants, while there was no difference among the treatments. The biggest root loss was recorded in the treatment with common infection with *H. fraxineus* and *P. plurivora*, and both fine and total root lengths were 2.3 and 2.27 times smaller than control group of plants, respectively. Also, the first mortality of young ash plants was observed in this treatment. Obtained results showed high aggressiveness of *H. fraxineus* to young ash plants, but also suggested that root infections with *Phytophthora* species may contribute to bigger damages of the plants in some cases.

Population genetic analysis of a parasitic mycovirus to infer the invasion history of its fungal host, the ash-dieback pathogen *Hymenoscyphus fraxineus* and other HfMV1 related studies

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Hymenoscyphus fraxineus is an introduced plant pathogen responsible for the devastating ash dieback epidemic in Europe. Recently, we described Hymenoscyphus fraxineus mitovirus 1 (HfMV1), which occurs in this introduced fungus. Here, we explored the prevalence and genetic structure of HfMV1 in order to elucidate the invasion history of both the virus and the fungal host. To do so, a total of 1298 *H. fraxineus* isolates (both from Europe, as well as from Japan, as an Asian origin of the fungus is assumed) were screened for the presence of this RNA virus. Subsequently, 301 virus-positive isolates were subjected to partial sequence analysis of the viral RNA polymerase gene. Our results indicate a high mean prevalence (78.7 %) of HfMV1 across European *H. fraxineus* isolates. This suggests an efficient spread of the virus, probably through sexual spores of its host. Furthermore, only 1.1 % of the Japanese isolates were tested virus positive. This is in accordance with an expected founder effect in the introduced fungal population in Europe. In Europe, HfMV1 shows low nucleotide diversity but a high number of haplotypes, which seem to be subjected to strong purifying selection. Phylogenetic and clustering analysis detected two genetically distinct HfMV1 groups, both present throughout Europe. This pattern supports the hypothesis that only two (mitovirus-carrying) *H. fraxineus* individuals were introduced into Europe as previously suggested from the bi-allelic nature of the fungus. Moreover, our data points to reciprocal mating events between the two introduced individuals, which presumably initiated the ash dieback epidemic in Europe.

Advanced phenotyping using FT-IR distinguishes disease resistance in *Fraxinus excelsior* against *Hymenoscyphus fraxineus*

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The invasive ascomycete fungus *Hymenoscyphus fraxineus* has caused large scale population decline of European ash (*Fraxinus excelsior*) throughout much of its distribution range in Europe. Large genotypic variation in susceptibility to the pathogen exists in the natural population, albeit resistance occurs at a low level. Damage traits associated with the pathogen are strongly genetically controlled, which suggests that considerable gain can be achieved through selection and breeding. Large potential exists for utilizing modern approaches or tools that can quantitatively identify phenotypes and help explain the genetic basis of important plant traits, such as disease resistance. One main obstacle to making such advances is the lack of viable tools for rapid resistance phenotyping. Vibrational spectroscopy is one approach that has been used successfully for rapid phenotyping for plant resistance. In this study, we used Fourier-transform Infrared (FT-IR) spectroscopy coupled with a chemometric model to discriminate between resistant and susceptible European ash genotypes. Non-infected leaves and stem samples from known susceptible and resistant *F. excelsior* genotypes

were collected from six European countries. Purified phenolic extracts were analyzed on a FT-IR spectrometer and soft independent modeling of class analogy (SIMCA) was used to discriminate between resistant and susceptible trees. The model built with stem samples, and subsequently validated using random blind samples, gives powerful evidence that FT-IR can clearly discriminate between susceptible and resistant genotypes. These results suggest that spectroscopic phenotyping tools may allow for superior genotypes to be quickly identified and employed in restoration efforts.

The airborne inoculum of *Hymenoscyphus fraxineus* seems to be an efficient transport means for Hymenoscyphus fraxineus mitovirus 1 in the Czech Republic

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Hymenoscyphus fraxineus is a devastating invasive fungal pathogen causing ash dieback (ADB) primarily on common ash (*Fraxinus excelsior*) and narrow-leaved ash (*F. angustifolia*) in Europe. Nowadays, the disease is found throughout almost the entire distribution of European ashes. The fast expansion of the pathogen is highly likely enhanced by its airborne ascospores, considered the main responsible for tree infection as well as for pathogen dispersal over long distances.

The description of the transmission of Hymenoscyphus fraxineus mitovirus 1 (HfMV1) by *H. fraxineus* is necessary in case of a possible use of this mycovirus as a biocontrol agent. Here, we studied the presence of the mitovirus in the airborne inoculum of *H. fraxineus* in four ecologically different ash forests of the Czech Republic using eight rotating-arm spore traps. The detection and quantification of *H. fraxineus* and HfMV1 were performed by direct DNA and RNA extractions, and subsequent qPCR and mitovirus-specific reverse transcription (RT) qPCR, respectively. The occurrence of HfMV1 was shown to be significantly correlated with its fungal host, as it was detected in 57% of *H. fraxineus* inoculum. Furthermore, the ratio of mitovirus-carrying ascospores was constant at any level of *H. fraxineus* infection pressure independently of the studied locality. Temperatures of 18-19 °C at the time of spore trapping correlated with the highest presence of both HfMV1 and *H. fraxineus*. This study points out *H. fraxineus* ascospores as an efficient transport means for HfMV1 in nature and describes similar climatic requirements of both HfMV1 and *H. fraxineus*, suggesting a long-standing relationship. Moreover, a new technology to directly study a mycovirus through its host aerospora is presented.

Population structure of *Dothistroma septosporum* in northern Europe and Asia

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The well known pine needle pathogen, *Dothistroma septosporum,* is widely distributed in many areas inhabited by pines (*Pinus* spp.) in the northern and southern Hemispheres. There are hypotheses regarding the native geographic origin of the pathogen, which currently remains unknown. Evans (1984) stated that *Dothistroma* spp. could be native to Central America, while Ivory (1994) suggested that the pathogen originates from Himalayas. Other studies have indicated that native range of the fungus could be found in Europe (Drenkhan et al. 2013; Barnes et al. 2014; Mullett et al. 2017). The pathways of movement and long distance dispersal of the pathogen on a continental scale and in Eurasia are poorly known.

To determine the possible migration events and population structure of *D. septosporum* in northern and eastern Europe, and some Asian populations on the continuous Eurasian forest belt from the Atlantic to the Pacific Ocean, 238 Eurasian *D. septosporum* isolates from 12 countries were analysed with 11 microsatellite markers. Isolates included 211 from northern Europe, 16 from Russian Far East and 11 from Bhutan. Results show that populations of *D. septosporum* in the center of the distribution area of Scots pine in Europe were highly diverse and less so in locations in Bhutan and the Russian Far East. The migration of the fungus in Europe was frequent, and on a continental scale, between Europe and Russian Far East and central Asia. Mantel tests detected significant correlation between Nei's genetic distances and geographical distances in Europe, but not in Eurasia. Additionally, unique genetic patterns were detected in the populations from Norway and Serbia, which is not inherent to other populations in northern and eastern Europe.

In conclusion, this study shows a lack of support for an Asian origin of *D. septosporum* but rather supports the hypothesis that the indigenous center of Scots pine forest in Europe might be the native area for the notorious pathogen.

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Dothistroma needle blight in Alberta, Canada

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Dothistroma needle blight has been recorded in Alberta in Canadian Plant Disease Survey reports from the late 1990s on lodgepole pine (*Pinus contorta* var. *contorta* Dougl. ex Loud.), Scots pine (*Pinus sylvestris* L.) and "pine". The pathogen has also been recorded on jack pine (*Pinus banksiana* Lamb.) in Newfoundland and Ontario by the Canadian Forest Insect and Disease Survey, as well as in the Czech Republic, but its status on jack pine in Alberta is unknown. Recently, the pathogen has been identified as infecting lodgepole pine in Alberta; however, the risk to jack pine in the boreal forest has not been assessed. We are currently conducting experiments under controlled conditions to confirm Koch's postulates on jack pine and we have also developed a LAMP assay that will allow us to identify the pathogen within infected pine needles during field surveys. Through these experiments and survey activity we are hoping to have a much clearer picture of the risk posed by *D. septosporum* to *P. banksiana* in Alberta and the broader boreal forest.

New perspectives and questions concerning the Swiss needle cast epidemic on the west coast of North America.

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Since the initiation of an epidemic in the 1990's, Swiss needle cast (caused by *Phaeocryptopus gaeumannii*, Ascomycete) has been causing growth loss of Douglas-fir (*Pseudotsuga menziesii*, Pinaceae) in coastal zones of NW North America. A 2016 aerial survey of coastal forests indicated that Douglas-fir on 221,057 ha in Oregon and 100,362 ha in Washington States, USA had visible symptoms of disease. Recent monitoring, research, and evaluations using reciprocal planting trials, have shed new perspectives on the epidemic but continued to raise new questions. Monitoring efforts show that the number of hectares with visible symptoms has flattened over the past 3 years in Oregon, and gone down significantly in Washington. However, we feel that an area along the Pacific coast from the California border north to the Olympic Peninsula of Washington State, representing about 4 million hectares, is diseased, with growth losses averaging about 15 - 20% across the region for Douglas-fir. Surveys in Northern California coastal Douglas-fir forests have documented no disease expression. Research on the epidemiology of disease has focused on winter temperature and leaf wetness during May - August. However, various studies indicate that the most important climatic factors influencing disease vary with geographic location in this maritime and mountainous region. Temperature is more important at higher elevations for example. July climate appears to be particularly important, and leaf wetness likely occurs through a number of mechanisms, including dew, fog, drizzle, rain, and adjacency to water. Investigation of a reciprocal planting study has provided evidence that the effects of climate on disease is interactive with Douglas-fir genetics and climate of the seed source. Disease expression was linked to movement of trees from drier environments to wetter environments, as well as from high elevations to low elevations. This is consistent with our general understanding of foliage diseases but does not explain why disease has emerged in the forests thought to be most tolerant of disease. One possible explanation is that changing weather/climate patterns have been improving for the fungus, including leaf wetness in May, June, and especially July, and increasing winter temperature. Preliminary results from new research comparing mature and old-growth trees (120 – 450 yrs) to adjacent young stands (10-20 yrs old) indicates that needle retention is greater in mature and old-growth, and that disease severity (based on incidence x % stomates occluded by pseudothecia in 2 yr old foliage) is much greater in young trees. A number of research projects are supporting the hypothesis that all Douglas-fir trees of a similar age (especially young trees) and in a similar location, are equally infected by *P. gaeumannii*, but that disease expression varies based on tolerance by the individual host. A new monitoring plot network is allowing epidemiological studies across the range of disease severity from California to SW Washington and 50 km inland. This will aid in monitoring of growth losses, refinement of predictive models, and provide insight into disease behavior across a range of severity, including un-impacted stands along the eastern margin of the epidemic.

Foliage diseases affecting the quality of noble fir boughs in the U.S. Pacific Northwest.

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The southern Cascade Mountains of Washington State represent the geographic center of noble fir (*Abies procera*) bough production for use in decorative greenery products in the U.S. Pacific Northwest (PNW). Noble fir occurs naturally at high elevation sites above 900 m and most boughs are harvested from extensive noble fir stands on public and private lands that came about, in part, as a result of reforestation efforts after the eruption of Mt. St. Helens in 1980. In recent years the demand for noble fir boughs and Christmas trees has increased markedly. The PNW leads the U.S. in the production of Christmas trees and noble fir represent about half of the production. Bough harvesting has also increased at former lower elevation noble fir Christmas tree plantations. In 2014, an estimated 45% of the 16 million pounds of noble fir boughs that were harvested came from former Christmas tree sites.

During the past few years, bough production trees have been severely damaged by needle cast diseases. Even at low levels, such diseases impact all stages of the decorative greenery products industry. Given that multiple years of foliage is highly visible on boughs, disease development on a single age class of needles can result in unmarketable boughs for several years. Surveys in WA and OR during the past three years revealed a complex of needle cast diseases on noble fir boughs. The three most common diseases were interior needle blight, purple needle eater, and Lirula needle cast. Interior needle blight, which is the most severe foliar disease of noble fir in Christmas tree plantations, was more common at former Christmas tree sites than higher elevation sites. *Rhizosphaera* spp. were the most common pathogen associated with this disease. Purple needle eater is the name used by landowners and harvesters for a disease that is characterised by a purple coloration of blighted new growth during the summer and was observed more frrequently at high elevation sites. Although this disease has been a problem at high elevation sites near Mt. St. Helens for a number of years, it was first observed at lower elevation sites and in Christmas trees in 2014. This disease appears to be caused by *Delphinella abietis*, which is known to cause severe shoot blight on *Abies* spp in Canada and Europe. It has previously been observed on noble fir in Europe, but not the PNW. Lirula needle cast was much more common on trees at high elevation sites than former Christmas tree sites. *Lirula abietis-concoloris* and *L. punctata* have been reported on noble fir in OR. Needle rust, typically caused by *Uredinopsis* or *Pucciniastrum* spp., was also observed on trees in about 10% of the sites examined. At one high elevation site, sequence data from fruiting bodies on needles exhibiting a light brown discoloration matched *Phacidiopycnis* sp.. This fungus has previously only been reported on *Abies beshanzuensis* in China. The impact this disease complex has on the management of diseases in bough production stands will be discussed during this presentation.

The long-term impact of foliar disease on *Pinus sylvestris* L. growth: case study of needle cast

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The aim of the study was to assess the long-term impact of damages caused by needle cast to the dimensions of Scots pine (*Pinus sylvestris* L.). The study was carried out in two full-sib family trials (including 80 crosses between Latvia's pine plus trees), Kalsnava (56°40´ N, 25°57´ E) and Zvirgzde (56°41´ N, 24°26´ E). Both trials are established in *Vacciniosa* forest type, 12-15 trees per family were planted in each of four replicates, spacing 2 × 1 m.

Tree height and diameter was measured for all surviving trees at the age of 5 and 17 years. In total 80 samples (one per family from random tree) were taken to identify needle cast causing fungi using fruit bodies on dead needles. Visual grading of damage caused by needle casts was done for all trees at the beginning of June of the sixth growing season, based on proportion of affected needles on the previous-year height increment: Grade 1 corresponded to 0–5%, Grade 2 to 6–35%, Grade 3 to 36–65%, Grade 4 to 66–95% and Grade 5 to 96–100% of the damaged needles.

Tree dimensions at the age of 5 years were similar in both sites; however, the proportion of severely damaged (Grades 4 and 5) trees was notably different: 52% in Kalsnava and 94% in Zvirgzde.

The proportion of severely damaged trees was significantly higher among the trees that died between the inventories (68%) than among the trees that survived (37%). This proportion also was higher among the smallest trees (in both inventories). However, hampering effect of needle cast on growth was demonstrated by larger height differences between the trees with contrasting damage grades at the age of 17 years than at the age of 5 years in Kalsnava (Fig 1).

Family had significant effect on tree height and diameter at ages of 5 and 17 years ($P < 0.001$) in both trials. No relation was found between proportion of damaged trees and survival at the age of 5 years (i.e. until the assessment of needle cast damage), but relation between proportion of damaged trees and survival from the age of 6 till age of 17 years were negative ($P < 0.001$; $r = 0.62$-0.70). Also relations between proportion of severely damaged trees and growth traits (height and diameter at both ages) were negative ($P < 0.05$; $r = -0.25...-0.72$).

GLM analysis of Kalsnava trial data, using height at the age of 5 years as covariate, demonstrate that tree height at the age of 17 years was affected by damage Grade and family (both $P < 0.001$), and their interaction ($P = 0.03$); model $R^2 = 0.47$. Thus needle cast at juvenile age have had a long-term impact on growth of trees.

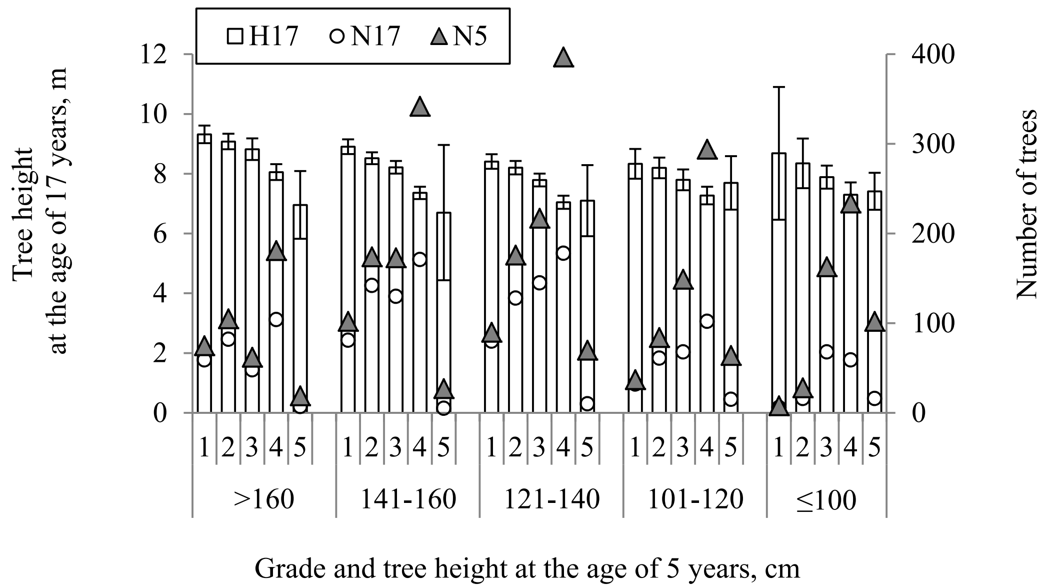

Figure 1. Number of trees at the age of 5 and 17 years (N5 and N17, respectively) and tree height at the age of 17 years (H17; ± confidence interval) according to damage Grade (1–5) in the 6th growing season and tree height (≤ 100, 101–120, 121–140, 141–160, > 160 cm) at the age of 5 years in Kalsnava.

Gemmamyces bud blight of *Picea pungens*: a sudden disease outbreak in Central Europe.

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Due to its high tolerance to acid rain, the North American Colorado blue spruce (*Picea pungens*) has been among the most frequent substitute tree species used in reforestation programmes in spruce mountain forests in the Ore and Sudeten Mountains in the Czech Republic after their destruction by sulphur dioxide pollution in the second half of the last century. This species was planted on more than 8800 ha of deforested area in the Ore Mountains alone. New plantations had prospered until a massive outbreak of the Gemmamyces bud blight at the beginning of millennium. The causal agent, *Gemmamyces piceae*, induced massive bud blight in infected trees – bud loss progressively increased to 70–80% or more, and because the trees were not able to replace the natural loss of older needles, they quickly withered and died. Many plantations disrupted by the pathogen had to be cut down. Although several resistant genotypes have been identified, the cultivation of this species in forest stands has no future in this area. Because this disease was also identified in several ornamental plantations in the area, the bud blight epidemic haunts public green space administrators and nursery and Christmas tree plantation owners. Other pathogens and pests, such as *Lophodermium piceae*, *Sirococcus conigenus* and *Elatobium abietinum*, have also been identified as involved in the damage to *P. pungens* (Černý et al. 2016)

Černý K., Pešková V., Soukup F., Havrdová L., Strnadová V., Zahradník D. and Hrabětová M. (2016): Gemmamyces bud blight of *Picea pungens*: a sudden disease outbreak in Central Europe. Plant Pathology. Doi: 10.1111/ppa.12513

Re-emergence of *Neonectria neomacrospora* on *Abies* spp. in Britain

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Neonectria canker of fir caused by the fungus *Neonectria neomacrospora* was first described from grafted white fir (*Abies concolor*) in a German nursery more than 100 years ago. In 2008 and 2011 high levels of damage were reported on fir trees in Norway and Denmark respectively. In Britain, there were occasional reports of the disease from the 1960s and from the 1990s, but then an absence of records until the re-emergence of the disease in 2015. The number of cases increased significantly in 2016 and tree death was reported on several affected sites. A survey was carried out to assess the current disease situation and to evaluate the damage. Site details, soil and climate data were evaluated to try to determine if there were any predisposing factors for the disease re-emergence. The presence of other pest and pathogens was also investigated. As the biology and epidemiology of this fungus remain largely unknown, one of the objectives was to investigate its infection process. A total of 56 forest sites and three tree collections were surveyed. *Neonectria neomacrospora* was detected in 24 of the forest sites and in all of the tree collections on a range of *Abies* species. Symptoms included dead tips or dead shoots, sometimes limited to the lower branches but in other instances throughout the crown. Affected branches or trunks showed cankers and resin flow that could be abundant, and entire branches or trunks could be girdled resulting in dieback and defoliation of the affected parts. In late autumn and winter and under humid conditions, characteristic perithecia were also observed. The fungus was detected on needles, on shoots, cankers, on male and female cones and in galls caused by the needle and shoot sucking aphid (*Adelges* sub gen. *dreyfusi*). Other fungi such as *Armillaria ostoyae* and *Heterobasidion annosum* were also present in one of the severely affected sites.

How similar are fungal communities invading bark stripping wounds of native *Picea abies* and introduced *Pinus contorta* in Europe?

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There are two economically important native conifer species in Latvia: *Pinus sylvestris* L. and *Picea abies* (L.) Karst. After successful introduction of *Pinus contorta* Dougl. ex Loudon in Sweden (Karlman 2001), experimental plantations of *Pinus contorta* were established in Latvia. At the same time (since the end of 20th century) the populations of *Alces alces* L. and *Cervus elaphus* L. have increased in Latvia and the risk of bark stripping to forest has grown (Baumanis 2013). Pines are usually characterized by relatively low susceptibility to wound decay (Vasilauskas 2001), but still introduction of tree species arise the question of resistance to diseases. Moreover the introduction of tree species may increase spread of native and invasive pathogens (Karlman 2001).

The aim of this research was to compare the extent of bark stripping wounds, assess the incidence of the subsequent discoloration of wood and analyse diversity of fungi in 30-year-old *P. contorta* and 30-year-old *P. abies* stems damaged by large game. In two studies (Arhipova *et al.* 2015; Burņeviča *et al*. 2016) fungi inhabiting *P. contorta* and *P. abies* were identified. In total, 90 *P. contorta* and 90 *P. abies* were evaluated in different sites. One wood sample was collected from each wound (1 cm under or bellow wound margin) of the stem. For each analysed tree, the diameter at breast height was measured, and the number of wounds per stem was recorded. Width, length, area, age, height from ground level of each wound was estimated. Discoloration of each wood sample was analysed and outgrowing fungi were isolated into pure cultures.

Bark stripping was more frequent in *P. contorta* stands - 170 wounds of different ages were recorded, whereas only 157 bark stripping wounds were determined in *P. abies*. Despite that wood discoloration was more common in *P. abies* stems (13-50 % of wounded trees), in comparison with wood samples of *P. contorta* (7-30 % of wounded trees). In total, 271 fungal isolates (representing 28 fungal taxa) were isolated from *P. contorta* wood samples, while isolations from *P. abies* wood samples were made less often (160 fungal isolates were obtained (representing 25 fungal taxa)). All fungal species were native.

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Eutypella canker of maple (*Eutypella parasitica*) in Europe.

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Eutypella canker of maple (*Eutypella parasitica*), a destructive disease of maples (*Acer* spp.) originating from North America, is known in Europe since 2005, when it was found in Slovenia (Jurc *et al.* 2006). It was added to EPPO Alert list and in subsequent years wider distribution of the disease was revealed: Austria in 2006 (Cech 2007), Croatia in 2007 (Ogris *et al.* 2008), Germany in 2013 (Cech *et al*. 2016), Hungary in 2015 (Jurc *et al*. 2016) and Czech Republic in 2015 (EPPO 2015). The disease was introduced to Europe probably with infected plants before second world war, since the oldest cankers found in natural stands were initiated in the beginning of sixties of the 20th century and at the edge of its distribution, the cankers are large, more than 1 m long (EPPO 2015, Jurc *et al.* 2016, Cech *et al*. 2016). In infected maple stands the disease incidence is similiar to the situation in North America (3–5 %), but there are also large uninfected areas between those territories. In Europe the disease is still spreading and its final distribution is likely to comprise the majority of the continent (Ogris *et al*. 2006). Old cankers are regulary found in urban environment which is indication for its long range transport with infected maple saplings. Susceptibility of european maple species differs, most infections occur on sycamore maple (*Acer pseudoplatanus*), folowed by field maple (*Acer campestre*) (Fig. 1) and *A. platanoides* but the disease has not yet spread enough to evaluate its impact to other european species of maples (Ogris *et al*. 2005). Comparison of the disease incidence in street plantings and forest stands revealed that in urban environment the disease incidence is two times lower than in the forest. Official measures against the disease are not implemented in any european country. Slow spread of the disease and its slow development provide good opportunity to mitigate the disease by intensive search and application of phytosanitary measures.

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Weather influences the severity of butternut canker in Québec

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Butternut (*Juglans cinerea*) belongs to the walnut family (Juglandaceae) that includes other important tree species such as *J. nigra* (black walnut), *J. regia* (Persian walnut), and pecan *(Carya illinoinensis*). Butternut is indigenous to North America and it is an ecologically and economically important component of the mixed hardwood forests of eastern North America. Of primary concern currently is the survival of butternut that is threatened by an exotic fungal pathogen, *Ophiognomonia clavigignenti-juglandacearum*. The disease was first reported from southwestern Wisconsin in 1967; currently, it is widespread and occurs throughout the range of butternut in North America causing severe dieback, trunk cankers, and eventually tree mortality. Given the potential for extirpation of this tree species primarily by the disease, butternut is designated as an 'Endangered' species in Canada. However, few studies have investigated the factors that contribute to the occurrence and severity of butternut canker over a coarse scale. For instance, impacts of weather on butternut canker have never been explored to our knowledge. In this study, we used butternut canker survey data from the province of Québec, Canada, to evaluate the relationships of percentage tree dieback and the occurrence of trunk canker with weather-derived variables. We first developed indices of trunk canker severity and overall disease, i.e., median percentage tree dieback and trunk canker severity combined into a single measure, over a 1 sq. km scale. Then, we investigated the relationships of the two disease indices with derived seasonal and annual weather variables, averaged over a 3-year and a 5-year time period, using regression models. Temperature and soil water deficit were positively associated with trunk canker severity; however, precipitation was not a significant predictor at the 1 sq. km scale. Temperature, precipitation, and spring water deficit were significantly related to the overall index of disease severity. Our results demonstrate that weather is one of the key variables that drives the severity of butternut canker over the landscape.

Incidence of Slime Flux in Southern Ontario Deciduous Trees

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Slime flux is caused by the bacterial infection of the heartwood of deciduous trees known as wet wood, which creates a pressure build up within the xylem of the tree and causes liquid to be exuded. The wet wood exudates from a tree are known as slime flux. While wet wood is a reasonably well studied subject, there is relatively little research on the occurrence of slime flux. The research conducted here in Ontario, Canada, used a visual survey to estimate the occurrence of bacterial slime flux in selected tree species. Local forests and parks in Southern Ontario were surveyed for the occurrence of slime flux, and if observed, then slime flux height, length, width, tree species and wounding were recorded. Among over 1700 trees inspected, 42 had visible signs of slime flux. Analyses showed that slime flux presence was positively correlated with tree age, and that incidence differed among tree species, with greater incidence in parks than in forests. Slime flux occurred mainly from bark cracks and at the bottom four meters. Future work will examine the microbiota associated with slime flux and wetwood.

Poster presentations

Major diseases of tropical plantation forests in Indonesia

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Reforestation program in Indonesia is aimed at sustaining forest product supplies and at the same time preserving natural forests to secure not only their economic importance, but also environmental and social roles. Productivity of plantation forests in the humid tropic areas is always challenged by pests and diseases. With the introduction of new plant species including fast growing plants such as acacias and eucalypts, new diseases become emerging threats. A number of pathogens have been recorded in plantation forests in Indonesia since their early establishment. They ignite various diseases such as foliage, shoot, and stem diseases. Major diseases in tropical Indonesian plantation forests include Ceratocystis wilt and top dieback caused by *Ceratocystis* spp., heart rot disease caused by *Phellinus noxius* and some other pathogens, phyllode rust caused by *Atelocauda digitata*, Fusarium wilt caused by *Fusarium* spp., bacterial wilt caused by *Ralstonia solanacearum*, and bacterial leaf blight caused by *Xanthomonas campestris*. This presentation elaborates discussion on the diseases. When available, field measures taken to mitigate losses due to the diseases based on the concept of integrated disease management are also provided.

Economic Impact and Fungal Communities Associated with Canker Damage on White Pine (*Pinus strobus*) in New England, U.S.A.

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Eastern white pine (*Pinus strobus*) is a signature species in eastern North America, particularly from economic and ecological perspectives. However, white pine has experienced unprecedented damage in recent years due to native pathogens. One increasing concern is *Caliciopsis pinea*, a native fungus that can result in thinner tree canopies, profuse resin secretions, and reduced wood quality. *Caliciopsis* represents a serious emerging threat, however its impact on pine remains poorly understood. Further, the extent and severity of the pathogen, along with associated fungi, have yet to be quantified. In order to confirm the presence of *C. pinea* and identify other fungal species in these cankers, our research team (1) intensively sampled 36 trees; (2) collected infected pine tissue from both thinned and unthinned sites, (3) tested a variety of sampling and DNA-extraction techniques, and (4) harvested an additional 60 trees for economic analysis.
Fungal species identification (using morphological assessment and PCR-based diagnostic assays) confirmed *Caliciopsis* was present in all stands, and associated with symptomatic white pine damage. Our sampling trials indicated that removing two layers of white pine bark and sapwood resulted in greater *C. pinea* yields, compared to removing just one layer. Further, younger cankers (those with fresh resinosous and closer to the bark) yielded more isolates of *C. pinea* than did older cankers. In addition to *Caliciopsis*, a wide range of other fungal species were isolated from necrotic tissue associated with *C. pinea* damage. However, *Caliciopsis* is the only species cultured that is a known pathogen of white pine.
Results from our economic analysis demonstrated that 28-48% of pine sawlogs had *C. pinea*, but only 7.5-12.5% of sawlogs had a loss in quality and economic value due to the pathogen. By documenting *Caliciopsis* extent and severity, identifying the fungal community associated with damage, and quantifying economic losses, we can in turn guide management prescriptions aimed at mitigating future damage and reducing loss.

Keywords: pathogen-native, Maine, New Hampshire, forest products industry, DNA extraction, PCR

Climatic conditions related to resent outbreaks of *Neonectria neomacrospora* on *Abies* spp. in Europe and USA

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During the last decade, Neonectria canker (*Neonectria neomacrospora*) has caused severe damage to true fir (*Abies* spp.) in Scandinavia, UK and western USA. Typical symptoms have been heavy resin flow and dieback of shoots and branches. On several hosts, e.g. white fir (*A. concolor*) and subalpine fir (*A. lasiocarpa*), mortality has often been observed, however, some fir species and/or provenances have proven to harbour certain degrees of resistance. Both an imperfect and a perfect stage of the fungus are known; conidia (macro- and micro conidia) and ascospores, respectively. The conidia may cause local infections within the same tree or neighbouring trees during wet periods (splash dispersion of spores). The ascospores, which are produced in characteristic read fruiting bodies (perithecia), are capable of spreading the fungus over longer distances (airborne spores) and may cause epidemics. The conidial stage of the fungus has been known for over 100 years, but no epidemics like those that we have experienced during recent years were reported. We have assembled climatic data (temperature and precipitation) for the last 25 years from Scandinavia (Norway, Denmark and Sweden), UK and USA, two locations per country. From Sweden, UK and USA an infested and a non-infested site were chosen. From Norway and Denmark, suitable non-infested sites were not found. The data are currently being analysed and the results will be presented at the conference. The aim is to reveal the weather conditions that are associated with an epidemic.

Diseases on subalpine fir (*Abies lasiocarpa*) in Norway and USA

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Subalpine fir is a very important Christmas tree species in Norway. It tolerates harsh climatic conditions and is appreciated for its narrow shape and pleasant scent. It originates from native stands in the Cascades and Rocky Mountains of western USA and Canada. The best seed sources for Christmas tree production in Scandinavia have been selected through a number of provenances trials. In USA, subalpine fir is not an important Christmas tree, but it has been planted on a smaller scale in some areas, e.g. in Idaho. Unfortunately, subalpine fir is prone to a number of fungal diseases on both continents. Several diseases are troublesome, with a major one being Delphinella shoot blight (*Delphinella abietis*). Interestingly, results from provenance trials both in Norway and Idaho, shows that southern provenances, which have thicker wax layers on the needles (bluish color), are more resistant to *D. abietis* than northern provenances. Other commonly found foliar fungi on subalpine fir in Norway are *Rhizosphaera kalkhoffii* and *Phaeocryptopus nudus,* causing needle cast and interior needle blight, respectively. Both pathogens are also known from USA. The shoot and foliar diseases may cause major damage and destroy the marketability as Christmas trees, but they will not kill the trees. However, the canker fungi *Neonectria neomacrospora* and *Grovesiella abieticola* may cause mortality to subalpine fir. The former has recently caused epidemics on fir species both in Europe and western USA, with subalpine fir being one of the most susceptible species, although, no damage by *N. neomacrospora* has thus far been seen in the native subalpine fir stands in USA. Grovesiella canker was a commonly detected disease in a subalpine fir provenance trial in Idaho, but has never been isolated from subalpine fir in Europe. In Norway, Armillaria root rot (*Armillaria* sp.) and Phytophthora root rot (*Phytophthora megasperma*) have also caused mortality on subalpine fir. They are both known diseases in USA. Due to fungicide application (copper oxide) in Christmas tree fields in Norway, most foliar and canker pathogens on subalpine fir are kept under control, but a seed orchard and some forest stands have been badly damaged by *N. neomacrospora*.

Identification of pathogenic and endophytic fungal populations in west coast Douglas-fir foliage

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Douglas-fir provides social, economic, and ecological benefits in the Pacific Northwest (PNW). In addition to timber, forests produce abundant biodiversity and provide socioeconomic viability for many communities. Products derived from Douglas-fir account for approximately 17% of the U.S. lumber output with an estimated value of $1.9 billion dollars. Employment related to wood production accounts for approximately 60,000 jobs in Oregon. Timberland not used for production supports water resources, recreation, and wildlife habitat. Minor defoliation has previously been linked to Swiss Needle Cast, associated with the fungus *Phaeocryptopus gaeumannii*. However, unprecedented large-scale defoliation began in the 1990s and has increased since, leading to decreased growth and yield. Affected areas exceed 500,000 acres in Oregon. Recent symptoms are inconsistent with predicted effects of *P. gaeumannii*, and targeted chemical control has had mixed results. While the microbiome community of conifer needles is poorly described to date, we hypothesize the full interstitial microbiome complex is involved in disease response in conifers. Additionally, we hypothesize that moisture and temperature are important climatic drivers of microbiome diversity and disease etiology, especially with regards to endophytes.

There are at least three known pathogenic endophytes of Douglas-fir, in addition to a large number of endophytes with undetermined host relationships. In order to understand the mechanistic dynamics of needle cast, it is necessary to uncover the underlying cause of the symptom. The first step is establishing a baseline inventory of endophytes in PNW Douglas-fir needles. Needles were collected from three sites in Oregon and Washington. Study sites varied in elevation (240 – 860m) and mean annual precipitation (250 – 1,575 mm/year).

Preliminary results suggest that the probability of endophyte occurrence at the cool, wet site was 2.6 ($p<0.0007$) times higher than at the warm, dry site, and 3.7 ($p<0.0001$) times higher than at the warm, wet site. Long-term silvicultural management of PNW forests will benefit as a result of this study. It is vital to understand the complete etiology of the needle cast disease affecting Douglas-fir, and whether to focus on mitigating a single-species pathogen, or a number of different pathogens. Because forests are a long-term strategy, it is critical to understand the ecological implications of disease in this important tree species.

Global diversity of foliar fungal communities in native and exotic pine (Pinus spp.) from arboreta: implications for invasive species introductions.

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The genus *Pinus* includes some of the most ecologically and economically significant forest tree species in Northern Hemisphere, and is also commonly planted in the southern hemisphere in industrial plantations. Because of this importance, pines are the focus of considerable research including mycological work to determine fungi associated with all parts of the trees, including mutualists, pathogens and endophytes. Knowledge of the diversity and biogeographic distributions of needle inhabiting fungi, as well as the role of these organisms and factors shaping these communities remain limited.

In recent years, several pine pathogens have increased in importance, including needle diseases such as Dothistroma needle blight or Brown spot needle blight, and *Diplodia sapinea* causing tip blight of pines. Reasons for these changes are unclear, but probably include combined effects of the introduction of new strains of the pathogens and climate change. Explaining these changes, however, is complex but not impossible. Recent advances in sequencing technologies have proved useful for exploring fungal diversity in environmental samples through metagenomic approaches and addressing determinants of fungal diversity and biogeographic patterns. Fungal communities are interdependent on other organisms for nutrition and habitat, thus determinants of fungal diversity and biogeographic patterns will differ between assemblages occupying different substrates. To our knowledge, fungal biodiversity and factors shaping the biogeographic patterns of fungi inhabiting foliage, including pine needles, has not been studied on a global scale to date.

As fungi exhibit strong biogeographic patterns of distribution, mainly driven by dispersal limitations and climate, investigations on fungal communities in tissues of related hosts, such as members of a single genus, from different geographical origins but growing in similar ecological conditions, provides a valuable opportunity to test the factors driving the biogeographic processes including those have been rarely addressed such as the impact of biotic interactions. Arboreta provide excellent resources for this work, with collections of closely related taxa from wide geographical ranges.

Work has been initiated on biogeographical differences between fungal population in pine needles, taking advantage of collections in arboreta and Botanical gardens in Sweden, Turkey, United Kingdom, Lithuania, Ukraine, Georgia and Canada, to determine the fungal communities of 1) healthy (current year) needles, (2) symptomatic needles (necrosis, discoloration), or (3) dead, cast needles of both native and exotic *Pinus* species. Next Generation Sequencing will be used to define communities in pine needles and following bioinformatic analyses, to compare fungal species diversities and richness amongst *Pinus* species within and between locations. While determination of healthy needles will extend knowledge on endophytic fungi inhabiting these tissues, parallel data will also be obtained from live needles exhibiting symptoms. Analysis of the data will enable, for example, the detection of 1) established pathogens, as well as possible pathogens; 2) relative susceptibility of pine species to various fungal taxa, particularly those known to cause needle damage and 3) the impact of biotic interactions on establishment and development of needle pathogens. While the first two cases have practical importance in forestry and biosecurity through improving our knowledge on needle diseases and their interaction with climate change and global movement of plants and the microorganisms they carry, the latest can serve as a valuable evidence on the impact biotic interactions between fungi may have on shaping biogeographic patterns of communities in needles.

Preliminary work on pine demonstrated the presence of several known fungal pathogens of shoots and needles, such as *Sphaeropsis sapinea* s. l., *Dothistroma septosporum* and *Leconisticta acicola* in two arboreta in geographically and climatically distinct regions (Southern Sweden and North western Turkey) on pine species originating from North America or East Asia, and on native species such as *P. sylvestris*.

Phomopsis juniperivora* identified in Greece causing dieback on *Juniperus macrocarpa

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Juniperus macrocarpa Sibth. & Sm. is a native species in Greece, very common in many coastal sand dunes of the Aegean islands, adapted to arid conditions of the region. On the island of Paros, Cyclades group of central Aegean Sea, symptoms of branch dieback were observed during the summer of 2014, on several naturally growing shrubs of *J. macrocarpa*. Affected branches examined in the laboratory showed elongated cankers with bark necrosis associated with wood necrosis under the bark, forming wedge-shaped necrotic sectors in cross section. Isolations were performed on PDA from the margins of cankers. A fungus of the genus *Phomopsis* was consistently isolated from infected branches collected from different areas of the island. Pycnidia with exuding creamy spore droplets were formed on the cultures after 2-3 weeks incubation at room temperature (23-24 ^{o}C) under natural day light. Characteristic alpha (α) and beta (β) spores were observed. Alpha conidia were hyaline, fusoid, 8-11 x 2.5-3 µm. Beta conidia were hyaline, filiform curved, 33-46 × 1–1.5 µm.

Inoculation tests were performed on 3-4 year-old potted plants of *J. macrocarpa*, *J. oxycedrus* and *Cupressus sempervirens* (Mediterranean cypress) on October 2014. The trees were wound-inoculated on the main stem with mycelial plugs from two-week old cultures, using one isolate of the fungus. All three plant species were infected by the *Phomopsis* isolate, forming elongated cankers on the stems of the inoculated plants, while no symptoms developed on control plants where sterile agar plugs were used instead of inoculum. In the majority of the inoculated *J. macrocarpa* plants the distal part of the stem above the developed canker was dead six months after inoculation, because the canker had girdled the thin stems (diameter 5-7 mm). When infected parts of stems were incubated in a moist chamber, pycnidia were developed on the cankered area with spores extruding in the form of tendrils.

Phylogenetic analysis of the nucleotide sequence of the ITS region of three isolates, compared with sequences available in the GenBank database was performed by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach. All isolates from *J. macrocarpa* clustered together with *Phomopsis juniperivora* G. Hahn (≡*P. juniperovora*) (about 1% difference); spore morphology and size were also very similar with this fungal pathogen. *P. juniperivora* is a significant pathogen of junipers in North America and has also been reported in Scotland, UK. Further research is needed to verify the identity of the fungus, using multi–gene sequence analyses with isolates from North America and Greece. No previous reports on juniper dieback from *Phomopsis* spp. exist for Greece and all available evidence suggests that this fungus is an invasive pathogen in the country.

Etiology and management of a Diplodia tip blight outbreak on slash pine (*Pinus elliottii*) in Florida

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Extensive dieback and mortality of slash pine (*Pinus elliottii*) was reported in 2012 in central Florida. To determine the causal agent and disease biology, field monitoring and greenhouse experiments were carried out. Based on sequencing of the ITS-rDNA, *Diplodia sapinea*, *Diplodia scrobiculata, Lasiodiplodia theobromae* and *Lasiodiplodia pseudotheobromae* were isolated from resinous cankers from trees in the field. *D. sapinea* and *D. scrobiculata* were consistently recovered from low, medium and high incidence plots. A foliar nutrient analysis revealed mean nitrogen levels were significantly higher ($p\text{-value}<0.01$) from samples from trees in high disease severity plots versus healthy to medium disease severity plots. Significant differences in lesion lengths were observed when *Pinus elliottii* var. *densa* and *Pinus elliottii* var. *elliottii* were treated with high levels of nitrogen and inoculated with *Diplodia sapinea.* Disease progression plots displaying different incidence levels (low, intermediate and high) illustrated that intermediate incidence level plots had a significantly ($p\text{-value}<0.05$) more rapid disease progression compared with low and high incidence level plots. Sanitation reduced disease levels in plots with high disease incidence. Random thinning significantly reduced disease severity in both disease incidence plots, when compared to the control. These results suggest that in Florida, care should be taken not to over-fertilize or plant slash pines too densely. The research reported here is being used to manage the disease and improve silviculture practices of slash pine plantings in urban areas of Florida.

Responses of Austrian pine to an opportunistic pathogen under drought stress

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Understanding the effects of climate change on host pathogen relationships in key to managing diseases in new weather extremes expected in the future, especially among long-lived perennials like trees. For example, trees under drought stress become more susceptible to pathogens as resources are allocated towards the needs of basic survival rather than chemical defenses, thus creating more favorable conditions for disease development. Our study investigates the physiological mechanisms underlying the responses of Austrian pine (*Pinus nigra*) to the tip blight and canker pathogens *Diplodia sapinea* and *D. scrobiculata* under elevated temperature and drought, two conditions that are projected to become the norm in many areas of the world. Among the defense mechanisms likely to be affected by temperature and water restrictions are those involving specialized metabolites, specifically phenolics, which are modulated, in part, by the particular amino acid pathways associated with the response to drought. We will analyze gene expression and amino acid metabolism, as well as accumulation/depletion of soluble phenolics and lignin. Increased understanding of the interactions between hosts and pathogens undergoing climate stress will contribute to the development of integrated management strategies, such as implementing updated monitoring/detection programs, creating predictive models, and furthering our understanding of host resistance mechanisms.

Host range, distribution and the future threat of *Diplodia sapinea* in Turkey

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Diplodia (Sphaeropsis) shoot blight, caused by two *Diplodia* species in the *Sphaeropsis sapinea* complex, *Diplodia sapinea* and *Diplodia scrobiculata*, is one of the most common and important diseases of Pinaceae, primarily of pines, but also of other coniferous hosts throughout the world. In Turkey, epidemic outbreaks of the Diplodia shoot blight caused by *D. sapinea* have been reported usually after droughts, especially in either naturally regenerated or planted *Pinus brutia* stands in Mediterranean regions. *D. sapinea* has also been detected, related initially to reductions in seed production and in some cases mortality of trees, in seed orchards and stands of both native and exotic pine species. While the occurrence and damage caused by the fungus in plantations of *P. taeda*, *P. radiata* and *P. pinaster* was documented, a recent survey in an Istanbul arboretum demonstrated the presence of the disease on numerous additional exotic *Pinus*, including species originating in North America, or East Asia, as well as on native *Pinus* taxa. Preliminary observations from this arboretum contribute to the known host range of the *S. sapinea* complex, and provide insight into the relative susceptibility of *Pinus* spp. against *D. sapinea.*

In Turkey, *D. sapinea* usually occurs sporadically (e.g. after drought) in native *P. brutia* stands; recovery of infected hosts after epidemics has been documented in *P. brutia* stands. The occurrence of pycnidia on cones of *P. brutia*, even during epidemics, was rare. These observations could suggest a co-evolved host pathogen interaction. In contrast, in forest areas where *P. brutia* is grown outisde its natural distribution, the same pathogen may result in tree death, along with abundant production of pycnidia on cones. The origin of *D. sapinea* foudn in Turkey is unknown at present. Analysis of populations using molecular markers will prove useful in determining the origins of Turkish *D. sapinea* populations. Efforts to examine population genetics of *D. sapinea* from infected forests and plantations of *P. brutia*, *P. nigra*, *P. sylvestris*, *P. radiata, P. pinaster* and *P. taeda* remain inconclusive.

Here, we share our current knowledge and experiences derived from research and observations on the occurrence of Diplodia shoot blight over the last 10 years in Turkey. The future threat posed by *D. sapinea* to Turkish forests, in relation to the impacts of climate change is discussed.

Undetected or rare to ubiquitous and damaging: a nonlethal "fungicide" and nursery seedlings in the proliferation of *Diplodia sapinea*

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Although undetected or rare in both forests and forest seedling nurseries of the Great Lakes Region until the mid- to late-1970's, *Diplodia sapinea* has since become ubiquitous and periodically damaging to *Diploxylon* pines in this region. Diplodia shoot blight, canker, and collar rot diseases have been particularly damaging to red pine (*Pinus resinosa*) seedlings in forest tree nurseries and recently established plantations, and natural regeneration in the understories of mature stands. Initial responses to sudden occurrence in nurseries included application of benzimidazole fungicides such as thiophanate-methyl which effectively reduced incidence of these diseases in nurseries. But in spite of treatments, asymptomatic seedlings bearing virulent strains of *Diplodia sapinea* were widely distributed, and ability of this latent pathogen to subsequently proliferate, cause disease, and produce inoculum at newly planted sites has been proven. We have completed *in vitro* dose-response studies of the nonlethal effects of the benzimidazole "fungicide" thiophanate-methyl on *Diplodia sapinea* in both brief and longer exposures. Frequencies of conidial germination were not reduced and mycelial growth was maintained for days, even at the highest concentration tested. In contrast, hyphal morphology was drastically altered. Total hyphal length and farthest extent of hyphae from germinating conidia were less at relatively low concentrations of the chemical, compared to nonamended medium. In addition, normal growth could be resumed when such altered colonies were transferred from amended medium to nonamended medium. The fungistatic, rather than fungicidal, effect of thiophanate-methyl may help explain the asymptomatic persistence of *Diplodia sapinea* on treated nursery seedlings, and the current ubiquitous and periodically damaging occurrence of the pathogen.

Effects of copper and silver nanoparticles on growth in selected species of pathogenic and wood-decay fungi *in vitro.*

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As research indicates a role for metal nanoparticles as fungicides, the work described here addresses the influence of CuNPs and AgNPs on the growth *in vitro* of pathogens causing damping-off, as well as wood-decay fungi; i.e. *Rhizoctonia solani* (2 strains), *Fusarium oxysporum*, *F. redolens* and *Phytophthora cactorum*, along with *Fistulina hepatica*, *Grifola frondosa*, *Meripilus giganteus* and *Sparassis crispa*. Fungi were cultured on three types of medium, i.e. PDA (*R. solani*, *F. oxysporum*, *F. redolens*), V8 (*P. cactorum*) and MEA (wood-decay fungi). Nanoparticles were added to the medium at concentrations of 5, 15, 25 or 35 ppm. Results indicate selective anti-fungal activity of the nanoparticles. While neither nanoparticle affected *P. cactorum* or *S. crispa*, both were found to inhibit growth in *R. solani* (2), *F. redolens* and *M. giganteus*. *R. solani* (1), *F. oxysporum*, *F. hepatica* and *G. frondosa* only showed sensitivity to higher concentrations of AgNPs, albeit with inhibitory impact on mycelial growth found to be greater than with CuNPs. *R. solani* strains differed markedly in responses to both nanoparticles. Overall, the considerable toxicity of AgNPs and CuNPs to certain pathogens and wood-decay fungi indicates possible use in protecting nursery seedlings and safeguarding trees and wood, if with an awareness that certain fungi prove insensitive to both kinds of nanoparticle.

Giant leaf blotch disease (*Pleuroceras pseudoplatani*) identified on new maple hosts (*Acer* spp.)

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In Scotland, large necrotic lesions were observed on the foliage of several maples (*Acer* spp.) which resembled giant leaf blotch disease caused by *Pleuroceras pseudoplatani* (formerly *Gnomonia pseudoplatani*; *Ophiognomia pseudoplatani*) on sycamore maple (*Acer pseudoplatanus*), a common disease in Europe. Other than *A. pseudoplatanus*, no other *Acer* species have previously been reported as hosts for this pathogen. Samples were collected from *Acer rubrum, A. rubrum* var. Somerset, *A. saccharinum, A. negundo, A. macrophyllum,* and *A. circinatum* (all North American origin) and from *A. griseum* (origin: central China), as well as from the known host of *P. pseudoplatani*, *A. pseudoplatanus* for comparison. DNA sequencing of ITS region from necrotic leaf samples confirmed presence of *P. pseudoplatani*. This is the first report of *P. pseudoplatani* causing leaf blotch on *Acer* species other than *A. pseudoplatanus*. Lesions caused by *P. pseudoplatani* on *A. griseum* were smaller than those on the other *Acer* species which may reflect a lower susceptibility to the disease in Asian *Acer* species. The newly reported damage caused by *P. pseudoplatani*, especially on North American *Acer* species, is of particular concern since several species of maple comprise a significant component of the mixed deciduous forests in northern North America, some having high economic value for timber products, syrup production and as ornamental trees in urban landscapes.

Seasonal development of lesions of young common ash in Latvia.

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Dieback of common ash (*Fraxinus excelsior*), which affects trees of different age, is considered as a serious threat for the existence of the species in Europe; the ascomycete *Hymenoscyphus fraxineus* has been considered as the trigger for this process. The symptoms of the dieback on young trees are macroscopic cankers on leaves and leafstalks, wilting of leaves and formation of lesions on shoots, branches, and stems. The lesions are expanding, often resulting in death of the affected parts of trees; nevertheless, not all trees are damaged equally and the development of lesions differs between parts of tree. In this study, we monitored development of lesions in three young stands of ash in Latvia during the vegetation season of 2015. Ten dominant trees with one or two initial phase lesions were selected in each of three studied stands that were affected by dieback.

During the summer, once per month, for each lesion area and location on tree was recorded. In autumn, sample trees were collected and area of all lesions under the bark was measured. From 17 trees, lesion samples were taken for isolation of *H. fraxineus*.

Vital *H. fraxineus* was isolated from 35 % of the studied samples, suggesting involvement of other agents in development of the lesions on young ash trees. During the observation period, the mortality of sampled trees was low, as only one tree died by the end of June, likely due to secondary infection after browsing damage. At the beginning of observation, each tree had one to three lesions. During the observation period, 0.99 ± 0.53 lesion per tree emerged. The accounted lesions were the necrosis on stem (39.8 %, 1.17 ± 0.84 per tree), branches (28.4 %, 0.86 ± 0.29 per tree), as well as necrosis, discoloration or dieback of tops (31.8 %, 0.96 ± 0.46 per tree) (Fig.1). From the studied 87 lesions, 74 % were active, i.e. showed increase in area during the observation period, while the others were latent. The activity of lesions differed among months and stands, suggesting local differences in their development. The development of newly emerged and existing (present before observation period) lesions differed. The newly emerging lesions rapidly increased after appearance, yet they development ceased considerably afterwards. The fastest increase of area of the existing lesion was observed in July, when the air temperature was the highest; yet the development of all lesions ceased in August. The increase of area differed according to the location of lesions. Top lesions showed the fastest expansion (6.0 ± 1.6 cm^2 per lesion per month), while lesions on branches and stems expanded slower (5.6 ± 1.3 and 2.2 ± 0.3 cm^2 per lesion per month, respectively). The area of lesions under the bark was slightly higher (6%) than the visible area, however they were strongly correlated. The development of lesions on branches (48 %) ceased as they reached the node on main axis (reached the stem) of tree.

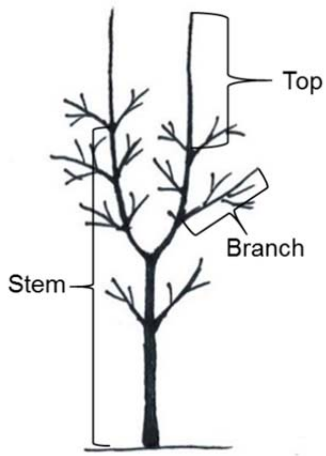

Figure 1. Lesion location on tree.

Prediction of *Hymenoscyphus fraxineus* impact in forests of the Czech Republic

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Ash dieback, caused by the ascomycete *Hymenoscyphus fraxineus*, has been rapidly expanding over large geographical areas in Europe in the last two decades, posing a considerable threat to native ash populations. In this study, we applied regression-based models trained by field data in conjunction with GIS to produce spatial predictions of ash dieback severity in Czech forests to emphasize landscape context in the implementation of effective disease management. Using an extensive dataset of disease extent and silvicultural and environmental characteristics of forest stands, we developed 1) a model of actual ash dieback severity and 2) a model of potential long-term disease risk that quantifies the relative susceptibility of sites to the disease independent of the current silvicultural characteristics. The final predictive maps identified the most endangered regions as fertile lowlands and humid areas bordering Poland and Slovakia. Areas at the lowest risk of damage were concentrated generally in dry areas and in highland and mountain areas in the western part of the country, usually with poor soils on acid bedrock. The maps also showed regions with high local variability in disease risk resulting from the high local variability in topography and silvicultural characteristics. Excluding the current silvicultural characteristics in developing the model, the predictive map enabled an easier identification of regions that differ in their susceptibility to the disease.

Host susceptibility to ash dieback shapes fungal communities of common ash, *Fraxinus excelsior* (L.)

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Common ash populations in Europe are currently threatened by the alien invasive pathogen *Hymenoscyphus fraxineus* that is causing extensive decline and mortality. Ash dieback was first detected in Sweden in 2001 and in few years it spread throughout the whole natural distribution area. In 2010, ash was first Red-listed in Sweden and by 2015 had become 'critically endangered'. The population decline will likely have cascading effects on obligate organisms, including fungal biodiversity associated with ash. We investigated the temporal variation of fungal communities in ash clones as it relates to different host susceptibility to the disease. We hypothesized that fungal communities of ash tissues (leaves, bark, and xylem) would differ among trees differing in their susceptibility to pathogen. We further hypothesized that the fungal communities would reflect a tissue-specific and temporal variation during the growing season. Bark, xylem, and leaves from high (H), intermediate (I) and low (L) susceptible clones were collected at four time points during summer 2015 in two areas in southern Sweden. Total genomic DNA was extracted and samples representing different host susceptibility, tissue types and time points were Illumina sequenced. Generally, fungal communities of leaves differed from those of bark and xylem that grouped closer to each other, however, this distinction was clearer during the beginning and the end of the growing season rather than throughout it. While at the two first sampling dates there was no community differentiation among susceptibility status of host genotypes, by the end of the growing season (during and after peak sporulation period of *H. fraxineus*), fungal community composition showed some differentiation between susceptible and resistant clones. The results provide some support to our initial hypotheses and showed the need of multiple samplings along the season in studies on linkages between fungal communities and susceptibility patterns.

Lonsdalea quercina subsp. _populi_ subsp. nov. a new bacteria canker on hybrid poplars in Hungary

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Different type of hybrid poplars are widely planted in Hungary. A special symptom has been detected in young hybrid poplar stands in the central part of Hungary since 2009. At first, the infested stands were only in the middle part of Hungary, but later in 2016 symptoms were detected all over the country. The extent of the disease varies significantly, sometimes reaching 70-80%, but on average it is 10-30%. First symptoms appeared at the end of spring/early summer period. The bark of the symptomatic trees is vertically cracked, and sticky, white and later brown-coloured foamy mucus bleeds out from the wounds of the stem. Wounds can appear on various heights of the stem, from the root swelling to crown. The length of a necrosis can add up to a few meters. Bark usually becomes discoloured, with brownish-purple or black areas, and with blisters. The bark dies under the mucus and the tissues under the bark also start to rot. White and stinky mucus develops under the bark. Many secondary organisms can colonize on the mucus: fly larvae, nematodes, bacteria, fungi etc. The mucus bleeding stops in the autumn, the dead bark tissue dries out and cracks up. In the next year the margins of the wound heal, but the centre of the wound remains usually uncovered, so the degradation of the timber may start here, which finally leads to the death of the tree.

In 2011 we were able to isolate a bacterium specie, which was abundant in every sample, so presumably the cause the symptoms. Later, we could induce the special symptoms artificially using this bacterial strain. The bacterium belongs to the species *Lonsdalea quercina* (former names: *Brenneria quercina*, *Erwinia quercina*), but has some special differences compared to *L. quercina*. The *Lonsdalea quercina* subsp. *populi* subsp. nov bacteria, which was identified beyond Hungary only in two countries, China (2006) and Spain (2002), but the origin of bacteria has been unknown until now.

Symptoms were observed on the fields only on 3 hybrid poplar clones (*I-214, Koltay, Pannonia*) in Hungary so far, but we could artificially infect more poplar clones in vivo in a nursery garden.

Key words: hybrid poplars, bacteria canker, *Lonsdalea quercina* subsp. *Populi*

Occurrence of *Botryosphaeria corticola* on oaks in the northcentral United States

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In the USA, diseased oaks (*Quercus* species) exhibit a variety of symptoms including tip blight, branch and stem cankers, bleeding cankers, and dieback that traditionally have been attributed to several *Botryosphaeria* species or various related anamorphic fungi. The emergence of *Botryosphaeria corticola* (anamorph: *Diplodia corticola*) as a pathogen of European oaks, and recent reports of this fungus from a number of *Quercus* species in the eastern and western United State prompted reconsideration of isolates in our collection that had been obtained from diseased oaks. Collected in the late 1990's and early 2000's, these isolates had been tentatively identified as *Diplodia* species based on anamorph characteristics. ITS sequence analysis of isolates in our collection indicates that *B. corticola* is common, with most of our Wisconsin isolates of this pathogen originating from northern red oak (*Quercus rubra*). Additional isolates that proved to be *B. corticola* had been collected from black oak (*Q. velutina*) and white oak (*Q. alba*) in Wisconsin. ITS sequence analysis also revealed that our collection includes *Botryosphaeria stevensii* (anamorph: *D. mutila*) from northern red oak in Wisconsin and *Botryosphaeria obtusa* (anamorph: *D. seriata*) from both northern red oak and bur oak (Q. *macrocarpa*) in Wisconsin. Finally, other isolates collected in Washington, D.C. and California in the early 1990's and provided by colleagues were also confirmed to be *B. corticola*. Thus, we can conclude that this oak pathogen has been present in North America, including the northcentral United States, for at least two decades, is well-established, and is transcontinentally distributed. The roles of *B. corticola*, other *Botryosphaeria* species, and influences of other environmental factors in deterioration of oak health in North America merit additional investigation.

Molecular assessment of the latent endophytic pathogen *Gnomoniopsis smithogilvyi* in chestnuts, rootstocks and grafts of six varieties of chestnut trees.

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Gnomoniopsis smithogilvyi is an endophytic fungus, recently identified in Europe and Switzerland, both as the main agent of chestnut brown rot and as a chestnut canker agent. It seems to be the main cause of the high mortality occurring in chestnut nurseries and orchards. The presence of this fungus and of the chestnut canker agent *Cryphonectria parasitica* was searched for in the propagation material of 6 chestnut tree varieties, used in Ticino to restore fruit orchards: *Torcione Nero, Lüina, Giacco, Marrone Lattecaldo, Marrone Michelangelo* and *Bouche de Bétizac* . The plant material was obtained from the Ticino Cantonal Nursery. Sixty root samples, 41 shoot samples from germinated chestnuts and 17 chestnut rootstock samples were analysed, along with 112 samples from 56 rootstock/graft pairs, in order to determine whether the pathogen was transmitted by the rootstock or the graft. DNA extraction was followed by specific amplification primers for *Gnomoniopsis smithogilvyi* and *Cryphonectria parasitica.* It was possible to detect the presence *of G. smithogilvyi* as an endophyte, but *C. parasitica* was never detected. Six of the 60 roots analysed from seed chestnuts were contaminated with *G. smithogilvyi* (in varieties *Lüina, Torcione Nero*, *Marrone Michelangelo*, *Marrone Lattecaldo* and *Bouche de Bétizac), as well as 2 out o*f the 41 shoots from seed chestnuts (*Lüina* and *Bouche de Bétizac*), and 2 out of 17 rootstocks (*Lüina* and *Torcione Nero* varieties). Regarding the 112 samples from 56 rootstock/graft pairs, *G. smithogilvyi* was found in 12% of the analysed rootstocks and 60% of the grafts. These results showed a weak presence of *Gnomoniopsis smithogilvyi* in rootstock propagation material and an important contamination of grafting material in all varieties, confirming the endophytic behavior *G. smithogilvyi.*

Molecular diagnostics of the chestnut canker agents *Gnomoniopsis smithogilvyi* and *Cryphonectria parasitica* in different tissues of *Castanea sativa.*

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Two fungi cause chestnut tree diseases (on *Castanea sativa* species) in Switzerland: *Cryphonectria parasitica*, the endemic chestnut canker agent, and *Gnomoniopsis smithogilvyi*, an endophytic fungus, recently identified in Europe and Switzerland as the main agent of chestnut fruit brown rot, also causing chestnut canker. The latter seems to be the main cause of the high mortality occurring in young chestnut nurseries and orchards. In order to evaluate the presence of these fungi in the plant material used for the multiplication of 6 varieties of chestnut trees in Ticino, specific molecular diagnostic tests were developed for both species. All sequences available in the GenBank for the internal transcript spacer (ITS) of the ribosomal DNA, the elongation factor 1-alpha (EF1a) gene and the beta-tubulin gene (TUBB), were collected for these two fungi. Significant differences between *Gnomoniopsis smithogilvyi* and *Gnomoniopsis spp.*, were sought, as well as between *G. smithogilvyi* and *C. parasitica*. After analysing 164 ITS, 90 EF1a and 45 TUBB sequences, only the TUBB gene sequences showed any significant differences between both species. Specific PCR primers for each species were then designed from the TUBB sequences alignment. *In silico* analyses with the BLAST tool (GenBank) confirmed the strict specificity of these primers. The two primer pairs were then tested with DNA extracted from previously characterised isolates of *G. smithogilvyi* and *C. parasitica* from Ticino, Wallis and Geneva, from roots and stems of germinated chestnuts or leaves of chestnut trees. These tests showed a great robustness and represent an interesting tool to describe the phytosanitary status of propagation material, especially for *G. smithogilvyi*, which is an endophytic fungus.

Pseudomonas putida and _Trichoderma harzianum_ may efficiently control the agent of chestnut brown rot and chestnut canker _Gnomoniopsis smithogilvyi_.

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In vitro challenge tests were carried out on Potato glucose agar (PGA) cultures between *Gnomoniopsis smithogilvyi* and 9 strains of antagonistic fungi: *Trichoderma asperellum, T. atroviride, T. aureoviride, T. hamatum, T. harzianum F1, T. harzianum B05, Aureobasidium pullulans, A. pullulans éch.5* and *Beauveria bassiana*. Similar tests on LBPGA medium were carried out with 7 strains of antagonist bacteria belonging to the following species: *Pseudomonas putida, P. viridiflava, P. graminis, P. xanthomarina, Bradyrhizobium elkanii, Bacillus amyloliquefaciens Ba2* and *B. amyloliquefaciens Ba4*. Two different genotypes of *G. smithogilvyi* from Geneva (GE1) and Ticino (TI1) and were used during these tests. These in vitro challenge tests allowed to select 5 fungal and 3 bacterial strains, which demonstrated a strong inhibitory activity on *G. smithogilvyi*'s growth. The organisms retained for biological control experiments on chestnut scions were: *T. harzianum B05, T. harzianum F1, T. hamatum, T. aureoviride* and *T. asperellum* for fungi; *P. putida, B. amyloliquefaciens Ba4* and *B. amyloliquefaciens Ba2* for bacteria. Batches of 8 chestnut scions (20 cm long; 1 cm diam.) were inoculated with each fungal or bacterial antagonist by soaking them for 48 hours in sterile bacterial or fungal suspensions in water, contained in 2 L sterile Duran bottles. After 48 hours' soaking at room temperature in closed bottles, the scions were transferred individually to an in vitro culture glass tube and placed in a climatic chamber (26°C, Photoperiod: 16 h, RH: 70%) for 3 weeks, in order to allow a uniform endophytic installation of the antagonist. A suspension of *G. smithogilvyi* was then applied to the scions of all modalities and half of the control scions. The developments of fructifications on the bark of the scions, as well as the aspect of the scions, were observed before and after inoculation for a total duration of 6 weeks. If most retained organisms did not maintain their efficiency in vivo, the bacterial strain *P. putida* UASWS0946 and the fungal strain *T. hamatum* UASWS1405 totally inhibited the growth of *G. smithogilvyi* and *C. parasitica.*

Assessment of defoliation on stem infections of birch seedlings with *Phytophthora plurivora*.

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P. plurivora is the most common pathogen of fine roots in many deciduous tree species (such as beech, oak, or ash), often found in forest ecosystems, nurseries, and plantations. Environmental stress usually increases susceptibility to diseases and it is hypothesized that insect stress may predispose birch tree to *P. plurivora* affection. Tree response on the defoliation factor consists of the responses induced by directly damaging effect, the changes following the hierarchy and changes resulting from the physiological and biochemical changes in the leaves.

To evaluate the effect of stress and infection of *Betula pendula* (1-year-old seedlings) artificial removal of all or partial foliage simulated insect damage to plants. Unstressed birch seedlings (non-defoliated) inoculated with *P. plurivora* and ones inoculated only with sterile plug of media served as control variants. *P. plurivora* infection inoculum (registered in NCBI under accession number KX618501) was produced by growing the oomycete on PDA for 7 days in Petri dishes at 25°C under laboratory conditions. One day after defoliation 10 plants were inoculated with *P. plurivora* in each treatment variant. Artificial inoculation at the base of each stem of birch with the pathogen was carried by cutting the bark tissue 5-7 cm above the soil. The level of stem damage was assessed after 70 days by measuring the dimensions of lesions, and the differences among variants evaluated with Kruskal-Wallis Test.

Our findings proved that *B. pendula* is the host of *P. plurivora*. The results of our investigation have shown the statistically significant difference of the lesions width on birch trunks after inoculation (50 and 100%). The small level of defoliation (50%) stimulated resistance of plants while the total defoliation stimulated growth of pathogen.

Understanding the phenology of *Fusarium circinatum* to predict future outbreaks in a changing climate

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The necrotrophic fungus *Fusarium circinatum* is the causal agent of pitch canker disease and is pathogenic to most pine species. High temperature and humidity conditions favor the occurrence of disease outbreaks, which may become more common in the future as global temperatures rise and precipitation regimes grow extreme. Resistance to this disease is possible to achieve, as this trait is quantitative and heritable, albeit relying mainly on breeding and selection of host material. It is therefore important to anticipate how current strains of this pathogen respond to future environmental conditions. For this purpose, we obtained *F. circinatum* isolates from 15 samples collected in Florida and Georgia, and evaluated their growth, sporulation, and germination in culture at 25, 28, and 31^{o}C. We also conducted pathogenicity tests at the USDA Resistance Screening Center (RSC) in Asheville, NC. We observed significant differences among isolates at different culture temperatures, as well as variations in pathogenicity, resulting in the RSC adopting the most virulent isolates for their current screening tests. We also conducted a survey of *F. circinatum* spore production throughout the 2016 growing season at three Florida locations. We placed custom-made spore traps within affected pine stands and recorded weather data at these locations and monitored spore production weekly. The presence of *F. circinatum* spores were determined and quantified by quantitative PCR using *F. circinatum*-specific primers, with an average of 18 and 114 pg among locations. Integration of weather data and a second installment of this experiment for 2017 will allow the development of epidemiological models that may predict pitch canker outbreaks under future environmental conditions.

Factors affecting the distribution of Pine Pitch Canker in Northern Spain

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Fusarium circinatum (teleomorph=*Gibberella circinata*) is the causal agent of Pine pitch canker, an important disease that is causing serious economical, ecological and social impacts in various parts of the world. The disease attacks several pine species and Douglas firs. In Spain it has been recorded for the first time in 1995 in nurseries in Galicia where it infected *P. radiata* and *P. halepensis*. In 1998 pitch canker was reported in north-west of Spain in the Basque Country and later in Asturias. Currently *Pinus radiata* is the pine species that was most affected by the disease in Spain. The main symptom are large resinous cankers on trunks and branches of pine trees. Pitch canker can also reduce seed germination, and cause seedling blight and canopy dieback. Several environmental factors may contribute to pitch canker severity such as drought, physical damage or other environmental stresses. In this study a total of 50 sites were surveyed in the Cantabria region, North of Spain, in order to evaluate the environmental and biotic elements that influences the epidemiology of pitch canker. We used univariate and multivariate statistics to evaluate the importance of local (e.g. trees height, soil) and landscape (e.g. distance to the sea, distance to the nearest infected stand) scales. The results of the statistical analysis showed the relationship among edaphic and stationary factors of the sites and the severity of the disease. The results of this study should be taken into account for future management of pine plantations.

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