Resilient Forests for the Future

EVOLTREE Conference 2023

12 – 15 September 2023
UNITBV, Brașov, Romania

Book of Abstracts

Transilvania University of Brașov

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Associate Professor Dr. Elena Ciocîrlan

Prof. Dr. Neculae Şofletea

Short program

Time (GMT+2; CET+1)	**Tuesday 12.09.2023**	**Wednesday 13.09.2023**	**Thursday 14.09.2023**	**Friday 15.09.2023**
08:30 - 09:30		Excursion to *Dealul Lempeș* forest and *Sânpetru* teaching and research station		
09:30 - 10:30			Lecture: Potential applications of remote sensing in genomics (Mihai Daniel Niță)	Lecture: Introduction to adaptive silviculture (Norocel Valeriu Nicolescu)
10:30 - 11:30	Registration & Coffee			
11:30 - 12:00				
Lunch Break	1:1 meetings	1:1 meetings	1:1 meetings	1:1 meetings
13:00 - 13:15	Welcome and Information	Information	Information	Information
	Session 1: Climate resilient forests		Session 4: Innovative methods and approaches	Session 5: Conservation genomics
13:15 - 14:00	Keynote	Poster Session A	Keynote	Keynote
14:00 - 14:40	Oral presentations Session 1		Oral presentations Session 4	Oral presentations Session 5
14:40 - 14:50	Short break		Short break	Short break
14:50 - 15:50	Oral presentations Session 1		Oral presentations Session 4	Oral presentations Session 5
15:50 - 16:20	Long break	Long break	Long break	Long break
	Session 2: Tree genomics & biotic interactions under climate change	Session 3: Evolutionary genomics	Poster Session B	Session 6: Tree breeding and sustainable use of forest genetic resources
16:20 - 17:05	Keynote	Keynote		Keynote
17:05 - 17:45	Oral	Oral		Oral

	presentations Session 2	presentations Session 3		presentations Session 6
17:45 - 17:55	Short break	Short break		Short break
17:55 - 18:30	Oral presentations Session 2	Oral presentations Session 3		Oral presentations Session 6
18:30 - 18:55			Departure to *Bran*	
18:55 - 19:15				
Evening	1:1 meetings	1:1 meetings	Conference Dinner	1:1 meetings

Categories

Scientific exchange
Networking
Teaching
Social event

Session 1:

Climate resilient forests

Tuesday 12 September 13:15 - 15:50

Chair: Dr. Katharina Birgit Budde, Georg-August University, Göttingen, Germany

Oral presentations

13:15	**Keynote** **Hamilton, Jill:** Hybrid zones as model systems to examine the genomic basis for climate adaptation
14:00	**Rellstab, Christian:** Identifying adaptive traits and genes to choose seed sources for climate resilient oak forests
14:20	**Müller, Niels A.:** Genomic variation of European beech across its distribution range reveals patterns of local adaptation and future maladaptation
14:40	***Short Break***
14:50	**Toomey, Madeline:** Improving climate resilience in silver banksia (*Banksia marginata*) through landscape genomics and common garden experiments
15:10	**Kansu, Cigdem:** Genomic scans detect evidence of positive selection using SNP data in rangewide populations of *Populus trichocarpa* and *P. balsamifera*
15:30	**Chakraborty, Debojyoti:** Utilizing assisted migration to enhance and preserve European forest carbon sink

Keynote Session 1:

Hybrid zones as model systems to examine the genomic basis for climate adaptation

Contribution ID: 101

Hamilton, Jill

Trees are foundation and keystone species in forest ecosystems and contribute to numerous ecosystem services, such as habitat for associated species, soil formation and water regulation but also timber products. Global climate change is rapidly advancing, especially with respect to long-lived species, such as forest trees. Within the lifetime of a single tree, mean annual temperature is currently expected to rise by 2-4°C. Apart from that, natural disturbance events, such as prolonged drought periods, heat waves, wind throws, as well as pest and pathogen outbreaks, are likely increasing. Here, resilience refers to the capacity of a forest ecosystem to tolerate and recover from such perturbations while maintaining a similar functioning and structure. Many factors, including species-specific characteristics, biotic interactions as well as management practices, influence forest resilience. Understanding the complex underlying mechanisms and processes affecting forest resilience is therefore crucial to develop suitable mitigation and adaptation strategies. In this interdisciplinary session we encourage contributions from various fields, such as forest genetics and genomics, silviculture, ecology and pathology, to foster a joint discussion about strategies to maintain and enhance forest resilience in the face of global climate change.

Keywords: hybridization, climate change, *Populus*, common garden experiments, whole genome sequencing

Identifying adaptive traits and genes to choose seed sources for climate resilient oak forests

Contribution ID: 107

<u>Rellstab, Christian</u>; Acar, Pelin; Jansen, Simon; Neophytou, Charalambos; Kaya, Zeki; Leigh, Deborah M.

Oak trees can live for over 1000 years. Fixed in place, the climate change-mediated environmental shift that individual oak trees experience is likely to be substantial and potentially harmful. European white oaks grow from the Mediterranean coast to Southern Scandinavia, a huge environmental gradient that has fostered local adaptations that could be beneficial under future climate scenarios like drought and extreme temperature. Assisted seed translocations from populations from drier and warmer sites, could ensure oak forest health by matching trees with their predicted future climates. However, an understanding of the geographical patterns and genomic architecture of environmental adaptation is needed as a guide. Particularly because it is unclear if the genomic basis of environmental adaptation is highly localized or even population specific in oak trees, or if it similar at a range wide scale.

To characterize local adaptation in white oaks (*Quercus robur*, *Q. pubescens*, *Q. petraea*), we have established three common gardens of oak seedlings (Switzerland, Turkey, Austria). Provenances were selected from both distributional and local environmental extremes (i.e. chronic soil drought vs wet soil), and seedlings measured at key productivity and water use efficiency traits. Analyses of trait data from across the gardens shows limited differences between provenances from local environmental extremes relative to distribution extremes. This suggests environmental adaptation is predominantly visible at a large geographical scale for the three species. The genomic architecture of these adaptations is now being explored through GWAS of key traits to identify if the same genes drive the trait differences observed.

Keywords: *Quercus*, climate change, common garden experiments, assisted gene flow, drought adaptation

Genomic variation of European beech across its distribution range reveals patterns of local adaptation and future maladaptation

Contribution ID: 108

Müller, Niels A.; Geßner, Cornelia; Mader, Malte; Blanc-Jolivet, Céline; Fladung, Matthias; Degen, Bernd

Local adaptation is key for ecotypic differentiation and species evolution. Understanding the underlying genomic patterns allows the prediction of future maladaptation and ecosystem stability. We used whole-genome resequencing to analyze 865 individuals from 100 range-wide populations of European beech (*Fagus sylvatica*), one of the most important forest tree species in Europe. We show that genetic variation closely mirrors geography. Adaptive variation identified by genotype-environment associations exhibits highly polygenic architectures, involving thousands of associated sequence variants across the genome. By modelling the 'genomic offset' of these sequence variants under projected future climate conditions, we identify broad- and fine-scale variation highlighting geographic regions as well as populations at potential elevated risk of mortality or local extinction. Our results emphasize the importance of considering natural genetic variation for forest conservation under climate change.

Keywords: population genomics, genotype-environment associations, local adaptation, genomic offset, *Fagus sylvatica*

Improving climate resilience in silver banksia (*Banksia marginata*) through landscape genomics and common garden experiments

Contribution ID: 109

<u>Toomey, Madeline</u>; Ahrens, Colin; Rymer, Paul; Miller, Adam

Climate change is expected to increase the severity and frequency of drought events around the world in the coming decades, putting many functionally important plant species and the ecosystems they support at risk. Evidence suggests many species will be unable able to track their ecological niches via migration, meaning their future persistence will likely depend on adaptation in situ, facilitated either by plasticity or genetic evolution. Consequently, a major conservation challenge is characterising the adaptive capacity of functionally important plant species and identifying interventions capable of rescuing plant populations threatened by drought stress. One such species showing signs of climate stress is the Silver Banksia (Banksia marginata, Proteaceae), a keystone species endemic to the savannas and forests of Australia that was once widespread but has suffered significant decline over the last century. Recent genetic studies show a high level of relatedness within populations with significant genetic structuring among remnant fragments, highlighting imminent risks of inbreeding and maladaptation under climate change. I will present the findings of recent landscape genomic and common garden studies aimed at testing for genotype x environment and genotype x phenotype associations among B. marginata populations spanning an aridity gradient. These studies are providing insights into the likely contributions of phenotypic plasticity and genetic adaptation in assisting the species to combat future climate challenges. This research will have an impact on future management, including the need for assisted gene flow strategies capable of improving the adaptive capacity of vulnerable populations.

Keywords: landscape genomics, common garden, climate change, local adaptation, banksia

Genomic scans detect evidence of positive selection using SNP data in rangewide populations of *Populus trichocarpa* and *P. balsamifera*

Contribution ID: 110

Kansu, Cigdem; Phannareth, Tommy; Bolte, Constance; Zhang, Qian; Hamilton, Jill A.; Fitzpatrick, Matthew C.; Keller, Stephen R.; Holliday, Jason A.

Populus trichocarpa and *P. balsamifera* are sister species that inhabit mostly temperate coastal and continental climates, respectively, in western and northern North America, with the Rocky Mountains roughly dividing their ranges and also encompassing a hybrid zone. Previous work suggests that introgression may be a conduit to pass adaptive diversity between these species, and we sought to characterize this process through sampling of six west to east transects that each span putative parental-type P. trichocarpa, the hybrid zone, and ending in putative parental type P. balsamifera. A total of 576 samples were sequenced at ~20X coverage of the whole genome. As a prelude to understanding the role of adaptive introgression in the evolution of these species, we sought to characterize how parallel and non-parallel selection has shaped the genomes of the parental species. We used genome-wide scans to detect evidence of positive selection in widely distributed populations of P. trichocarpa and P. balsamifera with the iHS (integrated Haplotype Score), which identifies genomic intervals undergoing selection in a given species in isolation, and the XP-EHH (cross-Population Extended Haplotype Homozygosity), which tests for selection unique to the focal species in comparison to a second species. A total of ~25M SNPs were screened from 318 parental individuals. We identified loci potentially under selection with a high-quality dataset of SNP markers across the genome. Furthermore, we compared the selection signatures between the northern and southern populations of *P. trichocarpa* to identify regions of the genome with rapid increases in allele frequency. Our findings illustrate genomic regions exhibiting signals of positive selection on both incomplete sweeps and sweeps near fixation. Functional annotation using gene ontology provided insights into the biological processes and molecular functions. The identification of those regions undergoing positive selection offers valuable knowledge for future studies aiming to explain the underlying molecular processes.

Keywords: *Populus*, WGS, SNP, selection signatures, positive selection

Utilizing assisted migration to enhance and preserve European forest carbon sink

Contribution ID: 111

<u>Chakraborty, Debojyoti</u>; Schueler, Silvio

The role of European forests as carbon sinks is increasingly endangered by climate change-induced droughts and disturbance events. On the policy level, European Union has an ambitious plan to increase the terrestrial carbon sink and achieve net zero emissions by 2050. Adaptive management strategies such as choice of species and planting materials are therefore crucial for maintaining forest carbon sinks and increasing forest resilience. Assisted migration (AM) of forest tree species and populations was suggested to avoid maladaptation and to maintain forest growth under future climate. We identified AM schemes for seven major European tree species based on 587 range-wide provenance trials, evaluating more than 3000 provenances. Using models that account for environmental and genetic factors of phenotypic trait variations, we estimated the annual aboveground carbon sink (CS) of 40-year-old trees under current and projected future climate by adapting species composition and seed sources.

To increase forest resilience under climate change, coniferous trees might need to be replaced by deciduous trees in large parts of their distribution, with significant consequences for ecosystem services and biodiversity. This change will result in a decrease of the current CS of 44 Tgyr-1 by 32-43% until 2061-80 if local seed provenances are employed. However, if seed provenances adapted to the future climate are utilized, current CS can be maintained or even increased to 46-55 Tgyr-1. Transnational AM can boost both resilience and the CS of European forests.

Keywords: adaptation, assisted migration, climate change, carbon sink, emission reduction

Session 1:

Climate resilient forests

Poster Session A: Wednesday 13 September 13:15 - 15:50

Posters

Neuwirthová, Eva:
Genetic variation of drought-stress tolerance in Scots pine

David-Schwartz, Rakefet:
Natural hybrids of *Pinus brutia* and *P. halepensis* and their resistance to drought in regenerating forests

Caicoya, Astor Toraño:
Species mixtures research for the study of the role of genetic diversity in stands of Scots pine

Lampei, Christian:
Beech seedlings from exposed dry sites show higher drought resistance

Hazarika, Reneema:
Stakeholder perception on risks and benefits of managing non-native tree species in the European alpine space

Jansen, Simon:
Large-scale genetic structure of European white oaks: on the search for climate-smart seed sources

Müller, Markus:
Association of genome-wide genetic variation with adaptation-related traits in European beech

Chevalier—Mairet, Arnaud:
Impact of abiotic factors on growth-related trait variability across populations of white oak species in Europe: applications to understanding future wood resources in managed forests

Fussi, Barbara:
Identification of potentially climate resilient beech seed stands (Fagus sylvatica L.) in Germany

Hurel, Agathe:
Searching for drought-resistant genetic variants in *Quercus cerris* for future Austrian climate

Suliman, Tammam:
The development of disturbance models on the basis of Austrian National Forest Inventory (ANFI)

Afifi, Lila:
Sorbus torminalis and the WILDOBST project: using genetic analysis to inform conservation

Korecky, Jiri:
Comparative multi-genotype LC-MS metabolite profiling of Norway spruce in distinct environments

Dominguez-Flores, Tania:
Analysis of pollen flow inferred from paternity analysis in *Quercus rubra* in an urban landscape in Germany

Vajana, Elia:
Unveiling convergent adaptation in Mediterranean pines to inform a new tool for the management of forest genomic resources — the MedForAct project

Avanzi, Camilla:
Tree decline of Italian pedunculate oak populations: a multidisciplinary approach for selecting and producing resistant forest genetic resources

Ciocîrlan, Mihnea-Ioan-Cezar:
Bud-burst monitoring in the European beech population (*Fagus sylvatica* L.) along an altitudinal gradient in the South-Eastern Carpathian Mountains

Genetic variation of drought-stress tolerance in Scots pine

Contribution ID: 112

<u>Neuwirthová, Eva</u>; Stejskal, Jan; Lhotáková, Zuzana; Čepl, Jaroslav; Korecký, Jiří; Albrechtová, Jana; Panzarová, Klára; Lstibůrek, Milan

Scots pine (*Pinus sylvestris* L.) is a species known for its low ecological requirements, wide distribution, and remarkable phenotypic plasticity under drought stress. This study aims to investigate the phenotypic plasticity of Scots pine, which makes it an ideal species for understanding responses to water deficit. Considering the genetically determined variability in photosynthesis observed in Scots pine, we hypothesize that other biophysical parameters will differ among populations and families during early drought and subsequent recovery phases. In this research, we examined the progeny of upland and lowland Scots pine ecotypes sourced from three seed orchards containing locally adapted populations in the Czech Republic. 810 seedlings from 130 families were analyzed. In a greenhouse experiment, we exposed two-year-old seedlings to induced drought stress and examined their response to water deficit and subsequent regeneration during new shoot development from February to August 2022. To test our hypothesis, we employed a high-throughput phenotyping facility equipped with a fully automated system. To assess seedling phenotype, we used biophysical parameters obtained as follows: 1) weekly sampling of fluorescence, infrared, and RGB cameras in 160 days; 2) sampling of individual seedlings after recovery for RCD, height, water content, specific leaf area, and needle length. A decrease in the heritability of biophysical parameters obtained through the image data was observed during the stress period. In addition, differences among the populations and families in the majority parameters were observed after recovery. Drought tolerance is a crucial trait in forest tree breeding; however, relying solely on phenotype for selecting drought-tolerant individuals may be insufficient. Stress conditions can obscure the heritability of physiological traits, and the genetic basis of drought tolerance in forest tree species remains poorly understood. This study provides insights to better understand the

Keywords: seed orchards, seedling screening, high-throughput phenotyping, image data, biophysical parameters

Natural hybrids of *Pinus brutia* and *P. halepensis* and their resistance to drought in regenerating forests

Contribution ID: 113

Houminer, Naomi; Osem, Yagil; Riov, Joseph; Sherman, Amir; Rozen, Ada; Sela, Hanan; David-Schwartz, Rakefet

Interspecific hybridization increases genetic diversity, which is essential for coping with changing environments. Hybrid zones, occurring naturally in overlapping habitats of closely related species, can be artificially established during afforestation. The resulting interspecific hybridization may promote sustainability in man-made forests, particularly in regions facing degradation due to climate change. However, there is limited evidence of hybridization during forest regeneration. Here, we studied the frequency of Pinus brutia Ten. x P. halepensis Mill. hybridization at three stages of forest regeneration in five planted forests in Israel: seeds before dispersal, emerged seedlings, and recruited seedlings at the end of the dry season. We found hybrids on *P. brutia*, but not on *P. halepensis*, owing to asynchronous flowering phenology. Using 94 single-nucleotide polymorphism (SNP) markers, we demonstrated that all stages included hybrids, most of which were hybrids of advanced generations. The hybrid proportions increased from 4.7±2.1 to 8.2±1.4, and to 21.6±6.4 percent, from seeds to emerged seedlings, and to recruited seedlings stages, respectively. The increased hybrid ratio implies an advantage of hybrids over P. brutia during forest regeneration. To test this hypothesis, we measured the seedling growth rate and morphological traits under controlled conditions and found that the hybrid seedlings exhibited selected traits of the two parental species, which likely contributed to the fitness and survival of the hybrids during the dry season. In addition, the results of a controlled drought experiment suggested that the response of the hybrids to drought stress was better than that of the parental species. This study highlights the potential contribution of hybrids to sustainable-planted forests and contributes to the understanding of genetic changes that occur during the regeneration of man-made forests.

Keywords: hybrids, drought stress, planted forests, forest regeneration

Species mixtures research for the study of the role of genetic diversity in stands of Scots pine

Contribution ID: 114

Toraño Caicoya, Astor; Pretzsch, Hans; Uhl, Enno; Climent, José María; Del Río, Miren

The research on species mixtures has shown how species diversity has an overall positive effect on productivity, as well as on the resistance and resilience of forest stands, especially when the complementary between species is high. In this work, we investigate whether these benefits occur also in genotypes mixtures. To this aim, we transfer the methodologies commonly used when analyzing species mixtures to study the impacts of mixing provenances on forest growth. We present models for the study of genetic diversity effect on growth, analyzed in a broad set of provenance plots, for *Pinus sylvestris*, in Spain and Germany. With the help of a moving window design, that selects the immediate vicinity of every tree, we calculated relevant tree and stand characteristics, together with the diversity of provenances inside of each moving circle. With this data we have fitted generalized linear models each growth and stand characteristic, accounting for the site as a random effect. A higher number of provenances has shown a positive and significant effect in the structural diversity (coefficient of variation of diameter at breast height - dbh). Our results have also shown a positive impact in the height growth, but not on diameter growth, potentially indicating a higher competition for light, at least noticeable in the young development phase of Pinus sylvestris. Although this may change with age, silviculture guidelines and management recommendations could be draws for young stands. In the future, we plan to extend these analyses to a diverse range of species like *Fagus sylvatica*, *Pinus pinaster*, *Picea abies* and *Abies alba*.

Keywords: forest management, resilience, forest growth

Beech seedlings from exposed dry sites show higher drought resistance

Contribution ID: 115

<u>Lampei, Christian</u>; Lambertz, Johannes; Heer, Katrin; Opgenoorth, Lars

The recently increased frequency of prolonged drought periods in late spring and early summer had visual negative effects on the health of the European beech (*Fagus sylvatica*) in many German forests. Already, foresters start searching for new, exotic tree species, that could substitute beech in the future. However, beech is known for high within stand genetic diversity and the observed damages may only show ongoing selection that will shift the population towards a more drought resistant state, if drought resistant genotypes are present in the population. To test whether the latter is true, we conducted a common garden experiment with seedlings from moderate and exposed-dry sites in the National Park Kellerwald-Edersee, and subjected the seedlings to a drought treatment. We found that, on average, the leaves of seedlings from the dry sites withered slower compared to the moderate sites. However, variation was strong among sites and the differences were driven predominantly by two of the dry sites. Notably, the seedlings with higher drought resistance showed reduced water consumption. We conclude that variation in drought resistance exists in German forests however, geneflow between sites may counteract local adaptation, which may be the reason for the high variation across tested sites. For German beech forests this may indeed indicate the potential for adaptation, though through a potentially painful period of selection.

Keywords: local adaptation, drought resistance, common garden

Stakeholder perception on risks and benefits of managing non-native tree species in the European alpine space

Contribution ID: 116

Hazarika, Reneema; Lapin, Katharina; Vacik, Harald

Discussion in forest management has increasingly focused on how humans can assist tree species adaptation /migration processes, especially when important forest ecosystem services are at risk. One option is to introduce non-native tree (NNT) species to help these forest ecosystems adapt to climate change. With potential invasiveness, NNTs face both socially and ecologically complex management challenges. Moreover, a lack of awareness and negative attitudes towards the NNTs can cloud conservation policies in cases where the NNT provides beneficial ecosystem services. In this study, we analyzed the perceptions of multiple stakeholders, associated with the urban landscapes and traditional forests, on the risks and benefits of NNTs and their management in the European Alpine Space. We surveyed 6 countries of the Alpine Space and received 457 responses. The results of this survey highlight that 90% of the respondents are aware of the NNTs in their region and among them, most believe that the NNTs pose a risk to the environment. NNTs and invasive NNTs occur mainly in urban areas with a perceived increase in their occurrence in the last 25 years. There was a clear relationship between the invasiveness of NNTs and their risks and benefits on ecosystem services. Respondents, who were not concerned about the invasiveness of NNTs, recognized a positive impact of NNTs on the provisioning ecosystem services such as timber. In contrast, respondents concerned about the invasiveness of the NNTs recognized a negative impact on regulating and cultural ecosystem services such as native biodiversity and landscape aesthetics, etc. Also, approximately 50% of the respondents believed that their understanding of the management policies of NNTs is inadequate.

Keywords: non-native trees, Alpine space, ecosystem services, perception, management

Large-scale genetic structure of European white oaks: on the search for climate-smart seed sources

Contribution ID: 117

Jansen, Simon; Semizer-Cuming, Devrim; Tourvas, Nikolaos; Blyth, Colette; Kansu, Cigdem; Funda, Değirmenci; Asiya, Uluğ; Leigh, Deborah M.; Acar, Pelin; Aravanopoulos, F.A. (Phil); Kaya, Zeki; Rellstab, Christian; Neophytou, Charalambos

In the face of climate change, forest tree provenances adapted to drought are gaining importance as seed sources. In this context, it is particularly meaningful to explore the genetic variation of species with wide ecological amplitude and distribution ranges, such as the three closely related white oak species Quercus robur, *Q. petraea*, and *Q. pubescens* in the European continent. In the framework of the BiodivERsA project 'ACORN', more than 120 populations of the aforementioned three species were sampled within a large area stretching from Central Europe to the Eastern Mediterranean Basin. A series of genetic and genomic tools are being applied, with the final goal of identifying populations with high adaptive potential. Current results based on nuclear and chloroplast microsatellite markers provide insights into the neutral genetic structure, demography, and diversity of the three species both at the regional and range-wide scale including refugial populations, which received little attention in the past. Moreover, they allow the taxonomic assignment and assessment of admixture level within this species complex. Our results elucidate the effect of evolutionary mechanisms on the gene pools of the oaks. Large geographic barriers, introgressive hybridization and the post-glacial range expansion were all important factors that shaped the neutral genetic structure and diversity. The analysis of neutral genetic structure delivers valuable information that can be directly used to inform forest conservation and management policies.

Keywords: spatial genetic structure, demography, genetic diversity, microsatellites, *Quercus*

Association of genome-wide genetic variation with adaptation-related traits in European beech

Contribution ID: 118

Müller, Markus; Leuschner, Christoph; Weithmann, Greta; Weigel, Robert; Banzragch, Bat-Enerel; Steiner, Wilfried; Hofmann, Martin; Schmidt, Daniel; Gailing, Oliver

European beech is already affected by climate change and a decrease in its growth is predicted for large parts of its distribution range. Therefore, knowledge about the genetic basis of environmental adaptation, especially with regard to drought stress, is of particular importance in European beech. The GenVarBuche project aims to increase the understanding of adaptation processes in beech. In close cooperation with the BEECHLIMITS project, beech populations along a precipitation gradient as well as additional populations from other regions in Germany were analyzed using genotyping by sequencing and genome-wide genetic variation was identified. A total of 13,493 high-quality single nucleotide polymorphisms (SNPs) were used for association analyses with environmental and tree physiological traits. This identified 33 SNPs that consistently showed significant associations using different methods and are thus potentially involved in environmental adaptation. These and other potentially adaptive and neutral SNPs are used to genotype 2000 individuals of 13 beech provenances from a provenance trial that is replicated at two different sites. These data will then be used for further association analyses. In the provenance trial, the traits height increment, diameter at breast height, bud break timing, fall leaf coloration, specific leaf area, and stomatal density were recorded. In addition to differences among provenances, some of the traits also showed differences at the two trial sites. For instance, while stomatal density showed very similar values at both sites, specific leaf area showed significant differences. This suggests a different amount of phenotypic plasticity of different traits. The results from the provenance trials are used for the validation of adaptive SNPs and will provide insights into the respective relevance of genetic and environmental effects on trait expression in European beech.

Keywords: adaptation, association study, genetics, adaptive traits, genotyping by sequencing

Impact of abiotic factors on growth-related trait variability across populations of white oak species in Europe: applications to understanding future wood resources in managed forests

Contribution ID: 119

Chevalier-Mairet, Arnaud; Lepoittevin, Camille; Bert, Didier; Nicolas, Loïc; Loiseau, Baptiste; Mathurin, Jean-Charles; Garnier-Géré, Pauline

Quercus robur and *Q. petraea* are two closely related European dominant forest species with major cultural, economic and ecological interests. There is much concern for their resilience to predicted abiotic and biotic selection pressures, due to recurrent dieback in recent decades. In order to address the fundamental issue of these species adaptive potential to future changes, we need to characterize the structure and magnitude of genetic diversity at both spatial scales (can we identify local adaptation among regions?) and evolutionary scales (are there different species patterns?). However, this knowledge is lacking in many regions potentially vulnerable to future droughts across Europe, such as the Limousin region (central France), known for its wood of high quality (e.g. elevated ellagitanins) used in the cooperage and spirits industry. The objectives are: (1) to identify the main ecological determinants of growth-related trait variation across regions, by combining data from both climate and National Forest Inventories; (2) To further explore growth patterns in the Limousin region, in comparison to contrasted Northern or Southern regions, using a dendroclimatic approach; (3) To quantify the genome-wide diversity and its structure across European populations, testing genotype-environment associations, while including new samples with very little data or absent from previous genetic studies. Focusing here on objective (1), the first results show that variation in climatic conditions across French regions is organized along three main independent axes, with the mean annual water balance explaining best the first axis in multidimensional analyses. The Limousin region shows a very large range of climatic conditions, with sub-regions showing less aridity than other forest regions. The first three axes also explain cumulatively and significantly between ~5% and ~11% of growth-related traits variation, depending on species or periods. We discuss how these factors could influence possible tree responses to future climatic scenarios.

Keywords: European *Quercus* species, adaptive potential, ecological factors, dendrochronology, population genomics

Identification of potentially climate resilient beech seed stands (*Fagus sylvatica* L.) in Germany

Contribution ID: 120

Fussi, Barbara; Mellert, Karl-Heinz; Kavaliauskas, Darius; Müller, Markus; Semizer-Cuming, Devrim; Schmied, Gerhard; Uhl, Enno; Gailing, Oliver; Šeho, Muhidin

The reaction of seed stands to climate change, in particular to increasingly frequent climate extremes such as severe drought, has not yet been sufficiently studied in Germany. The focus of previously established provenance trials was on the general suitability, growth, and wood quality of different provenances, with the main purpose of high yield. However, ongoing climate change threatens the stability, productivity, and survival of forest genetic resources (FGR). Therefore, it is crucial to identify climate-resilient provenances and forest stands that can be used as suitable seed sources for climate smart forestry. The "sensFORclim" project, funded by the Forest Climate Fund of the German Federal Ministry of Food and Agriculture, aimed to investigate the climate sensitivity of forest genetic resources of silver fir, Norway spruce and European beech in Germany and to verify the suitability for seed production in the future. For that reason, 624 trees (48 each) were sampled from 13 European beech stands and analysed with 11 nuclear microsatellite markers. Genetic variation at neutral loci between stands was low and no signs of clustering was found. Six out of 13 populations were analysed at 96 potentially adaptive SNP markers, showing correlations with drought stress and bud break in previous studies. The R package Boruta confirmed previous findings (e. g. significant correlation of the SNP marker CP10_377 with climate parameters related to drought stress susceptibility). The project results are expected to contribute to forest research and to a better understanding of forests adaptation to climate change by supporting the identification of resilient provenances.

Keywords: *Fagus sylvatica*, adaptation, resilient provenances, forest genetic resources, SNP markers

Searching for drought-resistant genetic variants in *Quercus cerris* for future Austrian climate

Contribution ID: 121

<u>Hurel, Agathe</u>; Feichter, Jonathan; Heinze, Berthold

In the current context of global change, forest ecosystems are among the most endangered. The main objectives of our study are (1) to identify the genetic variants associated with drought stress resistance across *Quercus cerris* natural distribution, and (2) to screen the Austrian populations for such genetic variation. We plan on a phenotype-genotype association analysis of tree-ring width on dry years as a proxy for drought resistance, by means of ca 90 K SNPs detected with Single Primer Enrichment Technology (SPET). The first step of this analysis is to find regions in the current distribution of Q. cerris where the climate is comparable to predicted future conditions in Austria (IPCC climatic scenario RCP8.5). We established partnerships with research institutions in 14 countries, providing 40 locations of interest. In addition, we included 6,348 locations distributed evenly over the natural range of *Q. cerris* into our dataset. To represent Austria, we selected 34 locations where *Q. cerris* has high probability of presence in 2095 according to RCP8.5. Mean annual temperature, continentality, summer temperature, total annual precipitation and accumulated growing degree days are among the most important climatic variables for Q. cerris. The CHELSA dataset delivers data observations from 1981-2010 as well as predictions for RCP8.5 in the timeframe 2071-2100. We retrieved the observed variables for the locations of interest and the predicted variables for the 34 Austrian locations. Using the Elbow method, we established k=4 as the optimal number of clusters for this dataset. Interestingly, using Ward's clustering algorithm with Euclidean distance, we observed that 3 of these clusters were represented in Austria. In sum, we report a meaningful approach to select relevant sampling locations to investigate the genetic variants underlying drought resistance in climatic regions similar to the future of Austria, bringing us one step closer to ensuring forest ecosystems sustainability.

The development of disturbance models on the basis of Austrian National Forest Inventory (ANFI)

Contribution ID: 122

Suliman, Tammam; Ledermann, Thomas

Disturbances such as wind, snow, and bark beetles have a significant impact on Austrian forests. Annually, storms and snow damage 1-3 million cubic meters of timber. However, major storms like Vivian/Wiebke in 1990, Kyrill in 2007, and Paula/Emma in 2008 caused 7-10 million cubic meters of damage. After these storms, bark beetle damage increased from 1 million to 2-3 million cubic meters. Considering the expected impact of climate change on disturbances, adaptive forest management and disturbance-based growth models are crucial for the future management of Austria's forests.

The aim is to develop the following sub-models at the plot and individual-tree level:

- The likelihood of random events (wind, snow breakage, bark beetle outbreaks).
- The breakage sub-model (damaged only by wind and snow).
- The other random events (damaged only by drought and bark beetles).

Methods: We categorized disturbance-related damages/mortality as "events" and analyzed an extensive dataset of 343,722 individual trees from 9,532 plots of the Austrian National Forest Inventory (ANFI) spanning the years 1981-2021. To investigate the influencing factors, we developed plot-level and individual-level sub-models that integrate climate data, site conditions, stand variables, and individual-tree characteristics. Logistic mixed-effect models were used to examine the relationships between these factors and the likelihood of random events.

Initial results: At plot level:

- The developed models indicate that reducing the proportion of *Picea abies* and *Pinus sylvestris*, while increasing the proportion of *Fagus sylvatica*, *Quercus* sp., and *Carpinus* betulus, can mitigate the risk and expected damage intensity resulting from random events.
- The occurrence of random events increases when wind speed interacts with the maximum stand height.
- Maximum temperature and snow increase the probability of further random disturbance events.
- Moderate interventions in the stand can mitigate the vulnerability of trees to random events, while excessive interventions can significantly increase the risk of random event occurrence.

Keywords: disturbance models, climate change, wind, snow breakage, bark beetle outbreaks

Sorbus torminalis and the WILDOBST project: using genetic analysis to inform conservation

Contribution ID: 124

Afifi, Lila; Tremetsberger, Karin; Lapin, Katharina; Konrad, Heino

As climate change progresses, so does our need to bolster forest resilience to lessen the burden of climate change in the future. So too, does our need to maintain drought resistant species that can act as ecosystem anchors. One such species, *Sorbus torminalis*, is the focus of this work. A light dependent, tolerant, post-pioneer species, *S. torminalis* has the potential to provide vital stability to more delicate forest ecosystems that are currently dominated by more sensitive species. Furthermore, models have shown that *S. torminalis* should be capable of expanding its range as climate change continues. But without adequate population connectivity, the genetic material necessary to allow this expansion will deteriorate before enough migration occurs. To that end, small, scattered populations of *S. torminalis* across Austria were analyzed for genetic diversity, population structure, and other genetic factors such as the fixation index and rarefaction. These analyses provide the first glimpse into the insights of the WILDOBST Project, which looks to analyze genetic diversity, structural, and functional connectivity of 3 scattered tree species: *Pyrus pyraster*, *S. torminalis*, and *S. domestica*. The goal of this project is to identify which populations to collect seeds for planting efforts from, as well as which conservation measures are necessary to maintain or improve functional and structural connectivity of these three species. With this information, more informed conservation and management policies can be recommended to foresters and organizations both across Austria and further across Europe.

Keywords: climate change, conservation, genetics, *Rosaceae*, *Sorbus torminalis*

Comparative multi-genotype LC-MS metabolite profiling of Norway spruce in distinct environments

Contribution ID: 125

Korecky, Jiri; Čepl, Jaroslav

The metabolite profiles of plants can vary significantly across genotypes, reflecting their inherent genetic diversity and responses to environmental stimuli. Understanding the metabolic responses might be essential for unraveling plant adaptation strategies. In this study, we performed comparative LC-MS metabolite profiling of three genotypes propagated in Norway spruce seed orchards at two contrasting sites. The robustness of the analysis was enhanced by analyzing each genotype in several replicates (ramets). By employing partial least squares discriminant analysis (PLS-DA), we identified variations in the metabolite profiles among genotypes within each site and between identical clones across sites. Similar metabolomic profiles among identical genotypes within site imply a genetic nature of metabolite profiling. In contrast, differences in the clonal metabolite profiles between the two sites indicated environment-driven metabolic adaptations.

Keywords: LC-MS metabolite profiling, *Picea abies* (L.) H. Karst., genetic and environmental variation, PLS-DA

Analysis of pollen flow inferred from paternity analysis in *Quercus rubra* in an urban landscape in Germany

Contribution ID: 126

<u>Dominguez-Flores, Tania</u>; Budde, Katharina Birgit; Gailing, Oliver

In the face of changing climatic conditions, it is essential to anticipate how different species might cope with associated stresses. Gene flow is a fundamental factor influencing the genetic diversity and structure of tree species. Planted tree species outside their natural distribution range, e.g. in arboreta or botanical gardens, provide an ideal setting to study the effect of severe fragmentation on gene flow patterns and distances. Paternity analysis based on microsatellite marker genotyping was used to analyse the effect of fragmentation on gene flow between individuals of *Q. rubra* distributed in a small, isolated group of trees (15 trees) planted in an arboretum on the north campus of the University of Göttingen. For paternity analysis, 365 seedlings from 4 seed parents were selected and genotyped using 16 microsatellites. The paternity analysis revealed a significant relationship between pollination frequency and distance, indicating that most pollen (84.89 %) was coming from neighbouring trees. The average distance of the four seed parents to the pollen donors ranged from 17.3 m to 103.6 m. Pollen influx from outside was significant and ranged from 8.64 to 26.26%. We observed high genetic differentiation among the four pollen clouds (G''ST = 0.407). In addition, four large full-sib families were identified. Overall, using an isolated patch of *Q. rubra* to estimate gene flow and mating system parameters we could observe that there was no self-fertilisation even in very small plantations. Gene dispersal was distance-dependent as expected and we observed a remarkable influx of external pollen from a large number of different donors (30), which may promote high genetic variation even in isolated stands. Long-distance pollen dispersal could explain high genetic variation even in isolated natural populations.

Keywords: gene flow, red oak, fragmented landscape, parentage, microsatellites

Unveiling convergent adaptation in Mediterranean pines to inform a new tool for the management of forest genomic resources — the MedForAct project

Contribution ID: 127

Vajana, Elia; Piotti, Andrea

An overview of the background, aims, workflow, expected impact and outcomes will be provided for the EU-funded project MedForAct (HORIZON Marie Skłodowska-Curie Action 2022-PF-01). The 2-yrs project will address the need of outlining new genomic-informed strategies to mitigate the impact of genetic erosion and adaptive lags in the Mediterranean forests as induced by climate change. Particularly, MedForAct will focus on three iconic pine species native to the Mediterranean basin (i.e., Aleppo pine, maritime pine and stone pine) to identify a core set of genes and gene networks that may have fostered their convergent adaptation in the face of severe ecological challenges and despite million years of independent evolution. To tackle this challenge, the project will rely on a newly produced genomic dataset composed of c. 800 individuals sampled throughout the main environmental gradients in Italy and genotyped at c. 100K SNPs, largely focusing on the same target regions in the three species. Then, inter- and intraspecific gene-environment association tests will be devised to screen the pine genomes for association with habitat so as to identify top candidate regions for convergent local adaptation. The potential characterization of such regions will advance our knowledge on the mechanisms underlying the adaptive potential in Mediterranean conifers with key implications for developing genomic-informed management strategies and conservation priorities. Following this, MedForAct envisages using the detected top-ranked candidates to develop new tools for forest management, with the aim of providing forest managers with a practical means of implementing targeted reforestation approaches by monitoring the expected adaptive lag of populations using genomics and future climatic predictions.

Keywords: convergent local adaptation, forest genetic resources, gene-environment association analysis, climate change, Mediterranean pines

Tree decline of Italian pedunculate oak populations: a multidisciplinary approach for selecting and producing resistant forest genetic resources

Contribution ID: 128

Avanzi, Camilla; Vajana, Elia; Pericolo, Osvaldo; Assini, Silvia Paola; Bagnoli, Francesca; Barcella, Matteo; Borghetti, Marco; Bracco, Francesco; Castellaneta, Maria; Pinosio, Sara; Tarzariol, Giulia; Vendramin, Giovanni G.; Ripullone, Francesco; Nola, Paola; Piotti, Andrea

In recent decades, climate change has induced chronic stresses and prompted episodes of tree decline and mortality, which are expected to further intensify, especially in the Mediterranean region. Tree decline and mortality profoundly affect forest functioning in both the short and long term, with serious consequences for the ecosystem services provided. Widespread phenomena of decline have been observed from the late 1990s in pedunculate oak (*Quercus robur* L.) populations of northern Italy, especially in the area with the largest presence of the species (along the Ticino River). The causes of such decline are still unknown, but probably lie in a complex interplay of biotic and abiotic factors, such as an increased frequency of drought episodes, increased competition with exotic species, and the action of fungi and other pathogens. We screened the oak genome to identify which genetic variants might contribute to providing some resistance to decline. To this purpose, we applied a novel experimental design, selecting pairs of nearby individuals, one in healthy conditions and one with clear symptoms of decline, for a total of 125 pairs from five study sites. Each individual was genotyped with a Single Primer Enrichment Technology (SPET) panel of 90k probes, that yielded a total of 352,459 SNPs. Individual decline was first assessed visually and, later, on the basis of growth dynamics by means of incremental core analysis. The potential confounding effect of environmental variation was considered through botanical and phytopathological surveys aimed at characterizing ecological features at the individual tree level. The ultimate goal of the work will be providing insights into how genomic information can be used to identify resistant genotypes and its usefulness for conservation and management programs, particularly at the material collection stage. The poster presents first results of ongoing genotype-phenotype association analyses.

Keywords: climate change, forest genetic resources, dendrogenomics, *Quercus robur*, oak decline

Bud-burst monitoring in the European beech population (*Fagus sylvatica* L.) along an altitudinal gradient in the South-Eastern Carpathian Mountains

Contribution ID: 129

<u>Ciocîrlan, Mihnea Ioan Cezar</u>; Ciocîrlan, Elena; Chira, Dănuț; Chira, Florentina; Mantale, Costel; Radu, Gheorghe Raul; Gailing, Oliver; Curtu, Alexandru Lucian

Under climate change, forest tree species are forced to react and adapt to new environmental conditions, even pushed to their limits of survival. European beech (*Fagus sylvatica*) is one of Europe's most widespread forest tree species and has great economic and ecological importance. Phenology data is important for forest management decisions. Spring phenology of European beech was monitored for three consecutive years, in five study sites, along an altitudinal gradient, from 550 m to 1450 m. Only the upper third of the crown was analyzed, based on Vitasse's scale which includes four stages of bud development (dormant winter bud, bud-swollen, bud-burst, and at least one leaf unfolding). In each study site, three sensors were installed for recording temperature and relative humidity. There is a gap between the populations located at the extremities of the altitudinal gradient (26 days in 2021, 30 days in 2022, and 26 days in 2023, respectively) and, also, from one year to another (Lempes site: 119 D.O.Y. in 2021, 102 D.O.Y. in 2022, and 114 D.O.Y. in 2023 and Ruia site: 145 D.O.Y. in 2021, 132 D.O.Y. in 2022, and 140 D.O.Y. in 2023). In the years in which the bud-burst occurs later, 2021 and 2022, the transition from one phenophase to another (the dynamics through the four stages of bud development) is much faster (6-11 days in 2021 and 2023, compared to 13 in 2022). The correlation of the meteorological data with the phenological ones showed that the start of the beech in the growing season (associated with the "bud-burst" stage according to the scale used) occurs when the average daily temperature value exceeds the thermal threshold of 10 °C. This study highlights the phenological differences among and within beech populations, from one year to another, bringing data about the adaptation of European beech along a complex altitudinal gradient.

Keywords: European beech, phenology, budburst, meteorological data, altitudinal gradient

Session 2:

Tree genomics & biotic interactions under climate change

Tuesday 12 September 16:20 - 18:35

Chair: Dr. Hilke Schröder, the Thünen Institute, Germany

Oral presentations

16:20	**Keynote** **Swenson, Nathan G.:** Functional genomics as a window into the drivers community structure and dynamics in temperate and tropical forests
17:05	**Kjær, Erik Dahl:** Resilience of European ash forests influenced by ash dieback
17:25	**Coq--Etchegaray, Domitille:** Genetic architecture of leaf specialized metabolites natural variation within sessile oak populations
17:45	***Short Break***
17:55	**Olofsson, Jill K.:** Can northern sessile oaks profit from southern genetic variants to face future climate change?
18:15	**Schröder, Hilke:** Surviving oaks as beacons of hope in climate change

Keynote Session 2:

Functional genomics as a window into the drivers community structure and dynamics in temperate and tropical forests

Contribution ID: 102

Swenson, Nathan G.

Tree community structure and dynamics are, ultimately, the emergent properties of differential individual-level performance. This differential performance is governed by interaction between the environment and organismal functional. Over the past two decades there has been an incredible increase in the use of functional traits to predict plant population and community structure and dynamics. However, the results of these studies have often been underwhelming with indications that richer and more dynamic assays of function are necessary. That is, functional traits are rough and static approximations of some organismal functions and, generally, do not consider functions of interest ad the dynamic response of organisms to changing environmental contexts. In this presentation, I will begin by discussing this fundamental problem in trait-based tree ecology. Next, I will argue that functional genomics provides a potential pathway for improving our understanding of tree populations and communities and I will buoy this argument by providing examples from our work in temperate and tropical tree communities. Finally, I will end the presentation with a vision for the future of tree community genomics that seeks to tackle multiple outstanding conceptual and practical issues.

Keywords: community ecology, forest dynamics plots, functional biology, gene expression, transcriptomics

Resilience of European ash forests influenced by ash dieback

Contribution ID: 130

Kjær, Erik Dahl; Lobo, Albin; Kosawang, Chatchai; Long, Feng; Thomsen, Iben; Doonan, James; Xu, Jing; Hansen, Lars; Nielsen, Lene; Hansen, Jon Kehlet

During the last century, several forest calamities has been caused by host shifts where an introduced fungus has become a severe pathogen on a native species that lacked co-evolutionary history with the new pathogen. This is considered to be the case for the European ash (*Fraxinus excelsior*) that in recent decades has become severely damaged throughout most of its natural distribution area by the introduced Asian ascomycete *Hymenoscyphus fraxineus*. Fortunately, genetic variation in resistance against the novel pathogen in Europe was identified early in the epidemic, and a substantial body of research has since focused on understanding the genetics of this resistance with the vision to promote resilience of ash forest based on wise genetic management practices. Here, we review knowledge obtained from common garden trials, inoculation tests, in situ field studies of mature ash forests, analysis of microbiomes, genomes, transcriptomes and analysis in relation to survival and reproductive fitness. Based on present the knowledge, we discuss how genetic considerations can be integrated into the management of natural and planted ash forests to enhance and protect their resistance and evolutionary resilience.

Keywords: ash dieback, biotic adaptation, *Fraxinus excelsior*, resilience, host-pathogen interaction

Genetic architecture of leaf specialized metabolites natural variation within sessile oak populations

Contribution ID: 132

Coq--Etchegaray, Domitille; Bernillon, Stéphane; Le-Provost, Grégoire; Kremer, Antoine; Ducousso, Alexis; Lalanne, Céline; Bonne, Fabrice; Moing, Annick; Plomion, Christophe; Brachi, Benjamin

Specialized or secondary metabolites (SMs) play a key role in plant resistance against abiotic stresses and defences against bioaggressors. For example, in sessile oaks *Quercus petraea*, phenolics contribute to reduce herbivore damage and improve drought resistance. In the context of global climate change the extensive diversity of compounds and variation of biosynthesis within species may play a key role to mitigate the increased frequency of stressful events such as drought, heat waves or emergent pathogens. Here, we study the genetic basis of leaf SMs natural variation in nine European provenances of sessile oaks and investigate signature of selections along the genome. We sampled mature leaves from high and low branches on 225 sessile oak trees located in a common garden and used untargeted metabolomics to characterise the variation of 219 leaf specialized metabolites. In addition, we used whole genome low-depth sequencing to genotype all individuals for 1.4M genetic markers. We then performed genome-wide association analyses, identified candidate genes underlying the variation of leaf SMs and compared signatures of selection at these genes to the rest of the genome. We found that leaf SMs displayed extensive within-provenance variation, but very little differentiation between provenances. For ∼10% of the metabolites we detected, most of this variation could be explained by a single genetic marker. Our results suggest that genetic variation of most leaf SMs is unlikely to be locally adaptive, and that varying selective pressures may act locally to maintain diversity at loci associated with leaf SM variation.

Keywords: leaf specialized metabolites, GWAS, *Quercus petraea*, balanced selection

Can northern sessile oaks profit from southern genetic variants to face future climate change?

Contribution ID: 134

Olofsson, Jill Katharina; Lobo, Albin; Hansen, Jon Kehlet; Nielsen, Lene; Budde, Katharina Birgit; Rellstab, Christian; Kjær, Erik Dahl

In addition to valuable renewable wood resources, oak forests are essential ecosystems hosting a large amount of biodiversity. Although oaks are predicted to be less affected by a shift in climatic conditions, including more frequent and severe drought spells, compared to other forest tree species, they will have to adapt fast to future climatic changes. Here we use classical landscape genomics to locate genes with a potential adaptive role in drought-resistance among pan-European provenances of sessile oak (*Quercus petraea*). We ask if an enrichment with alleles beneficial for dry conditions from southern provenances often subjected to drought – be it by natural dispersal, gene flow or human plantings – can enhance the adaptive potential of the native Danish Q. petraea populations to a future drier climate. We find numerous genetic loci (single nucleotide polymorphisms; SNPs) associated with bioclimatic variables describing local precipitation. While many of the associated SNPs are found in inter-genic regions, some are indeed located in, or close to genes, known to be involved in drought stress responses. Thus, beneficial alleles have the potential to spread across the landscape. We will present detailed analyses of these beneficial alleles in order to determine whether they are absent in the local Danish gene pool, or if they are already present at low frequency, and thus enabling adaptation to a drier climate based on standing genetic variation. In conclusion, beneficial alleles found among southern populations of sessile oak is a valuable source for future enrichment of northern oak seed sources and natural populations to ensure their robustness under future climate.

Keywords: climate adaptation, landscape genomics, local adaptation, oak, *Quercus*

Surviving oaks as beacons of hope in climate change

Contribution ID: 133

Schröder, Hilke; Mader, Malte; Orgel, Franziska; Nosenko, Tetyana; Schnitzler, Jörg-Peter; Kersten, Birgit

The pedunculate oak (*Quercus robur*) shows high potential of adaption and is therefore a prime candidate to become a pillar of resilient forests in the future to combat the challenges of climate change. The project “Survivor-Oaks” aims to identify oak trees that are tolerant to different biotic and abiotic stresses including herbivory, mildew infestation and drought stress. Tolerant trees will be selected for the installation of seed orchards. Here we present the characterization of oak trees based on their expression profiles with respect to herbivory. The goal of this study is to compare the transcriptome response of oak trees to infestation by two different insects: a specialist, the green oak leaf roller (*Tortrix viridana*) and a generalist, the gypsy moth (*Lymantria dispar*). In earlier projects, oaks tolerant or susceptible to *T. viridana* have been identified based on defoliation rates in infestation years with heavy defoliation levels. We conducted two separate feeding experiments with the two above mentioned insects using three tolerant and three susceptible oak clones. Combining biological (ramets) and technical (different leaves) replicates, in total the RNA of two distinct sets of 36 samples (18 fed and 18 control) was sequenced. Analysis of the RNA-Seq data included the detection of differentially expressed genes with Deseq2 and functional analysis based on Gene Ontology over-representation analysis and gene set enrichment analysis with the R package ClusterProfiler. First results indicate the presence of similar functional patterns of enriched Gene Ontology terms in the *Tortrix viridana* and *Lymantria dispar* RNA-Seq datasets compared to control sets (e.g. an enrichment of terpene synthase-related terms) but also differences in the reaction of *Q. robur* to feeding by the two different insects. Expression levels of selected candidate genes were further validated by RT-qPCR in the course of feeding.

Keywords: *Quercus robur*, RNA-Seq, herbivory

Session 2:

Tree genomics & biotic interactions under climate change

Poster Session A: Wednesday 13 September 13:15 - 15:50

Posters

Jakuš, Rastislav:
Predicting Norway spruce resistance to bark beetle attack with the use of satellite imagery

Chano, Victor:
Transcriptomic analysis of the short-term response to ash dieback in two ash genotypes with different susceptibility to the disease

Chano, Victor:
Transcriptomics of the Dutch elm disease pathosystem

Gathercole, Louise:
The Centre for Forest Protection - a new British collaboration for future resilient forests

Korolyova, Nataliya:
Why do some Norway spruce trees survive bark beetle outbreaks?

Predicting Norway spruce resistance to bark beetle attack with the use of satellite imagery

Contribution ID: 135

<u>Jakuš, Rastislav</u>; Trubin, Aleksei; Korolyova, Nataliya

Norway spruce (*Picea abies*) resistance to bark beetle (*Ips typographus*) consists of resistance to primary and secondary insect attacks. During the primary attacks, bark beetles firstly target physiologically weakened trees that are usually stressed by drought and acute heat. When colonization of primarily attacked individuals is finished, bark beetles “switch” to the neighboring trees using a pheromone mediated mechanism. Beetles may infest even relatively vigorous trees as their second host choices. In addition to strong constitutive and induced defense mechanisms against direct boring attempts, resistant tress should be able to tolerate drought and thermal stresses without major impairments in physiological processes. Acute moisture deficit and thermal stresses commonly occur at the fresh forest edges created by wind and/or bark beetle disturbances and harvesting. To study spruce resistance to bark beetle attacks, we analyzed multispectral time series PlanetScope satellite imagery covering forested area that belongs to the University Forest Enterprise Kostelec nad Černými lesy in Czechia. We also used the field survey data showing locations of bark beetle colonized trees. During the whole vegetation season, we were monitoring individual bandwidths (blue, green, red, and infrared) and selected spectral vegetation indices (SVIs) calculated for infested and non-infested trees. We found significant and consistent differences in Enhanced Vegetation Index (EVI) between non-attacked and attacked spruces. We argue that EVI can facilitate more accurate prediction of resistant and beetle-killed trees, and, thus, increase the efficiency of forest pest management.

Keywords: spruce, bark beetle, resilience, remote sensing, *Ips typographus*

Transcriptomic analysis of the short-term response to ash dieback in two ash genotypes with different susceptibility to the disease

Contribution ID: 136

Chano, Victor; Callegari Ferrari, Renata; Dominguez-Flores, Tania; Shrestha, Karuna; Ridley, Maia; Fussi, Barbara; Steiner, Wilfried; Gailing, Oliver; Budde, Katharina Birgit

The invasive ascomycete species *Hymenoscyphus fraxineus* is the pathogenic agent causing a severe decline in European populations of common ash (*Fraxinus excelsior*), so-called ash dieback (ADB). In Germany, the disease is prevalent and has spread throughout all regions where this tree species can be found. In this study, we conducted a controlled inoculation experiment under greenhouse conditions using two ash genotypes from a clonal common garden showing differences in the response to ADB, the tolerant genotype FAR3 and the susceptible UW1. Infected trees were inoculated using wood plugs infected with a highly pathogenic *H. fraxineus* strain, that were placed and wrapped with parafilm over open wounds (ca. 1 cm) made in the surface of the petioles of the leaves, whereas control trees were mock-inoculated with wood plugs without the pathogen. Seven days after the inoculation (short-term response), the inoculated and mock-inoculated petioles were harvested for total RNA isolation and transcriptome sequencing (RNA-Seq). Raw sequence files were pre-processed and filtered based on quality scores, and then mapped against the reference genome available for F. excelsior. A total-count expression matrix was generated considering all the samples (two genotypes, control and inoculated samples, and four biological replicates per group) and used for gene expression analysis. We found a total of 693 Differentially Expressed Genes (DEGs) in response to the infection with p-value below the standard 0.05, showing different patterns of expression among the targeted genotypes. Moreover, we also performed a differential gene expression analysis for the individual genotypes (without accounting for genotype differences), the transcriptomic response to the infection involved 545 DEGs in the susceptible genotype UW1 (465 upregulated and 80 downregulated), whereas 252 DEGs were found in the tolerant FAR3 (147 upregulated and 105 downregulated). From these DEGs, 11 were common for both genotypes. These results together suggest a very distinct transcriptomic short-term response between the tolerant and the susceptible genotypes used in this study.

Keywords: common ash, transcriptomics, gene expression, ash dieback, short-term response

Transcriptomics of the Dutch elm disease pathosystem

Contribution ID: 137

<u>Chano, Victor</u>; Sobrino-Plata, Juan; Perdiguero, Pedro; Martínez-Arias, Clara; Collada, Carmen; Rodríguez-Calcerrada, Jesús; Martín-García, Juan Antonio

Dutch elm disease (DED) is a vascular wilt caused by the pathogenic fungi *Ophiostoma novo-ulmi* and considered as a major forest pandemic degrading European elm populations. In this work, the transcriptomic of the DED pathosystem has been analyzed by means of dual RNA-Sequencing in three *Ulmus minor* genotypes, MDV-2.3 and VAD-2 which shows tolerance to the disease, and the susceptible MDV-1. In addition to these three genotypes, we followed a multifactorial design including four time points (time-series analysis; 6, 24, 72 and 144 hours-post-infection), and infected (inoculated in the stem with spores from the pathogen) and control plants (mock-inoculated with sterile water). Moreover, four clonal replicates were used for each study group. Harvested samples were used for RNA isolation and dual RNA-Seq. After pre-processing, sequencing reads were mapped against the reference genome available for O. novo-ulmi strain H327, and mapped reads were later used to create a total-count matrix for gene expression analysis. As *U. minor* is lacking a reference genome, those reads unmapped to the pathogen genome (and considered as elm reads) were first used for de novo assembly of a single reference transcriptome, which resulted in 51,904 transcripts or unigenes. Samples reads were then mapped against the reference transcriptome, creating another total-count matrix for gene expression analysis. On the one hand, we found 712 differentially expressed genes (DEGs) were induced in the pathogen against the susceptible genotype MDV-1, whereas 671 and 710 DEGs were upregulated against the tolerant genotypes MDV-2.3 and VAD-2, respectively. On the other hand, we found 3,771 DEGs in the susceptible MDV-1, while the tolerant genotypes MDV-2.3 and VAD-2 showed differential expression of 3,048 and 1,538 DEGs, respectively. This suggests a different transcriptional response in the two tolerant genotypes.

Keywords: field elm, dual RNA-Seq, differential gene expression, DED, DEG

The Centre for Forest Protection - a new British collaboration for future resilient forests

Contribution ID: 138

Gathercole, Louise

The new Centre for Forest Protection (CFP), jointly led by Forest Research and the Royal Botanic Gardens, Kew, was established to provide a unique hub and collaborative platform for tree health expertise and research, supporting the England Tree Action Plan. The mission of the centre is to protect the future of our forests, woodlands and trees from environmental and socioeconomic threats, through innovative science, interdisciplinary research, expert advice and training. Research is focusing on strengthening our forests and woodlands to withstand pests and diseases, while also limiting the entrance and spread of new pests and diseases and reducing the impacts of other pressures such as climate change. We have a range of projects, many of which see the lead partners working in collaboration, using the complementary strengths of the two organisations and our partners and collaborators to further the resilience of our woodlands. We are developing an education and training programme to build capacity and capability in forest protection. We will also develop a knowledge hub, of use to scientists, policy makers and practitioners, to promote the outcomes of our work and to gather information from other organisations in the field of forest protection. We are beginning to plan the next phase of our research and are actively looking to work with international collaborators working on woodland resilience.

Keywords: resilience, future, protection, interdisciplinary, genomics

Why do some Norway spruce trees survive bark beetle outbreaks?

Contribution ID: 139

<u>Korolyova, Nataliya</u>; Buechling, Arne; Ďuračiová, Renata; Lieutier, François; Yart, Annie; Cudlín, Pavel; Jakuš, Rastislav

Climate change intensified severity and frequency of landscape altering bark beetle disturbances worldwide risking forest ecosystem functioning. Using a combination of experimental and phenomenological approaches, we studied *Picea abies* resistance to *Ips typographus* mass attacks. In 2003, in natural spruce-monodominant forest located in the Vosgues mountains, France, we conducted a mechanical wounding experiment, coinciding with bark beetle outbreak, to investigate chemical defenses of 97 mature trees using high-performance liquid chromatography. In the Bohemian forest, at the cross-border of Czechia, Germany and Austria, we acquired remotely sensed and field survey data comprising 184 surviving and 414 reference trees to investigate the factors of spruce survival during herbivore disturbance. Spatial clustering of extant trees indicated that survival was a non-random process governed by multiple biotic and abiotic factors. Beetles' first targets were individuals with elevated initial concentration of taxifolin glucoside in phloem, higher total and primary crown defoliation ratios, and lower juvenile crown ratios than in trees that were secondarily attacked. Non-linear logistic regression models showed that survival largely depends on tree size and distance to a previously colonized individual. Trees with more extensive crowns were better buffered against colonization attempts. Crown defoliation, a proxy measure of tree vigor, and stem sun exposure were negatively associated with tree resistance. Stand competition had a strong negative effect on survival. Increase in moisture deficit (climatic water balance) compromised tree chances to persist through disturbance. Synthesis of catechin exponentially increased tree survival probability. However, even resistant trees with high catechin production were susceptible in late season due to high insect population growth. Using an integrated analytical approach, we demonstrate that forest outcomes will depend on complex cross-scale interactions between global climate trends and tree-level trait factors, as well as feedback effects associated with landscape patterns of stand structural diversity.

Keywords: drought, tree resistance, *Ips typographus*, climate change, tree defense

Session 3:

Evolutionary genomics

Wednesday 13 September 16:20 - 18:55

Chair: Dr. Annika Perry, UK Centre for Ecology & Hydrology, UK

Oral presentations

16:20	**Keynote** **Lind, Brandon M.:** The limits of predicting maladaptation to future climate using genomic data
17:05	**Gonzalez-Martinez, Santiago C.:** Genetic variation within and among populations underlies adaptation to climate in a Mediterranean pine species
17:25	**Tysklind, Niklas:** Plant mutations: slaying beautiful hypotheses by surprising evidence
17:45	***Short Break***
17:55	**Păun, Ovidiu:** The drivers of the adaptive radiation of persimmon trees on New Caledonia, a biodiversity hotspot
18:15	**Gathercole, Louise:** Genomic evidence for extensive introgression amongst British oaks and assessment of mal-adaptation
18:35	**Paulo, Octávio S.:** A landscape genomic approach on the cork oak and holm oak in the Western Mediterranean: insights into the species’ capacity to respond to climate change

Keynote Session 3:

The limits of predicting maladaptation to future climate using genomic data

Contribution ID: 103

Lind, Brandon M.; Lotterhos, Katie E.

Methods using genomic information to forecast population maladaptation to climate change (i.e., genetic offset methods) are becoming increasingly common, yet there has been little exploration into the factors that could potentially affect performance of these methods, or mislead inference with regard to model accuracy during validation. These knowledge gaps pose serious hurdles toward the incorporation of such methods into management and policy. We use an extensive set of simulated data that varies demography, selection, the number of adaptive traits, and underlying adaptive architecture to evaluate offset methods (Gradient Forests, the Risk Of-Non-Adaptedness, redundancy analysis, and lfmm2). We validate these methods using 100 in silico reciprocal transplant gardens across each simulated landscape by associating predicted offset with simulated fitness in each garden. Using these results, we discuss how both evolutionary and experimental parameters affect the performance these methods. Finally, we make recommendations for evaluating and incorporating offset inference into conservation decisions for natural populations.

Keywords: climate change, maladaptation, genomic offset, conservation, restoration

Genetic variation within and among populations underlies adaptation to climate in a Mediterranean pine species

Contribution ID: 140

Archambeau, Juliette; de Miguel, Marina; Changenet, Alexandre; Perry, Annika; Avanzi, Camilla; Bagnoli, Francesca; Barraquand, Frederic; Benito Garzon, Marta; Grivet, Delphine; Vendramin, Giovanni G.; Alía, Ricardo; Cavers, Stephen; Gonzalez-Martinez, Santiago C.

Genetic variation is the raw material for population adaptation to climate change. Although forest trees often exhibit extensive genetic variation within and among populations, they may be particularly at risk under climate change due to their long generation times and slow migration rates. We studied the genetic variation within and among 34 rangewide populations of maritime pine (*Pinus pinaster* Ait.) using about 10 000 single nucleotide polymorphisms (SNPs) and phenotypic traits from five clonal common gardens located within the species natural range. Within-population quantitative genetic variation for early height growth, a fitness-related trait, was lower in maritime pine populations from climates with cold winters. This reduced genetic variation may result from adaptation to harsh climates but may also hinder future adaptation to novel climates. Genetic variation among populations was also associated with large-scale climatic gradients, and we predicted the extent to which the current gene-environment relationships will be disrupted under climate change for each population, using a proxy of potential maladaptation, often referred to as the genetic offset. As the genetic offset predictions were highly dependent on the modelling approach used to generate them, we evaluated which approach best explained phenotypic data from common gardens and mortality rates from natural populations, using National Forest Inventory Data from France and Spain. Approaches to predict potential maladaptation in natural populations are still under development, in particular for species with strong population structure such as maritime pine, and our results confirm that their predictions should not be used in conservation or management strategies without validation steps based on independent data.

Keywords: climate change, population vulnerability, genetic variance, genetic offset, maritime pine

Plant mutations: slaying beautiful hypotheses by surprising evidence

Contribution ID: 141

Tysklind, Niklas; Schmitt, Sylvain; Heuret, Patrick; Troispoux, Valérie; Beraud, Mélanie; Cazal, Jocelyn; Chancerel, Émilie; Cravero, Charlotte; Guichoux, Erwan; Lepais, Olivier; Loureiro, João; Marande, William; Martin, Olivier; Vincent, Gregoire; Chave, Jérôme; Plomion, Christophe; Leroy, Thibault; Heuertz, Myriam

Mutation is the source of all genetic diversity, on which selection can act allowing adaptation. Early differentiation between soma and the germline in animal development protects the germline, and thus the offspring, from the accumulation of somatic mutations. In plants, somatic mutations are expected to occur and accumulate along the branches and the differentiation between soma and germline is debated. There are several predictions on the fate of somatic mutations occurring in plant tissues: exposure to UV radiation increases mutagenesis; mutations have generally low frequency in plant tissues; branching topology of the tree dictates mutation distribution; and mutations at high frequency have a higher chance of being transmitted to the next generation. We produced a unique plant dataset of 60 high-coverage whole-genome sequences of two tropical tree species (*Dicorynia guianensis* and *Sextonia rubra*) and identified 18,274 de novo somatic mutations on branches exposed to high and low light, almost all at low frequency in tissues. We demonstrate that: 1) mutation rates and mutation spectra are not demonstrably affected by differences in UV exposure; 2) mutation phylogenies deviate from the branching topology of the tree; and 3) low-frequency mutations are transmitted to the next generation. Altogether, our results suggest far more complex links between plant growth, ageing, UV exposure, and mutation rates than commonly thought. Specially, the transmissibility of low frequency mutations, which are the most abundant, indicates a non-negligible role of low frequency somatic mutations as heritable mutations fuelling plant evolution.

Keywords: mutation, tropical trees, genomics, evolution, heritability

The drivers of the adaptive radiation of persimmon trees on New Caledonia, a biodiversity hotspot

Contribution ID: 142

Khastgir, Teerna; Emelianova, Khaterine; Bruy, David; Munzinger, Jérôme; Păun, Ovidiu

Adaptive radiations are dynamic interplays between speciation, expansion and extinction, often starting from long distance migrations. However, it remains unclear whether such radiations are driven by a mere increase in ecological opportunity, or if an elevated 'genomic potential' is required, often linked to demographic events, hybridization and/or genome evolution. Due to its complex geological history, complemented by strong climatic zonation (dry East versus humid West) and sharp elevation gradient, New Caledonia hosts a rich and threatened biodiversity along its highly heterogeneous soils including ultramafic, serpentines, limestone and sedimentary. Diospyros (persimmon trees, Ebenaceae) colonized the archipelago four times during the last 20 million years, but only the second earliest long-distance dispersal event gave rise to a radiating clade of ca 35 extant species that at present take advantage of all niches within this biodiversity hotspot, except for mangroves. The other three New Caledonian Diospyros lineages remain highly restricted in area and types of habitats occupied. We show that, without a change in ploidy, the radiating group has on average twice the genome size and increased TE dynamics compared to non-radiating relatives. Using newly assembled genomes and whole genome resequencing data for over 350 accessions, we investigate the potential drivers of adaptive variation in this group, and found evidence for i) pervasive introgression across the history of the radiating group, including of adaptive alleles from related species that share similar environments, in particular those occupying heavy metal rich soils, ii) TE-induced structural variation with potential regulatory effects, iii) environment-specific sorting of ancestral genetic variation, and iv) lineage-specific de novo evolution of alleles. Although the evolution of island biotas is intuitively expected to be mainly shaped by drift rather than natural selection, our results suggest that adaptive processes, often linked to high genome dynamics, are playing important roles in the radiation of New Caledonian persimmons.

Keywords: introgression, genome evolution, structural variation, climate, serpetine soils

Genomic evidence for extensive introgression amongst British oaks and assessment of mal-adaptation

Contribution ID: 143

<u>Gathercole, Louise</u>; Brown, Nathan; Denman, Sandra; Nichols, Richard; Buggs, Richard

The two native species of oak in Britain, (*Quercus robur* L and *Q. petraea* (Matt) Liebl.) are resilient keystone species, supporting over 2000 macro species, and are a major feature of the British landscape, economic history and culture. Many observations suggest *Q. petraea* is found mostly in the north and west and *Q. robur* in the south and east, with slightly different environmental preferences, although the species are often sympatric and can hybridise. Hybrids are hard to identify based on morphology. Here, we report whole genome re-sequenced data from 418 oak trees sampled at 60 sites across England, Wales and Scotland. These sites were previously part of a long-term forest condition survey. We used genomic methods to allocate trees to species, and identify hybrids and introgression. We found large numbers of hybrids and extensive of introgression of *Q*. *robur* alleles into Q. petraea genomes. None of our sampled individuals from Scotland were pure *Q. robur*. Within each species we found little genomic population structure. To seek evidence for genetic adaptation to local environments, we used latent factor mixed methods models to identify associations between allele frequencies and nineteenth century climate parameters. We used genetic offset methods to assess potential future mal-adaptation within a changing climate. The resilience of UK oaks may be partly due to dynamic exchange of alleles between two species with slightly different niches. Adaptation to future climates may involve co-planting of the two species and changes to a “local is best” seed sourcing policy.

Keywords: oak, genomics, introgression, adaptation, mal-adaptation

A landscape genomic approach on the Cork oak and Holm oak in the Western Mediterranean: insights into the species' capacity to respond to climate change

Contribution ID: 144

Paulo, Octávio S.; Galhofa, Davide; Viegas, Mariana; Sousa, Filipe; Henriques, André; Sousa, Paulo; Pina-Martins, Francisco; Vanhove, Mathieu; Silva, Adriana; Batista, Dora; Goulier-Lagadec, Julien; Galinat, Florian; Rzigui, Touhami; Jalila, Aoujdad; Ouadji, Mohamed; Forte, Luigi; Cavallaro, Viviana; Saulle, Domenico; Dettori, Sandro; Cillara, Marcello; Guisso del Galdo, Gianpietro; Sciendrello, Saverio; Picó, Xavier; Marcer, Arnald; Belkadi, Bouchra; Costa, Augusta; Coelho, Ana Cristina; Branquinho, Cristina; Ingvarsson, Pär K.; Knowles, Lacey

The Mediterranean region has been described as a 'climate change hotspot', with increased temperature and decreased precipitation expected to affect the region in the forthcoming decades. Cork oak (*Quercus suber* L.), and Holm oak (*Quercus ilex* L. and *Quercus rotundifolia* Lam.) are considered keystone tree species of the western Mediterranean basin. This work uses Genotyping by Sequencing to obtain thousands of SNPs from samples collected throughout the species ranges, which were used (i) to investigate population structure, (ii)to detect evidence of local adaptation and (iii)to project the gene-environment relationship across space through Gradient Forest to identify areas more sensitive to climate change. Our results reveal a contrasting population structure and differentiation pattern in Holm oak and Cork oak. While the former shows marked structure and differentiation, the latter shows significantly less differentiation. Furthermore, a considerable degree of differentiation is observed between Iberian and Moroccan populations of *Q. rotundifolia*, but not in *Q. suber*. In fact, for the Iberian populations, both *Q. rotundifolia* and *Q. suber* species show a relatively unstructured pattern. Our results support the status of *Q. ilex* and *Q. rotundifolia* as two genetically distinct species. Regarding the detection of local adaptation, we identified a considerable number of putative SNPs under selection in both species. Most of these SNPs showed an association with multiple temperature and precipitation-related bioclimatic variables. Annotation of the SNPs under putative selection revealed several genes associated with heat and water stress. Most importantly, Gradient Forest approach allowed the identification of sensitive geographic areas within the western Mediterranean region under a changing climate: southwestern Iberia and northern Morocco. Our findings provide a preliminary assessment of the capacity of these species to respond to future climate change and contribute towards a potential management strategy for their conservation in the Mediterranean Basin.

Keywords: oaks, GBS, Western Mediterranean, climate change, evolutionary genomics

Session 3:

Evolutionary genomics

Poster Session A: Wednesday 13 September 13:15 - 15:50

Posters

Sergiadou, Dimitra:
Molecular dating and selection analyses of the European white oak plastomes

Bruxaux, Jade:
First population genetic study on Scots pine based on whole genome resequencing

Lazic, Desanka:
Detecting genomic signatures of ecological speciation, adaptive divergence and evolution in oaks

Čepl, Jaroslav:
Exploring genetic divergence of quantitative trait during range expansion

Lenga, Marieke:
TREEvolution

Szukala, Aglaia:
An integrative perspective of species limits, gene-flow and local adaptation in Southeast European white oaks

Hansart, Amandine:
Assessing the response of temperate fruit trees to climate change: insight from the cultivated and wild apples

Acar, Pelin:
Comparative genomics of Turkish endemic *Salix purpurea* subsp. *leucodermis* reveals the sequence variations, homologous genes, and synteny across the relatives

Molecular dating and selection analyses of the European white oak plastomes

Contribution ID: 146

<u>Sergiadou, Dimitra</u>; Kjær, Erik Dahl; Olofsson, Jill Katharina

Chloroplasts have originated from an endosymbiotic relationship of multi-cellular organisms with single-cellular cyanobacterium and their evolution allowed plants to photosynthesize and maintain life on Earth. As chloroplasts retained their own DNA and due to their characteristics, such as maternal inheritance and non-recombination in most Angiosperms, they make excellent molecular tools. Previous studies regarding European oaks (*Quercus*) have shown excessive chloroplast sharing between *Q. robur* and *Q. petraea* with no clear species delamination based on chloroplast genomes, assuming parallel chloroplast capture events during the recolonization of oaks from the refugia after the end of last glacial maximum (LGM) as the cause of this pattern. In this study, we aim to shed more light on the evolution of European oaks by looking at their chloroplast genomes. Using 69 chloroplast genes in a molecular dating analysis, we examine if the timing of the split among chloroplast lineages predates the LGM, while positive selection on 34 chloroplast genes is being tested as an ancillary factor of the observed low genetic diversity. The results reveal old splits among chloroplast haplotypes and younger splits within lineages, suggesting that chloroplast sharing already occurred prior to the LGM in some lineages and/or refugia. Selection analysis shows relaxed purifying selection for most of the genes, however, positive selection on ccsA and rbcl genes is found. Positive selection on the rbcl gene possibly related to the adaptive evolution of RuBisCo enzyme conceivably indicates a selective sweep as an additional interpretation of the limited genetic diversity between these species. Nevertheless, to fully explore these hypotheses the integration of nuclear genomes for the detection of introgression events is needed, while analysis on the protein level can further evaluate whether the replacements of positive selected amino acids are associated with environmental adaptations.

Keywords: *Quercus*, molecular dating, selection analysis, plastomes

First population genetic study on Scots pine based on whole genome resequencing

Contribution ID: 147

Bruxaux, Jade; Hall, David; Zhao, Wei; Wang, Xiao-Ru

Scots pine (*Pinus sylvestris* L.) has the widest distribution among pine species, ranging from southern Spain to northern Norway and from Scotland the Pacific coast of Russia. It has a very large ecological niche, tolerating drought as well as heavy rain, stable and very variable precipitation regimes, and cold to temperate climates. It is also highly planted to produce timber or paper, making it a major economic resource in Europe. It has therefore been intensively studied, and local to large scale studies point towards a moderate to high genetic diversity, with low differentiation among populations. However, due to the large size of its genome (estimated at 23Gbp), all results so far were based on a tiny fraction of the genome, thus obscuring our understanding of the fundamental population genetic parameters of the species. We have studied for the first time almost 200 trees from a population located in northern Sweden using whole genome resequencing at a sequencing depth of 4.5x (3.5-11x). Our goal is to perform in-depth population genetic analyses across the whole genome with a good sample size. We will estimate the population nucleotide diversity, the relatedness and inbreeding of the samples. Genome-wide scans of diversity will allow us to identify regions of selective sweep, as well as patterns of linkage disequilibrium. The genome-wide polymorphism will also allow us to reconstruct the demographic history of this population which represents the northern limit of the species distribution. Results from this study will be compared to previous studies based on reduced representation sequencing, such as RAD-seq / GBS or exome capture to understand the effectiveness of each method in population genetic studies. Most importantly the genomic data will facilitate genome-wide association studies of important breeding and adaptive traits in the future.

Keywords: Scots pine, whole genome sequencing, population genetics, genetic diversity

Detecting genomic signatures of ecological speciation, adaptive divergence and evolution in oaks

Contribution ID: 148

<u>Lazic, Desanka</u>; Hipp, Andrew L.; Carlson, John E.; Budde, Katharina Birgit; Cao, Hieu Xuan; Gailing, Oliver

Oaks arose as model organisms for studying species coherence in the face of gene flow. Previous research showed a highly heterogeneous differentiation across the genome in closely related oak species. Parts of the genome showing increased differentiation could give insight into which genomic regions are responsible for maintaining species integrity as result of divergent selection or reproductive barriers in spite of ongoing gene flow. We were interested if these divergent genes are repeatedly found in hybridizing white oak and red oak species across a wide phylogenetic divide indicating parallel evolution. Because of ongoing interspecific gene flow and adaptation to different micro-environments in sympatry, species pairs of *Quercus robur* L. - *Quercus petraea* (Matt.) Liebl. (section *Quercus*) and *Quercus rubra* L.– *Quercus ellipsoidalis* E.J. Hill (section *Lobatae*) are particularly suitable to study how selection impacts adaptation and speciation in trees. We sampled leaf material of 249 individuals in total. Leaves from 59 *Q. rubra* and 62 *Q. ellipsoidalis* adult trees were sampled in two locations in the United States. And 32 individuals of both *Q. robur* and *Q. petraea* in two locations in Germany. After whole genome resequencing we performed outlier analyses tests based both on non-overlapping genomic windows and SNP-by-SNP basis to detect potential candidate genes involved in adaptive divergence between both species pairs. Detected outlier genes had functions involved in both intrinsic and ecological barriers. We also found co-occurrence with 34 previously published outlier candidate genes in white oaks. Finally, using functional annotation, synteny and orthology approaches we checked for signatures of parallel evolution between these two sections. We found subset of orthologous genes between the sections and we discussed their potential functions in the context of speciation.

Keywords: Oaks, adaptive divergence, evolution, speciation

Exploring genetic divergence of quantitative trait during range expansion

Contribution ID: 149

Čepl, Jaroslav

This presentation aims to analyze and visualize the effects of range expansion on the genetic divergence of populations and the subsequent spatial distribution of quantitative traits. To examine this phenomenon, we employ an individual-based genetic simulation. Those individuals occupy cells on discrete hexagonal grid, where migration parameters are set to model the range expansion. By running various scenarios, we investigate how different levels of selection pressure, either uniform or varying spatially, or the absence of selection, affect the pattern of spatial variation. Our findings demonstrate that range expansion can indeed result in the divergence of founding populations. We also present distinct patterns of trait variation along the expanding front. We discuss the observed results in relation to existing trait variability.

Keywords: range expansion, genetic divergence

TREEvolution

Contribution ID: 150

Lenga, Marieke

Extreme weather events such as the dry years of 2018, 2019, and 2022 threaten the health and, thus, the ecosystem functions of temperate forests. Even tree species formerly thought to be resistant to climate change, like the European Beech (*Fagus sylvatica*), were found to be vulnerable. Drought affected individual beech trees within stands differently, suggesting a genotypic background for this pattern. Fagus sylvatica has a massive lifetime production of seeds. Though, only a tiny fraction of these seeds survives to maturity, leading to a considerable selection potential during early life stages that should favor adaption to the changing climate. In addition, forest management has pronounced effects on the stand structural complexity, which influences the microclimate and may enforce or attenuate beech climate adaptation. For example, beech saplings may experience enforced selection under an open canopy. In TREEvolution, we investigate the genetic adaptation potential of European beech saplings to new climatic conditions. While previous studies focused on adults, the younger generation may be better adapted to drought and heat. We will genomically examine one to five-year-old saplings and compare them with neighboring old trees to detect genomic changes over time and test whether micro- and macroclimatic environmental conditions or forest land use types affect these changes. We will collect leaf material from adult and juvenile trees (seedlings and saplings), measure whole plant and leaf traits (e.g. plant size, specific leaf area), and permanently mark the juveniles for future monitoring. From the collected material, we will extract DNA and prepare libraries for reduced representation sequencing (e.g. ddRAD) or low-coverage whole-genome sequencing. In the following, using bioinformatic- and population-genomic tools, we will investigate how forest structure, microclimate, forest management, and the year of establishment shape the genomic composition of the next generation.

Keywords: *Fagus sylvatica*, drought adaptation, genotype diversity, forest management

An integrative perspective of species limits, gene-flow and local adaptation in Southeast European white oaks

Contribution ID: 151

Szukala, Aglaia; Nicorescu, Adelin; Kovacs, Gyula; Curtu, Alexandru Lucian; Zhelev, Petar; Konrad, Heino

Oaks (genus *Quercus* L.) are considered potential winners under future drier and warmer climates. The white oaks species-complex includes some of the most widespread oak species in Europe – namely *Q. robur*, *Q. petraea*, and *Q. pubescens* – and is strikingly diverse in Southeast Europe, where a number of minor lineages have been reported. To date, it is unclear what evolutionary processes underlie this taxonomic richness. We hypothesize that local adaptation and (adaptive) introgression likely driven by post-glacial secondary contact play a major role. Our project features whole-genome resequencing (WGR) and leaf morphological data of 46 populations (ca. 15 individuals per population) scattered across Eastern Austria, Hungary, Croatia, Romania, and Bulgaria, including some white-oaks diversity hotspots. We test if leaf morphology can be used to discriminate among main and minor lineages and identify putative hybrids, extending knowledge from previous studies to a larger geographic scale. Further, we explore which demographic scenarios of secondary contact and gene-flow better explain the present white oak genetic composition. Lastly, we exploit populations growing under dry and warm conditions at the limit of the ecological range to better understand the adaptive potential of white oaks to the future climate. We show that leaf morphology can be used to characterize hybrids, which are intermediate between the parental species. While at least 7 leaf traits are significantly different between the main species, the same traits fail to discriminate between major species and minor taxa, mainly due to the large within-species variation. Ongoing analyses of WGR show very little to no reference-species bias when mapping genomic reads of different sample species to the *Q. robur* chromosome-level reference genome v. 3, likely as a consequence of frequent hybridization. These initial results support our approach towards a better understanding of the evolutionary processes underlying species and adaptive richness in white oaks.

Keywords: White oak, *Quercus*, species-complex, gene-flow, local adaptation

Assessing the response of temperate fruit trees to climate change: insight from the cultivated and wild apples

Contribution ID: 152

Hansart, Amandine; Lemarquand, Arnaud; Didelot, Frederique; Roman, Anamaria; Ursu, Tudor-Mihai; Cornille, Amandine

Climate change poses a significant threat to biodiversity and food security. To mitigate its impact on food production, it is crucial to harness the diversity of crops and their wild relatives. This is especially true for tree crops that were planted in orchards years ago under different climate conditions. We will assess the adaptive potential to climate change of crop and wild populations of an emblematic fruit tree, the apple, combining population genomics, modeling, and phenotypic data. This project benefits from the range of skills of those involved and the availability of data acquired over the years. This project will provide a comprehensive assessment of the vulnerability of fruit tree crops and their wild relatives to climate change, as well as a list of varieties that may be cultivated in different parts of Europe in the future, reservoirs of crop and wild genetic diversity in orchards across Europe that will be used for future breeding programs to meet the demands of food production in the context of climate change, increased public awareness of the impact of climate change on fruit trees, agrobiodiversity conservation, through community science initiatives.

Keywords: climate change, apple trees, population genomics, phenotype, crop and wild populations

Comparative genomics of Turkish endemic *Salix purpurea* subsp. *leucodermis* reveals the sequence variations, homologous genes, and synteny across the relatives

Contribution ID: 153

Acar, Pelin; Kaya, Yasin; Mavi İdman, Özlem

Salix purpurea subsp. *leucodermis* is an endemic shrub commonly known as fast-growing willow. It is considered a promising biomass feedstock and plays a vital role in maintaining wetland ecosystems. In this study, we sequenced the genome of S. purpurea subsp. *leucodermis* and compared it with the genomes of seven other tree species in the Salicaceae family. This is the first attempt to characterize the genome of this subspecies. Through comparative analysis of sequence variations, homologous genes, and syntenic arrays, we identified significant differences in genetic variation between *S. purpurea* subsp. *leucodermis* and its relatives. The total genome size of *S. purpurea* subsp. *leucodermis* was 392.7 Mbp, and 30.2% of the total length comprised repeated sequences. We identified structural variations, including translocations, duplications, and inverted duplications, in the genome of S. purpurea subsp. *leucodermis* that were linked to multiple physiological processes. Phylogenetic analysis indicated that *S. purpurea* subsp. *leucodermis* diverged from *S. purpurea*, and we discovered a large inter-chromosomal recombination between *S. purpurea* subsp. *leucodermis* and other Salicaceae species. Our findings also suggest the potential importance of transposable elements in shaping the evolution and diversity of the S. purpurea subsp. *leucodermis* genome. This study provides valuable insights into the genome diversity, evolutionary history, and relationships of endemic species among different *Salix* taxa and has significant implications for future functional genomic studies.

Keywords: Salicaceae, *Salix purpurea* subsp. *leucodermis*, genome assembly, comparative genomics, endemic to Turkey

Session 4:

Innovative methods and approaches

Thursday 14 September 13:15 - 15:50

Chair: Dr. Christian Rellstab, WSL, Switzerland

Oral presentations

13:15	**Keynote** **Schuman, Meredith Christine:** Leveraging remote sensing to support assessment of genetic variation in beech forests
14:00	**van Loo, Marcela:** Assessing drought stress adaptation potential in Norway Spruce seedlings: integrating high-throughput multi-sensor phenotyping (HTPP) approach with other -omics approaches
14:20	**Stejskal, Jan:** Revealing the hidden diversity: exploring genetic variation with hyperspectral phenotyping in Scots pine seedlings
14:40	***Short Break***
14:50	**Grigoriadou-Zormpa, Ourania:** Do we need high coverage whole-genome sequencing data to assess genetic variation and differentiation? A case study in *Fagus sylvatica* and *Quercus petraea*
15:10	**Xu, Jing:** Advancing drought stress assessment in trees: a fast and efficient method using drone-based remote sensing technologies
15:30	**Duvaux, Ludovic:** Testing pangenomic tools for detection of structural variant in populations of forest tree

Keynote Session 4:

Leveraging remote sensing to support assessment of genetic variation in beech forests

Contribution ID: 104

Schuman, Meredith Christine

To protect biodiversity, we must protect species genetic diversity. To protect genetic diversity, we must monitor it. Yet despite advances in sequencing, it remains resource-intensive to monitor genetic sequence variation within a species, requiring repeated sampling from many individuals and populations over time. Thus, there is growing interest in the potential of remote sensing to support assessments of within-species genetic diversity. The recently adopted indicators of genetic diversity for the monitoring framework of the Convention on Biological Diversity can be assessed in the absence of DNA sequence information, based on estimated census counts (above or below a threshold) of reproductively mature individuals in different populations. Remote sensing data from imaging spectrometry, providing high spectral resolution and thus rich biochemical information, is increasingly publicly available from open aerial datasets and new or upcoming public space missions. It is also becoming easier to acquire spatially continuous, high resolution data for targeted regions from cameras (photogrammetry) and sometimes laser scanning (LiDAR), using airborne or handheld systems, or from some (mostly commercial) spaceborne systems. Thus, it is increasingly feasible to characterize populations and their habitats from the air or from space, especially given complimentary ground-based knowledge of location, extent, and characteristics; and to overlay rich spectral information which can, combined with environmental data, provide additional proxies of genetic variation. Dominant, temperate forest trees are well suited to study these approaches because homogeneous stands and even individual canopies have fixed locations and can be differentiated even from space. For European beech, populations are known to harbor relatively high genetic variation, and increasing genomic resources and monitoring sites are established. I will present work from the UZH Spatial Genetics group developing methods and testing hypotheses towards leveraging remotely sensed observations to monitor differences in genetic diversity, and thus potential for resilience and adaptation, in beech forests.

Keywords: genetic diversity, chemodiversity, biodiversity monitoring, environmental interactions, *Fagus sylvatica*

Assessing drought stress adaptation potential in Norway Spruce seedlings: integrating high-throughput multi-sensor phenotyping (HTPP) approach with other -omics approaches

Contribution ID: 154

Ahmad, Muhammad; Stewart, Ethan; Seitner, Sebastian; Jez, Jakub; Espinosa-Ruiz, Ana; Carrera, Esther; Martínez-Godoy, Maria Ángeles; Baños, Jorge; Ganthaler, Andrea; Mayr, Stefan; Grubb, Emily Aline; Ufimov, Roman; van Loo, Marcela; Trujillo-Moya, Carlos

Drought stress is a significant constraint limiting the distribution of Norway spruce (*Picea abies* (L.) H. Karst.). 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. Here, we present a novel high-throughput multi-sensor phenotyping (HTPP) approach and protocol for evaluating the drought stress adaptation potential of Norway spruce provenances at the most critical tree´s life stage, the seedling stage. Here, two climatically contrasting Norway spruce provenances were studied by HTPP while exposed to 21 days of drought stress under controlled conditions. Multivariate analyses of data derived from the HTPP platform demonstrates that the HTTP approach enables estimation of more than 50 phenotypic traits (e.g. chlorophyll fluorescence) for differentiation of early and late drought stress responses between populations. We further linked the phenomic data with needle transcriptomics, metabolomics and stem anatomy. Consistent with the phenotypic results, we observed significant metabolic changes towards the later stages of the drought stress, with each provenance displaying a distinct metabolic signature under both well-watered and drought-stressed conditions. Analysis of mRNA-Seq data revealed over 4000 differentially expressed genes, most of them shared between the two populations. A small proportion of genes were provenance specific, aligning with the observed differences between the two provenances in the phenomics and metabolomics datasets. Finally, stem anatomical differences were identified between drought-stressed seedlings and control plants, and the proportion of specific stem tissues such as xylem was differentially affected on the studied provenances, which may compromise future wood production. In conclusion, our study highlights the relevance of the HHTP approach and introduces a standardized HTTP protocol for evaluating drought stress adaptation in Norway spruce seedlings, which can potentially be extended to other tree species.

Keywords: Norway spruce seedlings, high-throughput phenotyping, drought stress, metabolomics, transcriptomics

Revealing the hidden diversity: exploring genetic variation with hyperspectral phenotyping in Scots pine seedlings

Contribution ID: 155

Stejskal, Jan; Čepl, Jaroslav; Neuwirthová, Eva; Lhotáková, Zuzana; Chuchlík, Jiří; Albrechtová, Jana

Hyperspectral phenotyping is a state-of-the-art technology that utilizes hyperspectral reflectance to detect plant phenotypic variation, making it a useful tool for evaluating foliar traits indicative of a plant's physiological status. Through high-throughput phenotyping, hyperspectral reflectance can help tree breeders and nursery practitioners select seedlings with the desired adaptation potential to local environments. In our research, we compared two non-destructive methods for measuring hyperspectral reflectance on Scots pine seedlings from low-land and upland ecotypes in three different local populations in the Czech Republic. We evaluated the accuracy and efficiency of the contact probe and bare fiber optic cable measurements to differentiate individuals of two Scots pine ecotypes. The contact probe measures the bidirectional reflectance factor of a sample placed on a black background with a defined field of view, while non-contact measurement enables reflectance measurement in its actual appearance without the distortion caused by variable morphology. Although the optical cable allowed the measurement of the reflectance of entire individuals, it was susceptible to ambient light and atmospheric changes. Both spectral datasets showed statistically significant differences among all represented Scots pine populations and ecotypes. Contact measurements showed differences between ecotypes in the visible spectral region due to photosynthetic content. In contrast, non-contact measurements detected differences in the near-infrared part of the region due to the canopy structure of individual seedlings. Moreover, using Random Forest and Support Vector Machine learning algorithms, the proximal data obtained from the top of the seedlings offered higher accuracy (83%) in predicting three different Scots Pine populations. Our results indicate that both contact probe and non-contact measurements are viable for hyperspectral phenotyping and can be used to disentangle the phenotypic and underlying genetic variation within Scots pine seedlings. The findings offer valuable insights for tree breeders and nursery practitioners in selecting seedlings with desired adaptation potential to local environments.

Keywords: hyperspectral reflectance factor, *Pinus sylvestris*, high-throughput phenotyping, machine learning, random forest

Do we need high coverage whole-genome sequencing data to assess genetic variation and differentiation? A case study in *Fagus sylvatica* and *Quercus petraea*

Contribution ID: 156

Grigoriadou-Zormpa, Ourania; Wilhelmi, Selina; Ben Targem, Mehdi; Müller, Markus; Budde, Katharina Birgit; Götz, Jeremias; Scaglione, Davide; Scalabrin, Simone; Curtu, Alexandru Lucian; Wildhagen, Henning; Gailing, Oliver

Understanding genetic variation patterns of important long-lived tree species is crucial, especially under the new, increasingly warmer, and drier environmental conditions. In this study, European beech and sessile oak populations were selected from the Carpathian Mountains and western Romania, respectively, along altitudinal gradients. In addition, eight European provenances of sessile oak from a provenance trial located in Germany were included in this analysis. In total, 96 European beech and 96 sessile oak trees (48 originating from natural stands in western Romania and 48 from a provenance trial) were selected randomly and whole-genome sequencing (WGS) was performed to investigate the population genomic characteristics. As sequencing costs decrease, the number of studies performing WGS increases. However, even today, targeted alternatives such as genotyping arrays are more cost-effective and in many cases the first choice. A major drawback of those is the ascertainment bias occurring due to target design. As a cost-effective alternative, low coverage sequencing overcomes the ascertainment bias and could provide sufficient quality to analyse population genetic variation and structure, identify outliers, or perform genome-wide association studies. Here, a data set of single nucleotide polymorphisms (SNPs) obtained from WGS (coverage at ~15x and ~22x for oak and beech, respectively) is used and downsampled to lower coverages (8x, 4x, 2x, 1x, and 0.5x) for comparison. Preliminary results show that with increasing sequencing coverage, observed heterozygosity is increasing while the inbreeding coefficient is decreasing as well as the range of the pairwise genetic differentiation between populations.

Keywords: European beech, sessile oak, whole genome sequencing, low coverage, genetic variation

Advancing drought stress assessment in trees: a fast and efficient method using drone-based remote sensing technologies

Contribution ID: 157

<u>Xu, Jing</u>; Trepekli, Katerina; Ræbild, Anders; Hansen, Ole Kim

Studying drought resistance in trees presents a common challenge due to the complexity of physiological responses and the varying importance of traits based on drought intensity, duration, and timing. Traditional methods of quantifying drought stress rely on labor-intensive, time-consuming, and partly destructive sampling using portable equipment to monitor photosynthesis, transpiration rate, and water potential in trees. Furthermore, these methods are often limited to small sample forest areas. To address these limitations, we propose an innovative method that leverages state-of-the-art laser scanners, gas analyzers, thermal and multispectral cameras mounted on drones. This technology enables the simultaneous monitoring of a wide range of tree traits at centimeter resolution, offering a fast and efficient approach to exploit characteristics related to drought adaptation mechanisms. Our research focuses on establishing this method using Nordmann fir as a model species. In 2022, we created artificial drought conditions in potted Nordmann fir clones within a greenhouse, employing three treatments: control, medium dry, and very dry. We conducted both novel drone-based measurements and traditional techniques to compare their efficacy. In September 2022, we extended our investigation to a clonal Nordmann fir plantation by covering selected ground areas with plastic. During the 2023 growing season, we performed drone-based and ground measurements on the trees covered by plastic, with the trees outside the covered area serving as the control group. We will present the results of these two studies, highlighting the benefits of utilizing drone-based remote sensing technologies in forest tree management. The successful application of these sophisticated technologies will revolutionize conventional manual phenotyping of forest trees, replacing laborious and inconsistent methods. This advancement holds great potential for enhancing tree breeding efficiency for climate resilience and providing a valuable tool for assessing the health of forests.

Keywords: remote sensing; drought stress; phenotyping; forest health

Testing pangenomic tools for detection of structural variant in populations of forest tree

Contribution ID: 158

Denni, Sukanya; Trang-Bui, Quynh; Lapalu, Nicolas; Plomion, Christophe; Decroocq, Véronique; Duvaux, Ludovic

Recent advances in the field of pangenomics - e.g., development of tools to build and manipulate pangenome graphs - now allow to detect and genotype structural variants (SVs) at a population scale for a reasonable cost. However, most pangenomics tools were developed with the human genome in mind and it is currently unclear to which extent they can be applied to non-model organisms with different genomic features (e.g. higher genetic diversity, different transposable element content, whole genome duplications and polyploidy) and less resolved genome assemblies. Here, we tested the robustness - to various genomic conditions deviating from the human model - of SV genotyping from short reads mapped on a pangenome graph using vg Giraffe. Using three datasets of previously assembled genomes from species with heterogeneous levels of genome complexity and genetic diversity (a fungi, an apricot tree and a European white oak), we tested the capacity of vg Giraffe to robustly and accurately map reads for individuals with high divergence to the pangenome graph. By simulating reads with increasing mutation rates, we found that vg Giraffe is able to accurately map reads diverging by up to 3% from the graph and that mapping quality remains above 30 for divergence up to 2% confirming that this tool is suitable for forest tree species with high genetic diversity. In further investigations, we will evaluate pangenome graph building tools like minigraph and PGGB and their impacts on pangenome quality and SV genotyping. We will estimate the minimal depth of sequencing required for accurate SV genotyping using either approach and check the SV genotyping accuracy of vg Giraffe. The pipeline and tests used for these analyses are available on gitlab as Snakemake/Singularity workflows.

Keywords: pangenomics, structural variants, *Quercus petraea, Prunus armeniaca, Zymnoseptoria tritici*

Session 4:

Innovative methods and approaches

Poster Session B: Thursday 14 September 16:20 - 18:30

Posters

Imboden, Noemi:
Introduction of a forest strategy for the canton of Valais based on the theory of the commons - approach and challenges

Šķipars, Vilnis:
Use of low coverage whole genome sequencing to study DNA regions influencing transcription of disease resistance related genes in Scots pine

Roman, Anamaria:
The PHOTO module for rapid and accurate estimation of black locust (*Robinia pseudacacia*) inflorescence area

Šķipars, Vilnis:
Elucidation of flanking sequences of Scots pine candidate genes for resistance against root rot using non-standard approaches for a non-model organism

Fussi, Barbara:
MicroRNA-mediated regulation may play a role in the resistance of ash trees (*Fraxinus excelsior* L.) to ash dieback

Provazník, Daniel:
Addressing the altitudinal and geographical gradient in European beech via photosynthetic parameters

Krautwurst, Melina:
QTL analyses for bud burst and ash dieback susceptibility in common ash (*Fraxinus excelsior*)

Introduction of a forest strategy for the canton of Valais based on the theory of the commons - approach and challenges

Contribution ID: 159

Imboden, Noemi; Genoud, Stéphane

As pointed out by Elinor Ostrom, a large part of the forests in Valais (Switzerland) were managed as common goods. While its ownership has remained practically unchanged over the years, the aspect of common management has lost much of its importance, mostly due to the replacement of energy wood by fossil fuels and the consequent decline in the importance of the forest as a basis for survival. Today, most of Valais' forest is severely under-managed which results with the wood rooting in the forest instead of being exploited and thus contributing to the achievement of the energy strategy. Within the framework of the development of a new cantonal forest strategy, it is investigated within three test regions whether it is possible to place the community at the center of the strategy and to reintroduce the aspect of joint management of a common good as the foundation pillar of forest management, all while optimizing local forest management. This to ensure that forests are managed sustainably and for the common good, rather than for profit. Moreover, the new strategy goes a step further, analyzing the forest ecosystem services and ensuring they are taken into account, promoted as much as possible and other problems linked to the current forest management are also addressed. To elaborate the strategy, firstly, the evolution of forest management as a common good over the years was studied. Secondly, a bottom-up approach was chosen, in order to integrate stakeholders and local communities. Therefore, co-design workshops were carried out with those actors to identify and classify the forest ecosystem function and to point out the problems linked to the current forest management. Based on the results, a forest strategy was elaborated that respects the principles of Ostrom and thus allows a better management of the forest as a common good.

Keywords: forest management, common good, alpine forest, forest strategy

Use of low coverage whole genome sequencing to study DNA regions influencing transcription of disease resistance related genes in Scots pine

Contribution ID: 160

Šķipars, Vilnis; Vivian-Smith, Adam

Forests are one of Latvia's most important resources. The dominant tree species in large areas is Scots pine. Our long-term goal is to reduce the economic losses caused by Scots pine root rot. After identifying genes with importance in resistance to this disease, we focused on the study of the DNA regions regulating the activity of these genes. Since the Scots pine genome is poorly studied, this task is not easy and it was necessary to develop non-standard approaches to study the regions upstream of the genes involved in resistance in a targeted manner. In the poster we provide an overview of two experimental approaches which turned out to be inefficient but might be useful in species with simpler genomes:

- multiplex linear DNA amplification in combination with high-throughput sequencing
- modified terminal transfer amplification and sequencing (TTAS) method

We provide our results obtained with assistance of low coverage WGS which also explain some of the reasons for inefficiency of the methods mentioned above. We will use the obtained WGS data for further studies on approaches for targeted investigation of upstream flanking regions of candidate genes.

Keywords: whole genome sequencing, Scots pine, flanking regions of candidate genes, resistance

The PHOTO module for rapid and accurate estimation of black locust (*Robinia pseudacacia*) inflorescence area

Contribution ID: 161

Roman, Anamaria; Boamfă, Maria Ioana; Cetean, Horațiu; Mihuț, Liana Nicoleta; Milin, Vlad; Buzura, Loredana; Gălătuș, Ramona; Stoica, Adrian-Ilie; Ursu, Tudor-Mihai

The PHOTO module, along with the 3D-VEG (LIDAR point clouds) and SPEC (spectral data) modules, compose SPECTRAVEG, an open-source GIS tool developed for multi-sensor data analysis. They can be used for the quick evaluation of biometric vegetation traits with high potential of application within environmental monitoring and bioeconomy. We present the use of the PHOTO module for rapid estimation of black locust (*Robinia pseudacacia*) inflorescence area. The module includes two QGIS Graphical Processing Models (GPM). The Inflorescence_Area GPM performed the quick estimation of inflorescence area while the Accuracy_Assessment GPM tested the estimation accuracy. The tested database included digital photos of 110 inflorescences from 11 trees using a Canon EOS 500D camera. Several open-source scripts were developed within the Processing R provider QGIS plug-in and assembled into the RobiniaInflorescenceArea algorithm using SuperpixelImageSegmentation package (R-cran) functions for the segmentation and automatic classification of target pixels from the input image. This algorithm processes the RGB digital images and extracts the number of pixels from the target classes in two clusters: the white petals and the greenish rachis and bracts that, together, represent the inflorescences' area. For accuracy assessment, the binarized images were printed and reference measurements of the inflorescence area were taken with a leaf scanner. The estimated inflorescence area varied between 6.19 and 87.61 cm while the average area was 31.75 cm2 and the estimation accuracy was high (RMSE = 5.033, R2 = 0.859). The PHOTO module is free, effective, and easy to use for inflorescence area evaluation by users with basic GIS and scripting skills. Integrated with LIDAR metrics it can help estimate inflorescence area at forest level for bio-economic evaluation of ecosystem resources.

Keywords: digital image analysis, inflorescence area, *Robinia pseudacacia*, open-source scripts, segmentation

Elucidation of flanking sequences of Scots pine candidate genes for resistance against root rot using non-standard approaches for a non-model organism

Contribution ID: 162

Šķipars, Vilnis; Vivian-Smith, Adam

The forest is one of Latvia's most important resources. The dominant tree species in large areas is Scots pine. Our long-term goal is to reduce the economic losses caused by Scots pine root rot. In order to achieve the goal, we have focused on genetic research. After identifying genes differentially expressed in response to inoculation with *Heterobasidion annosum*, we focused on the study of the DNA regions regulating the activity of these genes, more specifically - distal 5' flanking sequences. Since the Scots pine genome is poorly studied, this task is not easy and it was necessary to develop non-standard approaches to study it specifically in the regions upstream of the candidate-genes. In the poster we provide an overview of experimental approaches for studies of these genomic regions:

- multiplex linear DNA amplification in combination with high-throughput sequencing
- modified terminal transfer amplification and sequencing (TTAS) method
- low coverage pine genome sequencing for the study of target sequences

The complex genome of Scots pine is one of the reasons why we encountered unexpected results and experimental difficulties, however, using low coverage whole genome sequencing, we have obtained new scientific information that is useful in the analysis of the DNA regions regulating the activity of genes involved in resistance. We consider the other methods useful for species with simpler genomes.

Keywords: gene regulation, low coverage genomic sequencing, candidate genes

MicroRNA-mediated regulation may play a role in the resistance of ash trees (*Fraxinus excelsior* L.) to ash dieback

Contribution ID: 163

Fussi, Barbara; Seidel, Hannes; Budde, Katharina Birgit; Callegari Ferrari, Renata; Chano, Victor; Gailing, Oliver

European ash (*Fraxinus exlcelsior* L.) had been considered a tree species with high potential for the adaptation of mixed forest stands to climate change. However, due to the rapid spread of the invasive, ash dieback causing pathogen, *Hymenoscyphus fraxineus*, natural ash populations are under threat. Epigenetic mechanisms act like switches and activate/deactivate gene transcription by changing the accessibility of the DNA (DNA methylation or histone modification) or by post-transcriptional regulation, e.g., through microRNAs. Although such mechanisms are known to play a role in plant-pathogen interactions, studies in forest tree species in relation to biotic stressors are still rare. Susceptibility of ash trees to the pathogen had been studied in a clonal study site in Bavaria during several years. Four genotypes, two showing high susceptibility and two showing low susceptibility, were selected and replicated through grafting for the present study. In spring 2022, four replicates of each genotype were inoculated with the pathogen and four were treated with sterile agar plugs (control) in a climate chamber. After 17 days, petioles were harvested and, additionally, diseased, and healthy leaves were collected directly in the clonal study site in Bavaria from each genotype. MicroRNA was isolated from all samples and sequenced on an Illumina NovaSeq6000. Differentially expressed microRNAs between inoculated and control samples, as well as affected and unaffected leaves, will reveal post-transcriptional response mechanisms of F. excelsior trees attacked by H. fraxineus in the early stage of infection. The epigenetic patterns could be used as an additional resource for the development of resistance markers and for a diagnostic test for contaminated trees. The project contributes to an improved understanding of the response and plasticity of ash trees to the invasive pathogen. Practical recommendations will then make an important contribution to the preservation and use of forest genetic resources of ash trees.

Keywords: epigenetic patterns, Ash dieback, *Fraxinus excelsior*, plasticity, resistance markers

Addressing the altitudinal and geographical gradient in European beech via photosynthetic parameters

Contribution ID: 164

Provazník, Daniel; Stejskal, Jan; Hansen, Ole Kim; Čepl, Jaroslav; Erichsen, Eva Roland; Hansen, Jon Kehlet; Zádrapová, Dagmar; Tomášková, Ivana

The knowledge about the photosynthetic performance within the European beech (*Fagus sylvatica* L.) provenances is essential for assessing their potential under assisted migration. As the previous studies compared only geographically distant provenances when addressing the altitudinal variation, we also focused on the within-provenance variation in gas exchange (GE) and chlorophyll fluorescence (ChlF) kinetics driven by the altitude. The experiment was conducted on seedlings replanted in a Danish common garden experiment comprising Danish and Italian populations. A cluster of provenances transplanted from Italy (Calabria region) represented Mediterranean beech refugia. The GE method yielded two parameters (net assimilation of CO2 - PN; light saturation point - LSP) that reliably detected the geographical distance among Italian provenances. Moreover, spring flushing scores repeatedly clustered the Italian provenance subgroups similarly to GE. Several ChlF parameters showed within-provenance differences mostly related to altitude, and some could also distinguish between the two Danish provenances. The most indicative ChlF parameter was the dissipated energy flux per reaction center (DI0/RC). In addition, the photosynthetic parameters served as a proxy for senescence variation related to origin. We conclude that ChlF is a less senescence-influenced proxy of photosynthetic performance than GE. ChlF can uncover variation on a finer scale as it reveals the provenance subgroups' altitudinal differences. Additionally, this method is much faster, limited mainly by the dark adaptation. Assessing within-provenance photosynthetic performance variation in young trees may help to utilize the full potential of provenances for different planting sites.

Keywords: OJIP, photosynthesis, common garden, phenology

QTL analyses for bud burst and ash dieback susceptibility in common ash (*Fraxinus excelsior*)

Contribution ID: 165

Krautwurst, Melina; Past, Franziska; Kersten, Birgit; Bubner, Ben; Müller, Niels

Common ash, *Fraxinus excelsior*, is threatened by the invasive pathogenic fungi *Hymenoscyphus fraxineus*. The pathogen is rapidly spreading throughout Europe with severe ecological and economic consequences. Typical ash dieback symptoms are leaf shedding and stem necrosis. Less susceptible individuals are likely to feature specific phenotypes. Studies have shown that bud burst timing is correlated with susceptibility and early-flushing individuals show fewer symptoms of ash dieback. In other tree species, bud burst exhibited polygenic inheritance. In our study we will use quantitative trait locus (QTL) analysis, to unravel the genetic architecture of ash dieback susceptibility and predict the effect sizes of the underlying genomic regions. Budburst timing and dispersion of necrosis are used as phenotypes. For generating a F1-generation the method “breeding-without-breeding” was used. It overcomes the need for artificial mating, by working with paternally unknown but maternally known material. Five full-sibling progenies were identified and used to generate genetic maps for the QTL analysis. Significant QTLs were detected for both phenotypes, which will be characterized in more detail. The results will contribute to elucidating the genetic basis of natural variation in ash and may support breeding and conservation of more robust forest ecosystems.

Keywords: Common ash (*Fraxinus excelsior*), breeding without breeding, QTL-Analysis, ash dieback, bud burst

Session 5:

Conservation genomics

Friday 15 September 13:15 - 15:50

Chair: Prof. Dr. F.A. (Phil) Aravanopoulos, University of Thessaloniki, Greece

Oral presentations

13:15	**Keynote** **Scotti, Ivan:** Resilience: can we define it in an evolutionary framework?
14:00	**Krutovsky, Konstantin V.:** Dendrogenomics - a new interdisciplinary field of research in forest tree conservation genomics integrating dendrochronology, dendroecology, dendroclimatology and genomics
14:20	**Westergren, Marjana:** Estimates of effective population size are highly dependent on sampling design
14:40	***Short Break***
14:50	**Farsakoglou, Anna-Maria:** The challenge of estimating effective population size: Can standard genetic parameters be of use?
15:10	**Theraroz, Adélaïde:** The genetic consequences of population marginality: a case study in maritime pine
15:30	**Belton, Sam:** Molecular analysis of the oak syngameon in Ireland – genetic characterisation of the *Quercus robur* (L.) and *Quercus petraea* (Matt.) Liebl. species complex at its western limit

Keynote Session 5:

Resilience: can we define it in an evolutionary framework?

Contribution ID: 105

Scotti, Ivan

The resilience framework is a general ay of interpreting the way systems respond to disturbance. To make it concrete, interpretable, and applicable, it has to be declined into particular resilience of a particular system to a particular disturbance. In this presentation, I will first look at what the resilience of a population may be in terms of population-genetic concepts. I will argue that, fundamentally, population-genetic resilience is the capacity of a population to recover its fitness after disturbance, and that this is related to the concept of “adaptive potential”. Next, I will review the available literature on the links between genetic diversity, adaptive potential, and resilience. Finally, I will propose a novel analytical framework that allows to link population dynamics and resilience through a re-interpretation of the components of fitness (survival, reproduction) computed for individual genotypes. This framework is generic and easily applicable both to field data and to modelling; I will provide an overview of its properties and propose to develop it collectively under the form of an open project.

Keywords: genetic diversity, population growth rate, population dynamics, survival rate, adaptation

Dendrogenomics - a new interdisciplinary field of research in forest tree conservation genomics integrating dendrochronology, dendroecology, dendroclimatology and genomics

Contribution ID: 166

Krutovsky, Konstantin V.

Dendrogenomics is a new interdisciplinary field of research that integrates dendrochronology, dendroecology, dendroclimatology, genetics and genomics. This novel approach allows joint analyses of dendrological and genomic data and opens new ways in forest tree conservation genomics to study temporal dynamics of forest treelines, to delineate spatial and temporal population structure and, most of all, to study the adaptive genetic potential of forest tree populations. These problems are especially relevant to predicting how climate change will shape distribution of boreal forest species. The data will be presented on an association analysis of the variation of individual dendrophenotypes, reflecting the individual response of a tree to stress, with variation of a large number of DNA markers identified by genotyping-by-sequencing using ddRADseq allows to identify genome regions and genes whose variation is associated with variation of important adaptive traits using as examples the studies of Siberian larch (*Larix sibirica* Ledeb.) and Siberian stone pine (*Pinus sibirica* Du Tour) populations.

Keywords: genomics, dendrochronology, genotyping-by-sequencing, larch, pine

Estimates of effective population size are highly dependent on sampling design

Contribution ID: 167

Westergren, Marjana; Bajc, Marko; Rok, Damjanić; Dovč, Natalija; Kraigher, Hojka

Effective population size (*Ne*), the size of an idealized Wright-Fisher population that has the same value of a given genetic property, such as inbreeding, variance or linkage disequilibrium, as the real population, has been the focus of scientific debate since it was proposed to be used as a genetic indicator under the Convention on Biological Diversity. Here, we present empirical estimates of contemporary Ne based on molecular-marker data using different methods and sampling designs for two widespread forest tree species with continuous distribution, European beech and silver fir. Using 14-16 nuSSR loci, we compared sampling designs covering between 1 and 100 ha and sample sizes from 25 to 250 individuals. In addition, we compared Ne estimates provided by widely used one-sample methods (as implemented in NeEstimator) with those based on the variance of reproductive success estimated by mating models (MEMM). We found that the usual sampling design used in population genetic studies (25 trees spaced one tree height apart) resulted in low estimates of *Ne* with NeEstimator, with values ranging from 150 to 320, depending on sample size. Expanding the sampling area to 100 ha resulted in much higher estimates, over 7,000 for beech. The ratio between Ne and census population size calculated from reproductive variance with MEMM was 0.19 for beech and 0.20 for fir, which translates to Ne of over 10 million. Thus, based on this study and available literature, when standard population genetic sampling designs and Ne estimation methods are used, many forest tree populations are at risk of falling below the Ne=500 threshold and being classified as endangered, even if they consist of millions of trees and they are not under any genetic or demographic threats.

Keywords: forest trees, Census population size, nuSSR, NeEstimator, MEMM

The challenge of estimating effective population size: Can standard genetic parameters be of use?

Contribution ID: 168

<u>Farsakoglou, Anna-Maria</u>; Scotti, Ivan; Fady, Bruno; Aravanopoulos, F.A. (Phil)

Effective population size (*Ne*), if estimated accurately, can serve as a valuable synthetic tool for conservation and genetic monitoring for forest tree species. However, estimating effective population size in natural forest populations using genomic data from high-throughput genotyping technologies has proved to be challenging, due to the demographic and life-history characteristics of forest trees. In this study, we explore the possibility of indirectly estimating effective population size using classical genetic parameters and their associated statistics; the mean and standard deviation of expected heterozygosity (H_S) and the standard deviation of inbreeding coefficient (F_{IS}). The mean and standard deviation of expected heterozygosity (H_S) were examined with regards to their relation to the population diversity parameter θ. Results suggest the potential of mean (*Hs*) and sd (*Hs*) as indirect estimators of *Ne*, under the assumption that mutation rates are equal over populations, and therefore, comparisons of relative effective population sizes can be made across populations. We have also explored the possibility of indirectly inferring differences in effective population size using the standard deviation of inbreeding coefficient (F_{IS}), by conducting forward-time population genetics simulations, using the SimBit software. However, this hypothesis was rejected since it was found to be significant only when the potential effect of the spatial distance was not considered. We suggest that the mean and standard deviation of expected heterozygosity can be used as indirect estimates of *Ne*, but as it is challenging to estimate nonetheless, continued research is needed to enhance our understanding of *Ne* dynamics and along with other parameters to contribute to the conservation genomics of forest tree species.

Keywords: conservation, genetic diversity, effective population size, expected heterozygosity

The genetic consequences of population marginality: a case study in maritime pine

Contribution ID: 169

<u>Theraroz, Adélaïde</u>; Guadaño-Peyrot, Carlos; Archambeau, Juliette; Bagnoli, Francesca; Vendramin, Giovanni G.; Alía, Ricardo; Grivet, Delphine; Westergren, Marjana; González-Martínez, Santiago C.

Geographical marginal populations are located at the edge of the species' range and fragmented into sparse isolates, often in non-optimal environments. Because of their location, marginal populations may harbour highly specific alleles for local adaptation, thus potentially constituting valuable genetic resources for biological conservation. However, we lack evidence of the extent to which marginal populations are affected by particular genetic processes related to their typically small size, such as genetic drift or the purge/accumulation of genetic load. In this study, we used Pinus pinaster Ait., a widely distributed and economically important conifer characterized by a fragmented range, as a model species to better understand the genetic processes at play in marginal populations, as well as to test some of the main predictions of the Central-Peripheral Hypothesis (CPH). Based on 81 populations (1,431 individuals) and 10,185 SNPs, we estimated five population genetic indicators potentially related to ecological resilience (genetic diversity, genetic differentiation and inbreeding) and population vulnerability to climate and adaptability (genetic load and genetic offset) and correlated them with eight geographical marginality indices computed following Picard et al. (2022). Our study showed some significant correlations between marginality indices and genetic indicators. Indeed, we observed a trend towards decreasing genetic diversity and increasing genetic differentiation with geographic population marginality, which is consistent with the range-wide patterns of genetic diversity and differentiation described for this species, and which supports the CPH. However, we did not find a clear relationship between inbreeding, genetic load or genetic offset and population marginality. Overall, our results suggest that marginal populations keep similar levels of genetic variation and adaptive capability as central populations, and thus may still be a valuable source of pre-adapted alleles to atypical environmental conditions in P. pinaster, a main forestry species in south-western Europe.

Keywords: population genetics, conservation genetics, marginal populations, *Pinus pinaster*, genetic indicators

Molecular analysis of the oak syngameon in Ireland – genetic characterisation of the *Quercus robur* (L.) and *Quercus petraea* (Matt.) Liebl. species complex at its western limit

Contribution ID: 170

<u>Belton, Sam</u>; Fox, Erica; Degen, Bernd; Kelleher, Colin

Ireland represents the western limit of pedunculate (*Quercus robur* (L.)) and sessile oak (*Quercus petraea* (Matt.) Liebl.), which are Ireland's only native oaks. Both support a rich biodiversity and readily hybridise across much of their overlapping range. Here, 549 *Q. robur*, *Q. petraea* and putative hybrids from 31 Irish populations were genetically characterised using 22 plastid (17 chloroplast SNPs and five mitochondrial SNPs) and 404 nuclear (403 SNPs and one indel) markers. These were combined with data from 4,780 trees spanning 438 populations across the European continent to the eastern boundary in Russia. Plastid DNA variation indicates that Irish oak belong to a northwest European haplotype group but interestingly, nuclear DNA diversity was amongst the highest across the entire range. This appeared to be a consequence of frequent introgression from *Q. robur* into *Q. petraea*, with the diversity of the latter and the frequency of genetic hybrids being higher in Ireland than anywhere else. These results show that whilst island populations are typically less diverse than mainland populations, this may not always be true when sympatric taxa frequently hybridise. Ongoing work funded by the Irish Department of Agriculture, Food and the Marine is now exploring whether there is also a high diversity in adaptive gene regions.

Keywords: population genetics, hybridisation, introgression

Session 5:

Conservation genomics

Poster Session B: Thursday 14 September 16:20 - 18:30

Posters

Budde, Katharina Birgit; Grigoriadou-Zormpa, Ourania:
Fine scale spatial genetic structure in *Fagus sylvatica* along a steep elevational gradient in the Carpathian Mountains

Vujnović, Zvonimir:
Selection of European black poplar burl wood trees with contribution to gene pool conservation

Maksimović, Filip:
In situ conservation of forest genetic resources at the locality „Duboka” in the National Park „Kopaonik” – Serbia

Maksimović, Filip:
Identification of the field elm gene pool in the protected natural area "KOSMAJ" (Serbia) as a basis for its conservation and sustainable use

Köbölkuti, Zoltan Attila:
Allelic variation and post transcriptional regulation of candidate genes associated with virus defence in *Fraxinus excelsior* L.

Moro, Laura:
Land-use change effects on habitat availability and genetic diversity of tropical trees

Papadopoulou, Aliki:
Elucidating white oak phylogeographic diversity in an unexplored region of the Southern Balkans

Lyrou, Fani:
Genetic monitoring of *Quercus robur* and *Quercus petraea* populations in northern Greece

Flores, Andrés:
Priorities for conservation of forest genetic resources in two Mexican pines

Żukowska, Weronika:
Getting further east: genetic resources and the conservation strategy for black poplar in Poland

Fine scale spatial genetic structure in *Fagus sylvatica* along a steep elevational gradient in the Carpathian Mountains

Contribution ID: 171

Grigoriadou-Zormpa, Ourania; Wilhelmi, Selina; Vucetic, Boban; Ciocîrlan, Mihnea Ioan Cezar; Müller, Markus; Ciocîrlan, Elena; Curtu, Alexandru Lucian; Ben Targem, Mehdi; Wildhagen, Henning; Gailing, Oliver; Budde, Katharina Birgit

In plant species, limited gene dispersal via pollen and seeds typically causes a clustering of more related individuals within a population. This decrease in relatedness with increasing distance is termed the fine-scale spatial genetic structure (FSGS). It reflects microevolutionary processes at the local scale and can inform management practices. High throughput sequencing is advancing our understanding of population genomic processes, also in non-model species, such as forest trees. Using Single Primer Enrichment Technology (SPET) we generated a genome wide SNP (Single Nucleotide Polymorphisms) data set to investigate the FSGS in five natural populations of European beech (*Fagus sylvatica* L.) collected along an elevational gradient, ranging from ca. 550 m to ca. 1450 m above sea level in the Carpathian Mountains, near Brasov city, Rumania. We compare the results obtained using genome-wide SNP markers with traditionally used nuclear Simple Sequence Repeat (SSR) markers. In each location ~100 individual trees were sampled (~500 trees in total), and a subset of ~30 trees per population was characterized for leaf phenological traits. The timing of bud burst development was assessed in spring 2021. Among others, our study showed similar patterns at SNP and SSR markers. We observed high genetic diversity with a slightly decreasing trend with increasing elevation, which might be explained by harsher conditions and lower population density at high elevations. The strength of the FSGS also showed a decline with increasing elevation, indicating stronger family structures in lower elevation populations. This is in agreement with previous findings from beech populations along an elevational gradient at Mont Ventoux, where a high canopy density in lower elevations was reported to act as a barrier to pollen flow. Additionally, high elevation populations flowered later, as indicated by a later flushing date, possibly facilitating pollen influx from lower elevations.

Keywords: *Fagus sylvatica*, elevational gradient, genetic diversity, fine scale spatial genetic structure, bud burst

Selection of European black poplar burl wood trees with contribution to gene pool conservation

Contribution ID: 172

<u>Vujnović, Zvonimir</u>; Lanšćak, Miran; Ivanković, Mladen

European black poplar in Croatia is distributed in the seed zones and spread directly along the courses of the largest Croatian rivers. Through many years, rivers have shaped the most valuable floodplain and riparian forests. Due to the threat of the species and the reduction of its distribution area, the remaining natural stands, groups, or individual black poplar trees are particularly specific, which is important to preserve the gene pool and biodiversity. During field work groups of trees and stands were found and 20-50 burl wood and plus trees were selected per location. The most important criteria for the selection of trees are the burl wood, while other criteria are good health status and the age of the tree, which should be at least 70 years to avoid crossbreeding with Euro-American poplars. In addition to the burl wood trees, other black poplar trees were also selected, which are phenotypically superior to the other trees. Also, Android application for field data collection Topole was developed and the data was entered into the application. Data contains detailed information about the selected trees (taxation measurements, health status, coordinates, etc.) and based on it a digital database was created with a public access web page where a map of the area and all the selected trees are visible. Each tree is permanently marked with numbered plastic tiles and georeferenced. Selected stands were proposed for register into the National Register of Forest Seed Objects in the categories of 'known origin' and 'selected'. Also, plant parts (leaves) were taken from selected trees for molecular analysis to determine intra-population and inter-population differences and obtain the genetic structure of black poplar in Croatia. By establishing a unique register of black poplars it contributes to the preservation of the European black poplar gene pool and expands knowledge about the genetic status of populations in the Republic of Croatia.

Keywords: black poplar, burl wood, gene pool, molecular analysis, conservation

In situ conservation of forest genetic resources at the locality „Duboka” in the National Park „Kopaonik” – Serbia

Contribution ID: 173

Nonić, Marina; Šijačić-Nikolić, Mirjana; Vilotić, Dragica; Maksimović, Filip; Šumarac, Predrag

In situ conservation in Serbia is mainly presented in protected areas, such as national parks. National Park „Kopaonik” is one of five national parks in Serbia, which covers a total area of 11,969.04 ha, including 13 localities with a protection regime of the first degree. Forest genetic resources in the National Park „Kopaonik“ are affected by various biotic and abiotic threats which lead to their genetic erosion. This research aimed to identify rare, endangered, relict, endemic, and vulnerable forest trees at the locality „Duboka”, to assess their degree of endangerment and propose conservation measures. The locality „Duboka” covers an area of 144.03 ha, at an altitude of between 1020 and 1780 m. By terrain reconnaissance, a total of 18 forest tree species, and 27 species in the shrub layer were identified, which indicates a significant biodiversity of this locality. Nine forest tree species belong to the categories of rare (rowan and wych elm), rare-endangered (silver birch), relict (European hop-hornbeam), endemic (Balkan maple), and vulnerable species (aspen, wild cherry, wild pear, and whitebeam) in Serbia. Among those species, it is very important to conserve the available gene pool of European hop-hornbeam (*Ostrya carpinifolia* Scop.), which is a very rare, relict species that occurs only in the locality „Duboka” in the entire area of Kopaonik, and the Balkan maple (*Acer heldreichii* Orph. ex Boiss.), an endemic species whose range is drastically decreasing on the entire Balkan peninsula. The measures of conservation and monitoring of individual genotypes or groups of trees have been defined, and an assessment of the variability of gene pool using genetic markers was proposed. In situ conservation units will include sites where all nine rare, endangered, relict, endemic, and vulnerable forest tree species were selected and georeferenced. The implementation of the proposed measures is expected in the following period.

Keywords: relict and endemic species, natural protected areas, conservation, genetic resources

Identification of the field elm gene pool in the protected natural area KOSMAJ (Serbia) as a basis for its conservation and sustainable use

Contribution ID: 174

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

The field elm (*Ulmus minor* Mill.) is an autochthonous tree species in Serbia that occurs as a secondary species in oak forests. In the forest fund of Serbia, this species is rare/endangered due to the genetic erosion and disappearance of elms from natural populations, mainly as a result of Dutch elm disease. In the protected natural area „Kosmaj“ the field elm was identified as one of the target species from the aspect of conservation. This research aimed to identify and assess the state of available field elm genepool in the protected natural area „Kosmaj“, as a basis for its conservation and sustainable use. By terrain reconnaissance a field elm gene pool was identified, representing almost 100 trees: 47 individuals and 8 groups of trees, on an area of 652.99 ha. All trees were georeferenced and mapped. The average height of the trees is 10.34 m, the diameter at breast height is 15.68 cm, the perimeter is 51.09 cm, while the average crown span is 3.95 m. Dry tops or dry side branches of trees, absence of yield for a long period, and weak natural rejuvenation were recorded. The selected trees will be included inconservation units, which were proposed to conserve the available gene pool in situ. To conserve the available genepool ex situ, the cuttings from selected mother trees were collected and the clonal test was established in the greenhouse of the Faculty of Forestry, University of Belgrade. This clonal test could be a basis for the establishment of a field gene bank in the future. It is planned to determine the variability of the selected trees, using morphological and molecular markers. The initiated activities should contribute to the conservation and sustainable use of the field elm gene pool in the protected natural area „Kosmaj“ and further breeding of the species.

Keywords: *Ulmus minor* Mill., natural protected areas, conservation, gene pool, clonal test

Allelic variation and post transcriptional regulation of candidate genes associated with virus defence in *Fraxinus excelsior* L.

Contribution ID: 175

<u>Köbölkuti, Zoltan Attila</u>; Eisen, Anna-Katharina; Buchner, Lisa; Jochner-Oette, Susanne; Rehanek, Marius; Köpke, Kira; Landgraf, Maria; von Bargen, Susanne; Al Kubrusli, Rim; Büttner, Carmen; Böhm, Jan W.; Kube, Michael; Fussi, Barbara

Across various European countries, *Fraxinus excelsior* L. is facing a decline caused by *Hymenoscyphus fraxineus*. The underlying mechanisms are still insufficiently understood in detail. Observations suggest that, in addition to the main pathogen, viral infections may also contribute to the decline of ash trees. The limited knowledge concerning the interaction between ash dieback and virus infections gives rise to a pressing need to thoroughly understand this interplay. Our study was performed to describe homologues in the F. excelsior genome of seven formerly annotated virus resistance genes, to test the applicability of these gene fragments in F. excelsior, and to genotype by PCR and Sanger sequencing cytorhabdovirus, ash shoestring-associated virus (ASaV), and privet leaf blotch-associated virus (PrLBaV) infected symptomatic and asymptomatic ash samples by revealing possible nucleotide variation at these loci. Further, prediction of cis-acting regulatory elements and transcription factor binding sites was accomplished, a co-expression network of the candidates was constructed, and an in-silico analysis was carried out to predict and annotate miRNAs that target these genes. After sequencing, the amplified products were analysed by considering the polymorphic sites and insertion/deletion events. In a total of 2256 sites 24 indels and 14 SNPs were found. 283 miRNAs were identified as RNA molecules with role in regulation of these seven genes. We found ABA Hypersensitive 1, ADP-ribosylation factor 8a, Microrchidia 2, phosphatase 2C 22, small RNA 2'-O-methyltransferase, NTM1-like 9 and Suppressor of gene silencing 3 as important nodes in a regulatory network with possible role in virus defence. The SNP markers developed on these nodes could be useful for the selection of individuals with various resistance to viral infections. The identification of trees with different virus resistance in ash dieback host populations could provide a route for a more thorough understanding of the ash dieback-virus resistance interaction.

Keywords: *Fraxinus excelsior,* ash dieback, virus defence, SNP markers*, miRNA*

Land-use change effects on habitat availability and genetic diversity of tropical trees

Contribution ID: 177

Moro, Laura; Muscarella, Robert; Milesi, Pascal

Land-use change presents major threats to biodiversity with impacts typically outpacing those from climate change. Habitat loss and fragmentation, key features of land-use change, can have direct and indirect consequences on plant species including reduced size and connectivity between populations, and reduction of genetic diversity. In Puerto Rico, for example, forest cover dramatically increased from ~6% in the early 1900's up to ~55% today. We quantified the impacts of land-use change on the area and configuration of suitable habitat patches for 267 native tree species in Puerto Rico to understand how land-use dynamics have affected their current geographic distributions, population sizes and genetic diversity. We built species distribution models (SDMs) for all native tree species in Puerto Rico (N=267) based on current geographic distribution and abiotic conditions. We then combined SDMs with available data on land-use change (based on historical aerial photos from the 1930s, 1950s, and 1970s, combined with more recent satellite imagery) to estimate habitat availability through time. We used Plot based data from the Forest Inventory and Analysis (FIA) Program of the US Forest Service to estimate current population sizes and forest cover. Our results provide species-specific information on (i) the areal extent (km^2) of climatically suitable habitat at different time points, (ii) fragmentation indices of suitable habitat at different time points and (iii) species responses to land-use change according to their life history strategies and phenotypic traits. Overall, 223 species gained and 44 species lost suitable habitat during the time period analyzed. Species-specific responses varied and depended on species' life-history strategies, phenotypic traits, and general habitat association. To more comprehensively assess both the short- and long-term effects of land-use change, we will integrate this information with population genetic data. We will use a comparative genomics approach to determine how land-use change has influenced patterns of genetic diversity for a focal set of 20 tree species with diverse life-history strategies and climatic associations. This will allow a broader understanding of the implications of habitat recovery for forest genetic resources.

Elucidating white oak phylogeographic diversity in an unexplored region of the Southern Balkans

Contribution ID: 178

<u>Papadopoulou, Aliki</u>; Malaspina, Alexia; Tourvas, Nikolaos; Aravanopoulos, F.A. (Phil)

The phylogenetic relationships concerning three of the most widespread European white oak species (*Quercus petraea*, *Quercus pubescens*, *Quercus robur*) were studied in continental (Macedonia, Thessaly) and insular Greece (Lesvos island, Aegean region). Reference samples from known maternal oak lineages (A - Balkan & Italian, B – Iberian, C – Italian, E – Italy through Russia) were used to study phylogeographic inferences. Out of 10 cpDNA microsatellite loci employed, six were polymorphic revealing 2-4 alleles. Eleven chlorotypes were detected and a minimum spanning tree analysis allocated them to lineages A (two haplotypes) and E (nine haplotypes). Chlorotype composition was not correlated with species identity. Most samples of lineage A, originated from Macedonia populations and were assigned to a known haplotype with high prevalence in the transect from Black Forest to the Balkans. A novel closely related haplotype was also revealed which was present in samples only from Lesvos island. In lineage E, two known haplotypes were detected in Macedonia and Thessaly, and seven novel haplotypes were identified throughout the study area. Notably, the populations from Lesvos presented two haplotypes with high mutational distance within this lineage. Haplotypic variation within populations (h_S=0.314) was substantially lower than overall (h_T=0.879), demonstrating high cytotype heterogeneity between regions, a result also supported by high genetic differentiation statistics (R_{ST}=0.695). Overall, these results contribute to the study of white oak post-glacial migration pathways and suggest the presence of a refugium in the extended Aegean region.

Keywords: cpSSR, maternal lineages, Greece, post-glacial migration*, Quercus*

Genetic monitoring of *Quercus robur* and *Quercus petraea* populations in northern Greece

Contribution ID: 179

Lyrou, Fani; Tourvas, Nikolaos; Papadopoulou, Aliki; Malaspina, Alexia; Neophytou, Charalambos; Aravanopoulos, F.A. (Phil)

Genetic monitoring, the quantification of temporal changes in population genetic diversity and structure, elucidates processes that maintain genetic variation in natural populations, introduces prognosis and helps define tools for the management of forest genetic resources. Genetic monitoring plays a crucial role in assessing the long-term persistence of natural populations and in understanding the impacts of environmental change on genetic diversity. Herein, we report the temporal evaluation of genetic diversity for two important oak species, *Quercus robur* and *Q. petraea*, employing two populations from northern Greece which belong to the Natura 2000 network, evaluated in a 16 years' time interval. We have employed 17 SSR markers and assessed observed heterozygosity (*Ho*), unbiased heterozygosity (He), and inbreeding coefficient (F_{IS}). Genetic diversity of *Q. robur* slightly declined, coupled with a more pronounced decline in the (close to neutral expectations) inbreeding coefficient. However, the differences observed were not statistically significant according to Mann-Whitney tests. Furthermore, baseline values for *Q. petraea* were *Ho* = 0.735, *He* = 0.781, and F_{IS} = 0.070, while present values were *Ho* = 0.682, *He* = 0.719, and F_{IS} = 0.050. Yet again, the differences observed were not statistically significant (Mann-Whitney tests). A slight decrease in genetic diversity is also seen for *Q. petraea*, while the inbreeding coefficient remains negligible. The present study emphasizes the importance of temporal genetic monitoring and provides valuable insights into the maintenance of genetic diversity in *Q. robur* and *Q. petraea* populations in protected areas.

Keywords: cpSSR, maternal lineages, Greece, post-glacial migration*, Quercus*

Priorities for conservation of forest genetic resources in two Mexican pines

Contribution ID: 180

Flores, Andrés; Buendía-Rodríguez, Enrique; Pineda-Ojeda, Tomás; Flores-Ayala, Eulogio; Méndez-González, Jorge

Genetic conservation priorities are based on the economic and environmental importance of a species. Although genetic studies of forest tree species have increased enormously throughout this century, there is still a lack of information for many of them, and decisions are mostly made in the absence of any genetic knowledge. Mexico is considered a center of pine diversity, but its genetic conservation efforts are not enough. To define genetic conservation units (GCU) and propose measures for the conservation and sustainable use of *Pinus cembroides* and *P. chiapensis*, we analyzed the distribution of the species at the national level and in germplasm transfer zones, and evaluated the pines with a set of minimum requirements for conservation and indicators from EUFORGEN program. We saw that 16 genetic zones harbored both species, in which *P. cembroides* was the most widely distributed. We defined 23 areas for establishing GCU for the target species studied; 61% of them were selected from areas with genetic information, and 39% in natural forests. We saw that most of the forest reproductive material used is collected from natural forests, and the use of seeds from breeding trials is scarce.

Keywords: conservation efforts, dynamic conservation, *Pinus*

Getting further east: genetic resources and the conservation strategy for black poplar in Poland

Contribution ID: 208

<u>Żukowska, Weronika</u>; Lewandowski, Andrzej

Black poplar (*Populus nigra* L.) is not popular among Polish foresters and breeders. This is mainly the consequence of unsuccessful attempts to establish poplar plantations in 1970s. Currently, black poplar occurs naturally along major river valleys in Poland, but the populations are usually small and fragmented. Unfortunately, many trees have reached terminal age. Natural regeneration is possible only in a few areas, where the river dynamics still allow periodic flooding. Using a set of 19 microsatellites, we analyzed the genetic variation of 24 black poplar populations (939 trees) located along the biggest river valleys in Poland. We detected clones in most stands, but only in close proximity. This indicates that the vegetative spread of black poplar through the river current is negligible. The level of genetic variation was generally high, but lower in downstream populations. The overall genetic differentiation was low (populations: Fst = 0.057; rivers: Fst = 0.029; $p < 0.001$). Nevertheless, trees occupying different river catchments formed separate genetic clusters. The genetic structure along the rivers was evident along the Warta and Oder, which are highly regulated. Contemporary gene flow occurs mostly downstream and between adjacent populations. The effective population sizes were very low (mean Ne = 35.59), with the lowest values in downstream locations. Our results will be accompanied by SNP genotyping and used to develop a comprehensive conservation strategy for the genetic resources of black poplar in Poland. As the species cannot regenerate naturally, we are making efforts to establish clone archives throughout the country. We believe that our results broaden our understanding of the genetic variability of European black poplar populations, as previous studies have focused on Western and Southern Europe. We welcome all researchers to use our material in their further research.

Keywords: *Populus nigra*, genetic variation, conservation, clone archive, adaptation

Session 6:

Tree breeding and sustainable use of forest genetic resources

Friday 15 September 16:20 - 19:15

Chair: Associate Professor Dr. Ole Kim Hansen, University of Copenhagen, Denmark

Oral presentations

16:20 **Keynote**
Sánchez-Rodríguez, Leopoldo:
B4EST: a collaborative research effort on adaptive BREEDING for productive, sustainable and resilient FORESTs under climate change

17:05 **Pers-Kamczyc, Emilia:**
Plant reproductive potential in the face of increased global nitrogen deposition

17:25 **Buggs, Richard:**
Genomic prediction for ash dieback resistance and the potential for a rapid cycle ash breeding programme

17:45 ***Short Break***

17:55 **Neophytou, Charalambos:**
Breeding sessile oak (*Quercus petraea*) for drought-stress tolerance

18:15 **Olsson, Sanna:**
Improving conservation and sustainable use of *Pinus pinea*, a multipurpose forest tree with narrow genetic base, by using genomic tools

18:35 **Liepe, Katharina J.:**
Accounting for phenotypic plasticity and local adaptation in species distribution models to support prescriptions on assisted migration

18:55 **Wu, Harry:**
Genomic selection progress in conifers

Keynote Session 6:

B4EST: a collaborative research effort on adaptive BREEDING for productive, sustainable and resilient FORESTs under climate change

Contribution ID: 106

Sánchez-Rodríguez, Leopoldo:

The strategic goal of B4EST was to increase forest resilience and productivity under climate change, while maintaining genetic diversity and key ecological functions. To cover the geographical, economic and societal needs of forestry in Europe, B4EST aimed to work with 8 conifer and broadleaves with advanced breeding programs or case studies of pest-threatened forests. To reach its goal, B4EST aimed to achieve the following scientific, technological and implementation breakthroughs: 1) enhance scientific understanding of species vulnerability to major disturbances and explore the trade-offs between production, resistance/resilience, and reproductive capacity; 2) diversify the portfolio of forest reproductive material (FRM); 3) make the portfolio of FRM accessible to forest managers through decision tools, recommendations and guidelines; and 4) integrate a landscape-level view and a transnational forest sector analysis of risks, costs and benefits. In this presentation, we propose a quick but complete overview of the most relevant results of this project.

Free and unrestricted access to historical and future climate databases is crucial for the scientific community to assess the impacts of climate change and develop effective adaptation strategies. In pursuit of this goal, B4EST has successfully created a Climate Matching and Climate Downscaling Tool, accessible at https://b4est.eu/tools. This tool has already proven invaluable in obtaining projections of tree performance under future climatic conditions and has been instrumental in designing new experiments using reaction norms. Additionally, B4EST has made significant strides in genetic analyses through the development of novel genotyping tools. Specifically, they have introduced three new 50K SNP arrays for six major species: *Fraxinus* spp, poplar spp, *Picea abies*, *Pinus sylvestris*, *P. pinea*, and *P. pinaster*. These cutting-edge tools have enabled unprecedented resolution of species' genetic structures, ensured FRM traceability, identified numerous key polymorphisms, and facilitated the implementation of genomic evaluation techniques.

During this project, many of the obtained results underwent evaluation within existing breeding programs. This evaluation facilitated the development of new breeding guidelines and decision support tools. The guidelines identified key innovations and predicted the potential impacts of these results under various scenarios, which will prove valuable for initiatives involving emerging species. Two decision support tools were created and are now accessible both as research platforms and operational tools for foresters. The first tool, called the Planter's Guide, emerged as a collaborative Nordic effort for Scots pine and Norway spruce. It enables the selection of optimal seed sources across Nordic countries, considering current and future climatic conditions. On the other hand, the Luberon2 simulation tool (accessible at https://b4est.eu/luberon2) facilitated the investigation of the impacts of different silvicultural scenarios on genetic diversity in the event of stochastic disturbance events.

In order to address future challenges effectively, tree breeding must be approached in a more collaborative manner, both at the national and European levels. B4EST played a pivotal role by offering current, research-based information that proved valuable for regional decision-making, policy formulation, and fostering a deeper comprehension of the diverse challenges and solutions across different regions within the EU. Even after the project's conclusion, communication about B4EST's work persists through its website, blog, and social media platforms, which serve as a central resource for ongoing engagement and dissemination of valuable insights.

Keywords: breeding, sustainability, new genotypes, adaptation profiles, genomic selection, deployment

Plant reproductive potential in the face of increased global nitrogen deposition.

Contribution ID: 181

Pers-Kamczyc, Emilia; **Kowalczyk, Anna; Suszka, Jan; Mąderek, Ewa; Kamczyc, Jacek**

The future of plant populations depends on their ability to adapt to changes in the environment. In both terrestrial and aquatic ecosystems, the deposition of significant amounts of nitrogen, phosphorus, and other elements is observed, which leads to the eutrophication of these environments. Plant species that through evolutionary changes have adapted to an environment of certain affluence are increasingly exposed to the long-term effects of higher availability of resources than those to which they have evolved through their adaptation. Dioecious plants may experience differential impact of global changes which can be related to sexual dimorphism. As it has been observed female and male plants may have different responses to environmental stressors and have different costs of reproduction. Increased anthropogenic deposition of nitrogen and phosphorus is observed and can affect environmental biodiversity. Thus both male and female plants of dioecious species have an equal impact on seed production and offspring performance, we performed long-term pot experiments with differentiated availability of fertilizer. We used clonal plants of males and female plants of two dioecious species - *Taxus baccata* L. and *Juniperus communis* L. We described reproductive potential by the quantitative and qualitative characteristics of pollen grains, seeds, and obtained seedlings. Our results indicated that long-term higher nutritional availability affects the reproductive potential and can have a great impact on species distribution.

Keywords: seeds quality, pollen grain quality, nitrogen deposition, dioecious plants

Genomic prediction for ash dieback resistance and the potential for a rapid cycle ash breeding programme

Contribution ID: 182

Buggs, Richard; Metheringham, Carey; Stocks, Jonathan; Wood, Daniel; Kelly, Laura; Nichols, Richard

European ash populations are being devastated by the alien invasive fungus *Hymenoscyphus fraxineus*, causing ash dieback. Using genome-wide association analysis we have found numerous SNP loci associated with resistance to this fungus. With thousand of loci, we have successfully made genomic predictions of ash dieback resistance in a planted trial. We demonstrated the relevance of these estimates in the natural environment by measuring shifts in the genomically estimated breeding values, under the natural selection imposed by the arrival of the fungus in an ancient woodland. We are now seeking further improvements in our predictions by including structural variants. This genomic knowledge could be used to select parents and progeny in an accelerated breeding programme. Other researchers have recently developed methods of somatic embryogenesis and genetic transformation in ash, opening up the potential for genetic modification, gene editing, or rapid cycle breeding. We suggest that rapid cycle breeding (in which early flowering is induced by genetic modifications that can be segregated out after a few generations of crossing and genomic selection) may be the most practical and socially acceptable way forward for European ash, to breed lines resistant to both ash dieback and the emerging threat of emerald ash borer.

Keywords: genomic prediction, genomic selection, *Fraxinus*, ash dieback, ash

Breeding sessile oak (*Quercus petraea*) for drought-stress tolerance

Contribution ID: 183

Semizer-Cuming, Devrim; Fussi, Barbara; Schlosser, Franziska; Seegmüller, Stefan; Rellstab, Christian; Michiels, Hans-Gerhard; Neophytou, Charalambos

Forest breeding programs have long been focused on highly productive sites as base populations. Although mostly irrelevant for forestry regarding productivity, relict sessile oak (*Quercus petraea*) stands on arid sites may have adapted to harsh local environmental conditions over many generations. Therefore, they are ideal study objects to investigate drought adaptation to face off climate change. Here, we studied 46 sessile oak stands in southern Germany and Alsace, France, with a multifaceted approach integrating ecology, genetics, genomics and physiology. Indicator species of flora and fauna supported the relict character of the stands. Microsatellite analyses backed our hypothesis of autochthony and showed a highly homogenous gene pool. In spite of this homogeneity, there were genomic and physiological differences among sites that can be attributed to local adaptation. Outlier and environmental association analyses applied on targeted genomic regions (all coding regions) revealed loci putatively under selection. Moreover, differences in physiological responses of progenies from dry vs. well water-supplied sites were detected in a common garden. Similarly, significant differences were observed at phenological and growth traits among progenies of the study stands in a common garden. This standing adaptive genetic variation is promising for the future selection of sessile oaks. Provenance-progeny tests established with 60 open-pollinated families from 25 stands at four sites along a drought gradient will enable selection within and among families and provenances. Our innovative breeding program aims to produce climate-smart oak reproductive material for sustainable use.

Keywords: adaptation, breeding, drought tolerance, reproductive material, sessile oak

Improving conservation and sustainable use of *Pinus pinea*, a multipurpose forest tree with narrow genetic base, by using genomic tools

Contribution ID: 184

Olsson, Sanna; Macaya-Sanz, David; Guadaño-Peyrot, Carlos; Pinosio, Sara; Bagnoli, Francesca; Avanzi, Camilla; Vendramin, Giovanni G.; González-Martínez, Santiago C.; Alía, Ricardo; Mutke, Sven; Grivet, Delphine

Stone pine (*Pinus pinea* L.) is an emblematic tree species within the Mediterranean basin, with great ecological and economical (edible seeds) relevance. Breeding programs (very active in Spain and Portugal) to improve the pine nut production started decades ago, but have been limited due to low level of genetic variation in the species. Therefore, there is the need to more accurately assess forest genetic resources (FGR) and their use in stone pine conservation and management programs. For this purpose, we used the recent genome-wide 4TREE array (5,671 SNPs). We first used the array for identification of 105 (registered and candidate) clones from the Spanish breeding program for pine nut production. We confirmed accurate clonal identification and better identity check (post-hoc traceability) than the currently used microsatellite markers. Second, we tested genetic differences among twenty Iberian populations, with the objective to improve the definition of gene pools in relation with the breeding and FGR conservation programs. The improved characterization of stone pine provenance regions will contribute to better define in situ conservation units. Finally, we successfully estimated kinship relationships among material from Spanish clonal collections and their F1 offspring, needed for low-input breeding strategies and genomic prediction.

Keywords: Mediterranean stone pine, pine nuts, clonal identification, breeding, SNP array

Accounting for phenotypic plasticity and local adaptation in species distribution models to support prescriptions on assisted migration

Contribution ID: 185

Liepe, Katharina J.; Liesebach, Mirko; van der Maaten, Ernst; van der Maaten-Theunissen, Marieke

The most common tool to predict future changes in species range are occurrence-based species distribution models. However, these models often underestimate the potential future habitat, as they do not account for phenotypic plasticity and local adaptation. These highly important processes in the response of tree populations to climate change are considered in trait-based models combining reaction norms of quantitative trait variation as a function of past climate experienced at seed source origin to which populations are genetically adapted, and simultaneously as a function of current climate experienced at the planting site to which they show plastic responses. We make use of extensive provenance trial series of Norway spruce and European beech to model future height growth potential and compare these predictions with classic species distribution models. For Norway spruce, both the occurrence-based and the growth-based model show a significant retreat towards northern latitudes and higher elevations (-55 % and -43 % by 2080). However, thanks to the species particularly high phenotypic plasticity, the decline is delayed. Increasing summer heat coupled with decreasing water availability limits performance, while a prolonged frost-free period enables an increase within the remaining area. Signals of local adaptation along climatic gradients are low, as they are masked by a strong influence of latitude. The latter reflects population differentiation for the Baltics, but does not capture the high phenotypic variation associated with heterogeneity in Central European mountain ranges and postglacial migration history. The model is used to provide recommendations for optimal provenance selection under future climate. In essence, seed transfer cannot mitigate the projected range decline of Norway spruce, but it can help to exploit potential opportunities for better growth associated with warmer climate conditions. A comparable model for European beech is currently under development and results will be presented.

Keywords: climate change, height growth, provenance trial, universal response function, TraitSDM

Genomic selection progress in conifers

Contribution ID: 186

Wu, Harry

Since the first publication of genomic selection concept in tree in 2010/11, genomic selection using cross-validation were studied in a dozen of commercially important conifers species. SNPs from low density array, exome sequencing, GBS and more recently from medium-density SNP array were used for genomic selection. Also, genomic selection from cross-validation were effective, with an average efficiency about 90%, relative to phenotype selection. The genomic selection across breeding population and across generation are much lower based on simulation and real data. Possible causes of low cross-population and cross-generation and proposed mitigation strategies are presented. Three cases of genomic selection along with the development of two 50K SNP arrays using whole genome re-sequencing in Norway and Scots pine are presented.

Keywords: Genomic selection, Breeding value, SNP array, Norway spruce, Scots pine

Session 6:

Tree breeding and sustainable use of forest genetic resources

Poster Session B: Thursday 14 September 16:20 - 18:30

Posters

Macaya-Sanz, David:
Applying genomics to the breeding for Dutch elm disease resistance

Ousmael, Kedra:
Genomic evaluation for breeding and genetic management in *Cordia africana* - a multipurpose tropical tree species

Blanc-Jolivet, Celine:
Should genetic tracking of geographical origin be required for reproductive material used in provenance trials and seed stands?

Szukala, Aglaia:
Ash in distress: results from a large experimental field trial on ash dieback in Austria

Postolache, Dragoș:
Exploring phylogeographic patterns of temperate broadleaved species in the Balkan Peninsula and the southeastern marginal range in Europe

Mittelberg, Hannah S.:
An insight into the current state of work on the population structure of *Carpinus betulus* L. in selected stands

Mohytych, Vasyl:
Estimating breeding values and genetic parameters in a series of Scots pine open-pollinated progeny trials in north-western Poland

Heinze, Berthold:
Oak seed stands and reproductive material genetics in Central Europe

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Yobu, Christi Sagariya:
Stochastic simulation of landscape breeding programs

Applying genomics to the breeding for Dutch elm disease resistance

Contribution ID: 187

Macaya-Sanz, David; Pallares-Zazo, Jorge; Baron-Sola, Angel; Martín-García, Juan Antonio

During the last century, several waves of Dutch elm disease eradicated elm stands from Europe, being Ulmus minor the most affected species. It was a member of lowland alluvial plains and other habitats and, thus, had a considerable ecological and cultural value. It was also a prevalent tree in urban parks, roadsides, and plazas. To protect the species and its heritage, several entities initiated conservation actions along breeding programs, although, in the latter their success has been limited to the date. Among other reasons, the low natural resistance of most European elms mustered a poor pool of founding resistant individuals to kick off breeding programs. Nevertheless, in Spain, an appreciable number of trees with high and moderate resistance were found, leading to the establishment of a low-input breeding program (i.e. Spanish elm breeding program). However, the program is facing the limitations inherent to breeding undomesticated, not economical organisms: lack of investment from industrial sector and reduced scientific information to guide it. That knowledge scarcity is even more pronounced in the genetics of the resistance. To cover this gap and speed up breeding, several research initiatives, brood from the collaboration of several public institutions, have emerged: (1) an U. minor draft reference genome using Illumina and PacBio sequencing platforms and state-of-the-art assembly software, attaining an acceptable genome quality (N50 > 1 Mbp); (2) combining it with whole-genome sequencing of 12 other genotypes to create several lists of SNPs amenable for target genotyping; (3) also, by means of restriction enzyme Genotyping-by-Sequencing, studying the population genetics of the species in Spain and evaluating interspecific introgression; (4) through genotyping and phenotyping crosses, analysing QTLs associated with resistance; (5) and finally, applying that information to the genomic prediction of the Mendelian sampling of the resistance in the crosses, to effectively accelerate breeding and reduce costs.

Keywords: Dutch elm disease, forest pathology, genomics, reference genome, *Ulmus*

Genomic evaluation for breeding and genetic management in *Cordia africana* - a multipurpose tropical tree species

Contribution ID: 188

<u>Ousmael, Kedra</u>; Cappa, Eduardo; Hansen, Jon; Hendre, Prasad; Hansen, Ole Kim

Planting selected and tested forest reproductive material is crucial to ensure increased resilience of intensively managed productive stands for the timber and wood products markets under climate change scenario. Single-step Genomic Best Linear Unbiased Prediction (ssGBLUP) analysis is currently being employed as an economic option for using genomic tools to enhance the accuracy of predicted breeding values and genetic parameter estimation in forest tree species. Here, we tested the efficiency of ssGBLUP in a tropical multipurpose tree species, *Cordia africana* Lam., by partial population genotyping. A total of 8,070 trees from breeding seed orchards (BSOs) established at three locations were phenotyped for height. We genotyped 6.1% of the phenotyped individuals with 4,373 high quality SNPs. Genotyping a subset of the study population provided insight into the level of relatedness in the BSOs, allowing for better genetic management. Due to the inbreeding detected within the genotyped provenances, we carried out the estimation of genetic parameters both with and without accounting for inbreeding. The ssGBLUP model showed improved performance in terms of additive genetic variance and theoretical breeding value accuracy. Both ABLUP and ssGBLUP models showed high predictive accuracy and low prediction bias. However, ssGBLUP showed improved predictive accuracy and lower bias compared to the pedigree-based relationship matrix (ABLUP). This study of *C. africana*, a species that has been declining by deforestation, fragmentation and selective logging, revealed inbreeding depression. The provenance that exhibited the highest level of inbreeding had poorest overall performance and the lowest percentage of trees that were considered candidates for selection in the top 10% ranking. At least 96% of the top 10% trees were consistently identified across all models used. Therefore, the use of different relationship matrices and accounting for inbreeding in the analysis did not have a significant effect on the ranking of candidate individuals. The implications of all these results for breeding and genetic management of *C. africana* in Ethiopia are discussed.

Keywords: *Cordia africana*, tropical tree breeding, genetic management, single-step GBLUP, quantitative genetic parameters

Should genetic tracking of geographical origin be required for reproductive material used in provenance trials and seed stands?

Contribution ID: 189

Blanc-Jolivet, Celine; Mader, Malte; Müller, Niels; Liepe, Katharina J.

Past records about the seed sources used for establishment of forest stands and provenance trials were often sparse, mainly limited to a broad sampling area and approximations of the number of harvested trees. Further information in terms of preceding seed transfers or their genetic assembly are lacking, but of high relevance for breeding programs and provenance recommendations. We used samples collected from spruce and beech provenance trials as well as in certified seed stands in Germany to study their spatial genetic structure in Europe. In Spruce, we ascertained SNP markers with ddRAD seq (Double digest restriction-site associated DNA) and genotyped 363 spatially informative loci with targeted sequencing (SeqSNP) in around 2,000 samples originating from across Europe as well as the Western part of Russia. In Beech, we genotyped 506 SNPs (SeqSNP) in 2,000 individuals, but also analysed another batch of 860 individuals for 3.6 million variants derived from whole-genome resequencing. The results revealed that, although spatial structure resulting from natural processes could be disentangled, some beech provenances or seed stands showed a contrasting origin compared to the overall patterns, and may sometimes even represent a different species. In Spruce, strong impacts of ancient seed transfer are prevalent, and raise the question of subsequent reproduction among individuals from autochthonous and planted stands. Several examples will be presented to discuss the potential risks of tacking the information of spatial origin for granted, and the needs and limitations of molecular tracking to select reproductive material for plantations and breeding programs.

Keywords: spatial genetic structure, SNPs, tracking, forest reproductive material, origin

Ash in distress: results from a large experimental field trial on ash dieback in Austria

Contribution ID: 190

Szukala, Aglaia; Unger, Gregor; Trujillo-Moya, Carlos; Kirisits, Thomas; Geburek, Thomas; Konrad, Heino

Common ash (*Fraxinus excelsior*) is a highly valuable broadleaved species, whose survival is threatened by the alien invasive ash dieback pathogen *Hymenoscyphus fraxineus*. Studies provided evidence that ash dieback tolerance has a polygenic basis and identified tolerance-associated genetic loci (Stocks et al., 2019). Here, we report on one of the largest extant field trials aiming at the identification and characterization of ash dieback tolerant genotypes, while encompassing the genetic diversity of common ash in Austria. Our genomic analyses are based on an ash-specific, newly developed 4TREE genotyping tool (Guilbaud et al., in prep) targeting 13,407 single-nucleotide polymorphisms (SNPs) and including a high proportion of those that were previously identified as associated with dieback tolerance. We observed that susceptibility in juveniles can strongly increase during the first three years following germination, whereas trees showing no disease symptoms towards the end of the third vegetation period are likely to remain symptomless or become only slightly damaged over the following years. We performed genotype-tolerance association analyses of over 1,000 individual trees including one susceptible and one putative tolerant progeny from tolerant mothers using the 4TREE array. Our genotype-tolerance association analyses overall failed to detect candidate loci that could be used for future genotype-informed breeding. Nevertheless, the array proves powerful to study genetic structure and detect introgression from the closely related species, as well as explore associations with environmental variables and other traits of interest.

Keywords: ash dieback, *Fraxinus excelsior*, ash, genotype-informed breeding, genotype-tolerance association analyses

Exploring phylogeographic patterns of temperate broadleaved species in the Balkan Peninsula and the southeastern marginal range in Europe

Contribution ID: 191

<u>Postolache, Dragos</u>; Zhelev, Petar; Paule, Ladislav; Ballian, Dalibor; Postolache, Gheorghe; Popescu, Flaviu

The Balkan Peninsula represents one of the largest and most significant glacial refuges in Europe. Nevertheless, there is still persist lack of understanding regarding the evolutionary history and phylogeographic patterns for most temperate tree species that survived in the Balkans refugia, as well as their contribution to the current genetic structure of populations in the Carpathian Mountains. To address this knowledge gap, we conducted a study utilizing various molecular markers and extensive population sampling. Our aim was to investigate the phylogeographic patterns of white oak species, *Tilia cordata*, *Carpinus betulus*, and *Carpinus orientalis*, both in the Balkan Peninsula and the southeastern marginal range in Europe. Our goal was to identify regions within the Balkans that facilitated the persistence of multiple genetic lineages of these forest species in refugial areas, which may help explain the high level of allelic and haplotypic richness. By sustainably using and preserving these forest genetic resources, we maintain not only the continuity of the forest ecosystems but also enhance our ability to understand evolutionary processes and phylogeographic patterns.

Keywords: genetic diversity, species diversity, glacial refugia, forest genetic resources

An insight into the current state of work on the population structure of *Carpinus betulus* L. in selected stands

Contribution ID: 192

Mittelberg, Hannah S.; Liepe, Katharina J.; Liesebach, Mirko; Liesebach, Heike

European Hornbeam (*Carpinus betulus*) is one of the indigenous deciduous tree species in Germany and temperate Europe which is considered a suitable alternative to the common tree species that are affected by rapid changing climatic conditions. It is largely distributed in Europe’s temperate forest ecosystems and shows ecologically valuable characteristics like drought and shade tolerance, a deep root system and easily decomposable litter, which has an ameliorative effect on soil conditions. These characteristics render it perfect e.g. for the conversion of pure coniferous forests into mixed stands. In conventional economically aligned management of forests Hornbeam is usually cultivated in oak-stands to promote a positive stem form. Current stands are often too small and spatially disjunct to realize notable increases through natural regeneration. Since October 2021 the project ‘Hornbeam’ works on improving the knowledge on genetic and phenotypic variation of European hornbeam and the identification of highly valuable and adaptive basic material for forest reproductive material, predominantly in the category “Selected”. A new provenance trial with approximately 30 provenances will be established. A particular focus lies on the genetics of European Hornbeam. Genetic analyses are scarce, which can be related to its octoploidy and because of its marginal economic importance. To understand the population structure and the mating system, new and powerful microsatellite markers for polyploid *Carpinus betulus* were developed. Knowledge of the genetic diversity of seed stands is crucial for quality control of reproductive material. An insight into the current state of work will be delivered.

Keywords: polyploid species, nuclear microsatellite markers, population structure

Estimating breeding values and genetic parameters in a series of Scots pine open-pollinated progeny trials in north-western Poland

Contribution ID: 193

Mohytych, Vasyl; Kowalczyk, Jan

In forest tree breeding programs, progeny testing is an essential part that includes estimation of breeding values (BLUP) and selection strategy of genotypes. Methods for calculating breeding values have been known for several decades and are constantly being improved by more advanced models that account for microsite variability and competition effects. Our aim was to estimate BLUP and selected genetic parameters in a series of progeny trials of Scots pine. In this series, 103 open-pollinated (OP) families were tested at four sites in north-western Poland. At each site, 100 seedlings per OP family were planted in a single-tree plot design. A base model (family information only) and three spatial models (pedigree information combined with different spatial approaches: block, B-spline, autoregressive) were tested for two growth traits: DBH (breast height diameter) and TH (tree height) measured after 10 years of growth. The model with the highest log-likelihood ratio was selected as the best model and used to calculate breeding values and genetic parameters for each trait at each site. The overall mean of the 10-year progeny of plus trees was 65.8 mm for DBH and 478.0 cm for TH. The advanced spatial models (B-spline and autoregressive) showed quite similar results and had a better fit than the base model or the spatial block model. For this series, the calculated difference between the total BLUPs of the parent trees based on their progeny performance was 14.5 mm for DBH and 50.0 cm for TH. Heritability was quite high for both traits and generally higher for models using B-spline or autoregressive approaches. This study confirms that microsite variability is an important factor that can influence the correct evaluation of BLUP and genetic parameters in breeding programs for Scots pine. Moreover, more advanced spatial models explain a higher proportion of total variance associated with microsite variability (6-27% for DBH and 18-34% for TH) than models assuming only a block effect (1-3% for DBH and 1-11% for TH).

Keywords: *Pinus sylvestris* L., heritability, microsite variability, forest tree breeding, BreedR

Oak seed stands and reproductive material genetics in Central Europe

Contribution ID: 194

Heinze, Berthold

This presentation will summarize results of various investigations into the genetics of oak (*Quercus robur* and *Q. petraea*) seed stands, seed harvests, nursery plant production, and selection of seed orchard clones. Microsatellites were used to characterize these populations genetically, and in their relation to forest reproductive material traceability, seed stand selection, selection of clones for future seed orchards, and suitability of relict populations for expanding the species' range in future, warmer climates. Stored acorn lots and nursery plant samples from the same harvested lot were compared for a German certification scheme. Genetic comparisons provided no direct evidence for any mishandling or errors along the chain of handling. Two *Q. petraea* stands near Vienna were compared genetically and in silviculture terms; only one of them was previously selected as a seed stand. The investigation suggested that the different trunk forms and general appearance of the stands were mainly due to different silvicultural treatment in the past, but not likely due to genetics. In various areas of the Carinthia province in Southern Austria, *Q. robur* "plus" trees were phenotypically selected and compared genetically to surrounding trees. While there was a slight genetic differentiation among valleys, no such differences of selected trees vs. neighbours could be detected. An ongoing study investigates the genetic make-up of small, relict oak stands in an Alpine valley system. Reproductive material from these stands can serve for restoring oak forests where they largely disappeared already in the distant past. Data on the genetic diversity of the relict stands will be compared to the accumulated database and will thus inform on the suitability of the potential seed stands.

Keywords: white oaks, genetics, seed stands, seed orchards, relict stands

Climate sensitivity of tree growth differs between northern red oaks (*Quercus rubra L.*) – a study in a 33-years-old provenance trial in Germany

Contribution ID: 195

Kormann, Jonathan M.; van der Maaten, Ernst; Liesebach, Mirko; Liepe, Katharina J.; van der Maaten-Theunissen, Marieke

Information about the resistance and adaptation potential of tree species and provenances is needed to select suitable planting material in times of rapidly changing climate conditions. Thereby, retrospective dendroecological analyses in provenance trials offer great potential, as they provide insight in growth reactions of tree populations to climatic fluctuations as well as extreme events. In this study, we evaluate such responses of provenances of northern red oak (*Quercus rubra* L.) from the natural distribution as well as from introduced stands in Germany planted in a provenance trial. We collected increment cores from 12 provenances at three trial sites with distinct environmental conditions that are located in northern, central and eastern Germany. In comparing provenance performance, we (1) established climate-growth relationships to identify main growth limiting factors, and (2) calculated pointer years and resistance indices to quantify growth responses in extreme years. We observe large differences in the climate sensitivity of red oaks between sites depending on the prevailing climate conditions, as well as differences between provenances within sites. At the northern site, for example, provenances originating from seed stands in Germany were found to be more drought sensitive than the provenances from the natural distribution. Overall, drought and low temperatures (i.e. frost events) were suggested to constrain growth of northern red oak.

Recommendations for the use of seed of the alternative tree species Norway maple (*Acer platanoides* L.) based on genetic studies

Contribution ID: 196

Bäucker, Cornelia; Liesebach, Mirko; Liesebach, Heike

In German forests, the consequences of climate change and globalization become evident and various native tree species of high forestry importance, such as spruce, beech or ash, show serious damage due to drought and/or the spread of pathogens. Regarding these problems, it is of increasing importance to expand the existing tree species spectrum and to promote so-called alternative tree species. For Germany, nine alternative tree species being relevant and promising for the future have been proposed – one of these is Norway maple (*Acer platanoides* L.). The potential of Norway maple is attributed to its certain drought tolerance and its wide site amplitude, suggesting high adaptability. Since 2020, therefore, the research project SpitzAhorn; at the Thünen Institute of Forest Genetics has been funded, with the aim of conducting marker-based population genetic analyses and establishing first provenance/progeny trails with Norway maple in Germany (project management organization FNR, grant number: 22040618). In the project, seed was collected over three years from a total of 29 Norway maple populations in Germany and abroad. The populations and seed orchards, most of which were harvested on a single-tree basis, fell into different categories of forest reproductive material: 'qualified', 'selected', 'source-identified'. Using species-specific nuclear SSR (Simple Sequence Repeats) markers, the individual maternal trees were genetically characterized in all populations. In case of eleven populations, at least 100 seedlings per population were genotyped and parentage analyses were performed with COLONY. Focus of these analyses were gene flow within populations, pollen input from outside and the proportion of selfing. Since ornamental cultivars of Norway maple were also genetically characterized in this project, it was possible to investigate whether Norway maple cultivars cross into natural populations. The results from the parentage analyses are discussed and seed from specific stands is recommended for diversification of the species spectrum in German forests.

Keywords: alternative tree species, forest reproductive material, parentage analysis, Norway maple, gene flow

Programme of breeding and protection of genetic diversity of Scots pine in Poland

Contribution ID: 197

<u>Kowalczyk, Jan</u>; Mohytych, Vasyl

Scots pine is the most important forest-forming species in Poland. It occupies more than 60% of the forest area. Pine growing throughout the country with the exception of a small part of the Bieszczady Mountains in the south-east. In Poland, research on identifying the genetic variation of the population has been conducted since the 1950s. Initially, a low-intensity selection was carried out with emphasis on population selection and identification of seed regions. In parallel, plus trees were selected and first-generation seed orchards were established based on phenotypic selection. Since 2010, a systematic programme of progeny testing of plus trees has been initiated. The programme is being implemented throughout the country in dedicated testing regions. Single-tree plots are established in a habitat gradient. The aim of work is to determine the breeding value and genetic selection of genotypes whose progeny have significantly better growth, quality traits and higher plasticity and lower susceptibility to adverse biotic and abiotic factors. Testing is an intrinsic part of the selection strategy being implemented as part of a programme stretching to 2035. Sixty-eight testing plots have been established. Data from measurements and observations in each plot were analysed according to a mixed model. Analyses were performed according to five possible models in order to select the model with the best statistical fit. The 'remlf90()' procedure in the '*breedR*' package, (Muñoz, 2017) was used. Corrected phenotypic values from individual parallel plots (within a set) were analysed jointly within a region. The value of the estimated BLUP random effect in the mixed model for each pedigree indicates its breeding value. This allows the use of backward selection and the selection of genotypes for the establishment of 1.5 generations of seed orchards. Conscious use in forest management of forest reproductive material selected as a result of breeding will result in increased productivity of newly established forest and increased stand stability, which is very important under conditions of observed climate change. The testing will also result in the development of principles for the rational use of the seed base by defining the area of possible transfer of forest reproductive material based on genetic bases

Keywords: Scots pine, breeding strategy, progeny testing, genetic diversity, genetic gain

Growth performances and transfer analyses of European beech (*Fagus sylvatica*) in two common garden experiments from Romania

Contribution ID: 198

Beşliu, Emanuel; Curtu, Alexandru Lucian; Apostol, Ecaterina Nicoleta; Budeanu, Marius

The provenance test is a valuable breeding technique that is widely used to assess growth performance and to estimate the adaptation capacity of forest tree species in different environmental conditions. One of the most important forest tree species for the European forestland is the common beech (*Fagus sylvatica*), which covers various environments. The main goal of this study was to test the growth performance and the transfer response of the 17 international beech provenances to the environmental conditions of two testing sites in Romania (Sacele and Carbunaru), after 27 years from planting. The growth performance was evaluated using trees height (Th), breast height diameter (Dbh), and survival (S). In the case of the transfer analyses, the ecodistance approach was applied. According to the results revealed by the Ellenberg climate quotient index, the two common garden experiments are placed in the ecological optimum of beech. However, the average of S was 13% higher in the Carbunaru trial and Dbh was higher in the Sacele trial by 15%, while no substantial differences were observed for Th. The best-performing provenances, selected for Dbh and S, were the German provenances 44 (Oderhaus), and 66 (Dillenburg) in the Sacele common garden, 44 (Oderhaus), and 92 (Elmstein-Germany) in the Carbunaru common garden, respectively. The general transfer response of common beech provenances revealed a similar performance across sites and suggested that provenances exhibited adaptation and acclimation to the testing site conditions in the Carpathian Mountains.

Keywords: European beech, common garden experiments, transfer analyses, growth performances, ecodistance

Insights into evolutionary history of landrace rice varieties in Thailand

Contribution ID: 199

Arunyawat, Uraiwan; Kuleung, Chatuporn

Understanding of genetic structure and genetic variation among landrace rice, recommended variety and its wild relatives is the fundamental data for crop planning and genetic resource management. In this study, molecular DNA marker is used to estimate the patterns of genetic diversity between landrace and cultivated rice in Thailand. The InDel markers showed a very low level of genetic variation in the cultivated rice variety. The genetic diversity parameter in 48 rice varieties ranges from 0.165-0.576 (on average 0.357). However, the low genetic diversity in recommended rice variety is perhaps due to the small sample size of recommended variety compared to the landrace rice. Moreover, the evolutionary genetic background based on genotyping by sequencing (GBS) data of landrace and recommended rice varieties in Thailand will be discussed.

Keywords: landrace rice varieties, genetic resource, genotyping by sequencing, evolutionary history, Thailand

A regional effort to develop ash trees with high tolerance towards ash dieback based on phenotypic selection

Contribution ID: 200

Kjær, Erik Dahl; Marciulyniene, Diana; Hansen, Jon; Nielsen, Lene; Tollefsrud, Mari Mette; Cleary, Michelle; Mateusz, Liziniewicz

Ash dieback (ADB) has become a major problem across European ash forests. The disease is caused by the invasive pathogenic fungus *Hymenoscyphus fraxineus* that results in sever crown damage, and especially in young ash trees often rapid mortality. Fortunately, several studies have found that a fraction of F. excelsior trees remain healthy with only few symptoms. Heritability and additive genetic variance in tolerance have been estimated from progeny trials to be moderate to high, with limited genotype x environment (GxE) interaction. High levels of infection pressure are often present in forest areas with newly planted trees revealing their level of tolerance within few years. These features make ADB tolerance suitable for phenotypic selection and led to the hypothesis that strong forward phenotypic selection can create a new generation of ash trees with substantial reduced susceptibility to the disease. As a coordinated effort, this approach is tested by establishing selection trials in Norway, Sweden, Denmark and Lithuania. The joint efforts include sharing of genetic material to estimate GxE, but the program is based on development of tolerant ash trees from local genetic resources. Here we present the concept, challenges, activities and some preliminary results from the field trials.

Keywords: ash dieback, resistance breeding, phenotypic selection, *Fraxinus excelsior*, *Hymenoscyphus fraxineus*

Analysing the transcriptional, anatomical, and physiological responses of trees to altered cambial dynamics in order to define the control and coordination of secondary growth and vascular continuity in the vertical growth axis

Contribution ID: 201

Woodward, George Malcolm; Fatz, Wiktoria; Räsänen, Matti; Ehonen, Sanna; Hölttä, Teemu; Mähönen, Ari Pekka; Kucukoglu Topcu, Melis

Plant vascular tissues are composed of continuous cell files that are aligned and connected with one another in the axial system. In secondary growth, the cambium generates conductive vascular tissues, depositing secondary xylem (wood) inwardly and secondary phloem (bast) outwardly, which drives radial thickening. Cambium activity is carbon-intensive, making it a significant carbon sink. The combined action of endogenous and environmental factors functions to regulate cambium dynamics and therefore sink strength, resulting in the phenological nature of cambium activity, and hence wood production, in trees. Research in *Populus* spp. has demonstrated that the carbon allocation capacity of tree cambia is somewhat reprogrammable, impacting wood development and total fixed carbon. As evidenced by WOX4 RNAi and tissue-specific cytokinin overproduction phenotypes, manipulating cambium dynamics significantly affects cambium size and vascular development. However, it remains to be understood how altering cambium sink capacity feeds back into whole-plant responses to sustain a functional three-dimensional vascular morphology. By causing whole-plant and localised cambial manipulations in hybrid aspen *(Populus tremula* x *tremuloides*), we intend to observe the transcriptional, morphological, and physiological responses which are elicited over time by a range of different cambium activities. These analyses will be used to elucidate how the strength of the cambium as a sink tissue controls and coordinates secondary growth and vascular continuity along the vertical growth axis of a model forest tree species. Furthermore, this data will help to establish a holistic model that will describe the relationship between source-sink interactions and multiple whole-plant responses across the physiological, anatomical, and transcriptomic scales, and how together they culminate in the regulation of tree growth.

Keywords: cambium, secondary growth, vascular continuity, *Populus*, sink strength

The response to drought of Norway spruce (*Picea abies*) provenances in Romania

Contribution ID: 202

<u>Alexandru, Alin Madalin</u>; Mihai, Georgeta; Stoica, Emanuel; Curtu, Alexandru Lucian

As the 1.5˚C limit of global warming might be reached in the next decades, severe and extreme weather events will become more frequent. Even though forests can have a large potential for climate mitigation, they are threatened by droughts and other extreme weather events. Although Norway spruce is sensitive to rising temperatures and water shortfall, it remains an economically important coniferous species in Europe, covering a distribution area of around 30 million ha. Selecting acclimated species and/or provenances is a good measure to mitigate drought's impact on forests. The objectives of our study were to (i) determine the genetic variation of wood traits among the Norway spruce provenances and (ii) evaluate the response to the drought of the Norway spruce provenances. We focused on three Norway spruce provenance trials installed in Romania in 1972, Zarnesti, Turda and Dorna Candrenilor, consisting of 10 Romanian provenances and 71 from other European countries. In the fall of 2020, four trees per plot were randomly selected. One core per tree was extracted on the slope line at breast height. The cores were then progressively sanded, scanned, and measured. After the years with meteorological droughts were identified using the Standardized Precipitation Evaporation Index (SPEI) for the 1972-2020 period, the following drought resilience indices were computed: Resistance, Recovery, Resilience and Relative resilience. Significant differences were found between provenances in all trials for ring width, latewood percentage, earlywood and latewood. Regarding the drought event from 2000, significant differences were found between provenances in all trials for at least one drought index. Evaluating the extreme event from 2003, significant differences regarding drought indices were found only in the Zarnesti field trial. Our results provide important input for the genetic breeding program of Norway spruce and the conservation of forest genetic resources to improve adaptability to climate change.

Keywords: Norway spruce, drought response, tree resilience, climate change, extreme events

Genome- and epigenome-wide association studies of wood quality and disease resistance-related traits in Norway spruce

Contribution ID: 203

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

In this work we studied the genetic and epigenetic basis underlying wood quality traits and resistance to the phytopathogenic fungus *Heterobasidium parviporum* in Norway spruce (*Picea abies* L. Karst.), one of the most important tree species in Europe. Exome-capture sequencing in combination with bisulfite treatment was used to genotype and epigenotype 620 individuals, including 218 half-siblings from 17 families currently used in breeding programs and 402 unrelated seedlings representing trees from natural stands in Finland. We identified 79,293 high-quality single nucleotide polymorphisms (SNPs) and 21,161 single methylation variants (SMVs), and these genetic and epigenetic markers were later used in genome- and epigenome-wide association studies (GEAS and EWAS) that included such important phenotypic traits as growth and length/width ratio of necrosis in phloem and xylem as a proxy of the response to the infection with *H. parviporum*. To this end, we used a mixed linear model (MLM) accounting for the confounding effects of genetic structure and kinship. We found 472, 2,225 and 2,146 genomic markers associated with growth, phloem necrosis, and xylem necrosis, respectively, while 70, 172 and 158 epigenomic markers were associated with the same traits, respectively. The obtained data help us understand the adaptive potential of Norway spruce and can be also used to assist breeding programs and for the genomic selection of trees with desirable phenotypes. Furthermore, the identification of epimarkers emphasizes the importance of epigenetic regulation in shaping the phenotype in Norway spruce. By considering both genomic and epigenomic factors, we gain a holistic understanding of the mechanisms driving important adaptive traits and develop more effective strategies for tree improvement.

Keywords: *Picea abies*, phenotyping, genotyping, epigenotyping, GWAS/EWAS

Genetic characterisation of selected *Fraxinus excelsior* L. trees with low susceptibility to ash dieback

Contribution ID: 204

Seidel, Hannes; Kunert, Gregor; Haapanen, Matti; Past, Franziska; Bubner, Ben; Budde, Katharina Birgit; Rentschler, Felix; Körtels, Elena; Dreist, Martin; Steinigen, Tino; Siemokat, Patrick; Fussi, Barbara

The use of common ash (*Fraxinus excelsior* L.) for climate resilient forest management is largely limited by the occurrence of the invasive, pathogenic fungus *Hymenoscyphus fraxineus*, which causes ash dieback. However, less damaged individuals are occasionally observed in otherwise severely infested stands. These individual trees seem promising in selection programmes to establish the basis for reproductive material with low susceptibility to ash dieback, e.g. seed orchards. In Central Europe, genetic diversity of common ash is high at the nuclear level and populations differentiate at the plastid level on a large scale. In general, the genetic characterisation of selected individuals is important for the management and the appropriate use of forest genetic resources. Moreover, the preservation of genetic diversity is crucial to maintain the adaptability to future challenges. In the joint project FraxGen, as part of the demonstration project FraxForFuture, around 650 apparently less susceptible ash trees were selected between 2020 and 2022 in severely affected stands based on a standardized damage score. All selected ash trees were genotyped with nuclear and plastid SSR-Markers. Additionally, around 50 adult trees each from 14 intensive monitoring sites were genotyped using the same markers. In total, the individuals originate from the German states of Brandenburg, Bavaria, Baden-Württemberg, Hesse, Lower Saxony, Mecklenburg-Western Pomerania, Saxony, Saxony-Anhalt, Schleswig-Holstein and Thuringia, which cover a wide range of climate and site conditions. Genetic variation patterns of the selected trees will be presented and placed in a national and European context based on the nuclear and plastid markers, respectively.

Keywords: population genetics, ex-situ conservation, resistance breeding, invasive pathogen, fungal disease

First study of native oaks in Denmark based on full genome sequencing

Contribution ID: 205

Muessig, Maxi Kristin Marie; Kjær, Erik Dahl; Olofsson, Jill Katharina

Widespread interpopulation hybridization can lead to outbreeding depression and homogenization of the wider gene pool. To benefit from local adaptation and to avoid interpopulation hybridization, recommendations and policies in European forestry are focused on the use of native and locally adapted seed sources in afforestation and reforestation. Defining a local or native provenance is predicated on knowledge about original seed sources. In places such as Denmark, where provenances of oak have been imported from many parts of Europe, lacking historical records can make this difficult. Advances in genomics have improved the resolution of detectable genetic differences between populations, giving us the opportunity to determine the source of provenances in the absence of written records. We compare whole genomes of 109 pedunculate oak (*Quercus robur*) samples belonging to provenances both native and nonnative to Denmark for the purposes of evaluating the suitability of these provenances for future use as native Danish seed sources. We analyze population structure and differentiation, admixture, and measures of genetic variation, and address the role of *Q. robur* in current and past Danish forestry, including the widespread introduction of foreign genetic material. We could not with certainty determine whether the studied provenances are native, but find that there are varying levels of admixture between provenances in the Danish *Q. robur* population. The Danish *Q. robur* population overall appears to be cohesive, although it acts as a continuous population rather than a group that is fully differentiated from foreign provenances planted nearby. We do not detect introgression from *Quercus petraea*. We conclude that the studied provenances represent diverse seed sources with little signs of inbreeding or previous bottleneck events and that they are therefore suitable for future use in Danish forestry.

Keywords: *Quercus robur*, single nucleotide polymorphism, full genome sequencing, provenance

Early pathogenesis – specific *Heterobasidion annosum* transcriptome in the *Pinus sylvestris - Heterobasidion annosum* pathosystem

Contribution ID: 206

Ramanenka, Maryna; Šķipars, Vilnis

Due to the economic and ecologic importance of Scots pine, studies of the most significant pathogen of this host – *Heterobasidion annosum*, are of big importance. We are investigating the first stages of plant – pathogen interaction in this pathosystem by studying *Heterobasidion annosum* transcriptome dynamics in early stages of infection. We have obtained transcriptome data from inoculated Scots pine seedlings from 1, 2, 3 and 4 weeks post inoculation. We used MGI sequencing to obtain sufficient number of reads to be able to make any statistics-based conclusions about *Heterobasidion annosum* transcriptomes in these samples (high number of reads is crucial as the fungal transcripts represent only a small proportion of the total transciptome). Our analysis is on-going but we have obtained evidence for importance of the following *Heteribasidion annosum* genes during the early stages of infection: glyceraldehyde 3-phosphate dehydrogenase, heat shock protein 70, polyubiquitin, P-loop containing nucleoside triphosphate hydrolase, ubiquitin-related domain-containing protein and several more.

Keywords: *Heterobasidion annosum*, transcriptome, early pathogenesis

Stochastic simulation of landscape breeding programs

Contribution ID: 207

<u>Yobu, Christi Sagariya</u>; Lstibůrek, Milan

A tree improvement program focuses on the genetic gains of forestry tree species' most economically profitable traits. The recurrent selection scheme of a conventional tree improvement program plays a vital role in developing genetically superior individuals without the detrimental effects of inbreeding. Designing an efficient breeding program to maximize genetic gain while maintaining sufficient levels of diversity is carried out in multiple cycles of mating, genetic testing, and selection. With the advancement of high-throughput phenotypic and genotypic platforms, additional information is available to boost breeding efficiency. Dynamic landscape gene resource management combining both utilization and conservation (Landscape Breeding) has been developed by Lstibůrek et al. (2017) based on the *Breeding without Breeding*, BwB concept by El-Kassaby and Lstibůrek (2009). Here we present our stochastic simulation model of the Landscape Breeding protocol developed on the earlier BwB model by Lstibůrek et al. 2015 and the Modular Breeding Program Simulator (MoBPS; Pook et al. 2020). The model provides a flexible framework to simulate Landscape Breeding considering numerous forest stands originating from a common breeding arboretum in advanced-generation tree improvement protocol. The modular structure of the program allows combining relatively coarse simulations, as needed to generate founder populations (generations of random mating, i.e., LD decay preceding the selection of plus trees) with detailed modeling of today's complex breeding programs, making use of all available biotechnologies (SNP chip, GBLUP evaluation, etc.).

Keywords: breeding program, stochastic simulation, genetic gain, landscape breeding, genetic gain

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Martínez-Godoy, Maria Ángeles	Institute for Plant Molecular and Cell Biology (IBMCP), Consejo Superior de Investigaciones Científicas (CSIC) - Universidad Politécnica de Valencia (UPV), Spain	154	63
Martín-García, Juan Antonio	ETSI Montes, Forestal y del Medio Natural, Universidad Politecnica de Madrid, Spain	137, 187	42, 105
Mateusz, Liziniewicz	Skogforsk, Sweden	200	118
Mathurin, Jean-Charles	Maison Rémy Martin, Centre Elaboration Produit, Merpins, France	119	23
Mavi İdman, Özlem	National Botanical Garden of Türkiye, Department of Collection, Ankara, Turkey	153	60
Mayr, Stefan	Department of Botany, University of Innsbruck, Austria	154	63
Mellert, Karl-Heinz	Bavarian Office for Forest Genetics, Germany	120	24
Méndez-González, Jorge	UAAAN, Mexico	180	92
Metheringham, Carey	RBG Kew, UK	182	98
Michiels, Hans-Gerhard	Forest Research Institute of Baden-Württemberg (FVA), Germany	183	99
Mihai, Georgeta	National Institute for Research and Development in Forestry “Marin Drăcea”, Romania	202	120
Mihuț, Liana Nicoleta	Unitatea de Suport pentru Integrare, Romania	161	71
Milesi, Pascal	University of Uppsala, Sweden	177	89
Milin, Vlad	Unitatea de Suport pentru Integrare, Romania	161	71
Miller, Adam	Deakin University, Australia	109	11
Mittelberg, Hannah S.	Thünen Institut of Forest Genetics, Germany	192	110
Mohytych, Vasyl	Forest Research Institute, Poland	193, 197	111, 115
Moing, Annick	Univ. Bordeaux, INRAE, UMR BFP, Bordeaux Metabolome, MetaboHUB, France	132	36
Moro, Laura	University of Uppsala, Sweden	177	89
Muessig, Maxi Kristin Marie	University of Copenhagen UCPH, Denmark	205	123

Müller, Markus	Forest Genetics and Forest Tree Breeding, University of Göttingen, Göttingen, Germany	118, 120, 156, 171	22, 24, 65, 84
Müller, Niels	Thünen Institut of Forest Genetics, Germany	108, 165, 189	10, 75, 107
Munzinger, Jérôme	IRD Montpellier, France	142	49
Muscarella, Robert	University of Uppsala, Sweden	177	89
Mutke, Sven	Instituto de Ciencias Forestales (ICIFOR-INIA), CSIC, Spain	184	100
Neophytou, Charalambos	Forest Reseach Institute of Baden-Württemberg (FVA), Freiburg, Germany	107, 117, 179, 183	9, 21, 91, 99
Neuwirthová, Eva	Czech University of Life Sciences, Faculty of Forestry and Wood Sciences Praha, Czech Republic	112, 155	16, 64
Nichols, Richard	QMUL, UK	143, 182	50, 98
Nicolas, Loïc	Office National des Forêts, agence Berry Bourbonnais, Bourges, France	119	23
Nicorescu, Adelin	Austrian Research Centre for Forests (BFW), Vienna, Austria	151	58
Nielsen, Lene	University of Copenhagen, Denmark	130, 134, 200	35, 37, 118
Nola, Paola	University of Pavia, Department of Earth and Environmental Sciences, Italy	128	31
Nonić, Marina	University of Belgrade, Faculty of Forestry, Belgrade, Republic of Serbia	173, 174	86, 87
Nosenko, Tetyana	Helmholtz Zentrum München, Germany	133	38
Olofsson, Jill Katharina	University of Copenhagen, Denmark	134, 146, 205	37, 53, 123
Olsson, Sanna	Forest Research Centre, INIA, CSIC, Spain	184	100
Orgel, Franziska	Thünen Institut of Forest Genetics, Germany	133	38
Opgenoorth, Lars	Philipps University Marburg, Germany	115	19
Osem, Yagil	Agriculture Research Organization, Volcani Center, Israel	113	17
Ouadji, Mohamed	Laboratory of ecophysiology of forest trees. Forestry Research Center, Rabat-Agdal, Morocco	144	51
Ousmael, Kedra	University of Copenhagen, Denmark	188	106
Pallares-Zazo, Jorge	ETSI Montes, Forestal y del Medio Natural, Universidad Politecnica de Madrid, Spain	187	105
Panzarová, Klára	Photon Systems Instruments, (PSI, spol. sr. o.), Czech Republic	112	16

Papadopoulou, Aliki	Aristotles University of Thessaloniki (AUTh), Greece	178, 179	90, 91
Past, Franziska	Thünen Institute of Forest Genetics, Germany	165, 204	75, 122
Paule, Ladislav	Technical University in Zvolen, Slovakia	191	109
Paulo, Octávio S.	Univiversity of Lisbon, Faculdade de Ciências, Portugal	144	51
Păun, Ovidiu	University of Vienna, Austria	142	49
Perdiguero, Pedro	Universidad Complutense de Madrid, Spain	137	42
Pericolo, Osvaldo	Department of Earth and Environmental Sciences, University of Pavia, Italy	128	31
Perry, Annika	UK Centre for Ecology & Hydrology (UKCEH), UK	140	47
Pers-Kamczyc, Emilia	Institute of Dendrology, Polish Academy of Sciences, Poland	181	97
Phannareth, Tommy	Virginia Tech, Translational Plant Sciences, USA	110	12
Picó, Xavier	Departamento de Biologia Evolutiva, Estación Biológica de Doñana (EBD), Consejo Superior de Investigaciones Científicas (CSIC), Sevilla, Spain	144	51
Pina-Martins, Francisco	Centre for Ecology, Evolution and Environmental Changes (cE3c) & CHANGE – Global Change and Sustainability Institute, Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal	144	51
Pineda-Ojeda, Tomás	INIFAP, Mexico	180	92
Pinosio, Sara	Institute of Biosciences and BioResources (IBBR), National Research Council (CNR), Italy	128, 184	31, 1
Piotti, Andrea	Institute of Biosciences and BioResources (IBBR), National Research Council (CNR), Italy	127, 128	30, 31
Plomion, Christophe	Univ. Bordeaux, INRAE, UMR BIOGECO, France	132, 141, 158	36, 48, 67
Popescu, Flaviu	National Institute for Research and Development in Forestry "Marin Drăcea", Romania	191	109
Postolache, Dragos	National Institute for Research and Development in Forestry "Marin Drăcea", Romania	191	109

Postolache, Gheorghe	National Botanical Garden (Institute) "Alexandru Ciubotaru", Republic of Moldova	191	109
Pretzsch, Hans	Technical University of Munich, Germany	114	18
Provazník, Daniel	Czech University of Life Sciences Prague, Czech Republic	164	74
Radu, Gheorghe Raul	National Institute for Research and Development in Forestry “Marin Drăcea”, Romania	129	32
Ræbild, Anders	University of Copenhagen, Department of Geosciences and Natural Resource Management, Denmark	157	66
Ramanenka, Maryna	Latvian State Forest Research Institute Silava, Latvia	206	124
Räsänen, Matti	University of Helsinki, Finland	201	119
Rehanek, Marius	Phytomedicine Division, Humboldt University, Berlin, Germany	175	88
Rellstab, Christian	Swiss Federal Research Institute WSL, Birmensdorf, Switzerland	107, 117, 134, 183	9, 21, 37, 99
Rentschler, Felix	Forest Research Institute Baden-Württemberg, Department of Forest Nature Conservation, Germany	204	122
Ridley, Maia	Julius Kühn-Institut, Germany	136	41
Riov, Joseph	Hebrew University of Jerusalem, Israel	113	17
Ripullone, Francesco	School of Agricultural, Forestry and Environmental Sciences, University of Basilicata, Italy	128	31
Rodríguez-Calcerrada, Jesús	Universidad Politecnica de Madrid, Spain	137	42
Rok, Damjanić	Slovenia Forest Service, Slovenia	167	79
Roman, Anamaria	Institute of Biological Research, Cluj-Napoca, Romania	152, 161	59, 71
Rozen, Ada	Agriculture Research Organization, Volcani Center, Israel	113	17
Rymer, Paul	Western Sydney University, Australia	109	11
Rzigui, Touhami	Laboratory of Management and Valorisation of Forest Resources. The National Research Institute of Rural Engineering, Water and Forestry (INRGREF), Tunes, Tunisia	144	51
Sánchez-Rodríguez,	INRAE, France	106	95

Leopoldo			
Saulle, Domenico	Department of Biosciences, Biotechnology and Environment, Botanic Garden Museum, University of Bari "Aldo Moro", Bari, Italy	144	51
Scaglione, Davide	IGA Technology Services, Udine, Italy	156	65
Scalabrin, Simone	IGA Technology Services, Udine, Italy	156	65
Schlosser, Franziska	Research Institute of Forest Ecology and Forestry of Rhineland-Palatinate (FAWF), Germany	183	99
Schmidt, Daniel	Northwest German Forest Research Institute, Department of Forest Genetic Resources, Germany	118	22
Schmied, Gerhard	Technical University of Munich, TUM School of Life Sciences, Chair for Forest Growth and Yield Science, Freising, Germany	120	24
Schmitt, Sylvain	INRAE - UMR AMAP, France	141	48
Schnitzler, Jörg-Peter	Helmholtz Zentrum München, Germany	133	38
Schröder, Hilke	Thünen Institut of Forest Genetics, Germany	133	38
Schueler, Silvio	Austrian Research Centre for Forests (BFW), Austria	111	13
Schuman, Meredith Christine	University of Zurich, Swizerland	104	62
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Scotti, Ivan	URFM, INRAE, Avignon, France	105, 168	77, 80
Seegmüller, Stefan	Research Institute of Forest Ecology and Forestry of Rhineland-Palatinate (FAWF), Germany	183	99
Šeho, Muhidin	Bavarian Office for Forest Genetics (AWG), Germany	120	24
Seidel, Hannes	Bavarian Office for Forest Genetics (AWG), Germany	163, 204	73, 122
Seitner, Sebastian	Plant Sciences Facility, Vienna BioCenter Core Facilities GmbH (VBCF), Vienna, Austria	154	63
Sela, Hanan	Agriculture Research Organization, Volcani Center, Israel	113	17

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Sergiadou, Dimitra	University of Copenhagen, Denmark	146	53
Sherman, Amir	Agriculture Research Organization, Volcani Center, Israel	184	100
Shrestha, Karuna	Georg-August-Universität Göttingen, Germany	136	41
Siemokat, Patrick	Staatsbetrieb Sachsenforst, Referat Forstgenetik/Forstpflanzenzüchtung, Germany	204	122
Šijačić-Nikolić, Mirjana	University of Belgrade, Faculty of Forestry, Serbia	173, 174	86, 87
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Šķipars, Vilnis	Latvian State Forest Research Institute Silava, Latvia	160, 162, 206	70, 72, 124
Sobrino-Plata, Juan	Universidad Complutense de Madrid, Spain	137	42
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Stocks, Jonathan	RBG Kew, UK	182	98
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Suliman, Tammam	Austrian Research Centre for Forests (BFW), Austria	122	26
Šumarac, Predrag	Public Enterprise „National Park Kopaonik", Republic of Serbia	173	86
Suszka, Jan	Institute of Dendrology, Polish Academy of Sciences, Poland	181	97
Swenson, Nathan G.	University of Notre Dame, USA	102	34
Szukala, Aglaia	Austrian Research Centre for Forests (BFW), Austria	151, 190	58, 108
Tarzariol, Giulia	Department of Earth and Environmental Sciences, University of Pavia, Italy	128	31
Theraroz, Adélaïde	Univ. Bordeaux, INRAE, BIOGECO, France	169	81
Thomsen, Iben	University of Copenhagen, Denmark	130	35
Tollefsrud, Mari Mette	NIBIO, Norway	200	118
Tomášková, Ivana	Czech University of Life Sciences Prague, Faculty of Forestry and Wood Sciences, Department of Genetics and Physiology of Forest Trees, Czech Republic	164	74
Toomey, Madeline	Deakin University, Australia	109	11
Toraño Caicoya, Astor	Technical University of Munich, Germany	114	18
Tourvas, Nikolaos	Aristotles University of Thessaloniki (AUTh), Greece	117, 178, 179	21, 90, 91
Trang-Bui, Quynh	BFP UMR, INRAE, France	158	67
Tremetsberger, Karin	University of Natural Resources and Life Sciences, Vienna, Austria	124	27
Trepekli, Katerina	University of Copenhagen, Department of Geosciences and Natural Resource Management, Denmark	157	66
Troispoux, Valérie	INRAE - UMR EcoFoG, France	141	48

Trubin, Aleksei	Czech University of Life Sciences Prague, Czech Republic	135	40
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Tysklind, Niklas	INRAE, UMR EcoFoG, France	141	48
Ufimov, Roman	Austrian Research Centre for Forests (BFW), Austria	154	63
Uhl, Enno	Technical University of Munich, Germany	114, 120	18, 24
Unger, Gregor	University of Natural Resources and Life Sciences (BOKU), Austria	190	108
Ursu, Tudor-Mihai	Institute of Biological Research, Cluj-Napoca, Romania	152, 161	59, 71
Vacik, Harald	BOKU, Vienna, Austria	116	20
Vajana, Elia	Institute of Biosciences and Bioresourses , National Research Council of Italy, Italy	127, 128	30, 31
van der Maaten, Ernst	Chair of Forest Growth and Woody Biomass Production, TU Dresden, Germany	185, 195	101, 113
van der Maaten-Theunissen, Marieke	Chair of Forest Growth and Woody Biomass Production, TU Dresden, Germany	185, 195	101, 113
van Loo, Marcela	Austrian Research Centre for Forests (BFW) - Department of Forest Growth, Silviculture & Forest Genetics, Vienna, Austria	154	63
Vanhove, Mathieu	Department of Immunology and Infectious Disease, Harvard T.H.Chan School of Public Health, Boston, MA, USA	144	51
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Vilotić, Dragica	University of Belgrade, Faculty of Forestry, Republic of Serbia	173	86

Vincent, Gregoire	UMR AMAP, France	141	48
Vivian-Smith, Adam	Norwegian Institute of Bioeconomy Research, Norway	160, 162	70, 72
von Bargen, Susanne	Phytomedicine Division, Humboldt University, Berlin, Germany	175	88
Vucetic, Boban	Forest Genetics and Forest Tree Breeding, University of Göttingen, Göttingen, Germany	171	84
Vujnović, Zvonimir	Croatian Forest Research Institute, Croatia	172	85
Wang, Kai	University of Helsinki, Finland	203	121
Wang, Xiao-Ru	Department of Ecology and Environmental Sciences, Umeå University, Sweden	147	54
Weigel, Robert	University of Göttingen, Department Plant Ecology and Ecosystems Research, Germany	118	22
Weithmann, Greta	University of Göttingen, Department Plant Ecology and Ecosystems Research, Germany	118	22
Westergren, Marjana	Slovenian Forestry Institute, Ljubljana, Slovenia	167, 169	79, 81
Wildhagen, Henning	HAWK, Faculty of Resource Management, Göttingen, Germany	156, 171	65, 84
Wilhelmi, Selina	Georg-August University Göttingen / Forest Genetics and Forest Tree Breeding, Germany	156, 171	65, 84
Wood, Daniel	RBG Kew, UK	182	98
Woodward, George Malcolm	University of Helsinki, Finland	201	119
Wu, Harry	Swedish University of Agriculture Sciences, Sweden	186	102
Xu, Jing	University of Copenhagen, Department of Geosciences and Natural Resource Management, Denmark	130, 157	35, 66
Yart, Annie	Institut National de la Recherche Agronomique, Zoologie Forestiere, Ardon, France	139	44
Yobu, Christi Sagariya	Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Czech Republic	207	125

Zádrapová, Dagmar	Czech University of Life Sciences Prague, Faculty of Forestry and Wood Sciences, Department of Genetics and Physiology of Forest Trees, Czech Republic	164	74
Zhang, Qian	Virginia Tech, Department of Forest Resources and Environmental Conservation, USA	110	12
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Zhelev, Petar	University of Forestry, Sofia, Bulgaria	151, 191	58, 109
Żukowska, Weronika	Institute of Dendrology, Polish Academy of Sciences, Poland	208	93