

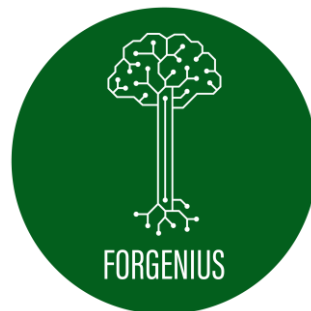
Integrative Diversity of Forest Ecosystems

EVOLTREE-FORGENIUS Conference

18 – 21 November 2025

CSIC, Madrid, Spain

Book of Abstracts



Short program

Time (CET)	Tuesday 18.10.2025	Wednesday 19.10.2025	Thursday 20.10.2025	Friday 21.10.2025
09:00-13:00	FORGENIUS ExCom General Assembly	Session 2: Forest Adaptation: Improving Resilience to Biotic and Abiotic Pressures	Session 3: Navigating Multiple Global Change Pressures: The Role of Phenotypic Variability	Session 5: Prioritising forest conservation through genetic diversity
13:00-14:00	Lunch break	Lunch break	Lunch break	Lunch break
	Welcome			
14:00-18:00	Session 1: New tools for science to reach practise	Field trip	Session 4: Breeding for Resilience: Integrating Novel Phenotyping & Genomics for Urgent Adaptive Solutions	EVOLTREE Governing board
18:00-19:00	Poster Session S1+S2		Poster Session S3+S4+S5	
		19:00-22:00 Social dinner		

Session 1 - New Tools for Science to Reach practice

Tuesday 18 November 13:30-17:00

Chair: Mari Rusanen, Natural Resources Institute Finland (Luke), Helsinki, Finland

Oral presentations

- | | |
|-------|--|
| 14:30 | Keynote - David O'Brien
Bridging the gaps between science, policy and practice |
| 15:15 | Michele Bozzano
The European Information System on Forest Genetic Resources (EUFGIS): A transnational tool for genetic conservation and policy support |
| 15:45 | van Moorsel Sofia
Using a planted tree biodiversity experiment to validate remote sensing of tree species |
| 16:00 | Coffee break |
| 16:30 | Neophytou Charalambos
Assisted Gene Flow for climate-smart forests: the gap between research and policy in Europe |
| 16:45 | Chludil David
Pollen-based assisted migration |
| 17:00 | Rellstab Christian
Lifting borders: The potential role of hybridization and adaptive introgression in drought resilience of mixed stands of European white oaks (<i>Quercus</i> spp.) |
| 17:15 | Blanc-Jolivet Céline
How can genomic data be useful for the timber market? |
| 17:30 | Gugerli Felix
Multifaceted tools for reaching out to conservation practitioners through teaching, infographics, and visualization of data on genetic diversity |
| 17:45 | Flash Poster session |

Keynote Session 1. Bridging the gaps between science, policy and practice

David O'Brien

Seldom has there been greater need for evidence-based policy and practice. Science has many of the answers to the current climate, biodiversity and societal crises. But we face a time of increased scepticism towards experts and a push back against science from many politicians, influencers and interest groups. This resistance often stems from a separation between scientists, policy-makers and practitioners or a perceived elitism. Practitioners can also be understandably reluctant to change established ways of working or to be told what to do on the land they manage.

In principle, integrating conservation genetics into policy and practice should be particularly challenging. We use a lot of jargon, and the concepts may seem theoretical and impractical to non-specialists. Many of the terms we use have links to quite polarising concepts like Genetically Modified Organisms and benefit sharing of genetic resources. In Europe, we have also seen a reaction against forestry conservation in the resistance to the EU Nature Restoration Law which led to significant modification of the final Regulations.

However, there are grounds for hope. David will introduce some successful, and some unsuccessful, attempts to bridge these gaps and move towards a nature-positive future for Europe's forests that incorporates genetic knowledge. He will draw examples from national policy through to individual sites to explore whether approaches can be made to work at multiple scales and will discuss how we measure success and learn from our experience.

S1.01. The European Information System on Forest Genetic Resources (EUFGIS): A transnational tool for genetic conservation and policy support

Michele Bozzano, Valentina Barbiero, Egbert Beuker, Simone Mori, Mari Rusanen, Ivan Scotti, Milko Skofic, Marjana Westergren

The European Information System on Forest Genetic Resources (EUFGIS), established in 2010 in the framework of the EUFORGEN Programme, is the only transnational information system dedicated to forest genetic resources (FGR) in Europe. It provides harmonised data on more than 3,500 Genetic Conservation Units (GCUs) representing over 100 tree species across 35 European countries. All GCUs included in EUFGIS comply with common pan-European minimum requirements for dynamic conservation, ensuring the comparability and reliability of information.

Since its inception, EUFGIS has become a cornerstone for monitoring and reporting on FGR conservation. Its data directly support Indicator 4.6 of the Forest Europe process on sustainable forest management and have been used in major assessments such as the State of Europe's Forests and the global State of the World's FGR. Beyond policy reporting, EUFGIS serves as a reference platform for conservation planning and the management of GCU networks.

From 2021, the EU-funded project FORGENIUS has been upgrading EUFGIS by developing a new interface, adopting modern technologies, and integrating complementary datasets. These include linkages with pan-European climate and environmental databases, the use of remote sensing, and the incorporation of genotype and phenotype data for 23 species. The upgraded system will allow more precise and comprehensive characterisation of GCUs, reinforcing Europe's capacity to conserve forest genetic diversity under changing environmental conditions.

In November 2025 EUFGIS will be made publicly available for conservationists, researchers, policy makers and all interested parties. We will present EUFGIS and its key functionalities.

S1.02. Using a planted tree biodiversity experiment to validate remote sensing of tree species

van Moorsel Sofia, Niederberger Michael, Schmid Bernhard, Damm - Reiser Alexander, Schuman Meredith

Forest biodiversity underpins ecosystem functioning but is declining rapidly. Effective conservation requires knowledge of which species are changing, where, and how fast. However, field-based monitoring of biodiversity and tree species composition is often sparse due to logistical constraints. Remote sensing offers a promising alternative, enabling repeated, spatially contiguous data collection across large areas. Yet, it remains unclear how accurately tree species can be identified from remote sensing data. We used two forest biodiversity experiments established 2002 in Germany (BIOTREE Kaltenborn and Bechstedt) to assess: (1) how well co-planted tree species can be identified using airborne imaging spectroscopy and (2) how tree species identification and predictions are influenced by tree species richness and composition. We acquired airborne imaging spectroscopy data at 1 m spatial resolution during peak growing season and applied discriminant analysis (DA) using reflectance values for 589 wavelengths between 400–2400 nm. In Kaltenborn, using nine principal components, we reliably distinguished conifers from angiosperms and correctly identified two species within each group with >77% accuracy. However, at Bechstedt, with 16 species, identification success dropped to around 50% using 59 principal components.

Our findings show that airborne imaging spectroscopy can effectively distinguish tree species in controlled, low-diversity settings. However, in more species-rich forests, identification accuracy decreases strongly. This suggests that while remote sensing is a powerful tool for forest biodiversity monitoring, its performance depends strongly on local species richness and spectral distinctiveness, highlighting the need to tailor approaches to forest complexity.

S1.03. Assisted Gene Flow for climate-smart forests: the gap between research and policy in Europe

Neophytou Charalambos, Blyth Colette, Pelin Acar, Bilela-Eckert Silvija, Jansen Simon, Kaya Zeki, Leigh Deborah M., Littmann Lars, Rellstab Christian, Rentschler Felix, Semizer-Cuming Devrim, Tourvas Nikolaos, Aitken Sally, Liesebach Mirko, Lowe Andrew, Aravanopoulos Filippou A

Experimental evidence suggests that the adaptation of native forest trees is increasingly lagging behind the current pace of climate change. Assisted Gene Flow (AGF) offers a strategy to enhance species' resilience. It is defined as the transfer of forest reproductive material (FRM) from areas matching a plantation site's anticipated future climate with both the seed origin and plantation area being located within the species' distribution range. Here, we ask i) to what extent research results are available that can inform AGF strategies and ii) whether current FRM transfer guidelines actively promote or even permit AGF implementation. We first conducted a systematic literature review yielding around 400 studies explicitly addressing AGF in forest trees. The methods used ranged from quantitative genetic approaches (e.g. response and transfer functions) to molecular genetics and genomics (e.g. genomic offset). Second, we examined FRM transfer guidelines across European countries sharing a common regulatory framework and found that provenance recommendations remain predominantly based on the 'local is best' paradigm. Despite substantial research, AGF is seldom incorporated into national or regional guidelines. Recent revisions of some national recommendations reflect only limited integration of AGF strategies, suggesting a persistent gap between research and practice. This likely stems from perceived risks of non-local FRM and practical obstacles, especially for imported FRM. However, given the risk of non-acting, policy adjustments are needed to address climate-change-driven needs. Current research results provide an important foundation for adapting current guidelines in order to promote the adaptive capacity of forest tree species, particularly in Europe.

S1.04. Pollen-based assisted migration

Chludil David, Lstibůrek Milan

Forests worldwide face increasing pressures from climate change, pests, and emerging diseases, underscoring the urgent need for adaptation strategies that are both scientifically sound and practically applicable. Conventional assisted migration (AM) with seeds or seedlings has been proposed to improve forest resilience, yet its use in many regions is constrained by regulations designed to conserve the unique genetic characteristics of local provenances, prevent invasiveness, and reduce phytosanitary risks. These regulations, together with long-standing forestry traditions, reflect legitimate concerns that must be addressed rather than dismissed.

We propose pollen-assisted migration as a complementary strategy that aligns with these concerns while enhancing the adaptive potential of forests. The approach builds on existing seed orchard infrastructure in source regions, supplying pollen that is then used in target-region orchards to hybridize with local genotypes. This process preserves a proportion of local adaptation in target regions, while also minimizing phytosanitary risks. Computer simulations focusing solely on adaptive response to climate variables showed that pollen AM could be an effective strategy under climate change, even without considering its additional practical advantages.

Pollen-assisted migration builds on current forestry practices while adding new possibilities for adapting to climate change. Because it uses familiar infrastructure and respects many of the principles behind existing regulations, it may be easier to include in ongoing management activities and future policy development. This approach provides a practical way to apply scientific knowledge directly in forest management and to support adaptation in a changing environment.

S1.05. Lifting borders: The potential role of hybridization and adaptive introgression in drought resilience of mixed stands of European white oaks (*Quercus* spp.)

Rellstab Christian, Reutimann Oliver, Zimmermann Felix, Baltensweiler Andri, Dauphin Benjamin, Walthert Lorenz, Olofsson Jill K., Gugerli Felix, Kremer Antoine

The current pace of climate change poses a threat to long-lived forest trees with long generation times, as they can only adapt slowly to environmental changes. Hybridization and introgression could increase the resilience to a warmer and drier climate through the exchange of beneficial gene variants. Here, we estimated levels of genetic admixture in three European white oak species: *Quercus robur*, *Q. petraea* and *Q. pubescens*. These ecologically, economically, and culturally important tree species generally occupy different ecological niches but are often found in sympatry and frequently hybridize. Using a newly developed diagnostic SNP set for accurate taxonomic assignment, we show that the three oak species, especially *Q. petraea* and *Q. pubescens*, exhibit extensive hybridization and backcrossing, resulting in a fine-scale taxonomic gradient among and within forest stands. Despite high levels of admixture, the three taxa have largely retained their species integrity. We then demonstrate that topography and soil properties are important factors for the taxonomic composition of trees and populations on regional and local scales. Even within a single stand, water availability and soil pH coincide with the spatial distribution of pure and admixed individuals. Moreover, our study suggests that admixture may play an important role in adaptation to more severe and frequent droughts under climate change through increased genetic diversity and adaptive introgression. In the future, conservation and management strategies for European white oaks should thus prioritize the entire species complex rather than focusing on taxonomic entities.

S1.06. How can genomic data be useful for the timber market?

Blanc-Jolivet Céline, Müller Niels, Schröder Hilke

Sustainability and legality of timber products is a growing concern, as forests and especially timber species play an important role in the mitigation of climate change. In situ conservation of genetic diversity of forest tree species is the first step to secure their adaptability and use in future breeding programs. However, the success of such strategies strongly relies on the sustainable management of forests. Illegal logging is the most important human threat to forest ecosystems, and not only in tropical areas. In Europe, the new Deforestation Regulation (EUDR), which will soon replace the EU Timber Regulation (EUTR), aims to prevent forest degradation caused by the expansion of agricultural activities and timber production. The competent authorities of each country are responsible for the enforcement of the EUTR/EUDR and conduct controls. Genetic testing is the most reliable technology to check both the geographical origin and species identity of timber products, but relies on species-specific large-scale and extensive reference data. Genomic resources from geolocalized autochthonous specimens are a pre-requisite for the development of genetic tracking methods and data from metabarcoding or phylogenetic studies provides important resources for species identification. We will show with examples from plastidial genome sequences and SNP array data in *Picea* sp. and WGS studies in *Fagus sylvatica* how scientific data can be valued through routine testing of timber products. Further, such NGS-based methods open the possibility to work more efficiently on mixed products such as wood pellets. Law enforcement and cutting-edge science can therefore benefit from each other.

S1.07. Multifaceted tools for reaching out to conservation practitioners through teaching, infographics, and visualization of data on genetic diversity

Gugerli Felix, Weber Alexandra A.-T., Feulner Philine G.D., Fischer Martin C., Grossen Christine, Naciri Yamama, Paczesniak Dorota, Pärli Rea M., Reutimann Oliver, Richman Sarah, Tschan Jasmine N., Widmer Alex, Buser Corine N.

To promote the recognition and implementation of genetic considerations in biodiversity conservation, it is essential to exchange with key practitioners using targeted communication tools. In a joint effort among four research institutions across Switzerland, (i) we developed a teaching course emphasizing the importance of genetic diversity, addressing fundamental concepts of molecular markers, the meaning and relevance of essential biodiversity variables (EBVs) for genetic composition, and best practices for transdisciplinary project planning. We provided introductory lectures, demonstrated case studies, and held group discussions to gradually guide participants towards interpreting genetic estimates and indicator values in the context of their biological background. In parallel to the three main course topics, (ii) we developed a set of infographics that summarize and illustrate conservation genetics concepts; this documentation can be openly accessed and used for manyfold purposes. Importantly, the course and the infographics are provided in different national languages, which is essential in a multi-linguistic environment like Switzerland. As a complementary long-term service, (iii) we are developing a national database on within-population genetic diversity data of wild species in Switzerland, GenDiB (<https://gendib.wsl.ch>). To this end, an interactive map gives an overview of hitherto available genetic data across Switzerland, with pertinent information on the respective study, scientific article, and data source when available. Soon, genetic datasets will be available for open-access download. Taken together, our multifaceted toolbox should serve to better value genetic diversity as a key component of biodiversity that needs to be integrated in conservation efforts a regional, national, and global levels.

Poster presentations

S1.P1. Assessing drought resilience of selected European forest plots in a future climate conditions using a hydraulic process-based modelling approach

Flash presentation

Oblišar Gal, Martin-StPaul Nicolas, Druel Arsen, De Cáceres Miquel, Marinšek Aleksander, Vilhar Urša, Mencuccini Maurizio, Delzon Sylvain, Cochard Hervé, Torres-Ruiz José, Eler Klemen

Forests play a crucial role in promoting global biological evolution and community succession, and maintain a delicate ecological balance at the global scale. The persistence and functionality of forests are highly dependent on their resilience, defined as their ability to withstand and recover from environmental disturbances. Increased evaporative demand and more frequent and prolonged dry spells, combined with rising air temperatures, provide a strong basis that conditions may worsen, and droughts are likely to become more frequent and intense in the future. To study the effects of drought stress on forest ecosystems, modeling becomes an indispensable tool. We will use trait-based plant hydraulic models such as SurEau and Sperry which hold great potential for studying the responses of individual trees or forest stands to drought. These models simulate the movement of water through the plant from roots to leaves, predict water flow and storage in different plant compartments, predicting the risk of hydraulic failure, which is a major cause of mortality under climate change. By combining simulations of future climate conditions with intraspecific trait variability, we aim to estimate drought resilience in selected European forest plots. Model parameters such as hydraulic traits, ecophysiological data and stand properties is measured on forest plots from a set of EUFORGEN (European Forest Genetic Resources Programme) genome conservation units of European beech (*Fagus sylvatica*), Scots pine (*Pinus sylvestris*), and maritime pine (*Pinus pinaster*). We anticipate that accounting for trait variability will alter estimates of the risk of hydraulic failure under climate change.

S1.P2. Spruce trees resistant to *Ips typographus* grow slowly and contain high sucrose and neoabietic acid in their constitutive defences

Flash presentation

Korolyova Natalie, Arne Buechling, Ishangulyyeva Guncha, Marešová Jana, Erbilgin Nadir, Mehdi Younessi Hamzekhanlu, Basheer Ahammed KK, Jakuš Rastislav

Climate change is increasingly exacerbating bark beetle outbreaks, posing a critical threat to the persistence of *Picea abies*. Despite widespread mortality, a small subset of individuals, “Last Trees Standing” (LTS), survive such disturbances, typically representing less than 1% of the population. Our previous studies investigated spruce survival drivers using remote sensing, genomics, and phenolic profiling via HPLC. In this study, we employed an interdisciplinary approach integrating dendroecology and analytical chemistry to identify physiological and ecological resistance traits during a prolonged *Ips typographus* outbreak in Central European protected forests. Using dendroecological data from 229 trees (110 LTS, 119 reference), we identified site-specific disturbance years and reconstructed pre-outbreak growth patterns. LTS trees exhibited significantly slower long-term radial growth, suggesting a trade-off between growth and defence, with survival probability increasing non-linearly among slower-growing individuals. Of 56 terpenes analysed via GC-MS in 80 trees (39 LTS, 41 reference individuals), neoabietic acid in uninoculated phloem was the strongest survival predictor, with a threshold-dependent effect. Methyl jasmonate application induced a 2- to 13-fold increase in terpene levels. In uninoculated phloem, LTS trees had elevated neoabietic acid, α -terpinolene, and γ -terpinene, while reference trees had more sabinene hydrate, methyl dehydroabietate, and dehydroabietal. Dehydroabietal was also lower in inoculated phloem of survivors. LTS individuals had significantly higher sucrose concentrations (positively and non-linearly linked to survival), while reference trees had more soluble starch (negatively linked). These findings provide key insights into traits promoting tree survival and offer valuable guidance for adaptive forest management and breeding strategies under a changing climate.

S1.P3. Implementing assisted migration (AM) at the example of fir species (*Abies* spp.) in a pilot region in south-western Germany

Flash presentation

Bilela-Eckert Silvija, Neophytou Charalambos, Badalamenti Lola, Blond Aurélien, Boulanger Vincent, De Ro Annelore, D'hondt Bram, Doucet Diane, Dounavi Aikaterini, Dufour Sophie, Olivier Fabes, Manuel Karopka, Maxime Lambinet, Olivier Leflon, Bénédicte Leguerroue, David Mathy, Brigitte Musch, An Vanden Broeck, Hannes Wilms, Nicolas Dassonville

The EU-funded Interreg NWE project MigFoRest (Assisted Migration to increase Forest resilience in North-West Europe) is an integrated effort bringing together private and public forest owners and practitioners to strengthen the resilience of the forests of Northwest Europe (NWE) in close cooperation with forestry research institutes. The project pursues a joint strategy to implement assisted migration (AM) for 20 tree species in three priority categories at the NWE level. To this end, the concept of a functional complex network will be implemented in a cross-border approach in pilot areas of the three partner countries (Belgium, Germany, and France). The aim of the project is to increase genetic diversity of the native populations by introducing highly diverse provenances from the specifically selected origins. *Abies* spp. is chosen as a genus of interest in the Swabian-Franconian Plateau, a German highland region chosen as pilot territory. There silver fir is particularly prone to climate change due to the limited altitude (less than 600 m). The introduction of climate-resilient provenances of silver fir and other fir species aims to increase the adaptive capacity of the genus in this area. An accompanying genetic analysis is employed to ensure a high genetic diversity of the used forest reproductive material. Additionally, the project will produce technical guidelines for policy makers, public authorities and associations of public and private forest owners and managers for implementing AM at their territory scale, including practical recommendations about genetic material selection.

S1.P4. A genetic database as a tool to provide proof of origin of autochthonous forest reproductive material

Flash presentation

De Ro Annelore, Wilms Hannes, Verschaeve Leen, Van Breusegem An, Neyrinck Sabrina, Vander Mijnsbrugge Kristine, Vanden Broeck An

The EU Forest Strategy for 2030 focusses on climate-resilient forest management. Planting the most suitable tree species and provenances is a key part of this approach. Moreover, a broad genetic base increases the likelihood that trees can adapt to future climate conditions. To ensure the origin and quality of forest reproductive material (FRM) of autochthonous Flemish origin, INBO has established a DNA database that enables traceability of the FRM throughout the entire production chain. Although some European countries already use molecular techniques to verify the origin of FRM, this is the first traceability system that is built on a comprehensive DNA database. The DNA database currently includes the genetic profiles of all mother trees in the Flemish autochthonous seed orchards of seven tree and shrub species: *Populus tremula*, *Corylus avellana*, *Frangula alnus*, *Ulmus laevis*, *Sorbus aucuparia*, *Carpinus betulus*, and *Tilia platyphyllos*. The genetic profiles were created using species-specific microsatellite markers. New genetic markers were developed for *Carpinus betulus* and *Ulmus laevis*. The DNA database was primarily made to verify the origin of forest reproductive material sold by nurseries through parentage analysis. But the DNA database has numerous other applications. By genetically mapping the seed orchards, we gained more insight into their genetic quality, such as genetic diversity and purity. The DNA database thus not only guarantees the origin of forest reproductive material but also serves as a tool for managing seed orchards and for the ex situ conservation of genetic diversity.

S1.P5. Genomics-driven monitoring for genetic conservation and breeding in forest trees

Flash presentation

Jill Hamilton

In a rapidly changing environment, maintenance of genetic variation within and across populations is increasingly important for conservation and restoration. A species' evolutionary potential is tightly linked to both the amount and distribution of genetic variation available through which natural selection may act. While there is growing emphasis on the importance of genetics in conservation, there is a need to pair genomic monitoring with range wide ex situ conservation collections as a foundation for breeding and restoration programs. Here, I will discuss the value of combining population genomic monitoring with conservation collections to understand species' evolutionary history, and the role different evolutionary mechanisms may play influencing neutral and adaptive processes across space and time using *Fraxinus* species as a case study. The decimation of eastern hardwood forests in North America in response to the Emerald Ash Borer and its continued expansion west emphasizes the need for proactive conservation of existing genetic resources and development of new genomic resources to pair with future breeding and restoration programs. I will discuss the need to safeguard biodiversity for species at risk, proposing genomic screening of seed and living collections for use in restoration, genecology, seed orchard establishment, and breeding program development.

S1.P6. Integrating science to public education curriculum: work done in Forgenius communication activities

Petteri Vanninen, Eero Kovanen, Egbert Beuker, Mervi Hiltunen, Katja Kavčič Sonnenschein, Urša Vilhar, Katja Winkler, Simona Miklavc-Pintaric, Saara Nissinen

To bring science closer to children aged 10–12, we used the connected learning pedagogy. This invites schools to choose common natural phenomena—like biodiversity loss—and explore them from both local and global perspectives. By sharing their approaches, schools inspire one another, and collaboration between pupils, teachers, and researchers sparks creativity, strengthens children’s grasp of the topic.

An online workshop was organized to introduce to FORGENIUS experts (GIS, LUKE, INRA, EFI, BFW) the connected learning method and to identify the learning phenomena in question for schools. Teachers were invited to this first workshop in order to ensure close alignment with the school curricula. The pedagogical support, planning and organization of the workshop was based on the research-based collaboration between Savonlinna schools and the teacher education unit at the University of Eastern Finland. In addition, the PlantNet application was presented by an expert from the Faculty of Education at the University of Ljubljana as a tested tool for this research-based learning project.

The start of activities was delayed by the COVID-19 pandemic. The learning project was finally implemented over a school year in Finland and Slovenia, involving national research institutes (Luke and GIS) and local primary schools. Teachers together with their classes selected the common learning task from the list of proposed phenomena and jointly tested the PlantNet application for observing spring phenomena in Finland and Slovenia. Researchers from the Forgenius project visited the schools and answered questions from pupils and teachers. Class excursions to local nature sites/study locations (Luke, GIS) representing the selected phenomenon were part of the learning process.

The pilot project was closely monitored and documented. It has since been opened up for broader application and possible European upscaling (<https://forgeniusforschools.metsabiotalous.fi/>). In addition, the cooperation will continue in a new project under Erasmus+ program “Forest for future - Science and environmental education for primary schools in Finland and Slovenia”, starting in 2026.

S1.P7. Forest Genetic Resources conservation strategy in Spain boosted by the FORGENIUS project.

Notivol Eduardo, Auñon Francisco, Callejas Marta, Chambel Regina, Barba Diana, Olsson Sanna, Alia Ricardo, Pérez Felipe, Grivet Delphine

In this presentation, the general context of the conservation of forest genetic resources in Spain is outlined. After a brief description of the country's forest characteristics, the national regulatory framework is addressed (including various aspects such as the national strategy, the plan, and the actions contemplated), the state of conservation of FGR, the methodologies and results of phenotypic, genetic, and physiological characterization to date, as well as the dissemination of actions. Special emphasis is placed on the role and methodologies implemented in the FORGENIUS project for the implementation of FGR conservation in Spain.

Session 2 - Forest Adaptation: Improving Resilience to Biotic and Abiotic Pressures

Wednesday 19 November 09:00-13:00

Chair: Marcela van Loo, Austrian Research Centre for Forests, Vienna, Austria

Oral presentations

- 9:00 **Keynote - Silvia Matesanz**
Phenotypic plasticity and adaptive evolution in Mediterranean gypsum
endemics: insights into climate change response
- 09:45 **Stejskal Jan**
Hyperspectral detection of genetic variation in Scots pine (*Pinus sylvestris*
L.): implications for forest resilience across environmental gradients
- 10:00 **Muhammad Ahmad**
Natural variation in drought sensitivity and associated metabolic
adaptations in European black pine (*Pinus nigra* Arnold s.l.): A step toward
integrated provenance selection
- 10:15 **Rezaie Negar**
Does intra-population genetic variability enhance productivity and drought
resistance in silver fir?
- 10:30 **Ramires Marcelo**
Mimicking bark beetle attacks: field and phytotron insights into Norway
spruce defense responses
- 10:45 Coffee break
- 11:15 **González-Martínez Santiago**
Adaptation to Climate in European Conifers: Lessons Learned
- 11:30 **David-Schwartz Rakefet**
Leveraging interspecific hybridization for drought adaptation in forest trees
- 11:45 **Garibay-Hernández Adriana**
Analysis of in situ performance of the European Beech (*Fagus sylvatica* L.)
through the lens of leaf proteomics
- 12:00 **Budde Katharina**
Loss of genetic diversity and signs of selection in response to ash dieback in
natural populations of *Fraxinus excelsior*
- 12:15 **Kremer Antoine - online**
Temporal genetic changes and evolutionary rates at contemporary
timeframes in oaks
- 12:30 **Flash Poster session**

Keynote Session 2. Phenotypic plasticity and adaptive evolution in Mediterranean gypsum endemics: insights into climate change response

Silvia Matesanz

Phenotypic plasticity and adaptive evolution in Mediterranean gypsum endemics: insights into climate change response

Climate change is a major threat to plant populations, especially in the Mediterranean. For gypsophiles—species restricted to gypsum soils—migration is a limited response due to specific edaphic needs, low dispersal, and fragmented distributions. Consequently, in situ processes like adaptive evolution and phenotypic plasticity are essential for their persistence. Future adaptive responses to climate change depend not only on historical evolutionary dynamics but also on the strength of selection and the evolutionary potential of functional traits and their plasticity. Our research investigates: i) the evolutionary potential of key functional traits and their plasticity; ii) whether past selection has shaped population phenotypes and plasticity patterns; and iii) the ability of gypsophiles to express adaptive transgenerational plasticity to drought. Using a quantitative genetics approach, our research shows that gypsophiles exhibit adaptive phenotypic plasticity to drought, sometimes aligned with selection patterns. High genetic variation for plasticity within populations supports their capacity to further evolve adaptive plasticity in response to climate change. This plasticity may have contributed to maintaining high genetic variation, enabling adaptation to contrasting climatic conditions. Populations of several Iberian gypsophiles display similar drought responses, likely shaped by natural selection in heterogeneous environments, and suggesting independent evolution of functional traits and their plasticity. Furthermore, gypsophiles express adaptive transgenerational plasticity to drought, though its extent varies among species. Our findings emphasize that, together, phenotypic plasticity and adaptive evolution (both past and future) play a key role in shaping population responses to changing conditions, particularly in stressful and spatially constrained habitats like gypsum outcrops.

S2.O1. Hyperspectral Detection of Genetic Variation in Scots Pine (*Pinus sylvestris* L.): Implications for Forest Resilience Across Environmental Gradients

Stejskal Jan, Provazník Daniel, Neuwirthová Eva, Korecký Jiří, Čepl Jaroslav, Červená Lucie, Lhotáková Zuzana

Scots pine (*Pinus sylvestris* L.) is a foundation species in European forest ecosystems, where its resilience to increasing biotic and abiotic stresses is critical under changing climate conditions. Yet, the physiological basis of its adaptive potential remains poorly characterized. Understanding intraspecific variation in key functional traits is essential for identifying genotypes capable of coping with environmental pressures. In this study, we combined hyperspectral phenotyping with genomic data to assess needle functional traits (NFTs) linked to foliar structure, water regulation, and pigment composition—traits closely associated with stress tolerance. Measurements were conducted across two growing seasons in clonal seed orchards using high-resolution hyperspectral sensing at needle and canopy levels, integrated with genotyping via a newly developed 50K SNP array. Linear mixed models revealed considerable genetic variation, with heritability estimates reaching 0.38 for structural and water-related traits, and up to 0.29 for pigment ratios such as carotenoid-to-total-chlorophyll—an indicator of oxidative stress response. Significant genetic correlations between stress-relevant NFTs and canopy-level reflectance highlight the potential of spectral data as a scalable proxy for selecting resilient genotypes. Low genotype-by-environment interactions and stable clonal performance across years further support the robustness of these traits for long-term adaptive breeding. Our findings underscore the utility of hyperspectral phenotyping and NFT-based selection for accelerating the identification of Scots pine genotypes with enhanced resilience to drought, heat, and pathogen pressures—offering a powerful strategy to support forest adaptation in the face of intensifying environmental challenges.

S2.O2. Natural variation in drought sensitivity and associated metabolic adaptations in European black pine (*Pinus nigra* Arnold s.l.): A step toward integrated provenance selection

Muhammad Ahmad, Almuth Hammerbacher, Clara Priemer, Albert Ciceu, Marta Karolak, Sonja Mader, Sanna Olsson, Johann Schinnerl, Selina Schöndorfer, Sebastian Seitner, Jakub Jez, Andrea Ganthaler, Stefan Mayr, Dominik K. Großkinsky, Stefanie Wienkoop, Carlos Trujillo-Moya, Marcela van Loo

European black pine is an ecologically and economically important tree species. Due to its presumed drought tolerance, it has been proposed as a candidate for assisted migration in Central European forestry. However, little is known about natural variation in drought sensitivity and the associated metabolic adaptations to drought at the seedling stage in this species. We applied automated high-throughput phenotyping to assess natural variation in drought sensitivity across nine black pine populations and integrated targeted and untargeted metabolomics to investigate associated metabolic signatures in a subset of contrasting populations. Our results revealed significant variation in drought sensitivity among populations. Climate–trait associations showed weak empirical trends, providing limited support for local adaptation. To investigate the metabolic basis of this variation, we selected four provenances (two drought-tolerant, two drought-sensitive). Targeted analysis confirmed the involvement of known drought-related metabolites, while untargeted metabolomics revealed clear metabolic separation between tolerant and sensitive populations, indicating distinct drought response strategies. Overall, our results highlight the potential of combining high-throughput phenotyping and metabolomics as a foundation for integrated provenance selection. The identified metabolic markers offer promising candidates for future screening and targeted selection of drought-tolerant material to support adaptive forest management and climate-resilient reforestation strategies.

S2.03. Does Intra-Population Genetic Variability Enhance Productivity and Drought Resistance in Silver Fir?

Rezaie Negar, D'Onofrio Gianluca, Piotti Andrea, Liberati Dario, d'Angelis Paolo, Pagliarani Sofia, Avanzi Camilla, D'Andrea Ettore

Consecutive drought is a major driver of regeneration failure in forest ecosystems, particularly due to its impact on seedling survival in the early establishment phase. Although the ecophysiological responses of plants to drought stress are relatively well characterized, the extent to which these responses are genetically determined remains little known. This study assessed the drought response of one-year-old seedlings from four populations in the Tuscan Apennines National Park (La Nuda, Lago Verde, Orsaro and Ventasso), grown under controlled hydroponic conditions. Two levels of water stress were applied to assess morphological, physiological, and growth-related traits. The hydroponic system allowed detailed monitoring of root dynamics and structure, key factors influencing field establishment. Over a growing seasons, biometric parameters were recorded, with particular attention to fine root development. La Nuda population consistently showed superior performance in organ development and biomass allocation, with a significantly higher root to shoot ratio, potentially indicating a drought-adaptive strategy. Morphological differences between populations suggest a genetic component, as populations with greater genetic variability demonstrated higher overall productivity. Root growth peaked early in the season (up to June), followed by a stabilization phase. Mild drought stress had limited impact on photosynthetic activity; however, intense drought led to an irreversible decline across all populations. Post-stress physiological performance did not differ significantly between populations, suggesting common physiological thresholds despite observed morphological divergence. Our findings underscore the importance of integrating genetic variability into reforestation strategies under increasing drought frequency, and highlight the value of root traits as early predictors of seedling resilience.

S2.04. Mimicking bark beetle attacks: field and phytotron insights into Norway spruce defense responses

Ramires Marcelo, Netherer Sigrid, Schebeck Martin, Hummel Karin, Schlosser Sarah, Razzazi-Fazeli Ebrahim, Ertl Reinhard, Ahmad Muhammad, Espinosa-Ruiz Ana, Carrera Esther, Arc Erwann, Martínez-Godoy Maria Ángeles, Baños Jorge, Caballero Teresa, Ledermann Thomas, van Loo Marcela, Trujillo-Moya Carlos

Norway spruce (*Picea abies* [L.] H. Karst.) is a keystone species of European montane and boreal forests, providing essential ecosystem services such as timber, water regulation, and biodiversity support. However, these forests are increasingly threatened by outbreaks of the Eurasian spruce bark beetle, *Ips typographus* (L.) (Coleoptera: Curculionidae: Scolytinae), which have intensified under ongoing climate changes. During early colonization, tree survival relies on a fast defense response, yet these molecular mechanisms remain poorly understood.

To address this, we conducted a controlled field experiment on 35-year-old clonal spruce trees using caged male beetles to simulate a natural attack. Multi-omics analyses at the site of attack revealed a robust local defense response, including upregulation of phytohormonal signaling, activation of defense-related genes and proteins, and accumulation of lignin, phenolic aglycones, and terpenoid compounds. These changes were absent in systemic tissues and control trees, emphasizing the specificity of early responses.

Field studies, however, have limitations, such as environmental variability and resource-intensive setups. Here we developed a complementary phytotron-based assay using beetle protein extracts applied to spruce seedlings. Remarkably, this “artificial” system elicited molecular responses closely mirroring those observed in mature trees, including activation of overlapping defense pathways, as revealed by RNA-seq. Together, these two approaches highlight a conserved early defense response in Norway spruce that can be triggered by beetle-derived cues. The integration of field-based realism with a standardized laboratory platform offers a powerful tool to dissect spruce resistance mechanisms and support breeding efforts aimed at enhancing forest resilience under increasing bark beetle pressure.

S2.05. Adaptation to Climate in European Conifers: Lessons Learned

González-Martínez Santiago, Archambeau Juliette, Francisco Thomas, Mayol Maria, de-Miguel Maria, Budde Katharina, Theraroz Adélaïde, Lesur-Kupin Isabelle, Riba Miquel, Westergren Marjana, Cavers Stephen, Perry Annika, Olsson Sanna, Benito-Garzón Marta, Jaramillo-Correa Juan Pablo, Grivet Delphine, Vendramin Giovanni G., Alía Ricardo

European conifers represent a diverse group of long-lived forest species occupying a broad range of climatic environments across the continent. In this talk, I will present insights from our research on past, present, and future climate adaptation in four conifer species with contrasting demographic histories: stone pine (*Pinus pinea*), maritime pine (*P. pinaster*), Scots pine (*P. sylvestris*), and English yew (*Taxus baccata*). The divergent demographic backgrounds have shaped distinct levels of genetic diversity and population structure—from exceptionally low diversity in stone pine to extensive standing variation observed in Scots and maritime pines; the two latter species having also contrasted capacity for adaptive evolution (higher in maritime pine than in Scots pine). Our analyses consistently reveal a polygenic basis for adaptive traits, with, for example, around 6% of SNPs showing non-zero effects on key phenotypes in maritime pine. This complex architecture presents challenges for pinpointing climate-associated candidate genes. Moreover, despite the prevalence of phenotypic clines in European conifers—particularly in traits such as growth phenology—rigorous tests for local adaptation often reveal adaptation lags and cases of population maladaptation. In English yew, such patterns appear to be exacerbated by strong population isolation. Furthermore, demographic history influences the dynamics of genetic load: from an excess of fixed deleterious alleles in stone pine to evidence of purging in marginal maritime pine populations, with no clear effects in Scots pine. Finally, I will discuss the application of predictive frameworks, such as the calculation of genomic offsets, across these species. While these approaches offer promising tools for forecasting climate vulnerability, I will argue that their interpretation must be contextualised and approached with caution. Moreover, using complementary statistics together with genomic offsets has the potential to provide more meaningful predictions.

S2.06. Leveraging interspecific hybridization for drought adaptation in forest trees

David-Schwartz Rakefet, Houminer Naomi, Shifrin Tom

Genetic variation is essential for the adaptation of forest species to increasingly stressful environmental conditions. Interspecific hybridization provides a potent, though often underutilized, mechanism to generate such variation. This study investigates the role of natural hybridization in enhancing drought adaptation in two forest systems: *Pinus* species in planted forests and *Acacia* species in wild populations. Using species-specific SNP markers, we identified fertile hybrids between *Pinus brutia* and *Pinus halepensis*, and sterile hybrids between *Acacia raddiana* and *Vachellia gerrardii*. In pines, hybrid fertility enabled us to track hybrid frequencies across three critical stages of forest regeneration: seed, emerged seedling, and drought-recruited seedling. The proportion of hybrids increased from $4.7 \pm 2.1\%$ in seeds to $8.2 \pm 1.4\%$ in emerged seedlings, reaching $21.6 \pm 6.4\%$ in recruited seedlings. These results suggest strong post-germination selection favoring hybrids under drought stress. In contrast, although acacia hybrids were sterile, they exhibited superior performance compared to both parental species, indicating their potential to buffer population decline under harsh conditions. Common garden and physiological experiments showed that pine hybrids consistently outperformed pure species seedlings, displaying higher total biomass, increased root-to-shoot and juvenile-to-total needle ratios, lower transpiration and stomatal conductance, and earlier stomatal closure during drought. These traits enhance water-use efficiency and drought survival, demonstrating that hybridization can confer a significant adaptive advantage under climate-induced stress. Our findings underscore the importance of spontaneous interspecific hybridization in forest ecosystems and support the inclusion of hybrids in conservation and management strategies aimed at fostering resilience to climate change.

S2.07. Analysis of in situ performance of the European Beech (*Fagus sylvatica* L.) through the lens of leaf proteomics

Garibay-Hernández Adriana, Utz Vanessa J., Sommer Frederik K, Ottaviani Maria, Ott Caroline, Venn Benedikt, Mühlhaus Timo, Seegmüller Stefan, Schroda Michael

Resilience and robustness are critical capacities for forest performance under current environmental conditions. The European beech (*Fagus sylvatica* L.) is a major deciduous tree species in Central Europe, whose population has been extremely damaged by recent droughts. However, the severity of drought-triggered symptoms varies among individuals, and the physiological mechanisms underlying these contrasting responses are poorly understood.

Implementing novel molecular approaches for in situ tree assessment provides an opportunity to deepen our understanding on tree physiology. To this end, we developed a proteomics workflow on beech leaves to investigate tree performance. We aim to integrate the resulting quantitative information on the relative abundances of more than 6,000 leaf proteins with physiological parameters such as photosynthesis, stomatal conductance, as well as with pigment and targeted metabolite content to associate the molecular changes to tree phenotypes.

To understand the physiological responses to drought, we conducted pilot experiments with beech seedlings subjected to controlled soil aridity settings like those experienced in the Rhineland-Palatinate. Aridities below 15 mm·°C⁻¹ reduced stomatal conductance, lowered chlorophyll a/b ratios, and impaired photosynthetic efficiency. The leaf proteomes showed decreased levels of core photosynthetic proteins and a higher abundance of Early-Response to Dehydration proteins.

As a proof of concept for in situ tree assessment, we analyzed the proteomes of sun leaves from 90-yr-old trees exhibiting contrasting vitalities in the Rhenish Hesse region near Mainz. Low vitality trees showed lower pigment levels, a decreasing photosynthetic efficiency, and leaf proteomes reduced in core photosynthetic proteins. Comparison of the leaf proteomes led to the selection of specific proteins as putative tree vitality markers.

Our first results underscore the enormous potential of leaf proteomics to assess and understand the season-specific performance of mature trees directly in the forest. We aim to apply this approach to additional locations to support decision-making in forest management.

S2.08. Loss of genetic diversity and signs of selection in response to ash dieback in natural populations of *Fraxinus excelsior*

Budde Katharina, Doonan James, Hanika Tom, Heuertz Myriam, Ulaszewski Bartożc, Verbylaite Rita, Kjaer Erik D., Nielsen Lene R

Common ash (*Fraxinus excelsior* L.) was considered a species with high adaptive potential to climate change, as it can tolerate a wide range of environmental conditions. However, ash dieback, an invasive fungal disease caused by *Hymenoscyphus fraxineus*, is provoking a sharp decline in common ash populations throughout Europe. Susceptibility to ash dieback is heritable but only a low proportion of ash trees are less susceptible to the disease. Taking advantage of trees growing in clonal plantations of common ash (in Denmark, Sweden, Germany, Austria, Ireland and Lithuania) affected by the pathogen, a previous genome wide association study (GWAS) revealed many loci with rather small effects on crown health. Here, we collected a total of 246 leaf samples from 18 natural common ash populations from Spain, France, Switzerland, Germany, Poland, Scotland, Denmark and Lithuania. In 2019 we randomly sampled leaves from saplings, that had already survived several years in the presence of the pathogen. From five locations, we had additional samples from adult trees collected in 2001 before any severe damages caused by the pathogen were visible. Therefore, we consider them as random samples of the old (2001) and young (2019) generations in these locations. Mortality due to ash dieback was strong between 2001 and 2019. Genome wide markers revealed a loss of genetic diversity in almost all populations. Based on loci significantly associated to crown health revealed by the GWAS study indicated a shift from higher to lower susceptibility in one generation especially in the eastern European populations

S2.09. Temporal genetic changes and evolutionary rates at contemporary time frames in oaks

Online

Kremer Antoine, Alexandre Hermine, Caignard Thomas, Truffaut Laura

What is the tempo, mode and direction of microevolution in present tree populations? While most temperate tree populations are in place since several millenia no genetic diachronic approach allowed so far to grasp the time span needed to achieve local adaptation. Did trees evolve gradually over several generations during the post-glacial period or did adaptation proceed over much shorter time frames as short temporal pulses? Similarly allochronic monitoring of evolutionary changes are missing at recent and present times scales, while forests are undergoing severe directional climatic changes. We will review recent studies assessing temporal genetic changes for traits of adaptive significance over different recent time scales in European oaks (*Quercus petraea* and *Quercus robur*). Significant genetic changes were found during the transition between the cold Little Ice Age (1450-1850) and the Anthropocene warming (1850-today) at the genomic and phenotypic level. In a second case study, genetic changes were tracked over two successive generations at contemporary time scales, during on-going climate change. Using quantitative genetic approaches in natura genetic shifts were observed for various adaptive traits. Taken together, these results suggest that adaptive evolution can be substantial, rapid, and fluctuating following environmental changes. We further dissect the genetic mechanisms at work in oak forests enhancing rapid evolution that ultimately contributes to the resilient responses to environmental changes. Overall these results have important implications for management decisions regarding regeneration of oak stands in the context of climate change.

Poster presentations

S2.P1. Genome-wide methylome stability and parental effects in the worldwide distributed Lombardy poplar

Flash presentation

Vanden Broeck An, Meese Tim, Verschelde Pieter, Cox Karen, Heinze Berthold, Deforce Dieter, De Meester Ellen, Van Nieuwerburgh Filip

Tree species rely on their ability to adapt to environmental change, with epigenetic mechanisms playing a key role by regulating gene expression. Understanding how epigenetic variation arises and persists across generations is essential to assess its evolutionary impact. The Lombardy poplar—a clonal variant of *Populus nigra* L. derived from a single 18th-century tree—is ideal for studying long-term epigenetic effects, as it has been widely propagated by cuttings across diverse climates. This study combines two observational methylome analyses and a phenotypic experiment to examine environmental and generational effects. In the first methylome study, we assessed seasonal and generational methylation changes. Methylomes in CG-contexts remained stable across locations and generations, while CHH-contexts showed seasonal variability. The second study tested whether methylation patterns in non-native environments reflected the parental climate but found no significant correlation. The third experiment evaluated phenotypic plasticity, focusing on bud set timing. A weak but statistically significant parental environment effect was detected, though it was overshadowed by the influence of the current environment. In conclusion, CG-context methylation appears stable and lineage-specific, making it a useful biomarker for tracing common ancestry and environmental history in Lombardy poplar.

S2.P2. Epigenetic Regulation of Tree Growth Reveals Climate-Resilient Genotypes in Douglas-fir

Flash presentation

Vu Giang, Cao Hieu, Schmidt Daniel, Hofmann Martin, Steiner Wilfried, Gailing Oliver

Understanding how forest trees adapt to climatic stressors is essential for predicting their long-term persistence under global change. While epigenetic regulation is increasingly recognized as a key driver of phenotypic plasticity, current understanding of its contributions to growth and climate resilience in forest trees remains limited. In this study, we integrate genomic, epigenomic and environmental data to investigate the regulatory basis of long-term growth performance in Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco), a species of major ecological and economic value. By comparing individuals with contrasting growth performance in provenance trials, we identified 650 differentially methylated loci (DMLs) and associated genetic variants (SNPs) distributed across the genome.

Machine learning models incorporating these DMLs, SNPs and environmental variables show strong potential for predicting growth responses, for example under recent extreme drought conditions. A targeted SNP assay developed from key loci identified demonstrates promise for identifying climate-resilient genotypes across both native and introduced provenances. Our findings highlight the role of epigenetic regulation in shaping adaptive growth strategies and provide a framework for advancing climate-smart conservation and breeding in long-lived forest species.

S2.P3. Oaks respond differently to infestation by generalist and specialist herbivorous insects

Schroeder Hilke, Mader Malte, Orgel Franziska, Nosenko Tetyana, Ghirardo Andrea, Schnitzler Jörg-Peter, Kersten Birgit

The pedunculate oak (*Quercus robur*) shows great adaptability and is therefore ideal for creating future resilient forests that can withstand the challenges posed by climate change. Our “Survivor-Oaks” project aims to identify oak trees resistant to herbivory, drought and powdery mildew, ensuring their survival under future climate. Here, we analysed the transcriptional responses in *Q. robur* leaves to infestation by the specialist moth *Tortrix viridana* and the generalist moth *Lymantria dispar*. Feeding experiments were performed using resistant (T) and susceptible (S) oak genotypes, identified based on defoliation rates during previous *T. viridana* outbreaks. Illumina RNA sequencing was performed from leaves 20 hours after start of feeding. Bioinformatic data analysis included mapping of short read against the oak reference genome (Darwin Tree of Life-Project), followed by analyses of differentially expressed genes and related functions. Overall, general changes in gene expression were observed as expected by herbivory, such as the activation of the jasmonate and ethylene signalling pathways mediated by the transcription factors MYC2, JAZ and ERF. Feeding by *L. dispar* triggered a broader and more intense transcriptional response, unlike the specialised profile induced by *T. viridana*. Additionally, comparing fed T- and S-oak genotypes revealed different expression patterns depending on the herbivore species. The changes in the transcriptome after feeding by the specialist were more influenced by the host genotype than those after feeding by the generalist. The results of the study are particularly relevant for selecting insect-resistant genotypes for forest management in a changing climate

S2.P4. Omic signature of local adaptation in Norway spruce

García-Gil M Rosario, Ranade Sonali S

Norway spruce (*Picea abies* L.) is one of the most economically important conifer species for the Swedish forest industry. Adapting to the local environmental conditions renders higher mean fitness to the plants. However, comprehension of the local adaptation strategies and detection of the underlying genetic basis of this adaptation is challenging in forest trees. Light is one of the environmental factors that plays a vital role in the regulation of plant growth and development. Norway spruce is shade tolerant which means it is well adapted to shade or the low red light (R): far-red light (FR) ratio. Due to Sweden's geographical location, the northern forests in Sweden daily receive more hours of FR-enriched light/twilight or shade-like conditions as compared to southern forests, during the growth season. Norway spruce has adapted to latitudinal variation in twilight characterized by a northward increase in FR requirement to maintain growth. Our group has demonstrated that the species also shows clinal variation to defence response. Recently, we have identified SNPs in Norway spruce that belong to the coding regions in the defence and light pathways indicating that adaptation to light and defence may be two related mechanisms in conifers.

S2.P5. Revealing mechanisms underlying variation in susceptibility in the Scots pine - *Dothistroma* pathosystem

Flash presentation

Annika Perry, Beth Moore, Diana Vinchira-Villarraga, Ninghui Du, Krisztian Nemeth, Rob Jackson, Sue Jones, Stephen Cavers

Understanding and predicting how trees respond to disease is essential for the successful management of existing and future forests. But, despite its vital importance, efforts to uncover mechanisms underlying host responses are often limited by the lack of robust estimates of variation in host susceptibility and trade-offs with other traits. Quantitative variation in susceptibility is controlled by the combined and interactive effect of multiple genes and is composed of tightly interlinked components and processes including: 1) genetic architecture underlying trait variation (genomics); 2) gene expression and regulation (transcriptomics); 3) biochemical synthesis (metabolomics). Each of these can provide valuable clues to the dynamics underlying tree health responses but independently they may lack the depth to reveal the complexity inherent in quantitative traits. Scots pine (*Pinus sylvestris*) is both economically and ecologically valuable but is threatened by the globally important pathogen, *Dothistroma septosporum*, causing *Dothistroma* needle blight (DNB). Although previous research has demonstrated that Scots pine shows quantitative variation in susceptibility to this disease, the specific mechanisms underlying the interaction are currently unknown.

A common garden progeny-provenance experimental trial of Scots pine, planted in 2012 and regularly assessed for susceptibility to DNB has enabled us to develop an increasingly comprehensive understanding of the mechanisms underlying variation in host response to disease, using metabolomics, transcriptomics and genomics. I will present the latest findings of this research as well as other ongoing research that will use this knowledge to improve management of the species into the future.

S2.P6. Generating a European beech pangenome to elucidate the genomic basis of environmental adaptation

Flash presentation

Lazić Desanka, Geßner Cornelia, Müller Niels A

Understanding the genetic basis of environmental adaptation is key to predicting species future maladaptation and ecosystem stability in the face of climate change. This is especially important for long-lived organisms like trees, which may struggle to keep pace with rapid shifts in environmental conditions. Here, we resequenced 1773 individuals from 100 range-wide populations in European beech (*Fagus sylvatica* L.), a widespread forest tree species in Europe. We found that genetic variation closely mirrors geography, with distinct isolation-by-distance patterns. Genotype-environment association (GEA) analyses identified a limited number of robust adaptive signals after accounting for extensive number of false positives. One high-confidence locus may drive winter temperature adaptation through modulation of spring phenology. Interestingly, reciprocal transplant experiments of trees supposedly adapted to the two contrasting climates suggest that phenotypic plasticity plays a major role. To better resolve the complexity of adaptive variation and address genotype-environment interactions, we are building a European beech pangenome, based on PacBio HiFi long-read sequencing of 70 diverse beech individuals. Using these data we generated high-quality haplotype-resolved genome assemblies with an average contig N50 of 25 Mb. This pangenome allows us to explore structural variation and serves as a more representative resource regarding genomic diversity. Together, these approaches highlight both the challenges and the potential of integrating genomic resources to better understand forest tree adaptation under climate change and guide current and future forest management and conservation strategies.

S2.P7. From many to one, if any – Elimination of rival embryos characterises Scots pine early embryogeny

Vakkari Eeva, McEvoy Susan, Cervantes Sandra, Vatén Anne, Savolainen Outi, Pyhäjärvi Tanja

Scots pine (*Pinus sylvestris*) ovules produce multiple egg cells which are fertilised by different pollen grains, resulting in polyzygotic polyembryony. In a mature seed, one dominant embryo survives, while the others are eliminated through developmental selection. Development may also result in an empty seed with no viable embryos. Several evolutionary explanations have been proposed: polyembryony has been suggested to compensate for embryo mortality, subject embryos to competition and maternal screening, and selectively eliminate selfed progeny (embryo lethal system).

We studied seed and embryo development using micro-CT imaging of ovules across 12 timepoints, covering stages from fertilisation to dominant embryo emergence. Our data reveal that initial polyzygotic polyembryony is followed by embryo cleavage producing genetically identical multipler. In an ovule exhibiting mixed polyzygotic and cleavage polyembryony, a rapid selective phase gives rise to a single dominant embryo proceeding into late embryogeny, while subordinate embryos fail to undergo organogenesis and are eliminated. Our results suggest that cleavage is a potentially important process in dominant embryo determination.

Fertilisation, pre- and post-cleavage early embryogeny, and the onset of late embryogeny, were studied using spatial transcriptomics to uncover genetic instruments of embryo competition and maternal screening. We tested the embryo compensation model by controlled crosses with varying self- and cross-pollen levels. Comparison of empty seed frequencies among cross types demonstrates that while inbreeding causes seed mortality, there is no indication of embryo compensation, making competition, maternal screening and embryo lethal system models more likely, non-exclusive, evolutionary explanations for polyembryony in Scots pine.

S2.P8. Fungal communities in Swedish elms: Implications for Dutch elm disease resistance

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

The native elms (*Ulmus* spp.) in Sweden are critically endangered because of the Dutch Elm Disease (DED). This wilt disease is caused by aggressive invasive fungi in the genus *Ophiostoma*. Although the disease is rapidly spreading, some elms show tolerance or possible resistance to the disease. Previous research has shown that certain microbial communities have a positive effect on their host, for example, they may support disease resistance by stimulating tree defence mechanisms. If similar communities could be found in the Swedish elms that show tolerance or resistance to DED, it could be possible to find new tools to push forward the breeding and support conservation of our native elms as a part of climate-resilient forests. The aim of our studies is to provide new knowledge about elm symbiotic microbial communities and their possible effects on the resistance and tolerance to DED, with the goal of identifying new tools to support breeding and conservation of native elm populations. Using a crowdsourcing approach, we located elms that show tolerance to DED. Sampling efforts and inventories targeted *U. glabra* population in Southern Sweden where the disease has been active for decades. The endophyte communities were studied using metabarcoding and isolation techniques. Approximately 80 isolates were recovered from visually healthy trees, including several *Fusarium* species. The results of biotests showing the activity of selected isolates against DED pathogens are discussed. Keywords: Dutch elm disease, *Ulmus* spp., *Ophiostoma*, microbial communities, fungi.

S2.P9. Microbiomes as Forest Health Indicators: Using Shotgun Metagenomics of Canopy Flowthrough to Investigate the Functional Composition of Phyllosphere Microbiomes in Danish Oak Forests

Hansen Kristina Egholm, Rostgaard Nielsen Lene, Doonan James

Danish forest management is transitioning from monocultures to mixed-species forests to improve biodiversity and ecosystem resilience. However, microbial diversity, especially in the phyllosphere, is often neglected in biodiversity assessments. The phyllosphere microbiome plays a crucial role in plant fitness and stress resilience, influencing desiccation tolerance, UV protection, nutrient cycling, and resistance to pests and pathogens. Disruptions in this microbial layer can reduce productivity and impair forest health. This study compares the phyllosphere microbiome of managed oak monocultures and unmanaged mixed forests to identify taxonomic and functional differences linked to forest type. Canopy flowthrough samples were collected during two autumn rainfall events in 2022 from paired forest sites in northern and southern Zealand, Denmark and shotgun metagenomic sequencing was used to analyze microbiome composition and functional potential. Preliminary results indicate that functional profiles (COG terms) cluster more strongly by geographic location than forest type, but forest type-specific differences were detected. Upregulation of COG terms associated with increased oxidative response (COG1858, COG2124 and COG1333) in mixed forests. This could imply increased oxidative stress response and detoxification capacity in this forest type compared to monoculture.

S2.P10. Integrating Leaf Morphology and Whole-Genome Sequencing to Resolve Species Boundaries in the White Oak Species Complex

Szukala Aglaia, Groot Crego Clara, Rellstab Christian, Nicorescu Adelin-Ionut, Kovacs Gyula, Curtu Alexandru Lucian, Zhelev Petar, Piotti Andrea, Avanzi Camilla, Kolbaia Sandro, Sandor Bordacs, Pelin Keske, Zeki Kaya, Nikolaos Tourvas, Filippas Aravanopoulos, Heino Konrad

Species discrimination within the white oak complex (*Quercus* sect. *Quercus*) has long been debated, yet accurate identification remains essential for forest management, conservation, and economic planning. While leaf morphology helps distinguish major species—particularly in allopatric contexts—its reliability diminishes in sympatric zones with frequent hybridization and when identifying local (sub-)species. Moreover, the relationship between leaf morphology and genomic patterns—shaped by ancient introgression and ongoing gene flow—remains poorly understood. This study investigates leaf morphological differentiation among four core species of the white oak complex (*Q. petraea*, *Q. robur*, *Q. pubescens*, and *Q. frainetto*), their putative hybrids, and related (sub-)species (*Q. polycarpa*, *Q. dalechampii*, *Q. pedunculiflora*, *Q. virgiliana*, *Q. iberica*, *Q. macranthera*, and *Q. imeretina*). We apply geometric morphometrics, trichome analysis, and unsupervised machine learning to assess morphological variation, comparing these patterns to genomic differentiation using whole-genome sequencing (WGS) data from over 70 populations, spanning from southern Switzerland and northern Italy to the Caucasus. Preliminary results reveal five leaf traits that significantly differ among species and highlight trichome type as a useful feature for distinguishing some of the subspecies. Morphologically intermediate individuals do not always match genetically admixed trees and hybrids and vice versa, indicating that leaf morphology may not reliably reflect levels of admixture and introgression. In combination with WGS data, we aim to analyse whether leaf morphological traits correlate with particular genomic regions. This study is the first to integrate whole-genome data and detailed leaf morphology across a broad geographic range to clarify white oak gene pools, offering a more informative perspective than traditional morphological classifications, especially for subspecies and admixed taxa.

S2.P11. Studies of range-wide introduction of Douglas fir after 50-200 years in Europe

Sergiadou Dimitra, Nørgaard Carsten Tom, Olofsson Jill Katharina, Kjaer Erik Dahl

Douglas fir (*Pseudotsuga menziesii*) is a conifer species native to western North America with high economic importance due to its high-quality timber and fast growth. In Europe, it was first introduced in the nineteenth century and has been increasingly cultivated in European forests since then, being one of the most abundant non-native tree species in several central European forests. A forest trial in Northeast Denmark, established in the '70s, includes trees from the range-wide distribution, offering the opportunity for a thorough study on the growth and adaptation potential of the species in Northern European climate conditions. Using quantitative genetic tools, along with an Axiom single-nucleotide polymorphism (SNP) genotyping array for Douglas fir, we aim to assess the species' performance in the Danish forests and detect any genetic variants linked to environmental adaptation. Additionally, the use of genome-wide genetic markers enables extensive investigations of population structure across the native range, as well as contributing to the identification and confirmation of the geographic origin of the Danish seed source. The results of this project are of high value for a better understanding of the genetics and survival potential of the species in a changing climate in Europe and for potentially improving tree breeding of one of the most ecologically and economically important trees in Europe.

S2.P12. Gene expression variation underlying local adaptation in silver birch (*Betula pendula*)

Sirén Jenni, Vuosku Jaana, Perraud Ysaline, Puntila Jenni, Kujala Sonja T., Kärkkäinen Katri, Verta Jukka-Pekka, Pyhäjärvi Tanja

For plants, adjusting the timing of growth and reproduction will be essential in the changing climate as the combinations of light, temperature, and biotic conditions change. Forest trees are excellent model species for understanding the genomic determinants of local environmental adaptation as they are often widely spread, occupy diverse conditions, and have hereditary, adaptive phenological differences among populations.

Silver birch (*Betula pendula*) is an ecologically and economically important forest tree species in Northern Europe. While its phenotypic adaptation across latitudinal gradients is well established, the gene regulatory mechanisms driving these patterns remain largely unknown. Silver birch has a relatively compact and well annotated genome compared to other boreal forest tree species such as conifers, making it well suited for investigating molecular patterns underlying local adaptation.

We conducted a large-scale growth chamber experiment with 1920 silver birch seedlings from four different populations to investigate population-level transcriptomic and gene regulatory responses to day-length changes. We sampled a time series of leaf material and conducted RNA-sequencing from 214 seedlings. Preliminary results show differential gene expression between populations, treatments and sampling points. While largest differences are observed expectedly between time points, patterns specific to combinations of population and treatment were also present.

Next, we intend to construct a gene expression network across time focusing on population-specific patterns to gain a better understanding of the transcriptional regulation underlying current local adaptation. Together, these results will provide insights into how trees respond to environmental change.

S2.P13. A population (epi)-genomic analysis of *Pinus nigra* populations with differential exposure to air pollution

Kotina Vasiliki Maria, Tourvas Nikolaos, Lyrou Fani, Aravanopoulos Filippos

In Western Macedonia and in the southeastern Peloponnese, the largest lignite mining and combustion centers in Greece have been operating for decades, resulting in the emission of large quantities of atmospheric pollutants, primarily SO₂, NO_x, and suspended particulate matter (PM₁₀). Using SPET genotyping and reduced representation bisulfite sequencing (RRBS), we analyzed natural black pine populations in these two areas under a factorial design with cohorts accounting for pollution exposure, age class and altitude. Preliminary results from SPET genotyping indicate no major differences in overall genetic diversity among populations, although polluted cohorts tend to exhibit slightly higher heterozygosity. A PCA also revealed greater divergence in the polluted cohorts, particularly in the Western Macedonia.

A differentiation analysis then focused on the targeted SNPs. Among these, two prominent outliers were discovered, possibly indicating loci associated with adaptation to air pollution. RRBS-seq was conducted on four cohorts with differential exposure to air pollution. CG methylation showed no significant differences among cohorts. This aligns with known patterns in conifers, where stress-related responses typically affect non-CG methylation. CHG methylation revealed 3 hypomethylated and 1 hypermethylated cytosine sites at single-base resolution, and 2 hyper- and 2 hypomethylated regions, while CHH methylation showed 25 hypomethylated sites, suggesting stress-related epigenetic responses. These findings point to possible genetic and epigenetic responses of black pine to sustained air pollution, underscoring the need for deeper investigation into their functional implications.

S2.P14. European beech growth responses to climate and altitudinal gradients in the Carpathian Mountains

Dominguez-Flores Tania, Miranda Jose Carlos, Chano Victor, Ciocîrlan Mihnea-Ioan-Cezar, Ciocîrlan Elena, Wildhagen Henning, Curtu Alexandru Lucian, Gailing Oliver

European beech (*Fagus sylvatica* L.) forests are facing an increase in extreme weather events, especially droughts and heatwaves, which affect their growth and survival. Understanding climate-growth relationships at the level of intra-annual wood formation across altitudinal gradients is essential for predicting forest resilience. Here, a dendroecological study was performed measuring tree ring width (TRW), earlywood (EW) and latewood (LW) increments of three populations (Lempes, Tampa, Solomon) in the Romanian Carpathians (1920-2020). Climate influence on growth was analysed through correlations with ring width index (RWI), earlywood (EWI) and latewood width Index (LWI), assessing temperature, precipitation, vapour pressure deficit (VPD) and Standardised Precipitation-Evapotranspiration Index (SPEI). Linear mixed-effects models were used to assess variation in wood production (BAI) as well as intra-annual components, earlywood (EWAI) and latewood (LWAI), in relation to climate variables. Results showed site-specific climatic sensitivities. Lempes, at the lowest altitude, showed late-season drought stress and increased latewood growth, suggesting adaptation to drought. Solomon, at higher altitude, was limited by spring temperatures, and earlywood growth benefited from atmospheric moisture, while latewood was negatively affected by wetter conditions. These results highlight different growth strategies along altitudinal gradients, with populations from the lowest altitudes being more vulnerable to drought and higher altitude populations being more temperature-limited but sensitive to humidity. Variation in the intra-annual patterns of wood growth among populations indicates a potential for adaptation, although long-term survival under climate change is uncertain. This underlines the need for site-specific management to improve the resilience of the European beech forest.

S2.P15. Remembering the past –a novel insight into pathogen resistance across generations of ash trees (EPI-FRAX)

Nielsen Lene Rostgaard, Hansen Kristina Egholm, Kosawang Chatchai, Kjær Erik Dahl, Yakovlev Igor, Magerøy Melissa

In long-lived trees, adaptation through natural selection can be too slow in contrast to rapid changes in their environment, and phenotypic plasticity based on fast adaptive mechanisms, like epigenetic modification, can prove important. Epigenetic modifications could also play a role for rapid adaptation to novel emerging pests or pathogens. Here, we present a new project on European ash (*Fraxinus excelsior*) that is threatened by the invasive Asian fungus, *Hymenoscyphus fraxineus*, causing severe ash dieback (ADB) in ash stands across Europe. The project aims to reveal whether transgenerational epigenetic modifications play a role in adaptation of the European ash towards the invasive fungus. We test if seedlings from seeds produced during the epidemic are less affected by the fungus than seedlings from seeds developed before the disease, due to changes in epigenetic marks, such as methylation patterns and histone modification, and are realized as alterations in gene expression.

S2.P16. Genetic diversity of oak species in Zvezdara forest

Kerkez Janković Ivona, Šijačić-Nikolić Mirjana, Aleksić Jelena

Artificially created forests can exhibit varying levels of genetic diversity, influenced by numerous factors such as source of planting material, breeding practices, and management strategies. Some studies revealed genetic diversity comparable to natural forests, while others showed reduced diversity due to selective breeding and limited genetic bases. Zvezdara Forest is an urban protected forest – IUCN Category III. This forest was artificially created by afforestation actions in different periods of mid XX century with seedlings of unknown origin. Two native oak species were planted: pedunculated and sessile oak. Aim of this study was to explore genetic diversity of adult populations of pedunculated and sessile oak, as well as in juvenile population of sessile oak. We analyzed 171 individuals: 62 adults and 50 juvenile sessile oaks, 59 adult pedunculated oaks. For genetic analysis 14 nSSRs were used. The observed heterozygosity (H_o) was similarly high across all three groups (~ 0.72 – 0.73), while the inbreeding coefficient (F) showed moderately positive and statistically significant values ($F \approx 0.14$ – 0.16). The lowest, yet statistically significant, F_{ST} value (0.0078) between adult and juvenile sessile oaks reflects genetic continuity, likely resulting from the reproductive contribution of adult trees to progeny. Conversely, the highest F_{ST} value (0.073) observed between pedunculated oaks and juvenile sessile oaks indicates moderate genetic differentiation. Despite their artificial origin, both pedunculated and sessile oak populations in Zvezdara Forest exhibit substantial genetic diversity, including in juvenile sessile oaks. This is a key factor for resilience and adaptive capacity under changing environment, especially in urban forest ecosystems.

S2.P17. A methodological framework for the conservation of the gene pool of woody species in urban forests: a case study of Zvezdara forest

Šijačić-Nikolić Mirjana, Nonić Marina, Maksimović Filip, Kerkez Janković Ivona

Gene pool conservation in forest trees has become essential and especially important in the context of adaptive potential of species and ecosystem stability regarding modern challenges. We developed a methodological framework for the conservation of the gene pool of woody species which is applied in Zvezdara Forest as a case study. Thanks to its specific location, heterogeneous flora, and ecological stability, Zvezdara Forest has become an important biodiversity refuge and a vital component of the city's green infrastructure. Framework is consisted of the following steps: 1) field reconnaissance and species inventory; 2) assessment of factors contributing to genetic erosion; 3) evaluation of the current state and degree of threat to the gene pool; 4) identification of target species; 5) georeferencing of target species individuals and/or groups; 6) determination of key traits of the georeferenced individuals; 7) mapping of the gene pool of target species; 8) creating a database for long-term monitoring, 9) assessment of variability using morphological and molecular markers, and 10) establishing a long-term genetic resource management strategy for the study area. In Zvezdara Forest applied framework resulted in 89 woody species recorded distributed in two in situ conservation units. All the data were saved in digital form for long-term monitoring purposes. Ex situ conservation, a progeny tests of wild cherry, pedunculated and sessile oaks, and field elm were established. As the overall result strategy for forest genetic conservation of the conservation of the gene pool of woody species in Zvezdara Forest is developed.

S2.P18. Genomic Prediction of Drought-Adaptation Traits in English Oak with Whole Genome Sequencing Data.

Aiyesa Leke, He Miao, Vu Thi Ha Giang, Müller Markus, Gailing Oliver

Genomic prediction is revolutionizing breeding programs by accelerating genetic gains, shortening generation intervals, and improving the accuracy of breeding value estimates. While this approach has gained substantial traction in forest tree species—with over 80 studies published between 2010 and 2022—there remains a noticeable gap when it comes to empirical applications in oak (*Quercus* spp.), a keystone genus in temperate forest ecosystems.

In this study, we explore genomic prediction in the English oak using whole-genome sequencing (WGS) data comprising 582,900 SNPs from 765 individuals collected across eight diverse geographic locations spanning four European countries. We focused on key ecophysiological traits— $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, their ratio, and stomatal density—that serve as indicators of drought adaptation. Our results show promising prediction abilities, ranging from 0.10 to 0.45, with the $\delta^{13}\text{C}$ trait exhibiting the highest predictive accuracy. To further enhance performance and practical utility, we are undertaking a comparative evaluation of prediction models, including both linear (e.g., GBLUP) and machine learning-based approaches, and assessing the role of non-additive genetic effects. Recognizing the computational challenges of working with large genomic datasets, we also explore three complementary strategies for dimensionality reduction by identifying and prioritizing non-neutral SNPs without sacrificing prediction accuracy. This work represents one of the first empirical demonstrations of genomic prediction in oak, marking a key advancement toward integrating predictive genomics into oak breeding and conservation strategies. It complements prior efforts in population genomics and marker-assisted selection, and opens the door to more efficient, data-driven tree improvement programs under climate change scenarios.

S2.P19. Simulated facilitation shapes intraspecific trait variation in *Quercus ilex* seedlings

Vizcaíno Palomar Natalia, Navarro Cano Jose Antonio, Alía Ricardo, Benito Garzón Marta, Goberna Marta

Variation in traits across a species' natural distribution is mainly due to local adaptation and phenotypic plasticity. Facilitation, positive plant-plant interactions, can also influence trait expression, particularly during early stages by enhancing recruitment in drought-prone ecosystems. Although trait variation related to facilitation is well studied at the species level, its role in shaping population-level variation remains poorly understood. To this end, we designed a semi-natural experiment to study early-stage recruitment, from seed to seedling, facilitation and climate. We assessed the interaction between intraspecific phenotypic variation in *Quercus ilex* L. (4 populations: North, South, West and Local; 40 families, 3,799 acorns), shrub facilitation (simulating the presence or absence of *Retama sphaerocarpa* L.) and climate (dry vs. wet summer) on seedling performance. We evaluated variation in emergence and mortality patterns over time, as well as in above- and below-ground traits. Preliminary results indicate that emergence and mortality over time were genetically determined. The effects of facilitation varied depending on population origin, climatic conditions, and the life stage (emergence vs. mortality). Facilitation significantly improved emergence only in the southern population, which experienced the greatest climatic shift between its origin and the test site, resulting in an 82.2% increase in emergence probability. In contrast, facilitation and wet climate consistently reduced mortality across all populations. Facilitation also significantly altered rhizosphere microbiota composition, suggesting below-ground impacts beyond survival. These findings indicate that facilitation can drive population-level trait variation, shaped by climatic stress, local adaptation, and microenvironmental conditions, underscoring the complexity of biotic interactions across environmental gradients.

S2.P20. Presence and distribution of the native white oaks (*Quercus robur* and *Q. petraea*) in two mixed oak forests in the Northern part of their native range

Sergiadou Dimitra, Larsen Mathilde Lundt, Olofsson Jill Katharina, Kjaer Erik Dahl

Two European white oaks, *Quercus robur* and *Q. petraea*, are native to Denmark, with *Q. robur* being more widespread across the country, whereas *Q. petraea* has a more restricted distribution, typically associated with western and drier habitats. Two mixed oak forests—one in the northwest (oak shrub forest in Kaas) and one in the southeast (Ulvshale forest)—were studied to investigate the spatial distribution, introgression levels, and signs of local adaptation in the two species. Using whole-genome sequencing data and a reduced single-nucleotide polymorphism (SNP) set, we found a high level of introgression in the Kaas forest, with the majority of sampled individuals showing varying degrees of admixture. *Quercus robur*-like individuals are mainly found along the coast and margin of this forest, and the spatial distribution of species in general appears to reflect ecological niches within the forest. In the Ulvshale forest, results were different; both species are also present, and a few individuals show signs of introgression. *Q. petraea* individuals form two spatially distinct groups in this forest, with high relatedness within the groups, but no obvious spatial relation to ecological conditions, possibly indicating signatures of past planting or recruitment from a few trees. Our findings provide insights into the local demographic histories of the two oak species and contribute valuable knowledge for effective conservation management strategies.

S2.P21. Genomic signatures of climate-driven (mal)adaptation in an iconic conifer, the English yew (*Taxus baccata* L.)

Thomas Francisco, Maria Mayol, Elia Vajana, Miquel Riba, Marjana Westergren, Stephen Cavers, Sara Pinosio, Francesca Bagnoli, Maurizio Marchi, Filippos A. Aravanopoulos, Anna-Maria Farsakoglou, Ivan Scotti, Bruno Fady, Giovanni G. Vendramin, Juliette Archambeau, Andrea Piotti, Santiago C. González-Martínez

The risk of climate maladaptation is increasing for numerous species, including trees. Developing robust methods to assess population maladaptation remains a critical challenge. Genomic offset approaches aim to predict climate maladaptation by characterising the genomic changes required for populations to maintain their fitness under changing climates. In this study, we assessed the risk of climate maladaptation in European populations of English yew (*Taxus baccata*), a long-lived tree with a patchy distribution where many populations are small or threatened. We found evidence suggesting local climate adaptation by analysing 8,616 SNPs in 475 trees from 29 European *T. baccata* populations, with climate explaining 18.1% of genetic variance and 100 unlinked climate-associated loci identified via genotype- environment association (GEA). Then, we evaluated the deviation of populations from the overall gene-climate association to assess variability in local adaptation or different adaptation trajectories across populations and found the highest deviations in low latitude populations. Moreover, we predicted genomic offsets and successfully validated these predictions using fitness proxies assessed in plants from 26 populations grown in a comparative experiment. Finally, we integrated information from current local adaptation, genomic offset, historical genetic differentiation and effective migration rates to show that Mediterranean and high-elevation *T. baccata* populations face higher vulnerability to climate change than low-elevation Atlantic and continental populations. Our study demonstrates the practical use of the genomic offset framework in conservation genetics, offers insights for its further development, and highlights the need for a population-centred approach to credibly assess climate vulnerability in wild plant populations.

S2.P22. Resilience of European Ash Forests influenced by Ash Dieback: the role of Genetic Diversity

Kjær Erik Dahl, Lobo Albin, Kosawang Chatchai, Xu Jing, Hansen Lars Nørgaard, Donnan James, Budde Katharina, Thomsen Iben M., Hansen Jon Kehlet, Nielsen Lene Rostgaard Nielsen

Forest health calamities often start with a host shift where an alien fungus becomes a severe pathogen on a native plant species. This is considered the case for the Asian ascomycete *Hymenoscyphus fraxineus* whose shift from Asian ash species to European ash (*Fraxinus excelsior*) has created severe damage throughout most of Europe's ash forests. Fortunately, common garden trials revealed genetic variation in tolerance early in the epidemic. This observation has initiated several studies of the level, inheritance and genomic background of variation in susceptibility, and its implication for fitness of the ash trees and long term stability of the forests. Here, we discuss what can be learned from recent Danish studies regarding these aspects with focus on new data from field trials established during the pandemic. Based on the findings, we discuss if and how genetic management of natural and planted ash forests can enhance and protect their resistance and evolutionary resilience. We reflect on general lessons when it comes to management of forests for resilience towards future emerging infectious diseases.

S2.P23. Signals of drought tolerance in *Quercus cerris*: insights for future Austrian forests resilience

Hurel Agathe, Depardieu Claire, Feichter Jonathan, Heinze Berthold

Austria, one of the most densely forested countries in Europe with 48% forest cover, faces growing threats from climate change, including droughts and pest outbreaks. Oaks are expected to largely contribute to future forest resilience, particularly *Quercus cerris* (Turkish oak) due to its relative tolerance to temperature extremes and drought. This study explores the genetic basis of drought tolerance in *Q. cerris* using a genotype–phenotype association approach.

We identified three climatically distinct clusters within the species' distribution and sampled 300 trees from a representative site in each: Croatia, Hungary, and Slovenia. Wood cores were analysed to detect responses to drought years, and several drought resistance indices were computed. These, together with models relating growth traits to climate variables, revealed population-specific drought response patterns, suggesting adaptive divergence across regions.

Leaves from the same trees were genotyped using a multispecies SPET probe panel developed by the FORGENIUS project. We aim to identify SNPs associated with dendroecological traits to uncover candidate variants linked to drought response. To assess the importance of these variants at the species' northern margin, 200 additional individuals from five Austrian populations were genotyped. This will allow us to screen for adaptive alleles potentially contributing to drought tolerance in Austrian forests. We anticipate our findings will reveal both genetic and phenotypic differentiation driven by climatic origin. These insights could inform conservation strategies, guide assisted migration, and help ensure forest sustainability under changing environmental conditions in Austria.

S2.P24. Evaluating Genomic Offset Predictions in *Abies alba*: Evidence from a Common Garden Experiment

Feichter Jonathan, Matziarli Paschialina, Reich Johanna, Heinze Berthold

Genomic offset is an increasingly popular concept for predicting the potential climatic maladaptation of forest tree populations in a changing climate. Recent genomic offset studies report high variability in GO predictions depending on the methods used, the markers selected and the climate scenarios considered. This emphasises the need for the empirical evaluation of these predictions. Here, we present an evaluation of GO predictions for *Abies alba*, an economically and ecologically important forest tree species in Europe, in an advanced-age common garden experiment. Genomic information and a wide range of phenotypic traits were obtained from 480 individuals originating from 20 populations, covering the entire species range. We found that GO predictions from RDA and Gradient Forest showed the expected negative correlation with most fitness-relevant traits, albeit barely significant. The strongest correlations were observed with a composite index combining the most relevant fitness traits. GO predictions generally explained the variability of fitness-relevant traits better than climatic transfer distance alone. While our results are promising for the implementation of GO concepts in forest management, they also highlight the need for larger sample sizes and more precise fitness proxies for evaluation.

S2.P25. Towards an integrative understanding of taxonomic diversity, climate adaptation, and introgression in Southeast European white oak species

Groot Crego Clara, Adelin-Ionut Nicorescu, Gyula Kovacs, Alexandru Lucian Curtu, Petar Zhelev, Sandor Bordacs, Andrea Piotti, Camilla Avanzi, Sandro Kolbaia, Pelin Keske, Zeki Kaya, Nikolaos Tourvas, Filippos Aravanopoulos, Heino Konrad, Christian Rellstab, Aglaia Szukala

The white oak species complex includes some of the most widespread European oak species and is strikingly diverse in Southeastern Europe, where several subspecies have been reported. However, the evolutionary processes underlying this taxonomic richness remain unclear. We hypothesize that climate adaptation and adaptive introgression during the divergence of white oak lineages played a major role. Our project features whole-genome resequencing (WGR) and leaf morphological data from over 70 populations sampled from Central and Southeastern Europe to Turkey and the Caucasus, including several white oak diversity hotspots. Sampling design includes pure and mixed-species stands to distinguish ancient from recent hybridization and determine each lineage's genetic composition. We aim at investigating the demographic history and the extent and direction of gene flow among white oak lineages. To investigate the role of gene flow in driving local adaptation, we will identify candidate loci for climate adaptation through genotype-environment association studies using publicly available climatic data, and evaluate whether they result from adaptive introgression. We will also study populations at the ecological range margins to assess white oak adaptive potential under future climates. Ongoing WGR analyses show clear genetic differentiation between species, but not among subspecies. The extent of introgression among species varies among chromosomes, indicating a non-random distribution of introgressed material that is maintained in the population. These results suggest different stages of differentiation among white oak lineages, allowing for investigation into local adaptation on multiple evolutionary scales. This large-scale study combining genomic, environmental and phenotypic data will significantly contribute towards a better understanding of adaptive potential in white oaks, and in hybridizing species complexes in general.

S2.P26. Mismatch between historical and contemporary gene flow indicates recent demographic disturbance in a tropical tree species

Bonnier Julien, Heuertz Myriam, Brunaux Olivier, Traissac Stéphane, Tysklind Niklas

Genetic connectivity is a key driver of forest resilience, yet it remains poorly understood in tropical trees facing increasing anthropogenic and environmental pressures. We assessed the spatial and temporal dynamics of gene flow in *Dicorynia guianensis*, a dominant canopy species of high ecological and economic value, across four natural populations in French Guiana encompassing protected and selectively logged forests. Using 66 nuclear and 21 chloroplast SSR markers genotyped on over 1,500 individuals, we combined parentage-based dispersal analyses with spatial genetic structure (SGS) metrics across juvenile, intermediate, and adult cohorts. Our results reveal strong variation in seed and pollen dispersal distances among plots and life stages, with logged populations showing reduced dispersal, higher inbreeding, and greater reproductive skew. In contrast, protected plots exhibited higher gene flow, lower SGS, and more equitable reproductive contributions. These patterns suggest that logging-induced demographic thinning and disrupted mating networks can precede detectable losses in genetic diversity, affecting the long-term adaptive potential of populations. By jointly analyzing contemporary and historical gene flow, reproductive success, and SGS across life stages, our study provides early indicators of demographic imbalance and connectivity loss. This integrative framework offers valuable tools for prioritizing forest conservation efforts based on genetic resilience, especially in tropical ecosystems where direct monitoring of reproductive processes is challenging.

S2.P27. Fungal assemblages in northern elms in light of Dutch elm disease

Jüri soo Liina, Agan Ahto, Tedersoo Leho, Witzell Johanna, Selikhovkin Andrey, Drenkhan Rein

Dutch elm disease (DED), caused by the ascomycete *Ophiostoma novo-ulmi*, continues to threaten elm (*Ulmus* spp.) populations across the Northern Hemisphere. Variation in host susceptibility may be partly shaped by differences in their twig-associated fungal endophyte communities. To explore the potential role of the mycobiome in tree resilience, we analysed fungal assemblages in symptomatic and asymptomatic individuals of highly susceptible *U. glabra*, less susceptible *U. laevis*, and disease-tolerant hybrids growing in contrasting environments in Estonia and Russia. Using PacBio long-read amplicon sequencing of the ITS1–5.8S–ITS2 region, we uncovered host-specific fungal community profiles. *Ophiostoma novo-ulmi* was found exclusively in symptomatic trees, dominating the community profile in *U. glabra* but entirely absent from hybrids, highlighting the latter's potential disease resistance. In contrast, *Sphaeropsis ulmicola*, a canker-associated pathogen, was present across all hosts regardless of their health status – dominant in *U. laevis*, prevalent in *U. glabra*. Interestingly, *S. ulmicola* was associated with increased fungal richness, while *O. novo-ulmi* presence did not affect diversity. Urban trees hosted significantly richer fungal communities than rural ones, suggesting that environmental context modulates endophyte composition and potentially disease dynamics. These findings suggest that host genotype and environment shape fungal assemblages in elms and may influence tree susceptibility to pathogens. Understanding these complex interactions offers valuable insights for forest adaptation strategies, including selection material for breeding for DED resilience.

S2.P28. Genome-wide association with the remotely assessed drought response of a beech (*Fagus sylvatica*) population

Flash presentation

Coq-Etchegaray Domitille, Helfenstein Isabelle, de La Harpe Marylaure, Moradi Aboubakr, Morsdorf Felix, van Moorsel Sofia, Schuman Meredith

European common beech (*Fagus sylvatica*) is a dominant broadleaf tree forming European temperate forests. European tree populations currently face an increasing number of extreme drought events. Understanding the response of today's forest trees to successive stress events is important for assessing their future under current climate scenarios. Using airborne imaging spectroscopy data collected over multiple years during peak greenness, we quantified the response of a temperate beech forest stand exposed to documented drought events in Switzerland in terms of changes in a spectral index of canopy water content. We then studied the link between the intraspecific genetic variation and the remotely sensed intraspecific trait variation. We performed a genome-wide association study using the genetic variation of 255 individuals and the remotely sensed reflectance information of the tree canopy. We aimed to 1) identify the total genetic contribution to the variation of remotely assessed drought responses and 2) find genetic differences associated with different drought responses of beech trees within a stand. We report on our findings as well as challenges inherent in estimating the genetic component of remotely sensed canopy trait variation by performing genome-wide association studies in real-world beech populations.

S2.P29. The genetic basis of spring phenology in European beech (*Fagus sylvatica*)

Geßner Cornelia, Lazic Desanka, Müller Niels A

Spring bud burst marks the start of the growing season that will be more advanced by climate change. The timing of bud burst is a critically adaptive process influencing the effective length of the growing season. Understanding the genetic basis of bud burst variation may contribute to predicting the adaptive potential in the face of climate change. Here, we explored spring phenology in a common garden in two consecutive years for 1800 individuals of European beech (*Fagus sylvatica* L.) originating from 100 populations from across the natural distribution range with greatly varying environmental factors. Interestingly, we observed that variation in spring phenology is mainly explained by individuals. A genome-wide association study (GWAS) with SNPs identified from whole-genome resequencing discovered a region on chromosome 6 that was strongly associated with bud burst. Notably, genotypic variation at this locus was not correlated with geographic origin of the individuals. Despite high trait heritability and a relatively large sample size our analyses reveal high missing heritability indicating high polygenicity. It will be exciting to use strongly increased sample sizes in future studies to finally elucidate the genetic architecture of a complex adaptive trait in a widespread forest tree species and assess predictive performance over large geographic distances. This may ultimately contribute to forest adaptation under climate change.

S2.P30. Identifying seed sources for highly adaptable oak forests at different spatial scales

Tourvas Nikolaos, Jansen Simon, Litmann Lars, Semizer-Cuming Devrim, Blyth Colette, Leigh Deborah Marie, Stepanovic Dawid, Rellstab Christian, Aravanopoulos Phil, Neophytou Charalambos

Given the pace of climate change, forest populations may become or already be maladapted to their local environment. Resilience in these populations may be enhanced through the translocation of forest reproductive material (FRM) that introduces adaptations from other populations already suited to future environmental conditions at the target site. However, large-scale FRM transfers involve risks ranging from climate model uncertainties to microenvironmental effects, outbreeding depression to mismatched biotic interactions. Leveraging adaptation at fine spatial scales for highly localized assisted gene flow is an overlooked resolution to these issues. Here, we used pooled whole-genome resequencing to genotype 114 white oak populations (*Quercus petraea*, *Q. pubescens*, *Q. robur*) across a large environmental gradient in Central Europe and in the Eastern Mediterranean basin. Our sampling strategy specifically targeted population pairs with contrasting soil water availability (high vs. low), within a close geographic proximity (<10 km). Using genotype-environment associations we identified genomic adaptation signatures with 29 topographic and bioclimatic variables (i) at the European continental scale and (ii) within the two distinct ecological study regions. Furthermore, utilizing our paired sampling design, associations between genomic regions and “arid”/“humid” ecotypes were investigated at the local scale. In many cases, comparing the results of the local vs the regional scale, we observed significantly more shared genomic regions associated with environmental adaptation than expected by chance. These findings indicate the potential of ecologically marginal sites as sources of pre-adapted FRM for low-risk assisted gene flow.

S2.P31. Being desiccation-sensitive in a warming climate: Insights into the germination and seedling development of European recalcitrant oak species

Carme Marion, Vicente Eduardo, Benito-Garzon Marta

The early life stages of trees are highly sensitive to climate change and crucial to fitness, but remain understudied compared to adults. This is particularly true for recalcitrant (desiccation-sensitive) seeds, which cannot withstand harsh climatic conditions after falling or be stored in seed banks, unlike orthodox seeds. To address this knowledge gap, we studied the effects of warming on germination and seedling development of three recalcitrant-seeded oak species – *Quercus suber*, *pubescens* and *petraea* – spanning Mediterranean, sub-Mediterranean, and temperate climates. We sowed 3,089 acorns from 8 populations per species at 15, 20, and 25 °C in climatic chambers. We assessed the effects of environment and population climate (historical: 1900-1960; maternal: 1960-2022; acorn maturation: 2023) on traits using generalized linear models.

Population climate and plasticity strongly shaped traits for all species, highlighting the need to consider early stages in climate resilience strategies. Warming reduced seedling fitness by lowering biomass, growth and survival. Germination percentage remained stable in this warming range, suggesting broader thermal tolerance. Populations and species responded differently to similar climatic drivers. Warmer populations germinated better in *Q. suber* - possibly reflecting an adaptation lag toward ancestral Miocene subtropical climates where the species emerged. *Q. petraea* and *Q. pubescens* were the most negatively impacted by warming, *Q. pubescens* being unexpectedly sensitive for a sub-Mediterranean species and showing contrasting population effects across traits (e.g. higher leaf protective pigments and root investment but lower germination and biomass in warmer populations). Reconsidering these patterns through the lens of species' evolutionary history invites further exploration.

S2.P32. Evaluating Genetic Variation in Leafing and Flowering Phenology in *Melia volkensii*

Musau Joshua, Kimiti Jacinta Kimiti, Cavers Stephen Cavers, Odee David Odee, Perry Annika Perry, Bush Emma Bush

Melia volkensii is a valuable tree species, indigenous to East Africa. It is of great interest for use in increasing tree cover in agricultural and degraded dryland landscapes. It is hardy to arid conditions and highly productive, delivering high quality timber. It is now the focus of a concerted effort to develop superior genotypes and improve seed production. In Kenya, two clonal seed orchards have been established as part of an improvement program, which bring together diverse genotypes of 100 clones sampled across the species' native range. While seed orchards rely on crossing among genotypes, concerted mating is only assumed and little is actually known about how factors like genetic variation, or seasonal and interannual environmental variation affect reproductive phenology in the species. To advance efforts to scale up quality seed production, this study aimed to quantify patterns of flowering and growth timing among genotypes in the seed orchards, compare patterns across sites, and determine the relationship between timing and seasonal and interannual climatic variation. Phenology was scored for every genotype weekly at both sites for a period of 108 weeks, and data were analysed to quantify patterns of leaf, flower and fruit production in *M. volkensii* and the environmental and genetic factors that govern their timing. With this detailed knowledge in hand, results were interpreted in terms of local adaptation, and recommendations for management of the orchards were prepared.

S2.P33. Genetic variation among progeny shapes symbiosis in a basidiomycete with poplar

Dauphin Benjamin, de Freitas Pereira Máira, Croll Daniel, Cardoso Anastácio Thalita, Fauchery Laure, Guinet Frédéric, Dutra Costa Maurício, Martin Francis, Peter Martina, Kohler Annegret

Forest trees rely on ectomycorrhizal (ECM) fungi for acquiring scarce resources such as water and nutrients. However, the molecular mechanisms governing ECM traits remain inadequately understood, particularly the role of intraspecific fungal variation in root-tip colonisation and trophic interactions. This study examined six ECM traits using *Pisolithus microcarpus*, an ECM fungus capable of forming ECM rootlets in poplar. A collection of 40 sibling monokaryons and their parental dikaryon was analysed through genome and transcriptome sequencing to examine quantitative trait loci, gene expression, and mating-type loci. These findings revealed a pronounced phenotypic continuum in poplar root colonisation by sibling monokaryons, ranging from incompatible to fully compatible strains. Genetic recombination among monokaryons was demonstrated, and genomic regions potentially involved in ECM-fungal traits were identified. Transcriptomic analysis revealed greater differentiation of transcriptomic profiles between fungal strains than between fungal tissues, and uncovered tissue-specific functional responses for ECM and free-living mycelia. Poplar exhibited distinct transcriptomic responses when interacting with different sibling monokaryons and the parental dikaryon. Allele sorting at 11 mating-type loci confirmed the species' heterothallic tetrapolar system. This study advances understanding of the genetic and transcriptomic mechanisms underlying ECM symbioses, highlighting intraspecific fungal diversity's role in forest ecosystem functioning.

S2.P34. Assessing the impact of *P. ramorum* to hybrid larch trees in Ireland

Guillardin Laura, O'Hanlon Richard, Newell Rory, Gibson Derek, Farrelly Niall

Japanese larch and European larch species have largely been affected by *Phytophthora ramorum* since its appearance in Ireland. However, there is a scarcity of studies looking at the level of tolerance or susceptibility of the hybrid larch towards this disease. Other studies have suggested that European larch may be more resistant to the pathogen, however, hybrid larch varieties produced in seed orchards may contain higher proportions of Japanese larch than European larch. Therefore, we aim to investigate the genetic makeup of the hybrids planted in three trial sites in Ireland that include trees from different sources. These sources include various geographic regions and are either pure European, pure Japanese or hybrid larch. Our hypothesis is that hybrids with maternal European genotypes may show higher levels of tolerance. To look into this, we will use molecular markers to identify the species and to define which type of hybrids exist in the trial sites. To confirm the presence of the fungus-like oomycete in the sites, we will place water containers and will use the *P. ramorum* LAMP detection kit. Finally, aerial images will be used to analyse the crown symptoms to assess the individual and species level of infection.

S2.P35. Dissecting Genetic Variation in Spectral Traits of Scots Pine Under Drought Stress

Čepl Jaroslav, Neuwirthová Eva, Chuchlík Jiří, Korecký Jiří, Stejskal Jan

Scots pine (*Pinus sylvestris* L.) spans across a wide ecological range, with local adaptations contributing to its extensive genetic diversity. To investigate population-specific drought responses, we conducted a 164-day drought and recovery experiment on seedlings from open-pollinated families originating from three seed orchards in the Czech Republic, representing contrasting provenances. Seedlings were cultivated under semi-controlled conditions and monitored using a high-throughput imaging platform capturing chlorophyll fluorescence and hyperspectral reflectance. A custom image-processing pipeline and machine learning approach enabled detection of both population identity and early drought effects based on spectral profiles. All 810 individuals were genotyped using the PiSy50K SNP array, which allowed reconstruction of genomic relationships and exploration of genetic variability in drought-related traits. We applied univariate linear mixed models to partition trait variance, estimate narrow-sense heritability, and quantify population-level differentiation (QST) across measured regions of the hyperspectral spectrum and experimental phases. The analysis across experimental stages revealed dynamic patterns of genetic variance linked to both family and population effects in hyperspectral traits. By integrating genomic data with physiological imaging, we observed population-specific responses and underlying genetic differentiation, suggesting regionally adapted variation that could aid Scots pine breeding for climate resilience and forest adaptation.

S2.P36. Pangenomics to study local adaptation and reproductive isolation in European white oaks

Couturier Florent, Piat Lucien, Denni Sukanya, Bezrukov Ilja, Weigel Detlef , Piotti Andrea, Magris Gabriele, Rellstab Christian, Valbuena Maria, Pinosio Sara, Szukala Aglaia, Plomion Christophe, Saez-Laguna Enrique, Duvaux Ludovic

European white oaks began diverging 10 million years ago and now differ in ecology, phenology, morphology, and adaptation. Despite this, they remain incompletely reproductively isolated, forming a species complex or syngameon. Traditional genomic approaches have failed to detect major regions of differentiation or adaptive genes, leaving their divergence largely unexplained. Structural variants (SVs), particularly inversions, have recently been shown to contribute to divergence by reducing local recombination. Here, we investigate their role using a pangenome variation graph approach. We generated 30 whole-genome haplotypes from eight oak (sub)species using long-read sequencing and built an oak pangenome graph with PGGB. This revealed striking contrasts among chromosomes in SV content and species discrimination. For example, chromosome 2 has low SV density, a high proportion of core nodes, and strong species resolution—harboring most known near-diagnostic SNPs. In contrast, chromosome 4 shows high SV density and weak species resolution. The lower SV density in more discriminating chromosomes suggests reduced local recombination and/or stronger selective constraints. These hypotheses are being tested by analyzing linkage disequilibrium, genetic divergence, and recombination rates along chromosomes, particularly around SVs. Annotation of the 30 haplotypes is underway to examine gene and transposable element content in candidate regions and identify relevant biological functions. To place these findings in a macroevolutionary context, we are developing a coalescent-based pangenome simulator. It will model various demographic and speciation scenarios while explicitly accounting for the role of SVs in the evolution of this long-lived species complex.

S2.P37. Elucidating the effect of single gene modifications on drought stress tolerance of poplars (*Populus*)

Alexander Fendel, Matthias Fladung, Tobias Bruegmann

Climate change and fast-changing fluctuations of local climate conditions strongly affect forest tree viability. Here, especially drought stress appears as a harmful factor; however, the underlying genes related to drought stress tolerance are still not well understood. The late initiation of reproductive organs in forest trees decelerates tree breeding and hinders the research for genetic characterizations. However, for suitable tree organisms, the in vitro culture and its subsequent biotechnological modification represents an excellent system for functional gene studies. We apply genetic engineering and genome editing mechanisms of single genes in in vitro-grown plants of the European poplar species *Populus × canescens*. Single genes, especially those potentially involved in stomatal aperture/density or proline accumulation, were either modified by CRISPR/Cas-generated loss-of-function mutations or constitutively overexpressed.

The rapid in vitro propagation of modified trees then provided optimal conditions for comparative genetic functional analyses. Modified trees were analysed on their altered drought stress tolerance under controlled stress conditions in the greenhouse. Amongst others, the improvement of survivability rates of more than 40 % could be observed in different genetically engineered trees compared to wild types. The in vitro culture approach enables the fast understanding of single gene contributions to the complex network of drought stress tolerance in trees. The identified key genes can be considered in targeted forest plant breeding approaches to obtain stress-tolerant trees, either by molecular selection from natural forests or via biotechnological approaches.

S2.P38. Genomic Diversity and Early Selection Between Trees and Offspring in *Fagus sylvatica*

Marieke Lenga, Christian Lampei, Katrin Heer, Lars Opgenoorth, Mona Schreiber

The health and ecosystem functions of temperate forests are threatened by extreme weather events such as the dry years of 2018, 2019, and 2022. Even European Beech (*Fagus sylvatica*), once considered less affected by climate change, shows increasing susceptibility to drought-induced dieback, crown thinning, and reduced growth. Notably, recent genomic studies have shown that individual trees within the same stand respond differently to drought, suggesting a potential genetic basis for drought resistance.

Fagus sylvatica produces vast numbers of seeds, of which only a few survive to maturity. This provides strong potential for natural selection, especially during years of climatic extremes. In such years, seedlings with stress-tolerant traits are expected to be favored, contributing to long-term adaptation.

While adult trees have been the focus of most genetic studies, much less is known about the younger generation and early selection dynamics. We investigated genetic differentiation between seedlings and adults to explore adaptation signals in natural beech populations.

We genotyped 540 seedlings and 540 adult *F. sylvatica* trees across the three regions of the Biodiversity Exploratories, a long-term ecological research platform with sites in northern, central and southern Germany. Using low-coverage whole-genome sequencing, we assessed genetic diversity and allele frequency differences to detect signatures of early selection and better understand the adaptive capacity of temperate forests.

Although seedlings and adults do not differ at the genome-wide level, PCA and Admixture analyses revealed weak but consistent regional structure, with partially overlapping genetic clusters. The southern population appears slightly more differentiated, possibly due to its higher elevation and distinct environmental conditions. While allele frequency differences were limited, genotype–environment associations with air temperature highlighted loci with contrasting patterns between seedlings and adults, suggesting possible signs of selection

Session 3 - Navigating Multiple Global Change Pressures: The Role of Phenotypic Variability

Thursday 20 November 09:00-13:00

Chair: Maurizio Mencuccini, Center for Ecological Research and Forestry Application - CREAM, Barcelona, Spain

Oral presentations

- 9:00 **Keynote - Mantova Marylou**
In the era of change: when genetics, physiology and modelling collide for more resilient forests
- 09:45 **Ramirez-Valiente Jose Alberto**
Plastic and evolutionary responses in hydraulic traits in a context of global change
- 10:00 **Tobias Brueggemann**
Ecophysiology meets molecular physiology and genetics: drought stress experiment with four European beech provenances
- 10:15 **Thomas Hay**
Architectural phenotyping of spruce trees based on TLS and QSMs
- 10:30 **Aida Solé Medina - online**
Genetic architecture and selection across populations and sexes in *Populus nigra*
- 10:45 Coffee break
- 11:15 **McNamara Simone**
Deciphering phenotypic variability in fitness-related leaf spectral traits in European white oaks
- 11:30 **Rozenberg Philippe**
From Annual Rings to Adaptive Response: Quantifying Phenotypic Plasticity in Douglas-fir
- 11:45 **Belmokhtar Nassim**
The use of Near Infrared Spectroscopy for high-throughput characterization of four European Forest Genetic Conservation Units
- 12:00 **Maurizio Mencuccini**
Environmental and genetic signals in continental scale variability in functional traits and growth of European trees
- 12:15 **Flash Poster session**

Keynote Session 3. In the era of change: when genetics, physiology and modelling collide for more resilient forests

Mantova Marylou, Castillo-Argaez Raiza, Perry Emily, Torres Eric, Clark Dylan J., Cinquini Andrew, Heintzelman Cross J., Ilinca Elisabeth, Cochard Hervé, Martin Timothy A., Peter Gary F., Sapes Gerard, Torres-Ruiz José M., Hammond William M.

Climate change is intensifying hotter-drought events globally, which threaten forest growth and increase tree mortality risk. Yet, the climate-resilience potential for growth and survival of many tree species remains largely unknown. Here we quantified physiological trait diversity across and within provenances, to identify trait combinations that may enhance climate resilience in *Pinus taeda* L, one of the most economically important forest species in the United States.

We sampled trees from provenances encompassing the species natural geographic and climatic range in a common garden located in Gainesville, FL, and phenotyped a suite of 20 traits associated with climate resilience. We predicted the time to hydraulic failure of each tree under a terminal drought, parameterizing a mechanistic model, SurEau, with observed trait values, and generated an ideotype tree in silico. We modeled tree performance across the Southeastern US under future climate scenarios.

Our results reveal high variability in traits across provenances with extreme values often exceeding 2 standard deviations from the mean. In our simulations, the ideotype outperformed the best existing provenance under terminal hotter-drought stress. However, the most climate-resilient existing provenance is projected to survive until the end of the century, even under worst-case climate scenarios. Nevertheless, it remains unknown to what extent *P. taeda*'s high intraspecific trait variation occurs in other species, including those restricted to much more narrow climatic distributions, or whether such variability reflects inherent plastic adjustments of traits to local environmental conditions.

S3.O1. Plastic and evolutionary responses in hydraulic traits in a context of global change

Ramirez-Valiente Jose Alberto, Poyatos Rafael, Blackman Chris J., Cabon Antoine, Castells Eva, Cochard Hervé, Creek Danielle, Delzon Sylvain, García-Valdés Raúl, Limousin Jean-Marc, Rosana López, Nicolas Martin-StPaul, Myriam Moreno, Lucy Rowland, Louis S. Santiago, Bernhard Schuldt, José M. Torres-Ruiz, Aude Valade, Jordi Martínez-Vilalta, Maurizio Mencuccini

Understanding how plants adjust their hydraulic system to the environment is essential to predict how these organisms will respond to global change. We compiled a dataset of more than 220 studies and conducted several meta-analyses to evaluate the plastic and evolutionary adjustments of hydraulic traits in response to air temperature, CO₂ concentration, irradiance, soil nutrient and water availability. We found that species plastically increased embolism resistance and sapwood area per leaf area under drier conditions, with a decrease in stem-specific hydraulic conductivity and water potential at the turgor loss point, which are consistent with adaptive responses. However, the increased embolism resistance was not sufficient to compensate the reduction in the minimum water potential implying lower safety margin from lethal hydraulic failure under drought. These results point towards a general critical increase in the risk of hydraulic failure in future drier environments. Plastic responses to increased soil nutrient content and irradiance not always aligned with those to drought, underscoring the potential of changes in irradiance and nutrition levels to modify plant hydraulic responses to climate change-driven droughts. Contrary to observation of trait conservatism in the studied traits in the phylogeny, responses to the environmental variation presented negligible phylogenetic signal, with species within the same evolutionary group presenting contrasting patterns of trait adjustments. Overall, our findings revealed that species exhibit phenotypic plasticity and evolutionary responses in hydraulic and drought tolerance traits that will be key to accommodating plant phenotypes to the new environmental conditions arising from ongoing global change.

S3.O2. Ecophysiology meets molecular physiology and genetics: drought stress experiment with four European beech provenances

Tobias Bruegmann, Alexander Fendel, Maike Woith, Friderieke Schwarzer, Alina Fomin, Sebastian Haß, Virginia Zahn, Boas Pucker, Matthias Fladung, Manfred Forstreuter

European beech trees (*Fagus sylvatica*) have a wide distribution range and face different climatic conditions. To investigate the varying drought stress tolerance of beech provenances, a provenance trial („Klimawald Berlin“) was established in Berlin, where individual experimental units (a group of trees) can be irrigated, while other units are influenced by naturally occurring drought stress in summer. Here, a drought stress experiment was initiated with one beech provenance each from Germany, France, Italy, and Spain. The trees were examined under different stress intensities and during the recovery phase after rewatering – using ecophysiological and molecular physiological analyses as well as RNA sequencing to analyse gene expression. The triad of analytical methods aims to provide a comprehensive picture of the stress response. The combination in this initial approach showed a differential picture of the provenances. While significant differences between the provenances were identified in some parameters (e.g., in the content of proline or malondialdehyde as markers for oxidative stress), other parameters showed uniform stress responses, e.g., in photosynthetic activity and stomatal conductance. Based on the sequenced leaf RNA, differentially expressed genes (DEGs) were identified for all provenances. The DEGs show differences and similarities in the genetic regulation of the stress responses of the four provenances. These insights into the different mechanisms by which beeches respond to drought provide approaches for further research on different provenances and the climate change adaptation of forest tree species.

S3.03. Genetic architecture and selection across populations and sexes in *Populus nigra*

Online

Aida Solé Medina, Nassim Belmokhtar, Philippe Rozenberg, Jonathan Feichter, Berthold Heinze, Camilla Avanzi, Andrea Piotti, Francesca Bagnoli, Sara Pinosio, Giovanni G. Vendramin, Maurizio Mencuccini, Christian Mestre Runge, Jill Sekely, Katrin Heer, Christopher Reudenbach, Lars Opgenoorth, Eduardo Notivol, Sanna Olsson, Ricardo Alia, Delphine Grivet

This study assesses the evolutionary potential of *Populus nigra* populations from Austria and Spain by integrating phenotypic variation, genetic architecture, trait correlations, and selection dynamics. Phenotypic traits were measured in 500 adult trees per population using field protocols, UAV imagery, and hydraulic vulnerability (P50) derived from near-infrared spectral curves. Genetic characterization of adults and juveniles with over 11,000 SNPs enabled estimation of trait heritability via Bayesian animal models incorporating spatial and environmental structure. A subset of SNPs was used to estimate individual effective fecundity.

Heritability estimates were generally low to moderate, yet posterior distributions revealed meaningful genetic control for key traits. P50 displayed sex- and population-specific heritability, particularly in Austrian males. DBH showed genetic determination in Spanish females and Austrian males, while height had moderate heritability in Spanish females. Crown area was non-heritable in Spain but strongly heritable in Austria, suggesting population-level genetic differentiation. Fecundity revealed moderate to high heritability in Spain but was mainly environmentally driven in Austria. Trait interdependence was revealed through Pearson and genetic correlations, especially among P50, DBH, and fecundity. Selection gradients, estimated via inverse Gaussian regression, indicated stronger selective pressures in Spain, particularly for growth traits in females. In contrast, weak selection in Austria suggests limited evolutionary response despite standing genetic variance. These results highlight the nuanced interplay between genetic variance and selective forces across environments and sexes. They underscore the value of integrative approaches for predicting tree responses to environmental change and reveal promising prospects for assessing adaptive evolution in natural populations.

S3.04. Architectural phenotyping of spruce trees based on TLS and QSMs

Thomas Hay, Tim Oberländer, Gaëtan Heidsieck

Norway spruce trees in Thuringia exhibit pronounced phenotypic plasticity, with lowland and highland ecotypes displaying distinct architectural adaptations. The highland ecotype is of particular interest because of its adaption to harsher winter conditions, which are likely to intensify due to climate change. This study aims to quantify architectural traits influencing physical resilience of spruce and to develop structural models reflecting phenotypic variability across ecotypes in central Germany. Using terrestrial laser scanning (TLS) data from 42 trees, we implemented an analysis pipeline leveraging and comparing three quantitative structural modelling (QSM) tools: TreeQSM, Simpleforest, and Treegraph. Outputs were standardized, and the precision of trait estimation and ecotype discrimination was assessed. Based on the QSMs, we analyzed stem profiles via polynomial fitting. We described primary branches as parabolas, and related their shapes to branch insertion height. Whorl patterns and tree silhouettes were quantified through point cloud reprojection, clustering, and machine learning methods. These analyses informed a synthetic, parametric 3D tree model. Among QSM tools, TreeQSM yielded the most robust and biologically plausible reconstructions, whereas Simpleforest and Treegraph had systematic deficiencies. The overall approach accurately captured major ecotypic differences, but occlusion in upper crown regions limited trait recovery. Overall, this framework supports robust stand-level architectural assessments and sets the stage for future work on second-order branching characterization and resilience testing. In particular, we will assess the resilience of synthetic tree models to snow and wind loads in physics simulations to guide breeding and conservation strategies under climate change.

S3.O5. Deciphering phenotypic variability in fitness-related leaf spectral traits in European white oaks

McNamara Simone, Blyth Colette, Graf René, Jansen Simon, Neophytou Charalambos, Rellstab Christian, Schuman Meredith C, Leigh Deborah M

Understanding how genetic and environmental factors shape fitness-related phenotypic traits is essential for selecting tree provenances adapted to future climates and preserving forest resilience. Quantitative genomics is a powerful tool to partition phenotypic variability into its additive genetic (which allows to estimate heritability) and environmentally driven (plasticity) components, especially when applied to multiple common gardens with replicated families. We developed a novel approach that incorporates genomic relatedness from low-coverage whole-genome sequencing into the “animal model” of quantitative genetics.

We applied this approach to two ecologically significant European white oak species, *Quercus pubescens* and *Q. robur*, which are expected to become increasingly important under future European climates due to their high temperature and (in the case of *Q. pubescens*) drought tolerance. We grew acorns from Central and Southern European provenances in two common gardens in Austria and Switzerland. Using spectral leaf reflectance measurements, commonly used in remote sensing, we derived traditional spectral indices such as chlorophyll concentration or the Normalized Difference Water Index (NDWI). We complemented this top-down approach with a data-driven, assumption-free analysis that leverages the full spectral signature to infer additional leaf traits. We found substantial phenotypic plasticity and moderate heritability in leaf spectral trait variation. We further show that using genomic relatedness from low-coverage whole-genome sequencing instead of pedigree-based estimates systematically shifts heritability estimates. This approach provides more robust insights for guiding adaptive forest management in the face of climate change.

S3.O6. From Annual Rings to Adaptive Response: Quantifying Phenotypic Plasticity in Douglas-fir

Sergent Anne-Sophie, Chauvin Thibaud, Dalla-Salda Guillermina, Cochard Hervé, Martinez-Meier Alejandro, Rozenberg Philippe

Climate change poses major challenges for long-lived forest trees, whose adaptive capacity may rely more on phenotypic plasticity than on evolutionary change. Phenotypic plasticity—the ability of a single genotype to modify its phenotype in response to environmental variation—may help trees cope with rapid changes such as drought, though it is not always adaptive. In this study, we assess whether phenotypic plasticity in Douglas-fir (*Pseudotsuga menziesii*) contributes to drought resistance and survival, using a retrospective approach based on annual ring microdensity profiles. Trees from four U.S. provenance regions (Washington, Oregon, coastal and interior California) were planted in two French common gardens. Reaction norms were constructed by regressing annual wood density variables against climatic variables to estimate inter-annual plasticity. We selected traits showing significant plasticity across a large number of individuals and tested their relationship with survival, a proxy for fitness. We further examined whether plasticity is linked to hydraulic traits such as cavitation resistance, known to influence drought-induced mortality in Douglas-fir, and whether provenance origin explains variation in plasticity. Results suggest that phenotypic plasticity of some tree-ring variables is adaptive, contributing to survival under drought, and varies among provenances in relation to the climate of origin. This supports the idea that plasticity can be under selection and evolve, offering short-term adaptive potential in the face of rapid environmental change. Our approach demonstrates how microdensity profiles can be used to assess adaptive plasticity and guide the selection of drought-resilient genetic material for forest management under climate change.

S3.07. The use of Near Infrared Spectroscopy for high-throughput characterization of four European Forest Genetic Conservation Units.

Belmokhtar Nassim, Boizot Nathalie, Touzet Orlane, Oumarou-Mahamane Ismael, Rozenberg Philippe

The phenotyping of extensive populations of European forest genetic resources is a key step in studying and understanding their potential for adaptation. However, traditional measurement methods are time-consuming and labor-intensive. To overcome these limitations, we explore the potential of Near-Infrared Spectroscopy (NIRS), which offers a rapid and cost-effective alternative for assessing growth- and function-related traits across entire genetic conservation units. A comprehensive chemometric workflow was applied, including spectral preprocessing to correct for additive and multiplicative effects, outlier detection and removal based on Principal Component Analysis, and the application of multiple regression algorithms Partial Least Squares Regression, Support Vector Machines, and Random Forests to assess the predictive performance of the four calibration datasets. For each species, two entire GCUs were fully sampled using short wood cores and analyzed by FT-NIR; these datasets were reserved as independent prediction sets. The performance of the developed models varied, with some achieving R^2 values exceeding 0.90. Predictive accuracy was primarily influenced by the number of available reference measurements and the range of trait variability. The validated models were then applied across the full GCUs, making them suitable for further and complementary ecological or genetic studies. Our study indicates that FT-NIR spectroscopy is a promising tool for predicting a wide range of traits in European forest species, providing valuable support for the research community, forest managers, breeders, and policymakers. These models can be further improved by increasing the size and diversity of the calibration datasets and by testing their transferability to portable devices, which would facilitate their use directly in the field.

S3.08. Environmental and genetic signals in continental scale variability in functional traits and growth of European trees

Maurizio Mencuccini, Ivan Scotti, Francois Lefevre, Laura Stewart, Forgenius consortium.

The relative roles played by plasticity and genetic differentiation in the intra-specific variability of plant functional traits and growth are generally investigated using replicated comparisons of provenances grown at common garden sites. Conversely, large-scale spatial patterns of intra-specific phenotypic variation (i.e., combining plasticity with extant genetic variability) are generally quantified using *in-situ* comparative studies. To determine the relative contribution of environment and genetics in determining large-scale spatial variability in the measured traits and growth, we used multivariate techniques borrowed from phylogenetics, by combining data on site-level variability in a set of functional traits with environmental and genomic data measured across 140 sites of seven common European tree species. We focused on the analysis of three functional dimensions, the leaf economics spectrum, a structural axis constituted by tree architectural traits and a third axis of carbon use efficiency in leaves and wood. In addition, we examined how the sensitivity of tree annual growth rates to an index of water availability across a 50-year period varied along the same gradients.

Intra-specific phenotypic variability was significantly related to environmental variables for all three functional trait axes. However, the explanatory power of these relationships was poor, with a high level of unexplained variance. Adding the genomics information from SNPs substantially increased the explanatory power of the model for all three trait axes. For the axis representing the leaf economics spectrum, the Bayesian BLUPs resulting from the multivariate models showed a highly significant association between inter-site climatic variability and trait values predicted from the SNPs distance matrix, suggesting that the environment-trait association was strongly moderated by genetic distance. For the remaining two axes, environment-trait associations driven by genetic distances were lower. However, highly significant associations between genetic distances and trait values were also found for these axes.

Although the study design does not neatly allow the separation of contributions of plasticity and genetic differentiation, our study suggests that continental-scale spatial variability in trait values and in growth of seven major European trees displays a significant genetic signal of population differentiation.

Poster presentations

S3.P1. Scaling of hydraulic capacitance at the organ-level and its ecological role in drought response

Flash presentation

Hernando Sonia, Martin-St. Paul Nicolas, Binks Oliver, Martinez-Vilalta Jordi, Mencuccini Maurizio

Pressure–volume (P–V) curves provide insights into plant water relations, characterizing phenotypic traits related to drought and climatic stress, such as hydraulic capacitance. Scaling analyses of plant hydraulic traits are essential for understanding plant ecophysiology and for their application at different scales from organ to ecosystem level. In this study, we use P–V curves to compare the scaling relationships of hydraulic capacitance before turgor loss between branches and twigs across ten tree species (*Populus nigra*, *Fagus sylvatica*, *Pinus pinaster*, *Pinus sylvestris*, *Abies alba*, *Picea abies*, *Pinus halepensis*, *Quercus robur*, *Pinus pinea* and *Malus sylvestris*). We also examine how these scaling patterns are associated with key functional traits related to drought tolerance, including turgor loss point, osmotic potential at full turgor, relative water content at turgor loss, bulk modulus of elasticity, symplasmic water fraction, and specific leaf area. Our dataset includes measurements from approximately 340 branches and twigs collected across 40 European sites. The results show that some species exhibit similar scaling patterns between organs, while others differ in slope or intercept. Although isometric scaling is predominant, allometric relationships are observed in certain species. In many cases, a higher intercept in the capacitance–size relationship in twigs suggests improved water retention. At the species level, this variation in hydraulic scaling is linked to traits that reflect both drought tolerance and resource-use strategies. Overall, our findings indicate that hydraulic capacitance scaling is organ- and species-specific, shaped by adaptive responses to water availability and climatic stress.

S3.P2. Different phenotypic plasticity for male and female reproductive allometry among *Pinus pinaster* provenances.

Flash presentation

Jose Climent, Nikolay Ivanov, Regina Chambel, Ricardo Alía

The modification of the allocation of resources between vegetative growth and reproduction is one of the most puzzling adaptive responses to climate change in forest trees, still poorly understood. This allometric change can indeed occur through genetic change across generations, but also in the short term by phenotypic plasticity. Previous research (Santos-del-Blanco et al 2012) confirmed an interesting ecotypic differentiation in male and female reproductive allocation among *Pinus pinaster* populations in a single test environment. In other species, unfavorable environments have been reported to induce greater (plastic) investment in early female reproduction. The objective of this study is to confirm whether the limiting environment induces higher relative investment in female reproduction compared to the male function in *Pinus pinaster*, and whether this pattern is consistent across provenances or, alternatively, with differences that can be interpreted as part of the ecotypic differentiation of this species. We used basic data on tree height and female and male strobili counts at the onset of the reproductive stage in two environmentally contrasted sites within a multi-site provenance trial. Results broadly fulfilled our hypothesis, yet with intriguing different behaviour of some provenances, even within genetic groups.

S3.P3. Early-age drought stress legacy in field grown Scots pine seedlings

Flash presentation

Štěpánová Kristýna, Lhotáková Zuzana, Neuwirthová Eva, Stejskal Jan, Čepl Jaroslav, Albrechtová Jana

Temperate forests are increasingly affected by climate change, particularly by more frequent and intense droughts. This raises demands on the drought resilience of tree species used in forest regeneration. Scots pine (*Pinus sylvestris* L.) is commonly planted in the Czech Republic and shows moderate drought tolerance, though local populations (provenances) differ in their response to water availability. The aim of this study is to explore whether young Scots pine in the field exhibit a stress legacy effect in the physiological and growth response related to drought exposure in very early age. Almost 800 seedlings of two Czech provenances (one upland and two lowland), whose genetic relationship is known from the genomic array, were planted in the forest plot at the age of two years. Half of these individuals were exposed to controlled drought in the growing season 2022 in the phenotyping unit. The seedlings were evaluated for growth traits (height, root collar diameter) and functional leaf traits (needle mass per area, fast chlorophyll fluorescence kinetics, photosynthetic pigment content, and VIS-NIR needle reflectance). Results show that early-age drought legacy remains detectable two years after stress, especially in growth traits. The legacy effect in leaf traits was found in needle water content, chlorophyll a/b ratio, and chlorophyll content. Needle reflectance showed no legacy effect but revealed significant differences among provenances. Heritability of growth traits was low (< 0.1), while some leaf traits, especially pigment ratios (Car:Chl_{a+b}), showed moderate heritability.

S3.P4. FORSOMICS: Studying Conifer Resistance Mechanisms to Bark Beetles in a Changing Climate: From Genes to Trees

Flash presentation

Rastislav Jakuš, Miroslav Blaženec, Natalie Korolyova

This research investigates the physiological and molecular mechanisms underlying Norway spruce (*Picea abies*) resistance to bark beetle (*Ips typographus*) attacks, with a focus on responses to abiotic stressors such as drought and heat. The primary aim is to identify genomic and transcriptomic markers associated with resistance by integrating controlled experiments and field studies on natural populations. Through advanced 'omics' approaches, the study examines variation in radial growth, secondary metabolite production, and gene expression among trees with differing resistance phenotypes. Experimental treatments under controlled conditions simulate environmental stress—drought, heat, and methyl jasmonate (MeJA) application—to assess biochemical and molecular responses. These insights are extended to mature trees in beetle-affected natural stands. Particular attention is given to classifying trees as primarily attacked, secondarily attacked, or surviving/resistant, using an integrated framework of genetic, dendroecological, and chemical analyses. The project also addresses challenges linked to the large and complex Norway spruce genome and inter-population variability in stress responses. Novel methodologies, including high-throughput sequencing, metabolomic profiling, and remote sensing, are employed to identify morphological and spectral indicators of resistance.

S3.P5. A reproducible geospatial tool for multi-scale mapping of canopy seed and productivity indicators in temperate forests using drone imaging and supervised machine learning

Flash presentation

Christian Mestre Runge, Jill T Sekely, Elliot Samuel Shayle, Dirk Zeuss, Christoph Heer, Lars Opgenoorth

Seed productivity is a key trait for understanding reproductive dynamics and forest resilience, yet direct field assessment is labour intensive, hard to scale and depending on the species not feasible. Consumer-grade, low-cost drones that capture visible-spectrum imagery at very low canopy height offer an alternative for detecting seed signals in structurally complex forests with strong spatial heterogeneity and asynchronous phenology. We developed and tested a reproducible, transferable workflow, orchestrated with link2GI, that integrates orthorectified images with 1.5–8 mm ground sampling distance and a machine-learning classification method to produce multi-scale maps of seed distribution in temperate forests. The approach begins with careful semantic indexing of training areas, proceeds with the derivation of synthetic predictors from the principal components of the imagery, and trains supervised models with class balance, parsimonious feature selection, and spatially blocked cross-validation. Reliability is mapped using a similarity indicator and an area-of-applicability surface. Applied to maritime pine (*Pinus pinaster*), European beech (*Fagus sylvatica*), Scots pine (*Pinus sylvestris*), and black poplar (*Populus nigra*) across eight genetic conservation units, the workflow attains robust classification accuracy and delivers multi-scale outputs: canopy-level maps of seed distribution and relative abundance, and, by aggregation, indicators of seed productivity and spatial distribution at the genetic conservation unit scale. These products are comparable across species and units, supporting adaptive management and providing an ecological basis for assessing resilience.

Session 4 - Breeding for Resilience: Integrating Novel Phenotyping & Genomics for Urgent Adaptive Solutions

Thursday 20 November 14:00-17:00

Chair: Jan Stejskal, Czech University of Life Sciences Prague, Czech Republic

Oral presentations

- 14:00 **Keynote - Fikret Isik**
Tree Breeding in the Age of Genomics for Climate Change: Challenges and Opportunities
- 14:45 **Carlos Trujillo-Moya**
Harnessing High-Throughput Phenotyping and Metabolomics to Reveal Intraspecific Variation in Drought Sensitivity of Norway Spruce (*Picea abies* (L.) H. Karst.) for Climate-Resilient Forestry
- 15:00 **Hayatgheibi Haleh**
Are fast growth and drought tolerance two opposed properties in conifers? Scots pine case
- 15:15 **Soto Álvaro**
Use of natural hybrids for *Q. suber* and *Q. ilex/Q. rotundifolia* breeding
- 15:30 **Chuchlík Jiří**
From Subjective to Objective Bud-burst Assessment: CNN-Assisted RGB Imaging in Norway Spruce Seed Orchard
- 15:45 **Milan Lstibůrek**
A dynamic breeding framework for bridging local adaptation and assisted migration
- 16:00 Coffee break
- 16:30 **Zavala-Paez Michelle**
The role of climate and interspecific gene flow in stomatal evolution across a *Populus* hybrid zone
- 16:45 **Sagariya Christi**
Genotyping error and its consequences for heritability estimation
- 17:00 **Chano Victor**
Genome-wide genotyping and epigenotyping strongly correlated in Norway spruce breeding material
- 17:15 **Irene Cobo-Simón**
Benchmarking Genomic Selection Methods for Nut Yield in Stone Pine (*Pinus pinea*)
- 17:30 **Flash Poster session**

Keynote Session 4. Tree Breeding in the Age of Genomics for Climate Change: Challenges and Opportunities

Fikret Isik

Climate change, rising demand for forest products, and increasing biotic and abiotic stresses pose major challenges for sustainable forestry. Advances in genomics, computing, and high-throughput phenotyping now offer powerful tools to address these issues. Forest geneticists can leverage these modern technologies to manage genetic diversity, enhance long-term adaptability and develop resilient tree varieties. Using locally adapted species is essential to mitigate biotic and abiotic stresses on both natural and managed forests.

This talk highlights examples of applying genomics and computational approaches in *Pinus taeda* breeding in the southern United States.

Fusiform rust disease remains a major threat to pine forestry. Two QTL linked in repulsion on linkage group two were identified and validated using GWAS and bulked-segregant transcriptome analyses. Progeny inheriting both QTL exhibited near-complete immunity to diverse pathogen isolates.

The efficiency of genomic selection (GS) was evaluated in a two-generation *P. taeda* population, achieving realized genetic gains per year higher than conventional breeding. Genetic relatedness and training population size were key determinants of prediction accuracy ($r = 0.51$). Recurrent GS is planned for implementation in 2026.

A major QTL on linkage group eight was associated with dwarfism across eight *P. taeda* families, following Mendelian 1:1 segregation. These heritable mutations may enable the development of dwarfing rootstocks for seed orchards.

For parentage analysis, an AgriSeq-targeted GBS panel and an R package were developed. The original C++ code of Grashei et al. (2018) was consolidated into a single, efficient, cross-platform framework and integrated with the Rcpp interface in R. The improved software provides visualization tools, handles large genotyping datasets, and achieves parentage assignment accuracies exceeding 99%.

S4.O1. Harnessing High-Throughput Phenotyping and Metabolomics to Reveal Intraspecific Variation in Drought Sensitivity of Norway Spruce (*Picea abies* (L.) H. Karst.) for Climate-Resilient Forestry

Ahmad Muhammad, Roach Thomas, Kranner Ilse, Arc Erwann, Seitner Sebastian, Jez Jakub, Chakraborty Debojyoti, Ciceu Albert, Espinosa-Ruiz Ana, Martínez-Godoy Maria Ángeles, Clara Priemer, Marta Karolak, Sonja Mader, Marcela van Loo, Carlos Trujillo-Moya

Drought stress is a major constraint limiting the distribution of Norway spruce. Provenance trials, a common approach to assess adaptive variation among populations, are limited due to the finite number of sites and seed sources involved, as well as their labour-intensive nature. To face this challenge our group developed a novel multi-sensor high-throughput plant phenotyping (HTPP) approach to assess the drought stress adaptation potential of Norway spruce provenances (Ahmad et al. 2025) at the most critical life stage of the tree, the seedling stage. Using this HTPP approach, we assessed natural variation in drought sensitivity across 66 populations (4,000 individuals) spanning the species' entire distribution. This was combined with targeted metabolomics to investigate associated metabolic signatures. Our results revealed substantial variation in drought sensitivity among populations. Climate-trait associations support the role of local adaptation in shaping growth-related sensitivity. Targeted metabolomic analysis confirmed the involvement of known drought-associated metabolites in drought mitigation such as glutathione derivatives, xanthophylls, carotenoids, and tocopherols. In addition, monoterpenes and sesquiterpenes clearly differentiated contrasting populations based on their photosynthetic performance under drought, revealing divergent physiological response strategies present across all climatic clusters and confirming the absence of a consistent latitudinal cline in drought sensitivity, contrary to expectations. In summary, our findings highlight the value of combining HTPP and metabolomics to explore the intraspecific variation of Norway spruce germplasm and guide provenance selection. The identified metabolic markers offer strong candidates for future screening and targeted breeding, supporting adaptive forest management strategies resilient to climate change.

S4.02. Are fast growth and drought tolerance two opposed properties in conifers? Scots pine case

Hayatgheibi Haleh, Gil Muñoz Francisco, Niemi Juha M, Ranade Sonali, García Gil Rosario

Genetic degradation is a significant ecological and economic threat to forest ecosystems. In Sweden, forests result from a mix of natural regeneration and planting with both unenhanced and genetically improved seeds from domestic and foreign sources. However, the long-term effects of tree breeding on forest resilience, adaptability, genetic diversity, and wood quality remain poorly understood. To investigate this, six Scots pine (*Pinus sylvestris*) forests in northern Sweden—three naturally regenerated and three planted with seed orchard-derived material—were selected. Seeds were collected and evaluated under controlled greenhouse conditions using a common garden assay to assess potential for early selection for drought tolerance.

A novel, machine learning-based, high-throughput phenotyping platform was employed to monitor growth and development under both drought and control conditions. In addition, a root phenotyping experiment was conducted to assess root system architecture, enabling evaluation of root traits associated with drought resilience and their genetic basis. Complementing these assays, xylem core samples from mother trees are being analyzed to identify physiological and structural traits linked to historical drought response. This integrative approach, combining greenhouse phenotyping, root architecture analysis, and xylem core data, aims to identify early, heritable indicators of drought tolerance, supporting climate-adaptive breeding and reforestation strategies in conifer species.

S4.03. Use of natural hybrids for *Q. suber* and *Q. ilex/Q. rotundifolia* breeding

Moya Eva, Arribas Claudia, Agüera Sonia, de Burgos Gonzalo, López de Heredia Unai, Soto Álvaro

Cold and drought are the main climatic factors limiting cork oak occurrence and productivity. Hybridization with holm oak could provide cork oak with a higher tolerance to these factors, but it can also mean a decrease in cork quality, since hybrid individuals have lower quality cork and are usually discarded for production. ddRADseq analysis of natural hybrid progenies have allowed us to identify a large number of discriminating markers between both species, distributed along the genome, and have selected a subset of markers for the precise estimation of introgression levels. As a secondary outcome, we have also selected markers for the unequivocal discrimination of genotypes at the individual level (even between half-siblings) in a routine and affordable manner, useful for the registration and control of basic materials in breeding and production programs. Monitoring of common-garden trials including hybrid progenies showed considerable variability in the morphometric, stomatal density, growth, and cold resistance characteristics of the hybrid progenies. Among them, some families and individuals showed high performance, with characteristics superior to the parental ones. These results suggest that the selection of hybrid material is feasible for its integration into genetic improvement programs aimed at increasing cold resistance in cork oaks. In addition, we have identified candidate genes for bark formation by RNAseq analysis of pure and hybrid individuals, and targeted sequencing is allowing the identification of SNP and structural polymorphisms. Epigenetic, additive and non-additive effects are currently under study, with the final goal of helping in marker-assisted breeding programs for cork production.

S4.O4. From Subjective to Objective Bud-burst Assessment: CNN-Assisted RGB Imaging in Norway Spruce Seed Orchard

Chuchlík Jiří, Čepl Jaroslav Čepl, Stejskal Jan

As climate change intensifies, the need for resilient forest systems and adaptive breeding strategies becomes increasingly urgent. Norway spruce (*Picea abies*), a cornerstone species in European forestry, is vulnerable to phenological mismatches driven by shifting climatic cues. Accurate phenotyping of adaptive traits like bud-burst timing is essential for breeding programs targeting climate resilience. However, current practices rely on subjective visual scoring methods such as the Kruttsch index, which are prone to observer bias and inconsistency across scorers and time. This reduces precision in genetic evaluations and obstructs the identification of resilient genotypes. To address this, we developed a high-throughput phenotyping pipeline integrating RGB imaging with deep learning. Using a custom-trained YOLOv7 convolutional neural network (CNN), we segmented and quantified bud-burst phenology in a clonal seed orchard. Bud-burst progression was expressed as the ratio of bud-burst pixels to total needle area. Our CNN-based assessment correlated strongly ($r = 0.75$) with traditional methods, yet the imperfect correlation underscores observer-induced variability in subjective scoring. The proposed method results, analyzed by linear mixed model, exhibited higher broad-sense heritability ($H^2 = 0.55$) than subjective scoring ($H^2 = 0.45$), retaining the same standard error. This study shows how novel phenotyping tools can enhance the selection of climate-adaptive traits. By improving potential reproducibility and scalability, CNN-assisted RGB imaging supports robust genetic analysis and the development of resilient tree populations. Our work contributes to an integrated framework where phenomics, genomics, and environmental modeling converge to accelerate forest adaptation.

S4.O5. A dynamic breeding framework for bridging local adaptation and assisted migration

Milan Lstibůrek

Assisted migration is increasingly promoted as a strategy to adapt forest ecosystems to climate change by moving populations across large spatial scales to match projected climatic conditions. While this approach provides a practical way to utilize existing natural adaptation across a species' range, it may overlook the importance of maintaining and enhancing local adaptation. Therefore, ongoing breeding efforts are still needed to strengthen local adaptation within breeding populations that are periodically enriched with genetic material from distant sources, ideally using the pollen-based assisted migration. To address this need, a novel breeding concept called Rolling Front Landscape Breeding was introduced. This framework adapts conventional recurrent selection strategies for outcrossing species by embedding them within a shifting environment. Continuous genetic evaluation across forest stands of consecutive age classes across a range of ecological conditions is integrated with genomic tools and drone-based phenotyping to enable real-time tracking of adaptive performance. Optimization algorithms support spatial planning and timely replacement of genotypes, enabling a continuous adaptive response without reliance on fixed breeding cycles.

S4.06. The role of climate and interspecific gene flow in stomatal evolution across a *Populus* hybrid zone

Zavala-Paez Michelle, Keller Stephen, Holiday Jason, Fitzpatrick Matt, Hamilton Jil

Stomata play a key role in regulating plant responses to changing environmental conditions. Where sister species differ in stomatal traits, interspecific gene flow can shape the evolutionary trajectory of these traits by generating novel recombinant genotypes upon which selection can act. To test how gene flow and selection influence stomatal trait variation, we sampled 544 genotypes across six latitudinally distributed transects spanning the natural hybrid zone between *Populus trichocarpa* and *P. balsamifera*. Each genotype was whole-genome re-sequenced and clonally propagated across multiple common garden environments. Phenotypic data suggested that species-specific differences have evolved between *P. balsamifera* and *P. trichocarpa*, with *P. balsamifera* having stomata primarily restricted to the lower leaf surface and *P. trichocarpa* showing a more even distribution across both surfaces. Hybrids more closely resemble *P. trichocarpa* but exhibit greater variability. Using admixture mapping, we identified several candidate genes associated with stomatal trait variation in hybrids including TWIST, a candidate gene for stomatal distribution. Geographic cline analysis for TWIST and additional candidate genes suggests that climate variation across the six latitudinally distributed contact zones has influenced the distribution of genetic ancestry underlying stomata distribution, rather than species barriers. These results emphasize the importance of climate in shaping the evolution of stomatal traits in *Populus* and demonstrate how interspecific gene flow generates novel recombinant genotypes that may enhance adaptive potential in changing environments.

S4.07. Genotyping error and its consequences for heritability estimation

Sagariya Christi, Lstibůrek Milan

Genomic relationship matrices are increasingly used across the biological sciences to estimate genetic parameters. Although genomic data provide powerful insights, their vulnerability to genotyping error is overlooked. In this study, we investigate how different types and levels of error in SNP data affect estimates of heritability. We found that even small error rates, within the range of current genotyping technologies, can introduce substantial bias. These distortions are particularly evident with dense SNP panels. Our findings emphasize the need for rigorous data quality control and the continued development of statistical approaches that account for uncertainty. This work serves as a caution: genomic-based relationships are valuable, but their effectiveness depends on the accuracy of the marker data on which they rely.

S4.08. Genome-wide genotyping and epigenotyping strongly correlated in Norway spruce breeding material

Chano Victor, Asiegbu Fred O., Haapanen Matti, Krutovsky Konstantin V., Wang Kai, Gailing Oliver

Norway spruce (*Picea abies* (L.) Karst.), one of the most important tree species in Europe, is nowadays threatened by challenging environmental conditions and associated pests and diseases. Leveraging breeding programs and genomic selection strategies for this species are crucial, and their efficiency can be greatly enhanced by incorporating both genome- and epigenome-wide variation in breeding families and natural populations. In this work, we used exome-capture and targeted-bisulfite sequencing to both genotype and epigenotype 620 Norway spruce seedlings from two sample sets: 218 individuals from 17 breeding full-sib families, and 402 individuals from 26 open-pollinated natural stands as source of new (epi)genetic material. Data filtering yielded a set of high-quality single nucleotide polymorphisms (hqSNPs), which clustered according to the genetic lineages established by controlled breeding crosses, whereas individuals from natural stands exhibited no genetic structure. These SNPs were used to perform both genome- and epigenome-wide association studies (GWAS and EWAS) with disease resistance. Clustering of differentially methylated positions (DMPs) across CpG, CHG, and CHH methylation contexts showed a strong correlation with genomic data in the breeding families. In contrast, the correlation between SNPs and DMPs in natural samples was weaker, particularly for CHG and CHH epimarkers. EWAS also revealed epimarkers significantly associated with disease resistance. The strong correspondence between genetic and epigenetic variation in breeding families indicates that DNA methylation patterns might be under genetic control, and a combined analysis of genomic and epigenomic data provides a more comprehensive framework for genomic selection in Norway spruce breeding programs.

S4.09. Benchmarking Genomic Selection Methods for Nut Yield in Stone Pine (*Pinus pinea*)

Irene Cobo-Simón, Francisco Gómez-Prieto, Ainhoa Calleja-Rodríguez, David Macaya, Sanna Olson, Sven Mutke, Ricardo Alía, Juan J. Robledo-Arnuncio

Stone pine (*Pinus pinea* L.) is an emblematic Mediterranean species valued for its edible nuts. Despite long-standing breeding efforts in Southern Europe, genomic tools have only recently become available to accelerate selection for nut production. Here, we compare three genomic prediction approaches—genomic best linear unbiased prediction (GBLUP), a Bayesian regression model (BayesC π), and a machine-learning algorithm (Random Forest)—to predict key traits in *P. pinea*. We genotyped 250 trees from diverse Iberian provenances planted in a common-garden trial using a commercial SNP array (5,671 markers). Phenotypic data comprised diameter at breast height (DBH), total number of mature cones per tree, and mean cone weight, each assessed in multiple years. Using stratified cross-validation, we will estimate predictive ability (Pearson's r) and accuracy (root-mean-square error, RMSE) for each trait and method, and benchmark computational requirements. We anticipate that GBLUP will serve as a robust baseline, BayesC π may enhance prediction for traits with unequal marker effects, and Random Forest will capture complex, nonlinear genotype-phenotype relationships. By identifying the optimal prediction framework, this study aims to enable early selection of superior genotypes for high pine-nut yield. Our results will provide a practical blueprint for integrating genomic prediction into stone pine breeding programs, ultimately accelerating genetic gain for seed production in this commercially important species.

Poster presentations

S4.P1. Environmental impact on gene expression activity during *Fagus sylvatica* L. seed germination

Flash presentation

Pers-Kamczyc Emilia, Suszka Jan, Pawłowski Tomasz A

The occurrence of a species is contingent upon the reproductive capabilities of its individuals, as evidenced by seed quality. Recent observations have indicated a decline in the seed quality of woody plants, including the common beech (*Fagus sylvatica* L.). The European beech thrives across a diverse range of environmental conditions and has developed various physiological adaptations, one of which is the presence of deep physiological seed dormancy. The geographical distribution of beeches, coupled with the environmental heterogeneity, has facilitated the emergence of ecotypic variation to accommodate local environmental conditions. Given that global climate change may alter species distribution, it is important to understand the biology of beech seed germination, particularly in terms of gene expression activity.

In our study, we collected common beech seeds from four distinct populations, each characterized by unique habitat conditions, to elucidate the influence of environmental factors on seed dormancy regulation. The seeds underwent stratification, and their germination capacity was assessed. Our analysis included beech embryonic axes isolated from seeds before stratification, post-dormancy, and during germination. We employed next-generation sequencing (RNAseq, Illumina) for transcriptome analysis, followed by differential gene expression (DGE) analysis. The data obtained facilitated the identification of marker genes corresponding to specific stages of the beech seed germination process, as well as potential markers related to seed quality in response to environmental conditions.

S4.P2. Transcriptomic Differences in Early Drought Responses among *Cryptomeria japonica* Genotypes

Flash presentation

Nose Mine, Nagano Soichiro, Matsushita Michinari, Takashima Yuya, Hirao Tomonori

Climate change is predicted to increase not only average temperatures but also the number of consecutive dry days, thereby exacerbating drought risk for forest trees. *Cryptomeria japonica* (sugi), a commercially and ecologically important species in Japan, may be particularly vulnerable during the early post-planting phase when water availability is critical for seedling establishment. To simulate such conditions, we conducted a drought stress experiment in which irrigation was withheld after initiation of the experiment. A broad range of drought tolerance was observed among genotypes. To elucidate the molecular mechanisms underlying this variation, we performed transcriptome analysis to compare the early stage of drought responses of several genotypes of *C. japonica*. Shoot samples were collected at multiple time points (0, 9, 16, and 23 days after irrigation was withheld), prior to the onset of visible wilting. Total RNA was extracted and subjected to RNA sequencing to examine gene expression dynamics during the early phase of water stress. Differential expression analysis revealed distinct transcriptional profiles between genotypes. These results provide mechanistic insight into the early molecular responses associated with drought tolerance in *C. japonica* and contribute foundational knowledge for the selection and breeding of climate-resilient genotypes.

S4.P3. Evaluation of comparative trials of the *Pinus sylvestris* Seed Orchard at the Valsaín CNRGF

Flash presentation

Miguel Nemesio Gorriz, Jose Climent Maldonado, Enrique Sastre Callejo, Ángel Sanz Martín, Pilar Duránte Jiméñez, David León Carbonero, Cruz Anegón Esteban, Felipe Pérez Martín

Scots pine (*Pinus sylvestris*) is a pine species that covers approximately 900,000 hectares primarily in mountainous areas of Spain. In the forests of Valsaín, Scots pine predominates over most of its 10,672 hectares and is managed for timber production, with the wood from the Valsaín pines being of excellent quality. There is a *Pinus sylvestris* seed orchard at the CNRGF of Valsaín composed of selected mother trees from the Valsaín forests based on their vigor, form, and growth with the aim of producing quality seed. To assess the superiority of the reproductive forest material originating from the seed orchard, two progeny trials (Riaza and Vaquerizas) and two comparative trials (Mujer Muerta and Pradera de Navalrey) were established. After analyzing the progeny trials in 2017, the evaluation of the seed orchard materials in the two comparative trials remains. This study presents the results of the analysis of dendrometrical data collected in these trials, comparing them with previous results from the progeny trials.

S4.P4. Dissecting the Genetic Architecture of *Ulmus minor*'s Resistance to Dutch Elm Disease.

Flash presentation

Miguel-Pizarro Adrián, Robledo-Arnuncio Juan José, Cobo-Simón Irene, Macaya-Sanz David

Dutch elm disease (DED), caused by the fungal pathogen *Ophiostoma novo-ulmi*, has devastated populations of field elm (*Ulmus minor*) across European lands. Despite significant breeding efforts, the underlying genetic architecture conferring resistance remained largely unresolved. In this study, we conducted a quantitative trait loci (QTL) analysis using controlled crosses of *U. minor* to identify genomic regions associated with resistance to DED. Phenotypic and genotypic data were obtained from a population of 563 individuals, including five parents and two controls. The experimental population, derived from multiple families with varying but overall high resistance levels, was phenotyped for resistance through artificial inoculation in the fourth growth season. High-density SNP genotyping was performed using restriction site-associated DNA sequencing (RAD-seq), and a high-resolution genetic linkage map was constructed. The integration of phenotypic and genotypic data enabled the identification of QTLs associated with resistance-related traits across families. These findings enhanced our understanding of the polygenic nature of DED resistance in *U. minor* and provided molecular tools for marker-assisted and genomic selection. Moreover, this study shed light on the potential for pyramiding resistance alleles in future breeding programs and contributed to the ecological restoration of elm populations affected by DED.

S4.P5. Landscape Breeding: A new paradigm in forest tree management using remote sensing and AI.

Flash presentation

Nordström Annica, García Gil Rosario,

Our main goal is to develop a digitized game-changing Norway spruce breeding strategy that overcomes the limitations of conventional breeding. Landscape breeding aims to accelerate forest tree improvement by operating directly on commercial forests and accounting for climatic and environmental variables. We will build models from ultra-high-resolution remote sensing data to access canopy, branch allometry, stem volume and quality in forest field trials. Then construct predictive models to access frost damage and phyllosphere diseases traits from airborne multispectral high-resolution images in sapling field trials. Finally, we will integrate ultra-high resolution laser scanner phenotyping, multispectral images, and molecular markers to monitor genetic diversity, estimate realized genetic gain and increase the accuracy of selection to accelerate tree selection. To achieve this, we have five work packages. One for finding new methods for the assessment of canopy branch allometry, stem volume and quality (remote sensing). Another one to develop new models to predict abiotic damage. One to develop a new remote sensing model to predict phyllosphere diseases. One to find the best genomic tool for tree selection, and finally, one for implementation of Landscape Breeding in commercial plantations.

S4.P6. Resilience to drought events in Finnish Scots pine breeding populations

Flash presentation

Kavlak Alper, Kärkkäinen Hanni, Mäkinen Harri, Tikkasalo Olli-Pekka, Haapanen Matti, Kärkkäinen Katri, Kujala Sonja

Climate change is increasing the frequency and severity of drought events in Nordic forests, posing significant risks to tree growth and forest health. We investigated genetic variation in drought resilience indices within Finnish Scots pine (*Pinus sylvestris*) breeding material. Our study included 1,457 progeny trees from controlled-cross breeding trials in Tuusula and Hankasalmi, representing distinct breeding zones. Tree-ring widths were measured from wood cores using microdensitometry to calculate yearly Basal Area Increment (BAI). We primarily evaluated resilience using general resilience indices—resistance, recovery, resilience, and relative resilience. Additionally, two complementary indices—average growth reduction and average recovery rate—will be calculated and included in subsequent analyses.

Drought intensity was quantified using the Standardized Precipitation Evapotranspiration Index (SPEI), with June SPEI best explaining the average annual BAI in the trials. Genetic markers (31,329 SNPs) were genotyped to assess heritability through genomic BLUP mixed models, incorporating block and trial age as fixed factors. Heritabilities varied between sites, indices, and stress years, with a stronger genetic component identified in Hankasalmi ($h^2 = 0.15\text{--}0.32$) compared to Tuusula ($h^2 = 0.03\text{--}0.16$). These preliminary findings demonstrate a meaningful genetic basis for resilience in Scots pine, suggesting promising opportunities for enhancing drought resilience through selective breeding. Further research with expanded datasets and additional locations is essential to confirm these findings and explore genetic correlations with conventional breeding traits

S4.P7. The triad of tree biotechnology

Tobias Bruegmann, Virginia Zahn, Alexander Fendel, Alice-Jeannine Sievers, Susanne Jelkmann, Matthias Fladung

Tree breeding is slow due to the long generation cycles of forest trees. The use of biotechnological methods for gene characterization could significantly accelerate tree breeding, which could become necessary for climate change adaptation. However, biotechnological methods are not available for the vast majority of forest tree species. Thus, we seek to transfer biotechnological methods such as tissue culture, genetic transformation, and genome editing to recalcitrant tree species. Based on the working technologies in poplars (*Populus*), the currently severely impaired European beech (*Fagus sylvatica*) in particular is in focus for expanding the molecular toolbox. In addition, work is ongoing on pedunculate oak (*Quercus robur*), common ash (*Fraxinus excelsior*), and the invasive tree species *Ailanthus altissima*. The goals of tissue culture include establishing sterile cultures from wild populations and testing protoplast isolation and regeneration. Genome editing involves testing different transformation methods such as Agrobacterium-mediated transformation and protoplast transformation. If one of these methods is successful in the recalcitrant tree species, vectors for genome editing will be used to knock out selected candidate genes. In addition to simple CRISPR/Cas9 genome editing, advanced techniques such as the use of Cas12a or D10A nickase are carried out. Among others, one aim is to knock out selected candidate genes using CRISPR/Cas editing vectors in order to characterize the involvement of individual genes in drought stress tolerance in trees. The results can contribute to breeding research and accelerate the adaptation of trees to climate change.

S4.P8. Use of high-throughput plant phenotyping in Norway spruce seedlings to study early differentiation of crown morphotypes

Chano Victor, Trujillo-Moya Carlos, Hay Thomas, Ahmad Muhammad, Jez Jakub, Seitner Sebastian, Schöndorfer Selina, Helfenbein Paula, Müller Markus, Gailing Oliver

In Norway spruce (*Picea abies* (L.) H. Karst.), trees from low-elevation provenances usually show broad crown phenotypes with comb-like branches, while high-elevation trees display narrow crown phenotypes with flat branches. This variation in crown morphology is suggested to reflect adaptive differentiation imposed by environmental selection, mainly driven by temperature and altitude gradients. Understanding these phenotypes at early developmental stages is crucial for predicting responses to different environmental scenarios. In this work, we used high-throughput plant phenotyping (HTPP) to analyse differences between Norway spruce seedlings from a high- and a low-elevation provenance. We first found significant differences in germination rates between the two morphotypes. In addition, 300 ten-weeks-old seedlings per provenance were evaluated using HTPP, measuring and collecting data on 3D structure (e.g., height, diameter, projected crown area and convex hull area), RGB imaging (i.e., needle color indices), hyperspectral imaging (VNIR and SWIR), and chlorophyll fluorescence. We found significant differences between the two morphotypes in a wide range of phenotypic parameters, including structural growth (as measured by height and convex hull area), needle color indices, and key chlorophyll fluorescence parameters such as non-photochemical quenching (NPQ), and various indicators of Photosystem II (PSII) activity and efficiency (e.g., Φ PSII and QYmax). These findings highlight early divergence in morphology and physiology between Norway spruce ecotypes from contrasting altitudinal environments, detectable through advanced phenotyping methods.

S4.P9. Pathogen as Partner: Integrating Fungal Effectors into Tree Improvement for Bioadaptive Timber Systems

Andrew Gennett

While breeding for resistance continues to deliver resilient forests through genomic technologies, new frontiers now ask how tree improvement programs will adapt to transformative applications beyond the forest. From the perspective of Engineered Living Materials (ELMs), the *Cronartium–Pinus* pathosystem offers a model for next-generation biomaterials to expand our concepts. Rather than pursuing resistance, we seek for tolerance as a breeding goal for living mass timber systems, where pathogens act as biological agents inducing phenotypic plasticity beyond the classical botanical form. At the intersection of Mass Timbers and Baubotaniks, host–pathogen interactions offer morphogenetic signals as emerging frontier to explore spatial logic for breeding beyond the forest. Specifically, *Cronartium quercuum* f. sp. fusiforme (Cqf), the causal agent of fusiform rust in *Pinus taeda*, induces increased vascular architecture and secondary growth. Both traits are critical for successful grafting and integrative living structures. Systems-level applications of plant tissue and fungal co-cultures are emerging as readily applicable directions, yet interpreting these living materials in a design-integrated context presents novel technical, ecological, and cultural challenges. As forests and cities alike continue warming under a changing climate and declining biodiversity, this project draws together forestry, fungal developmental biology, and architectural biomaterials to propose expanded breeding goals for bioadaptive timbers in the urban setting. By reconceiving pathogens as biodesign agents, this project contributes a speculative but actionable vision for resilient plant system, one where emerging genomic insight is coupled with creative ecological integration for live botanical architecture.

S4.P10. Inheritance of stem endophytic fungi and their correlation with resistance to Dutch elm Disease

Macaya-Sanz David, Martin Juan Antonio

Since the beginning of 20th century, Dutch elm disease pandemics have decimated elm populations across Europe and North America. Research has hypothesized some mechanisms of pathogenicity of the fungus and of resistance of the tree, but there is still a considerable lack of knowledge that hinders efficient tailored breeding. Among the sources of resistance, elements of the stem **endophytic** fungal flora have been found to covary with resistance. This opens new avenues to fight the disease. One of them is using the endophytic composition as a phenotype to select for in breeding programs, provided that narrow-sense heritability is high enough. Using these traits as phenotype for indirect selection, this approach could offer two advantages: (i) evaluating fungal composition is much cheaper and can be evaluated earlier than the traditional assessment of disease resistance, accelerating breeding turns; and (ii) providing that the genetic correlation among endophytic composition and resistance is high, it could produce elevated selection gains. Here, we present an evaluation of the narrow-sense heritability and additive genetic correlation with resistance of the stem endophytic mycoflora using a set of controlled crosses of resistant elms with large progeny numbers

Session 5 - Prioritising forest conservation through genetic diversity

Friday 21 November 09:00-13:00

Chair: Giovanni Giuseppe Vendramin, Institute of Biosciences and BioResources, National Research Council of Italy, Florence, Italy

Oral presentations

- 09:00 **Keynote - Victoria Sork**
Genetic and genomic strategies for conservation of natural populations of California oaks
- 09:45 **Fady Bruno**
Native trees of the Mediterranean region: distribution, diversity and conservation challenges
- 10:00 **Kravanja Marija**
Does genetic diversity underpin forest resilience?
- 10:15 **Farsakoglou Anna-Maria**
Can we detect genomic drivers of performance in natural conifer tree populations?
- 10:30 **Vajana Elia**
Uncovering the genetic origin and diversity of Mediterranean pine forests in the Italian peninsula
- 10:45 Coffee break
- 11:15 **Olsson Sanna**
Tracking forest material: Assessing the impact of managed materials on genetic diversity in Spanish forest trees using National Forest Inventory
- 11:30 **Mead Alayna**
Genetic variation associated with climatic extremes in the southern range of a model tree species
- 11:45 **Robledo-Arnuncio Juan J**
Using genotypic data for monitoring recent and contemporary seed and pollen migration and their environmental determinants
- 12:00 **McEvoy Susan**
Site Frequency Spectrum-based Inference of Demography and Fitness Effects as a Conservation Metric
- 12:15 **Olofsson Jill K**
Comparative genomics reveals extensive structural variants within and among European white oak species (*Quercus* spp.)
- 12:30 **Flash Poster session**

Keynote Session 5. Genetic and genomic strategies for conservation of natural populations of California oaks

Victoria Sork

California oaks are comprised of natural populations that have not undergone serious bottlenecks for over 200,000 years, and maybe longer. Oaks in California differ from managed forests in Europe in that they occupy a variety of ecosystems, occur in uneven-aged, naturally recruited populations, and have experienced many types of anthropogenic disturbance over the last 300 years, including fragmentation, invasive pests and pathogens, fires, and climate change. To preserve oak populations, restoration ecologists and oak managers could benefit from knowledge to the adaptedness of populations to warmer climates. Using a quantitative genetic approach, provenance studies and common garden experiments can document the extent to which individuals distributed across a species' range are genetically differentiated due to local adaptation. The first goal is to report findings of a long-term provenance study of valley oak (*Quercus lobata*), a foundational California oak, and demonstrate how climate-associated traits and current levels of maladaptation can inform management of oak populations. The second goal is to analyze genomic patterns of climate-associated adaptive variation across the landscape in three other California oak species and integrate models of future climate change to predict which regions are more likely to be maladapted in the future and which regions will be good seed sources for oak restoration and management project. Findings from both common garden and landscape genomic studies can inform strategies for transfer of seeds to enhance the response of California oak populations to climatic and environmental pressures.

S5.01. Native trees of the Mediterranean region: distribution, diversity and conservation challenges.

Eady B., Farsakoglou A-M., Caron M., Abulaila K., Aleksic J., Alipour S., Balian D., Bedair H., Bogunić F., Cheikh Albassatneh M., David-Schwartz R., Delgado Clavero C., Dönmez A.A., Fennane M., Gateble G., Gauquelin T., Hachi Illoul M., Khaldi A., Mahfoud-Saad I., Médail F., Mezni F., Muhammed J.J., Muys B., Perovic M., Saaed M., Seregin A.P., Stephan J., Vela E., Zhelev P., Bou Dagher Karrat M.

While 38% of tree species are at risk of extinction worldwide, their inventory and occurrence at ecologically and biogeographically meaningful scales is lacking in many parts of the world, including the biodiversity-rich Mediterranean region. Here, we provide presence/absence, extinction risk, biogeography and genetic diversity data of trees in 39 climatically and ecologically Mediterranean territories (so-called “botanical territories”) in North Africa, Western Asia and Southern Europe.

The inventory includes 496 species and 147 subspecies from 50 families and 111 genera, including 48 species and 8 subspecies previously not considered as trees. We show that native tree species distribution is highly skewed across the tree of life with a few species-rich families such as the Rosaceae and the majority with less than 1% of all species. Endemism was not evenly distributed among botanical territories and neither was extinction risk, an assessment of which was lacking in almost half of the species. While no geographic trends were detectable, species richness was found to be positively correlated with botanical territory area and, when standardized by area, with habitat heterogeneity. Information on genetic diversity was lacking in two thirds of the species inventoried and mostly focused on species with economic importance.

Our findings identified major native tree richness hotspots as well as key knowledge gaps and biases related to extinction risk and genetic diversity. Our findings also emphasize the importance of increased collaboration to support the conservation of Mediterranean forest trees. Our data are open access and can be used by researchers and stakeholders for a wide range of purposes, including conservation and restoration.

S5.O2. Does genetic diversity underpin forest resilience?

Kravanja Marija, McEvoy Susan, Olsson Sanna, Avanzi Camilla, Pinosio Sara, Pickering Mark, Alfá Ricardo, Cescatti Alessandro, Cavers Stephen, Bagnoli Francesca, Delphine Grivet, Berthold Heinze, Andrea Piotti, Annika Perry, Tanja Pyhäjärvi, Ivan Scotti, Giovanni G. Vendramin, Santiago C. Gonzalez-Martinez, Marjana Westergren

Forest environments are changing rapidly, resulting in increasing climate-induced selection pressures. Therefore, it is critical to understand the genetic basis of adaptation to ensure the long-term resilience of forests. In this study, we analysed genetic diversity and its distribution for 23 tree species on a pan-European scale. We used genomic data produced within EU H2020 FORGENIUS project for over 6,000 trees from more than 300 Genetic Conservation Units to calculate various genetic diversity and differentiation indices. Then, we tested for their correlation with resilience metrics based on remote sensing data (i.e. on Normalized Difference Vegetation Index). For this, we used multivariate statistical methods and generalized linear mixed models. Main findings, related to the potential contribution of genetic variability to resilience, are interpreted in the context of the conservation and use of Forest Genetic Resources in Europe.

S5.03. Can we detect genomic drivers of performance in natural conifer tree populations?

Farsakoglou Anna-Maria, Fady Bruno, Scotti Ivan, Aravanopoulos Filippou,

Whether heterozygosity or genetic load drive tree performance in natural populations has been a long-standing question in forest genetics. Here, we explored how these genomic drivers affect performance, using two phenotypic traits (basal area and height) as proxies for fitness in 54 natural populations species of five conifer tree species (*Abies alba*, *Pinus cembra*, *P. halepensis*, *P. nigra*, and *Taxus baccata*). Using SPET genotyping data, we estimated the proportions of heterozygosity and the proportions of recessive and additive genetic load, the latter after a SNP annotation, that were used as genomic drivers. We then performed multidimensional scaling (MDS) and Principal Component Analysis (PCA), using a relevant subset of axes from each to control for genetic relatedness. We constructed a custom-made bioinformatics pipeline in R to perform model selection analyses. For each model, individual phenotypic trait data were considered as dependent variables, while environmental (19 bioclimatic variables) and genetic data (genomic drivers and genetic relatedness controls) were considered as independent variables. The results showed no positive correlation for heterozygosity in any of the species. However, we detected a negative correlation for recessive and additive genetic load with basal area in *Pinus halepensis*. These findings highlight the potential of genetic load as a driver of performance and suggest that genomic drivers can assist as indicators in guiding monitoring strategies for both conservation and breeding purposes, especially under climate change scenarios.

S5.04. Uncovering the genetic origin and diversity of Mediterranean pine forests in the Italian peninsula

Vajana Elia, Avanzi Camilla, Bagnoli Francesca, Pinosio Sara, Castellani Maria Beatrice, Frascella Angela, Spanu Ilaria, Bonari Gianmaria, Calvia Giacomo, Francisco Thomas, La Mantia Tommasop, Iorio Giorgio; Conticelli Maurizio, González-Martínez Santiago C., Mercati Francesco, Misano Giuseppe, Tonelli Laura, Sabatti Maurizio, Tomaselli Valeria, Vendramin Giovanni Giuseppe, Piotti Andrea

Mediterranean pines provide a wide range of ecosystem services, such as protecting the soil, regulating the climate, producing food and wood, and playing a key ecological role as a foundation species. Despite their ecological relevance and widespread distribution, little information is currently available on the origins and genetic diversity of pine forests in Italy, a key biogeographical crossroad and multi-refugial area of forest trees. Here, we tackled this gap by carefully selecting 97 putatively autochthonous *Pinus halepensis*, *P. pinea* and *P. pinaster* populations densely covering their natural distributions in Italy and including several previously unsampled areas (e.g., central Italy, Sicily and Sardinia). More than 1,500 adult trees were characterized through SNP arrays (*P. pinaster* and *P. pinea*) and the newly developed FORGENIUS SPET panel for *P. halepensis*. After removing populations of likely artificial origin, judging by the genetic data, we investigated their patterns of molecular diversity using genetic structure and admixture analyses, and estimating historical gene flow. In agreement with recent, dense investigations of forest genetic resources from the Italian peninsula, we found a heterogeneous genetic diversity distribution with previously unsampled areas often characterized by peculiar genetic lineages. Despite the widespread presence of plantations along the Italian coasts, we found little evidence of genetic translocations in the past. These results demonstrate that sparse sampling, particularly of species with fragmented ranges, can result in a biased characterisation of existing genetic resources, which in turn could be detrimental for their use and conservation in the face of climate change.

S5.05. Tracking forest material: Assessing the impact of managed materials on genetic diversity in Spanish forest trees using National Forest Inventory

Olsson Sanna, Iciar Alberdi, Isabel Cañellas, Sara Pinosio, Santiago C. González- Martínez, Juan J. Robledo-Arnuncio, Delphine Grivet, Ricardo Alía

Introducing genetically selected material for forest regeneration or restoration may reduce long-term adaptability and genetic diversity compared to natural populations. Conversely, mixing selected and local materials could increase genetic diversity and adaptability. Identifying the origin of forest reproductive material is crucial for the conservation and adaptive management of forests, yet the use of genetic assignment for this purpose remains limited due to methodological and logistical constraints. We genotyped 1,299 individuals of maritime pine (*Pinus pinaster*) using the 4TREE SNP array and 1,056 individuals of holly oak (*Quercus ilex*) using SPET genotyping, with samples collected from plots included in the Fourth Spanish National Forest Inventory (NFI). Our goals were to: 1) compare genetic diversity between managed and autochthonous populations; 2) assess genetic structural differences between them; and 3) in *P. pinaster*, determine whether populations were autochthonous and, if not, infer their origin. _ We calculated ancestry coefficients, genetic diversity metrics, and used the R package rubias for genetic stock identification. For *P. pinaster*, we leveraged a genomic baseline from previous studies; for *Q. ilex*, forest density data served as a proxy for management history due to the absence of an existing genomic baseline.

We identified 20 of 36 *P. pinaster* populations as autochthonous, while 16 were of non-local or mixed origin. Our results show the value of genomic tools in characterizing NFI plots. NFI-based sampling offers a more realistic picture of genetic diversity in Spanish forests than studies based solely on genetic conservation units. Newly genotyped autochthonous populations enrich the genomic baseline.

S5.06. Genetic variation associated with climatic extremes in the southern range of a model tree species - CANCELLED

Mead Alayna, Phannareth Tommy, Fitzpatrick Matthew, Holliday Jason, Keller Stephen, Hamilton Jill, Sork Victoria

Genetic variation in stress tolerance will likely be necessary for forest tree populations to persist under climate change. *Populus trichocarpa*, or black cottonwood, is a model species in genomic research of forest trees. As an ecologically important riparian species and economically important biofuel source, it is critical to understand how responses to climatic stressors vary among populations or genotypes. Previous studies have identified genetic and phenotypic variance associated with drought and heat tolerance across its range in western North America. Yet, very little research has been conducted at the southernmost edge of the range. Populations in California likely experienced more stability during glacial periods, and currently experience warmer and drier climates than northern regions, and thus may contain unstudied genetic variation. Here, we present results of whole-genome sequencing of 130 individuals sampled from California, combined with a previously published dataset of samples from Canada and the northern United States. California populations appear genetically divergent, particularly southern California, which forms a separate genetic cluster. We used genotype-environment associations to identify SNPs that may contribute to local adaptation to climate within California. If variants conferring higher fitness in warmer and drier climates are present as standing genetic variation throughout the range, populations may be able to adapt rapidly to warming climates. Alternatively, if California harbors unique genetic diversity, it could be leveraged through breeding and assisted gene flow to ensure that natural and managed populations are resilient to future climates.

S5.07. Using genotypic data for monitoring recent and contemporary seed and pollen migration and their environmental determinants

Robledo-Arnuncio Juan L., Chybicki Igor J.

Dynamic conservation of genetic diversity involves monitoring and preserving natural evolutionary processes determining genetic variation and adaptation. Conservation management requires in particular accurate measurements of migration patterns under current demographic and environmental conditions, in order to understand and mitigate global change impacts on population genetic and demographic connectivity. We present two Bayesian methods to infer seed and pollen migration rates among tree populations using genotypic data. One of the methods uses adult-offspring samples to estimate contemporary seed and pollen migration rates during one or several reference dispersal episodes. The other method requires only adult samples and estimates recent seed and pollen migration rates during the last generation, along with spatial and environmental effects on migration. The two methods can be used alone or in combination, to assess for instance potential changes in migration patterns between the last and present generations. Additionally, the methods provide estimates of population allelic frequencies, population divergence, inbreeding coefficients, individual ancestries and genotyping error rates. We present simulation results indicating that the methods can provide reliable estimates of seed and pollen migration rates and allow accurate inference of spatial effects on migration at affordable sample sizes (50-100 individuals/population and 1,000 SNPs) even under relatively weak levels of divergence ($F_{st} = 0.025$). We apply the two methods to *Taxus baccata* population remnants, revealing sustained low levels of seed and pollen migration across the last and present generations, as well as a negative effect of interpopulation distance on migration that was detectable for pollen but not for seeds.

S5.08. Site Frequency Spectrum-based Inference of Demography and Fitness Effects as a Conservation Metric

McEvoy Susan, Kastally Chedly, Pyhäjärvi Tanja

Mutations can be neutral, deleterious, or beneficial, and range in strength from nearly neutral to highly deleterious or beneficial. A Distribution of Fitness Effects (DFE) analysis uses the site frequency spectrum (SFS) to characterize proportions of new mutations by their type of effect and strength of effect on fitness. When comparing species or populations, proportional differences in weak, nearly neutral versus highly deleterious or beneficial mutations can vary, which can be interpreted based on expectations from population genomics theory through the effects of varying N_e . These differences, combined with other assessments of diversity, may contribute to conservation monitoring at the genetic level. Methods to accurately estimate DFE are still evolving. We estimated DFEs for multiple species throughout Europe using pre-filtered SNP datasets provided by the FORGENIUS project and derived from SPET target capture sequencing. We used randomly designed probes to reduce bias and filtered these to remove hybrids, clones, and loci where over 50% of the genotypes have missing data. SNPs were grouped into two subsets by site-fold degeneracy: those potentially under selection (0-fold), and putatively neutral (4-fold, intronic or intergenic). Est-sfs was used to generate an unfolded SFS using the Kimura 2-parameter model. Depending on reference availability, either one or two outgroup species were used to identify the derived allele. We tested different models within PolyDFE, estimating both deleterious-only or full DFEs, and used the recommended maximum likelihood methods to compare models. We then compared the results with other conservation metrics to assess DFE metrics as a conservation indicator.

S5.09. Comparative genomics reveals extensive structural variants within and among European white oak species (*Quercus* spp.)

Olofsson Jill K, Müssig Maxi KM, Sunde Johanna, Kjær Erik D

Advances in sequencing technologies in the last decade have made it possible to assess genetic variants beyond classical single nucleotide polymorphisms and smaller insertions-deletions. In particular, long-read sequencing has revealed that most plant genomes are characterized by larger structural variants (SVs). While many SVs span repetitive regions of the genome, there is evidence from crops and model organisms that SVs also include functional genes and that they can have regulatory functions. Thus, SVs have a large impact on the phenotype upon which natural selection acts. Using newly produced long-read sequences, we present nine de novo genome assemblies representing four European white oak species (*Quercus robur*, *Q. petraea*, *Q. pubescens*, and *Q. frainetto*). Comparative genome analyses show evidence for a large number of SVs spanning genes in all four species. We demonstrate that these SVs are variable both within and between species. Thus, we show that SVs have the potential to significantly contribute to the genetic diversity of both species and populations. Finally, using population level whole genome data of *Q. petraea* we demonstrate that there indeed are variations in the distribution of SVs among populations and that they significantly contribute to the genetic variation among individuals. Taken together, our study shows the need for development of novel pangenomic resources for oaks, that take genetic diversity within SVs into account. Such novel resources would greatly improve our ability to predict responses of trees to future climates and contribute to our understanding of local adaptation in forest trees.

Poster presentations

S5.P1. Assessing range-wide neutral and adaptive genetic diversity within and between populations of black ash (*Fraxinus nigra*)

Flash presentation

LoPiccolo Kyra, Hamilton Jill

Temperate forest tree populations often exhibit signatures of climate adaptation, pointing towards the influence of historical climates in shaping the distribution of standing genetic variation. However, given the current pace of climate change, there is increasing probability that historical climates may be decoupled from contemporary climates, impacting the fitness of populations adapted to historical conditions. Given this, incorporating an understanding of the distribution of standing genetic variation and genotype by environment (G*E) relationships into management plans for restoration, breeding, and conservation is needed. Black ash, a foundational wetland species native to northeastern North America, faces dual threats from climate change and the invasive emerald ash borer. Despite its ecological importance, there have been no assessments of its genetic diversity or adaptive genetic variation along climate gradients. This study addresses that gap by analyzing 42 natural populations (n = 994) across the species range using ddRADseq. To assess diversity across the species' range, we used population level allele frequencies to estimate genetic diversity metrics (e.g., Fst, Fis, Ne, heterozygosity). To quantify the impact of environment and geography on genetic variation, we conducted a partial redundancy analysis (RDA). Genetic variants associated with historic climate gradients identified by RDA were then used to quantify potential genetic maladaptation under future climate scenarios using gradient forest (GF) to calculate projected genomic offset between current and future climate. Together, these analyses identified patterns of neutral and adaptive genetic variation across the species range to guide restoration, seed sourcing, and conservation in a changing climate.

S5.P2. Investigating the Role of PnCesA4 Gene Expression in Cellulose Biosynthesis and Growth Traits in Populus nigra L.

Flash presentation

Taskiran Bircan, Akkad Raitha, Kansu Cigdem, Kaya Zeki,

Populus nigra L. (European black poplar) is a fast-growing, ecologically valuable tree species with significant potential for biomass and bioenergy production. Although cellulose biosynthesis is a critical component of secondary cell wall formation in woody plants, the regulatory mechanisms underlying this process remain poorly understood. This study aims to elucidate the relationship between the expression of the secondary cell wall-related cellulose synthase gene, PnCesA4, and traits such as cellulose content, related enzyme activities (UGPase, SuSy), and growth parameters (height, diameter) across diverse *P. nigra* clones. A total of 44 five-year-old genotypes, representing a wide geographical distribution in Turkey, were sampled from a clonal bank in Ankara. RNA was extracted from stem tissues and analyzed via qRT-PCR to quantify PnCesA4 expression, while biochemical assays were used to determine cellulose, glucose, and enzyme activities. Statistical analyses revealed significant variation among clones. While UGPase and SuSy activities showed strong positive correlations with cellulose content, PnCesA4 expression was unexpectedly not correlated with cellulose levels and was negatively associated with tree height and diameter. These findings suggest that PnCesA4 may not act independently in regulating cellulose biosynthesis and highlight the potential compensatory roles of other Cesa subunits. This research provides novel insights into the genetic and enzymatic regulation of cell wall biosynthesis in poplar and identifies promising genotypes for future breeding programs focused on wood quality and bioenergy potential.

S5.P3. Spatial and temporal patterns of genetic variation of North European pedunculate oaks populations assessed based on whole genome sequencing

Flash presentation

Müssig Maxi MKM, Kjær Erik D, Olofsson Jill K

Long-lived forest trees are challenged by the speed of the ongoing climate crisis, and options and limitations for assisted gene flow are therefore important to explore. Improved insight into the genetic variation within and between forest tree populations sampled across environmental gradients is therefore essential. Genetic characterization of origins also facilitates studies of the degree of and outcomes of past provenance transfer, and its implications for the adaptive potential of existing forests. Using population level whole genome data, we estimate population structure across the northern distribution range in Europe of the ecologically and economically important pedunculate oak (*Quercus robur*). We associate population structure with environmental gradients. Our results support that population structure and local adaptation is widespread in present day oak forests. Based on our findings, we discuss the implication for assisted gene flow as a means to reduce adverse effects of climate change on forest health. However, direct measurements of changes in gene pools over time can give a more complete picture. Using a unique set of whole genomes of Danish veteran oaks (400 years old), we show that the veteran Danish gene pool expands beyond the contemporary gene pool. We discuss to what extent this could be the result of Danish forestry practices, and/or reflect past selection pressures. Our results highlight the importance of comparing contemporary gene pools across large distribution ranges as well as between age groups to get a better picture of how species and populations will respond to future changes in their local environments.

S5.P4. Population structure and genetic diversity in Norway spruce: insights from genomic SSRs and EPIC markers

Flash presentation

Vijayan Thapasya, Rupprecht Christina, Curto Manuel, Splechtna Bernhard, Sonnenberg Sabastian, Meimberg Harald

Norway spruce (*Picea abies*) is one of the most widespread and economically important conifers in Europe. While several studies have explored its genetic structure, the distribution of diversity across Central European populations remains incompletely resolved, especially at finer spatial scales. In this study, we analysed 400 individuals from diverse regions of Central Europe to explore spatial patterns of genetic variation and structure. Using a newly developed GBAS system targeting microsatellite and intronic regions, we examined genetic variation with high resolution. Our findings show that, although overall differentiation is low, as expected for a wind-pollinated conifer, subtle geographic structure is still detectable. The dataset includes individuals from the Rothwald primaeval forest, providing a valuable comparison to managed and reforested stands, and highlighting the conservation value of such old-growth remnants. We also observed substantial within-population variation, underscoring the genetic richness maintained across the range. Instead of relying on a single type of genetic data, we integrated complementary marker systems to provide a more complete view of diversity. This strategy proved useful for detecting both broad and fine-scale patterns in a species where genetic structure is often difficult to resolve. By advancing our understanding of how genetic variation is organised in *P. abies*, this study contributes to broader efforts to monitor and preserve the evolutionary potential of European forest trees, especially under growing environmental pressures.

S5.P5. Regeneration dynamics and genetic variation of black and white poplar in a transformed riverine ecosystem

Flash presentation

Robak Dominika, Lewandowski Andrzej, Żukowska Weronika Barbara

Black poplar (*Populus nigra* L.) and white poplar (*Populus alba* L.) are key components of riparian forests. Regeneration of black poplar in contemporary riverine ecosystems is rare, largely due to habitat transformation, whereas white poplar regenerates much more intensively, but predominantly through vegetative reproduction. We analyzed a sympatric population of both species (944 individuals) growing in the middle section of the Warta River in Poland. The studied trees represented multiple age classes; however, in white poplar, young individuals were more abundant. We aimed to: (1) assess genetic variation, (2) compare the regeneration strategies of both species, and (3) compare their gene pools. The analyses were carried out based on the polymorphism of 15 common nuclear microsatellite markers.

The results revealed markedly lower clonality in black compared to white poplar (37.37% vs. 98.26%). In white poplar, clonality gradually decreased with tree age. It appears that black poplar regenerated partly generatively, whereas white poplar regenerated exclusively vegetatively. Furthermore, black poplar exhibited greater genetic variation. Nevertheless, the parameters of genetic variation were generally comparable across age classes within both species.

The predominance of vegetative regeneration and low genetic variation in white poplar may limit its adaptive potential and threaten its long-term viability. Black poplar, by contrast, retains high genetic variation, but most populations consist of old individuals in poor condition. Our findings highlight the importance of maintaining sexual reproduction and initiating ex situ conservation efforts for both species. The research was funded by the Polish National Science Centre (grant no. 2021/41/B/NZ9/00722).

S5.P6. Relationship between Genetic Diversity and Marginality in four European Conifers

Flash presentation

Guadaño-Peyrot Carlos, Olsson Sanna, Francisco Thomas, Three pines Consortium*, FORGENIUS Consortium**, Vendramin Giovanni G., Benito-Garzón Marta, González-Martínez Santiago C., Marchi Maurizio, Alía Ricardo, Grivet Delphine

* Olsson et al. 2025 (doi)

** Pinosio, Bagnoli et al. 2025 (<https://doi.org/10.1101/2025.08.08.669074>)

Marginal and peripheral forest populations – defined in relation to their geographic and ecological characteristics, as well as demographic history – are acknowledged as highly valuable genetic resources where adaptive processes occurred differently from non-marginal ones (i.e. those located closer to the distribution core). Thereby their contribution on intra-specific genetic variation is highly valuable. Furthermore, marginal populations can be subject to specific demographic and genetic processes, such as inbreeding and genetic drift, which may adversely affect their long-term viability and vulnerability, particularly in the context of climate change. The objective of this study is to assess the relative importance of marginality drivers on genetic indicators. The study considered 244 native populations, and four conifer species selected based on their different demographic histories and evolutionary strategies, in order to identify common patterns. Two species have a restricted distribution within the Mediterranean basin (*Pinus pinea* and *Pinus pinaster*), whereas *Pinus sylvestris* and *Taxus baccata* extend beyond the Mediterranean region, growing also in central, northern, and eastern Europe. We evaluated the relationship between 10 genetic parameters estimated with SNP markers (e.g., genetic diversity, population-specific genetic differentiation, genetic load, and genomic offset) and nine geographic, environmental, and historical indices related to the marginality status. For instance, geographic isolation proved to be a good predictor for genetic diversity and differentiation within and among populations. Our findings could be useful for defining and prioritising conservation strategies for forest genetic resources in Europe.

S5.P7. Prioritising of in situ Genetic Conservation Units for ex situ conservation based on marginality and threats

López Peralta Ana María, Barba Ejido Diana Cristina, Prieto Estávez Laura, Mondelo Falcón Rubén, Alía Miranda Ricardo, Pérez Felipe

Royal Decree 159/2022, of March 1st, on the conservation of forest genetic resources and wild flora, establishes the basic rules on the conservation and sustainable use of forest genetic resources of national interest and, specifically, the planning, coordination and collaboration instruments for their in situ and ex situ conservation. Regarding the in situ conservation of forest genetic resources it has been defined a Network of in situ Genetic Conservation Units (GCU Network) that is made up of a set of populations of the 20 main forest taxa that try to conserve their maximum genetic diversity. The Spanish National Genebank carries out technical support activities related to the management and conservation of genetic materials. Ex situ conservation must be conceived as a complement to in situ conservation of natural populations. Therefore, these populations will be preferential for ex situ conservation. Within the GCU Network, priority populations must be established for ex situ conservation. These priorities are based on the geographic and climatic marginality of the population and the degree of threat due to size, climate change, and fire risk. Currently, 36 accessions of seeds and pollen from 9 taxa and 26 GCUs are conserved in the Spanish National Genebank.

S5.P8. Incorporating genetic diversity into the sustainable use of pedunculate oak forest genetic resources in Romania, Bulgaria and Republic of Moldova

Postolache Dragos, Petar Zhelev, Postolache Gheorghe, Titica Ghenadie, Miron Aliona, Plesca Bogdan, Popescu Flaviu

Forest genetic resources (FGR) of pedunculate oak identified as *Quercus robur* ssp. *pedunculiflora* (or *Q. pedunculiflora*) from Romania, Bulgaria, and the Republic of Moldova were sampled to investigate genetic variation using eight chloroplast microsatellite markers (cpSSRs) and fourteen nuclear microsatellite markers (nSSRs). The resulting phylogeographic patterns based on chloroplast DNA provide valuable insights into the evolutionary history in the eastern Balkan Peninsula, offering a scientific basis for potential assisted forest migration in the region. Assessing standing genetic variation through different molecular markers enhances the characterization of FGR, informs the development of effective monitoring strategies, and supports the sustainable use of FGR in the context of long-term adaptive forest management.

S5.P9. Assessment of the productive potential of field elm for ex situ conservation in the protected area "Zvezdarska šuma" (Belgrade, Serbia)

Filip Maksimović, Marina Nonić, Kristina Đorđević, Mirjana Šijačić-Nikolić, Ivona Kerkez Janković, Dragana Skočajić

In Serbia, *Ulmus minor* Mill. (field elm) is categorized as a rare and endangered species, being impacted by Dutch elm disease. Within the protected area "Zvezdarska šuma" (Belgrade, Serbia), remaining individual trees and small groups (59 georeferenced trees in total) persist in a fragmented spatial pattern, representing gene pool potentially valuable for the future species' adaptive potential. This study aimed to assess the productive potential of field elm trees in the protected area "Zvezdarska šuma" as a basis for ex situ conservation of the endangered gene pool. Hardwood cuttings were collected from 18 phenotypically healthy trees during February–March 2025. The experimental setup for propagation was conducted in March 2025 under controlled glasshouse conditions, using containers (35x25x14 cm) filled with peat and perlite (1:4 ratio) as substrate and treated with rooting hormone (dry-dip method, 0.4% IBA). Following root initiation observed in May 2025, the plants were transferred to a controlled nursery environment for acclimatization. Preliminary data collected in June 2025 indicated significant variation in rooting success among 18 genotypes, with an average rooting rate of 18.44%, ranging from 10.00% to 45.31%. The productive potential of the test trees will be further assessed in a green cuttings clonal trial and a generative progeny test, both established in the nursery of the Faculty of Forestry in Belgrade. The results presented herein represent only the initial phase of ex situ conservation, which should be further expanded through the integration of in situ conservation methods and continuous monitoring of the existing gene pool.

S5.P10. Assessing Genetic Diversity and Structure of Norway Maple (*Acer platanoides*) in Belgium (Wallonia) to Support a new Seed Orchard Design

David Mathy, Sophie Dufour, Yordan Muhovski, Eleonore Scholzen, Alain Servais, Marc Lateur

Norway maple (*Acer platanoides*) is a native broadleaved noble hardwood species gaining interest due to its putative better drought tolerance and positive impact on biodiversity. Because of its scattered distribution, no seed stands or other sources of Forest Reproductive Material (FRM) have yet been registered for this species in Belgium. To support seed stand selection and establish a high-quality seed orchard, we conducted extensive surveys in publicly owned forests across Wallonia, locating individuals or populations of this species. We identified 218 trees spread across 14 populations in eight of the ten bioclimatic zones in Wallonia. For each tree, we collected cambium samples and measured height, girth, and stem form. All 218 individuals were genotyped using 11 polymorphic SSR markers. We computed genetic diversity metrics and assessed population structure through Bayesian clustering. Sibship relationships were inferred with COLONY to avoid selecting related individuals for both seed stands and orchard composition. Results will be presented and discussed in the context of comparable Austrian and German studies that used the same SSR marker set. Ultimately, we aim to develop a selection method combining genetic and phenotypic data that will maximize seed orchard genetic diversity while ensuring high silvicultural quality. This study provides critical baseline data for developing certified FRM for *Acer platanoides* in Wallonia and demonstrates how integrating genetic and phenotypic information can enhance forest reproductive material programs under climate change.

S5.P11. Searching for the sex-determining region in the *Taxus baccata* L. genome

Bross Daniel, Mittelbach Jannes, Pippel Martin, Mader Malte, Uelze Laura, Schroeder Hilke, Pers-Kamczyk Emilia, Kurtz Stefan, Winkler Sylke, Müller Niels, Kersten Birgit

Dioecious species have distinct female and male individuals, and the sex is usually determined genetically through a sex-determining region (SDR). In plants, such SDRs have mostly been studied in angiosperms, even though dioecy is relatively more common among gymnosperms.

The TaxGen project set out to localize and characterize the SDR in the conifer species *Taxus baccata*, the European yew. Two haplotype-phased chromosome-level reference genomes (of one female and one male individual) were assembled from PacBio HiFi and Hi-C Illumina sequencing data. For the annotation, PacBio IsoSeq data and Illumina short read data from RNA of different tissues were generated and used together with public datasets. On average, the four haplotypes are 10.04 Gbp long (ranging from 9.87 Gbp to 10.19 Gbp), showed a contig N50 value of 12.9 Mbp and had 1,601 gaps. The new reference genomes, together with short-read whole genome sequencing data from 100 phenotyped yew samples (partially from autochthonous regions), are being used as the basis for traditional SNP-based GWAS, k-mer based GWAS and an analysis of differential coverage, to search for the SDR. Preliminary results show no evidence of an SDR, opening the exciting possibility of environmental sex determination in *Taxus*.

S5.P12. Investigating the genetic effects of introducing Honduran mahogany (*Swietenia macrophylla*) into Cuba: implications for the conservation of the native species of mahogany

Rodriguez Coca Liuder Isidoro, Ciocîrlan Elena, Curtu Alexandru Lucian

Hybridization between closely related species can compromise the genetic integrity of endemic taxa, especially following the introduction of non-native species. In Cuba, the introduction of *Swietenia macrophylla* (Honduran mahogany) in the 1970s—due to its fast growth and valuable timber—has raised concerns regarding its potential genetic impact on the native and endangered *S. mahagoni*, including the possibility of natural hybridization and introgression. Here, we aimed to estimate the genetic differentiation between *S. mahagoni* and *S. macrophylla* and to identify putative hybrids between the two species. A total of 357 individuals were sampled across five localities in Cuba, including two naturally regenerated populations of *S. mahagoni*, a remnant stand of *S. macrophylla*, and two plantations in which intermediate forms were observed. Eight nuclear microsatellite markers, previously validated for *S. macrophylla*, were employed. Analyses revealed marked genetic differentiation between species, with well-defined clusters and evidence of population subdivision. The populations of *S. mahagoni* showed greater allele numbers ($N_a = 12.4\text{--}13.3$) and greater expected heterozygosity ($H_e = 0.73\text{--}0.78$) compared to the remnant of *S. macrophylla* ($N_a = 5.75$; $H_e = 0.59$). The observed heterozygosity was systematically lower than expected in all populations, resulting in positive inbreeding coefficients ($F_{is} = 0.179\text{--}0.263$). Spatial genetic structure was more evident within *S. mahagoni* populations, suggesting that, within each site, seed and pollen dispersal is limited, favoring genetic clustering. Our results may be useful for developing a strategy for the conservation and sustainable use of *S. mahagoni* genetic resources in Cuba.

S5.P13. Mapping the Hybrid Zone: Simulations of Hybridization in Heterogeneous Landscapes and its Impact on Genetic Diversity

Medzihorská Michaela, Čepl Jaroslav

Hybridization plays a dual role in shaping genetic diversity, with both positive and negative ramifications for crossing populations. Gene flow between two populations can elevate heterozygosity, mitigate bottleneck effects, and facilitate adaptive introgression. On the other hand, extensive hybridization may lead to demographic swamping of endemic gene pools, erosion of local adaptations, and outbreeding depression that undermines long-term fitness. We simulated the spread of two hybridizing species across a landscape, considering varying levels of hybridization. The simulation explores how different levels of hybridization influence key genetic parameters such as heterozygosity, fitness or effective population size during the range expansion across heterogeneous environments. The fitness consequences of hybridization are particularly important, as hybrid populations may exhibit increased fitness caused by hybrid vigor. To analyze these dynamics, we utilize the AlphaSimR, a powerful tool for stochastic simulations of genetic processes at the DNA level for every individual. Custom functions were developed to incorporate spatial dynamics, allowing for more realistic modeling of how hybridization can influence the rate of spread and development of adaptive traits. Additionally, the model integrates complex genetic architectures of traits, considering not only additive genetic value but also dominance and epistasis. This enables a more comprehensive understanding of how hybridization affects the genetic structure of crossing populations. This model aims to explore the role of hybridization in divergent populations, if it can facilitate adaptive potential or range expansion, and its long-term implications for biodiversity conservation.

S5.P14. What can we learn from genomic analyses of local adaptation in forest trees?

Desanka Lazic, Cornelia Geßner, Niels A. Müller

Local adaptation is key for ecotypic differentiation and species evolution. The broad distribution range and large environmental amplitude of many forest tree species indicate that adaptive differentiation of local populations across the landscape may be crucial. To elucidate the underlying genetic basis, we re-sequenced almost 2000 individuals from 100 range-wide populations of European beech (*Fagus sylvatica*). We show that genetic variation closely mirrors geography. Genotype-environment association (GEA) analyses identify genomic regions strongly associated with environmental variation, especially for winter cold. Interestingly, allelic variation at these regions does not result in any apparent fitness differences in a common garden. More generally, reciprocal transplant experiments suggest extensive phenotypic plasticity over large environmental distances. While genomic offset estimates indicate a heterogeneous distribution of potentially adaptive alleles across the landscape, the plastic response and limited phenotypic differentiation of beech populations raise questions about the relevance and applicability of such estimates. In conclusion, we emphasize the importance but also the complexity of natural genetic variation for forest conservation under climate change

S5.P15. Uncovering genetic diversity and local adaptation in Norway spruce using SNP array data

Korecký Jiří, Čepl Jaroslav, Stejskal Jan

Understanding the genetic structure of Norway spruce (*Picea abies*) is vital for predicting its adaptive capacity under ongoing climate change. In this study, we analyze populations representing three morphologically and ecologically defined spruce ecotypes (acuminata, europaea, obovata) across the Czech Republic, using high-resolution SNP data from the *Picea abies* 50K genotyping array. Additional samples originate from provenance trials spanning multiple geographic regions. A total of ~1000 individuals were genotyped, with ~35,000 high-quality SNPs retained after filtering. Our primary aim is to resolve the population structure and assess genetic differentiation using Discriminant Analysis of Principal Components (DAPC) and complementary methods, including PCA and clustering algorithms. Genetic diversity metrics are computed to evaluate intra- and inter-ecotypic differentiation. Initial results reveal genetic clusters with low to moderate differentiation. Samples from the provenance trial often form more distinct clusters compared to the Czech ecotypic groups, which may be attributed to greater geographic distances or signals of local adaptation. Beyond characterizing population structure, we explore genotype-environment associations to identify candidate loci potentially underlying local adaptation along altitudinal gradients. The integration of landscape-genomic tools enhances our understanding of the adaptive differentiation in spruce and informs management strategies aimed at maintaining evolutionary potential.

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Heuertz, Myriam	National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux; BIOGECO, Cestas, France	S2.O8.,S2.P26.	28,55
Hiltunen, Mervi	Municipality of Savonlinna, Talvisalo comprehensive school (Finland)	S1.P6.	17
Hirao, Tomonori	Forestry and Forest Products Research Institute, Japan	S4.P2.	95
Hofmann, Martin	Nordwestdeutsche Forstliche Versuchsanstalt, Abteilung Waldgenressourcen, Hann. Münden, Germany.	S2.P2.	31
Holliday, Jason	Virginia Tech University	S5.O6.	111
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Jakuš, Rastislav	Inst. of Forest Ecology, SAS, Slovakia; Global Change Research Inst., CAS, Czechia	S1.P2.,S3.P4.	13,81
Jansen, Simon	Universität für Bodenkultur Wien, (BOKU), Vienna, Austria	S1.O3.,S2.P30.,S3.O 5.	7,59,74
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Jelkmann, Susanne	Thuenen Institute of Forest Genetics, Genetic Technologies, Grosshansdorf, Germany	S4.P7.	100
Jez, Jakub	Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), Vienna, Austria	S2.O2.,S4.O1.,S4.P8 .	22,85,101
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Karolak, Marta	Austrian Research Centre for Forests BFW - Department of Forest Growth, Silviculture & Genetics; Forest Genetics, Vienna, Austria	S2.O2.	22
Karopka, Manuel	Forest Research Institute Baden- Württemberg (FVA)	S1.P3.	14
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Kavčič Sonnenschein, Katja	GIS, Gozdarski Inštitut Slovenije , SFI, Slovenian Forestry Institute, Slovenia	S1.P6.	17
Kavлак, Alper	Natural Resources Institute Finland (Luke)	S4.P6.	99
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Kerkez Janković, Ivona	University of Belgrade, Faculty of Forestry	S5.O6.,S2.P16.,S2.P 17.	111,45,46

Kersten, Birgit	Thuenen Institute of Forest Genetics, Germany	S2.P3.,S5.P7.	32125
Khalidi, Abelhamid	INRGREF Tunis, Tunisia	S5.O1.	106
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Kjær, Erik Dahl	University of Copenhagen, Department of Geosciences and Natural Resource Management, Frederiksberg, Denmark	S5.O9.,S5.P10.,S2.O 8.,S2.P11.,S2.P15.,S 2.P20.,S2.P22.	114,117,28,4 0,44,49,51
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Kohler, Annegret	Université de Lorraine, Institut national de recherche pour l'agriculture, l'alimentation et l'environnement, UMR Interactions Arbres / Microorganismes, Centre INRAE Grand Est-Nancy, 54280 Champenois, France	S2.P33.	62
Kolbaia, Sandro	National Botanical Garden of Georgia, Tbilisi, Georgia	S2.P10,S2.P25.	39,54
Konrad, Heino	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.P10.,S2.P25.	39,54
Korecký, Jiří	Department of Forestry Genetics and Physiology, Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Czech Republic.	S2.O1.,S2.P35.,S5.P 15.	21,64,129
Korolyova, Natalie	Inst. of Forest Ecology, SAS, Slovakia; Global Change Research Inst., CAS, Czechia	S3.P4.	81
Kosawang, Chatchai	University of Copenhagen, Denmark	S2.P15.,S2.P22.	44,51
Kotina, Vasiliki Maria	Aristotle University of Thessaloniki (AUTh), Thessaloniki, Greece	S2.P13.	42
Kovacs, Gyula	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.P25.	54
Kovanen, Eero	Municipality of Savonlinna, Talvisalo comprehensive school (Finland)	S1.P6.	17
Kranner, Ilse	University of Innsbruck, Department of Botany, Sternwartestraße 15, 6020 Innsbruck, Austria	S4.O1.	85
Kravanja, Marija	Slovenian Forestry Institute (GIS), Slovenia	S5.O2.	107
Kremer, Antoine	INRAE, Pierroton, France	S1.O5.,S2.O9.	9,29
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Lambinet, Maxime	Royal Forestry Society of Belgium (SRFB)	S1.P3.	14
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Lazić, Desanka	Thuenen Institute of Forest Genetics, Germany	S2.P6.,S2.P29.,S5.P14.	35,58,128
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Leguerroue, Bénédicte	National Forests Office (ONF), France	S1.P3.	14
Leigh, Deborah M.	Swiss Federal Research Institute WSL, Birmensdorf, Switzerland; Senckenberg Research Institute, Frankfurt; Institute of Ecology, Evolution, and Diversity, Faculty of Biosciences, Goethe University	S1.O3.,S2.P30.,S3.O5.	7,59,74
Lenga, Marieke	Philipps University Marburg, Germany	S2.P38.	67
León Carbonero, David	Ministerio para la Transición Ecológica y Reto Demográfico (MITECO)	S4.P3.	96
Lesur-Kupin, Isabelle	INRAE, France	S2.O5.	25
Lewandowski, Andrzej	Institute of Dendrology, Polish Academy of Sciences, Parkowa 5 St., 62-035 Kórnik, Poland	S5.P12.	119
Lhotáková, Zuzana	Department of Experimental Plant Biology, Faculty of Science, Charles University, Prague, Czech Republic	S2.O1.,S3.P3.	21,80
Liberati, Dario	Università della Tuscia (DIBAF)	S2.O3.	23
Liese, Mirko	Thünen Institute of Forest Genetics, Germany	S1.O3.	7
Limousin, Jean-Marc	University of Montpellier, CNRS, France	S3.O1.	70

Litmann, Lars	Forest Research Institute Baden-Württemberg (FVA), Freiburg, Germany	S2.P30.,S1.O3.	59,7
Littmann, Lars	Stockholm University	S1.O3.	7
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Lowe, Andrew	University of Adelaide, Australia	S1.O3.	7
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Macaya-Sanz, David	Institute of Forest Sciences (ICIFOR-INIA-CSIC)	S4.O9.,S4.P4.,S4.P10.	93,97,103
Mader, Malte	Thuenen Institute of Forest Genetics, Germany	S2.P3.,S5.P7.	32125
Mader, Sonja	Austrian Research Centre for Forests BFW - Department of Forest Growth, Silviculture & Genetics; Forest Genetics, Vienna, Austria	S2.O2.	22
Magerøy, Melissa	Norwegian Institute of Bioeconomy Research	S2.P15.	44
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Mahfoud-Saad, Ilène	(1) Office National des Forêts, Avignon, France and (2) Latakia University, Latakia, Syria	S5.O1.	106
Mäkinen, Harri	Natural Resources Institute (Luke), Finland	S4.P6.	99
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Marešová, Jana	Inst. of Forest Ecology, SAS, Slovakia	S1.P2.	13

Marinšek, Aleksander	Slovenian forestry institute	S1.P1.	12
Martin, Francis	Université de Lorraine, Institut national de recherche pour l'agriculture, l'alimentation et l'environnement, UMR Interactions Arbres / Microorganismes, Centre INRAE Grand Est-Nancy, 54280 Champenoux, France	S2.P33.	62
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Martin, Timothy A.	School of Forest, Fisheries, and Geomatics Sciences, University of Florida, Gainesville, FL, 32611, USA	Keynote Session 3	69
Martínez-Godoy, Maria Ángeles	Institute for Plant Molecular and Cell Biology (IBMCP), Consejo Superior de Investigaciones Científicas (CSIC) - Universidad Politécnica de Valencia (UPV), Calle Ingeniero Fausto Elio, s/n, 46022 Valencia, Spain	S2.O4.,S4.O1.	24,85
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Martinez-Vilalta, Jordi	CREAF, Spain	S3.P1.	78
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Mayr, Stefan	University of Innsbruck, Department of Botany, Sternwartestraße 15, 6020 Innsbruck, Austria	S2.O2.	22
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Mestre Runge, Christian	Philipps University Marburg, Germany	S3.O3.,S3.P5.	72,82
Mezni, Faten	INRGREF, Tunis, Tunisia	S5.O1.	106
Miguel-Pizarro, Adrián	ICIFOR-INIA, CSIC, Spain	S4.P4.	97
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Mühlhaus, Timo	Computational Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
Müller, Markus	University of Göttingen, Germany	S2.P18.,S4.P8.	47101

Müller, Niels A.	Thuenen Institute of Forest Genetics, Germany	S1.O6.,S2.P6.,S2.P29.,S5.P7.,S5.P14.	10,35,58,125,128
Musau, Joshua	UK Centre for Ecology & Hydrology, Edinburgh, EH26 0QB	S2.P32.	61
Musch, Brigitte	National Forests Office (ONF), France	S1.P3.	14
Müssig, Maxi KM	University of Copenhagen, Denmark	S5.P9.,S5.P10.	114117
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Naciri, Yamama	Conservatoire et Jardin Botaniques, Genève, Switzerland	S1.O7.	11
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Nemeth, Krisztian	UK Centre for Ecology & Hydrology, Edinburgh, EH26 0QB	S2.P5.	34
Neophytou, Charalambos	Forest Research Institute Baden-Württemberg (FVA), Freiburg, Germany; Universität für Bodenkultur Wien, (BOKU), Vienna, Austria	S1.O3.,S1.P3.,S2.P30.,S3.O5.	7,14,59,74
Netherer, Sigrid	BOKU University, Austria	S2.O4.	24
Neuwirthová, Eva	Department of Experimental Plant Biology, Faculty of Science, Charles University, Prague, Czech Republic	S2.O1.,S2.P35.,S3.P3.	21,64,80
Newell, Rory	Teagasc Forestry Development Department, Teagasc	S2.P34.	63
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Nicorescu, Adelin-Ionut	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.P25.,S2.P10.	39,54
Nicorescu, Adelin-Ionut	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.P25.	54
Niederberger, Michael	Department of Geography, University of Zurich, Switzerland	S1.O2.	6
Nielsen, Lene Rostgaard	University of Copenhagen, Department of Geosciences and Natural Resource Management, Frederiksberg, Denmark	S2.O8.,S2.P9.,S2.P15.,S2.P22.	28,38,44,51
Niemi, Juha M.	SLU, Sweden	S4.O2.	86
Nissinen, Saara	Municipality of Savonlinna, Talvisalo comprehensive school (Finland)	S1.P6.	17

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Nordström, Annica	SLU, Sweden	S4.P5.	98
Nørgaard, Carsten Tom	Department of Geosciences and Natural Resource Management, University of Copenhagen, Denmark	S2.P11.	40
Nose, Mine	Forestry and Forest Products Research Institute, Japan	S4.P2.	95
Nosenko, Tetyana	Helmholtz, Research Unit Environmental Simulation	S2.P3.	32
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O'Hanlon, Richard	Department of Agriculture, Food and the Marine, Ireland	S2.P34.	63
Oberländer, Tim	Georg-August-Universität Göttingen, Department of Ecoinformatics, Biometrics and Forest Growth, Germany	S3.O4.	73
Oblišar, Gal	Slovenian Forestry Institute (GIS), Slovenia	S1.P1.	12
O'Brien, David	Inverness, UK & Royal Botanic Garden Edinburgh, United Kingdom	Keynote Session 1.	4
Odee, David	UK Centre for Ecology & Hydrology, Edinburgh, EH26 0QB	S2.P32.	61
Olofsson, Jill Katharina	Department of Geosciences and Natural Resource Management, University of Copenhagen, Denmark	S5.O9.,S5.P10.,S1.O5.,S2.P11.,S2.P20.	114,117,9,40,49
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Opgenoorth, Lars	Philipps University Marburg, Germany	S2.P38.,S3.O3.,S3.P5.	67,72,82
Orgel, Franziska	Thuenen Institute of Forest Genetics, Germany	S2.P3.	32
Ott, Caroline	Computational Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
Ottaviani, Maria	Molecular Biotechnology and Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
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Pagliarani, Sofia	Università della Tuscia (DIBAF), Italy	S2.O3.	23
Pärli, Rea M.	Swiss Federal Research Institute WSL, Birmensdorf, Switzerland and Translational Centre Biodiversity Conservation, Birmensdorf, Switzerland	S1.O7.	11
Pawłowski, Tomasz A.	Institute of Dendrology Polish Academy of Sciences	S1.O7.	11
Pérez Martín, Felipe	Ministerio para la Transición Ecológica y Reto Demográfico (MITECO)	S1.P7.,S4.P3.,S5.P1.	18,96,121
Perovic, Marko	University of Belgrade, Belgrade, Serbia	S5.O1.	106
Perraud, Ysaline	Northwest German Forest Research Institute (NW-FVA)	S2.P12.	41
Perry, Annika	UK Centre for Ecology & Hydrology, Edinburgh, EH26 0QB	S2.O5.,S2.P5.,S2.P3 2.,S5.O2.	25,34,61,107
Perry, Emily	School of Natural Resources and Environment, University of Florida, Gainesville, FL, 32611, USA	Keynote Session 3	69
Pers-Kamczyk, Emilia	Institute of Dendrology, Polish Academy of Sciences	S5.P7.	125
Petar, Zhelev	University of Forestry, Sofia, Bulgaria	S5.P2.	122
Peter, Gary F.	School of Forest, Fisheries, and Geomatics Sciences, University of Florida, Gainesville, FL, 32611, USA	Keynote Session 3	69
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Phannareth, Tommy	Virginia Tech University	S5.O6.	111
Piat, Lucien	National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux; BIOGECO, Cestas, France	S2.P36.	65
Pickering, Mark	European Commission, Joint Research Centre (JRC)	S5.O2.	107
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Pippel, Martin	Uppsala University, Department of Cell and Molecular Biology	S5.P7.	125
Plesca, Bogdan	National Institute for Research and Development in Forestry “Marin Drăcea”, Romania	S5.P2.	122
Plomion, Christophe	National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux; BIOGECO, Cestas, France	S2.P36.	65
Popescu, Flaviu	National Institute for Research and Development in Forestry “Marin Drăcea”, Romania	S5.P2.	122
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Prieto Estávez, Laura	Ministerio para la Transición Ecológica y Reto Demográfico (MITECO)	S5.P1.	121
Provazník, Daniel	Czech University of Life Sciences, Prague	S2.O1.	21
Pucker, Boas	(1) Technische Universität Braunschweig, Plant Biotechnology and Bioinformatics, Braunschweig, Germany and (2) University Bonn, Bonn, Germany	S3.O2.	71
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Pyhäjärvi, Tanja	Department of Forest Sciences, University of Helsinki, Finland	S2.P7.,S2.P12.,S5.O8.	36,41,113
Ramires, Marcelo	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.O4.	24

Ramirez-Valiente, Jose Alberto	ICIFOR-INIA, CSIC, Spain	S3.O1.	70
Ranade, Sonali S.	SLU, Sweden	S4.O2.,S2.P4.	86,33
Razzazi-Fazeli, Ebrahim	University of Veterinary Medicine Vienna	S2.O4.	24
Reich, Johanna	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.P24.	53
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Rentschler, Felix	FVA Baden-Württemberg	S1.O3.	7
Reudenbach, Christoph	Philipps University Marburg, Germany	S3.O3.	72
Reutimann, Oliver	ETH Zürich, Switzerland	S1.O5.,S1.O7.	9,11
Rezaie, Negar	CNR IRET	S2.O3.	23
Riba, Miquel	CREAF-UAB, Spain	S2.O5.,S2.P21.	25,50
Richman, Sarah	(1) ETH Zürich, Switzerland and (2) Translational Centre Biodiversity Conservation, Birmensdorf, Switzerland	S1.O7.	11
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Robledo-Arnuncio, Juan José	Instituto de Ciencias Forestales (ICIFOR-INIA), Consejo Superior de Investigaciones Científicas, Madrid 28040, Spain	S4.O9.,S4.P4.,S5.O5.,S5.O7.	93,97,110,112
Rodriguez Coca, Liuder Isidoro	Department of Silviculture, Transilvania University of Brasov, Romania	S5.P8.	126
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Rozenberg, Philippe	INRAE, France	S3.O3.,S3.O6,S3.O7.	72,75,76
Rupprecht, Christina	BOKU University, Department of Ecosystem Management, Climate and Biodiversity, Institute for Integrative Nature Conservation Research, Vienna, Austria	S5.P11.	118

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Sagariya, Christi	Czech University of Life Sciences, Prague	S4.O7.	91
Sandor, Bordacs	Hungarian Institute of Agriculture and Life Sciences	S2.P10.,S2.P25.	39,54
Santiago, Louis S.	Department of Botany and Plant Sciences, University of California, Riverside, Riverside, CA, USA	S3.O1.	70
Sanz Martín, Ángel	Ministerio para la Transición Ecológica y Reto Demográfico (MITECO)	S4.P3.	96
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Savolainen, Outi	Ecology and Genetics Research Unit, University of Oulu, Finland	S2.P7.	36
Schebeck, Martin	BOKU University, Austria	S2.O4.	24
Schinnerl, Johann	Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, Vienna A-1030, Austria	S2.O2.	22
Schlosser, Sarah	University of Veterinary Medicine Vienna	S2.O4.	24
Schmid, Bernhard	Department of Geography, University of Zurich	S1.O2.	6
Schmidt, Daniel	Nordwestdeutsche Forstliche Versuchsanstalt, Abteilung Waldgenressourcen, Hann. Münden, Germany.	S2.P2.	31
Schnitzler, Jörg-Peter	Helmholtz, Research Unit Environmental Simulation	S2.P3.	32
Scholzen, Eleonore	Public Service of Wallonia, Dept. Nature and Forest	S5.P6.	124

Schöndorfer, Selina	Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), Vienna, Austria	S2.O2.,S4.P8.	22101
Schreiber, Mona	Philipps University Marburg, Germany	S2.P38.	67
Schroda, Michael	Molecular Biotechnology and Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
Schroeder, Hilke	Thünen Institute of Forest Genetics, Germany	S1.O6.,S2.P3.,S5.P7 .	10,32,125
Schuldt, Bernhard	Technical University of Dresden, Germany	S3.O1.	70
Schuman, Meredith C.	Department of Geography, University of Zurich, Switzerland	S1.O2.,S3.O5.	6,74
Schwarzer, Friderieke	Technische Universität Braunschweig, Plant Biotechnology and Bioinformatics, Braunschweig, Germany	S3.O2.	71
Scotti, Ivan	National Research Institute for Agriculture, Food and the Environment (INRAE), URFM, Ecology of Mediterranean Forests, Avignon, France	S3.O2.,S1.O1.,S2.P2 1.,S3.O8.	71,4,50,77
Seegmüller, Stefan	Forschungsanstalt für Waldökologie und Forstwirtschaft Rheinland-Pfalz	S2.O7.	27
Seitner, Sebastian	Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), Vienna, Austria	S4.O1.,S4.P8.	85101
Sekely, Jill	University of Freiburg, Germany	S3.O3.,S5.P5.	72,82
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Semizer-Cuming, Devrim	Forest Research Institute Baden- Württemberg (FVA), Freiburg, Germany; Bavarian Office for Forest Genetics (AWG), Teisendorf, Germany	S1.O3.,S2.P30.	7,59
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Sergiadou, Dimitra	Department of Geosciences and Natural Resource Management, University of Copenhagen, Denmark	S2.P11.,S2.P20.	40,49

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Shayle, Elliot Samuel	Philipps University Marburg, Germany	S3.P5.	82
Shifrin, Tom	The Hebrew University of Jerusalem	S2.O6.	26
Sievers, Alice-Jeanine	Thuenen Institute of Forest Genetics, Genetic Technologies, Grosshansdorf, Germany	S4.P7.	100
Šijačić-Nikolić, Mirjana	University of Belgrade - Faculty of Forestry, Kneza Višeslava 1, 11030 Belgrade, Serbia	S2.P16.,S2.P17.,S5. P4.	45,46,123
Sirén, Jenni	Department of Forest Sciences, University of Helsinki, Finland	S2.P12.	41
Skofic, Milko	European Forest Institute (EFI)	S1.O1.	4
Solé Medina, Aida	Instituto de Ciencias Forestales (ICIFOR-INIA), Consejo Superior de Investigaciones Científicas, Madrid, Spain	S3.O3.	72
Sommer, Frederik K.	Molecular Biotechnology and Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
Sonnenberg, Sabastian	BOKU University, Department of Ecosystem Management, Climate and Biodiversity, Institute for Integrative Nature Conservation Research, Vienna, Austria	S5.P11.	118
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Spanu, Ilaria	Institute of Biosciences and Bioresources (IBBR), National Research Council of Italy (CNR)	S5.O4.	109
Splechtna, Bernhard	BOKU University, Department of Ecosystem Management, Climate and Biodiversity, Institute for Integrative Nature Conservation Research, Vienna, Austria	S5.P11.	118

Steiner, Wilfried	Nordwestdeutsche Forstliche Versuchsanstalt, Abteilung Waldgenressourcen, Hann. Münden, Germany.	S2.P2.	31
Stejskal, Jan	Department of Forest Genetics and Physiology, Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Prague, Czech Republic	S2.O1.,S2.P35.,S3.P3.,S4.O4.,S5.P15.	21,64,80,88,129
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Stepanovic, Dawid	Universität für Bodenkultur Wien, (BOKU), Vienna, Austria	S2.P30.	59
Stephan, Jean	Lebanese University, Fanar, Lebanon	S5.O1.	106
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Suszka, Jan	Institute of Dendrology Polish Academy of Sciences	S4.P1.	94
Szukala, Aglaia	Austrian Research Centre for Forests (BFW), Vienna, Austria	S2.P10.,S2.P25.,S2.P36.	39,54,65
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Theraroz, Adélaïde	National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux; BIOGECO, Cestas, France	S2.O5.	25
Thomas, Francisco	National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux; BIOGECO, Cestas, France	S2.O5.,S2.P21.,S5.O4.,S5.P13.	25,50,109,120
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Torres, Eric	Agronomy Department, University of Florida, Gainesville, FL, 32611, USA	Keynote Session 3	69
Torres-Ruiz, José M.	Instituto de Recursos Naturales y Agrobiología de Sevilla (IRNAS), Consejo Superior de Investigaciones Científicas (CSIC), Seville, 41012, Spain.	Keynote Session 3,S1.P1,S3.O1	12,69,70
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Truffaut, Laura	INRAE, France	S2.O9.	29
Trujillo-Moya, Carlos	Austrian Research Centre for Forests BFW - Department of Forest Growth, Silviculture & Forest Genetics, Vienna, Austria	S2.O2.,S2.O4.,S4.O1.,S4.P8.	22,24,85,101
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Utz, Vanessa J.	Molecular Biotechnology and Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
Vajana, Elia	Institute of Biosciences and Bioresources (IBBR), National Research Council of Italy (CNR)	S2.P21.,S5.O4.	50109
Vakkari, Eeva	Department of Forest Sciences, University of Helsinki, Finland	S2.P7.	36
Valade, Aude	CIRAD, France	S3.O1.	70
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Van Breusegem, An	Research Institute for Nature and Forest (INBO), Belgium	S1.P4.	15

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van Moorsel, Sofia	Department of Geography, University of Zurich	S1.O2.	6
Van Nieuwerburgh, Filip	Laboratory of Pharmaceutical Biotechnology, Ghent University, Belgium	S2.P1.	30
Vanden Broeck, An	Research Institute for Nature and Forest (INBO), Belgium	S1.P3.,S1.P4.,S2.P1.	14,15,30
Vander Mijnsbrugge, Kristine	Research Institute for Nature and Forest (INBO), Belgium	S1.P4.	15
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Vatén, Anne	Organismal and Evolutionary Biology Research Programme, University of Helsinki, Finland	S2.P7.	36
Vela, Errol	University of Montpellier, France	S5.O1.	106
Vendramin, Giovanni Giuseppe	Institute of Bioscience and Bioresources (IBBR), National Research Council (CNR), Firenze, Italy	S2.P21.,S3.O3.,S5.O 2.,S5.P13.	50,72,107,12 0
Venn, Benedikt	Computational Systems Biology, Rheinland-Pfälzische Technische Universität Kaiserslautern-Landau	S2.O7.	27
Verbylaite, Rita	Lithuanian Research Centre for Agriculture and Forestry, Institute of Forestry, Kaunas, Lithuania	S2.O8.	28
Verschaeve, Leen	Research Institute for Nature and Forest (INBO), Belgium	S1.P4.	15
Verschelde, Pieter	Research Institute for Nature and Forest (INBO), Belgium	S2.P1.	30
Verta, Jukka-Pekka	Faculty of Biosciences and Aquaculture, Nord University, Norway	S2.P12.	41
Vicente, Eduardo	INRAE, France	S2.P31.	60
Vijayan, Thapasya	BOKU University, Department of Ecosystem Management, Climate and Biodiversity, Institute for Integrative Nature Conservation Research, Vienna, Austria	S5.P11.	118
Vilhar, Urša	GIS, Gozdarski Inštitut Slovenije , SFI, Slovenian Forestry Institute, Slovenia	S1.P1.,S1.P6.	12,17

Vinchira-Villarraga, Diana	University of Birmingham	S2.P5.	34
Vizcaíno Palomar, Natalia	ICIFOR-INIA, CSIC, Spain	S2.P19.	48
Vu, Giang Thi Ha	Forest Genetics and Forest Tree Breeding, University of Göttingen, Göttingen, Germany	S2.P2.,S2.P18.	31,47
Vuosku, Jaana	Ecology and Genetics Research Unit, University of Oulu, Finland	S2.P12.	41
Walthert, Lorenz	WSL, Birmensdorf, Switzerland	S1.O5.	9
Wang, Kai	University of Helsinki, Finland	S4.O8.	92
Weber, Alexandra A.-T.	Eawag, Dübendorf/Kastanienbaum, Switzerland	S1.O7.	11
Weigel, Detlef	Max-Planck-Institute for Biology, Tübingen, Germany	S2.P36.	65
Westergren, Marjana	Slovenian Forestry Institute (GIS), Slovenia	S1.O1.,S2.O5.,S2.P21.	4,25,50
Widmer, Alex	ETH Zürich, Switzerland	S1.O7.	11
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Wilms, Hannes	Research Institute for Nature and Forest (INBO), Belgium	S1.P4.	15
Winkler, Katja	Elementary school Spodnja Siska (Slovenia)	S1.P6.	17
Winkler, Sylke	Max Planck Institute of Molecular Cell Biology and Genetics	S5.P7.	125
Witzell, Johanna	Linnaeus University, Sweden	S2.P8.,S2.P27.	37,56
Woith, Maïke	Freie Universität Berlin, Plant Ecology, Berlin, Germany	S3.O2.	71
Xu, Jing	University of Copenhagen, Denmark	S2.P22.	51
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Yordan, Muhovski	Walloon Agricultural Research Centre (CRA-W)	S5.P6.	124
Zahn, Virginia	Thuenen Institute of Forest Genetics, Genetic Technologies, Grosshansdorf, Germany	S4.P7.	100
Zavala-Paez, Michelle	Pennsylvania State University, USA	S4.O6.	90

Zeuss, Dirk	Philipps University Marburg, Germany	S3.P5.	82
Zhelev, Petar	University of Forestry, Sofia, Bulgaria	S2.P25.	54
Zimmermann, Felix	WSL, Birmensdorf, Switzerland	S1.O5.	9
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