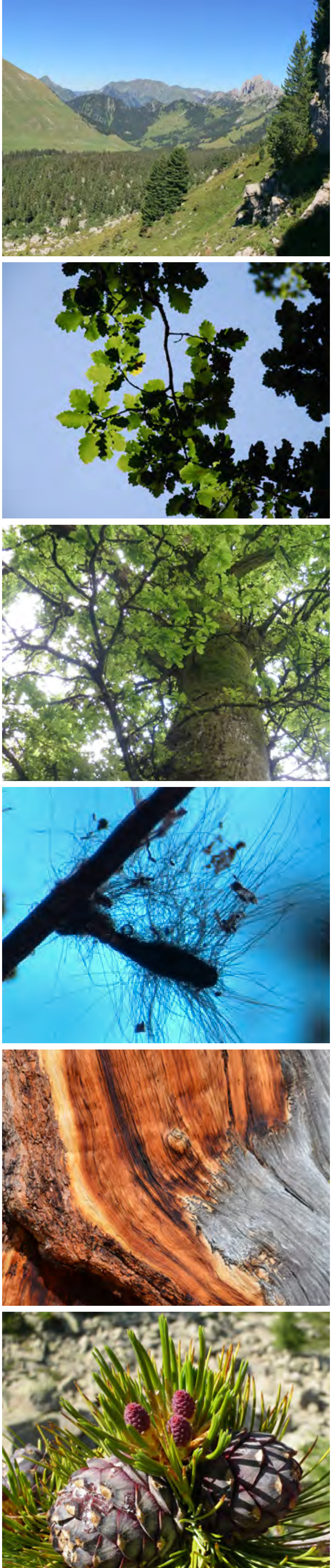

Genomics and Adaptation in Forest Ecosystems

EVOLTREE Conference 2021

14–17 September 2021
WSL, Birmensdorf, Switzerland

Book of Abstracts

Swiss Federal Institute
for Forest, Snow and Landscape Research WSL

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Content

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Short program

	Tuesday 14.09.2021	**Wednesday 15.09.2021**	**Thursday 16.09.2021**	**Friday 17.09.2021**
08:30 - 09:30		Excursion		
09:30 - 10:00			Lecture: Environmental data in landscape genomics (Benjamin Dauphin)	Lecture: Introduction to NEMO (Frédéric Guillaume)
10:00 - 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 4: Innovative methods and approaches			Session 5: Conservation strategies
13:15 - 14:00	Keynote	Poster Session A	Poster Session B	Keynote
14:00 - 14:40	Oral presentations Session 4			Oral presentations Session 5
14:40 - 14:50	Short break			Short break
14:50 - 15:50	Oral presentations Session 4			Oral presentations Session 5
15:50 - 16:20	Long break	Long break	Long break	Long break
	Session 1: Climate change genomics	Session 3: Demography and post-glacial recolonization	Session 2: Genomics of interactions	Session 6: Towards climate-smart forests
16:20 - 17:05	Keynote	Keynote	Keynote	Keynote
17:05 - 17:45	Oral presentations Session 1	Oral presentations Session 3	Oral presentations Session 2	Oral presentations Session 6
17:45 - 17:55	Short break	Short break	Short break	Short break
17:55 - 18:55	Oral presentations Session 1	Oral presentations Session 3	Oral presentations Session 2	Oral presentations Session 6
Evening	1:1 meetings	1:1 meetings	Conference Dinner	1:1 meetings

Categories
🟩 Scientific exchange
🟦 Networking
🟧 Teaching
🟨 Social event

Session 4:
Innovative methods and approaches

Tuesday 14 September 13:00–15:50

Chair: Dr. Katrin Heer, Philipps University Marburg, Germany

Oral presentations

13:15	**Keynote:** **Lotterhos, Katie:** Adaptation and climate change: what are we missing?
14:00	**Karunarathne, Piyal:** An improved and more sensitive detection of copy number variants (CNVs) from SNPs: An R package for detecting paralogs
14:20	**Cervantes, Sandra:** Haploid selection in predominantly diploid *Pinus sylvestris*
14:40	***Short Break***
14:50	**Wade, Abdou Rahmane:** eQTLs are key players in the integration of genomic and transcriptomic data for phenotype prediction.
15:10	**Robledo-Arnuncio, Juan Jose:** Genomic scans of selection from prospective cohort mortality studies in trees
15:30	**Zacharias, Melanie:** Genetic signatures of drought stress tolerance in contrasting treeline ecotones of a widespread conifer in Alaska

Keynote Session 4

Adaptation and climate change: what are we missing?

Contribution ID: 171

Lotterhos, Katie

Two critical questions in natural resource management are how to identify the genetic basis of adaptation and how to leverage this information for management decisions under climate change. Associations between genetic and environmental influences on phenotypes can affect responses to environmental change. Yet to date, nearly all research has focused on genetic-by-environment interactions (GxE) and linear associations between genotypes and environments. This keynote talk will highlight two understudied phenomena that have consequences for our understanding of how organisms will respond to environmental change. First, we will highlight that GxE is not the only way that “G” and “E” can be associated – covariance can exist between the genetic and environmental influences on phenotype (CovGE). CovGE is commonly called countergradient variation (negative CovGE) or cogradient variation (positive CovGE), but the field has previously lacked statistical methods necessary to quantify CovGE. We will introduce a standardized metric that estimates the magnitude, direction, certainty, and significance of CovGE for phenotypic data generated by common experimental designs. Second, we will highlight how genetic architecture and demography can result in the evolution of phenotypic clines without clines in causal allele frequencies. This finding suggests that commonly used methods to study genetic-environment associations may be limited in their ability to discover the genetic architecture of adaptation, and motivates the need for new algorithms.

Keywords: adaptation, climate change, countergradient variation, cogradient variation, statistical advances

An improved and more sensitive detection of copy number variants (CNVs) from SNPs: An R package for detecting paralogs

Contribution ID: 115

Karunarathne, Piyal; Milesi, Pascal

The evolutionary impact of copy number variants (CNVs: regions of the genome that vary in copy number) in organisms has been overlooked since its first discovery. Recent work shows that base pairs impacted by CNVs can be multi-fold compared to their mutual counterpart SNPs (single nucleotide polymorphisms). As a major source of genetic variation, CNVs contribute to phenotype variation, adaptation, and fuel organisms' evolution. However, the detection of CNVs in genomes, especially in non-model organisms, is challenging to researchers as it requires costly and extensive genomic resources and complex computational infrastructure. On the other hand, the unaccounted-for paralogous copies in the data can affect SNP calling and introduce biases to population genetic estimates. Based on McKinney's (2017) seminal work, we have further developed a comprehensive and reliable framework for detecting CNVs from SNP data. Our framework is particularly well adapted for target capture and genotyping-by sequencing (GBS) sequencing, two of the most commonly used sequencing approaches today. As such, it allows calling CNVs from genomes of any size and complexity. The framework is reinforced with an R package (rCNV) that not only can automatize the analysis with ease, but is also able to handle substantially large genomes. The methods implemented in the framework use read-depth variation from high-throughput sequence data, detect the excess of expected heterozygosity, allelic ratio variation within heterozygotes, and is sensitive to sample size and inconsistent depth of coverage values. Using this framework and rCNV, we detected CNVs in five species (i.e., American lobster – *Homarus americanus*, Chinook salmon – *Oncorhynchus tshawytscha*, Parrotfish – *Scarus niger*, Mountain barberry – *Berberis alpine*, and Norway Spruce – *Picea abies*) and compared them with previously published CNVs in each species. Our implementation of the method not only detected the CNVs with greater accuracy, but was also successful in identifying low-confidence samples/regions and eliminating them, reducing false positives (2-10% of SNPs).

Keywords: CNVs, SNPs, R-Genomics, GBS, GWAS

Haploid selection in predominantly diploid *Pinus sylvestris*

Contribution ID: 138

Cervantes, Sandra; Kesälahti, Robert; Helanterä, Heikki; Pyhäjärvi, Tanja

There is a wide variation on ploidy level among organisms. However, the evolutionary mechanisms underlying these differences are still not well understood. One of the most studied ploidy systems is the alternation of haploid and diploid life phases. Theory predicts that haploid and diploid stages will be affected differently by selection. Genes expressed in haploid stage will respond faster to selection, as deleterious mutations will be immediately expressed and beneficial mutations will reach fixation faster. In contrast, selection will be less efficient in genes expressed in diploid stage, where the fitness effects of recessive deleterious or beneficial mutations can be hidden from selection in heterozygous form. Theory expectations have been confirmed in yeast and *Capsella grandiflora*, however, results from studies in *Arabidopsis thaliana* and the moss *Funaria hygrometrica* do not support theoretical expectations.

A simple way to test theory expectations is to look at the genetic diversity of genes expressed at different ploidy levels, as we expect for genes expressed in haploid tissues or stages to have a reduced diversity compared to genes expressed in diploid tissues or stages. Here we used RNA seq data and the tau index to identify tissue-specific genes in haploid (megagametophyte) and diploid tissues (embryo, bud, needle, and phloem) from *Pinus sylvestris*. Next, we generated genomic data of some of the tissue-specific genes by using targeted resequencing. We then, using information at population level, analyzed the genetic diversity (theta Watterson and theta pi) and the distribution of fitness effect (DFE) of tissue-specific genes expressed in haploid and diploid stages to study the effect of selection on them. So far, our preliminary results do not seem to support theory expectations; this may be due to confounding factors as breadth and level of expression. Overall, we expect our results to contribute to the understanding of evolutionary dynamics affecting different ploidy levels.

Keywords: haploid selection, conifers, *Pinus sylvestris*, DFE, genetic diversity

eQTLs are key players in the integration of genomic and transcriptomic data for phenotype prediction

Contribution ID: 108

Wade, Abdou Rahmane; Duruflé, Harold; Rogier, Odile; Segura, Vincent; Sanchez, Leopoldo

Uncertainties posed by climate change, in terms of the adaptability of species, stress the need of developing sounding predictions of individual performances. Multi-omics offer new data for backing genomic predictions and provide an interesting way to link phenotypes and genome variation. Few studies yet address the integration of different -omics to gain understanding into genetic architecture and phenotype predictability. In our study, we used 241 *Populus nigra* genotypes phenotyped in two common garden experiments located on contrasting sites, and with their xylem and cambium RNA sequenced at one site, yielding large phenotypic, genomic and transcriptomic datasets. For each trait, prediction models were built with genotypic or transcriptomic data as predictors and compared to those integrating both -omics by concatenation. The advantage of combining the two -omics varied across traits. In order to better understand such differences, we made an eQTL analysis to classify the predicting features into CIS or TRANS relationships and further assessed their relative importance in the different models according to this typology. Across traits, a high and significant correlation was found between the change in predictability and the change in predictor importance for eQTL TRANS effects and CIS regulated transcripts. Such relationship was mainly observed for the traits evaluated in the site of transcriptomic sampling. In conclusion, beneficial integration appears to operate through a change in the weighting of important genes and SNPs, notably those showing already mutual associations through eQTLs, and consequently by minimizing the redundancy between predictors. To our knowledge, our work is the first to show such behavior, and delineates a promising way to explore data integration for multi-omics through differential weighting of features.

Keywords: poplar, genomic prediction, muti-omic integration, genomic, transcriptomic, eQTL analysis

Genomic scans of selection from prospective cohort mortality studies in trees

Contribution ID: 111

<u>Robledo-Arnuncio, Juan Jose</u>; Unger, Gregor Maximilian

Scans of selection from genomic time series data may allow detecting loci associated with adaptation to temporal environmental changes. Longitudinal multi-generation time series data are hard to obtain in forest trees, and rapid alternatives such as cross-sectional sampling suffer limitations for accurate selection inference. On the other hand, longitudinal cohort studies, by sampling a cohort of same-age individuals as they age and die, offer more potential for analysis of contemporary viability selection in trees. Previous models used to infer selection coefficients from longitudinal cohort studies require tracking and sampling exhaustively every individual in the cohort, rarely feasible in natural tree populations. We present a temporal neutrality test and a Bayesian method to infer stage-specific viability selection coefficients using sequential random genotypic samples drawn from a longitudinal cohort mortality study. The approach is suitable for investigating selective mortality in large cohorts in which individual tagging and tracking are unfeasible. Simulation results indicate that the method can discriminate loci under strong viability selection and, provided samples are large, yield accurate estimates of the corresponding selection coefficients. Genotypic frequency changes are largely driven by sampling noise under weak selection, however, compromising inference in that case. As an example, we analyze viability selection operating at early recruitment stages in a natural *Pinus pinaster* Ait. population. We measured temporal genotypic frequency changes at candidate-gene SNP loci among seedlings sampled from the time of emergence in autumn until the summer of the following year, a period with high elimination rates. We detected a few loci undergoing allele frequency changes larger than expected from stochastic mortality and sampling, with putative functions that could influence survival at early seedling stages. Our results illustrate how new statistical and sampling schemes can be used to conduct genomic scans of contemporary selection on specific tree life stages.

Keywords: contemporary adaptation, selection coefficient, longitudinal study, neutrality test, selective mortality

Genetic signatures of drought stress tolerance in contrasting treeline ecotones of a widespread conifer in Alaska

Contribution ID: 114

Zacharias, Melanie; Pampuch, Timo; Wilmking, Martin; Opgenoorth, Lars; Bog, Manuela; Schnittler, Martin; Heer, Katrin

In the course of climate change, many boreal forest ecosystems will experience an increase in drought intensity as well as frequency. Since trees are sessile and long-lived, the question remains how forests will cope with such extremes. As former studies on tree growth responses to drought stress show a high inter-individual variation, it is important to understand the underlying genetic structure of drought tolerance. Therefore, we investigated natural populations of the widely distributed boreal conifer white spruce (*Picea glauca*) in Alaska. The three investigated populations represent one drought-limited and two cold-limited treelines with a paired plot design of one forest and one treeline plot each, resulting in six plots. We obtained individual increment cores of 500 trees to determine their reaction to drought stress events. Based on these tree-ring series and climatic data, we identified growth declines caused by drought stress in each population independently. For the association of the dendrophenotypes with genetics, we genotyped 3,000 SNPs using the single primer extension technology (SPET). Genotype–phenotype associations were done using mixed models and the Random Forest algorithm to account for polygenic adaptation. Furthermore, we used outlier detection to identify loci potentially under selection in the drought- and cold-driven treeline ecotones. As last step we annotated significantly associated SNPs to confirm their biological relevance. We discuss if the individual growth response to drought stress differs in contrasting treeline ecotones and if these differences can be associated with genetic signatures potentially shaped by selection processes in the contrasting environments. With that we deepen our understanding of the underlying genetic signatures of drought stress tolerance.

Keywords: genotype-phenotype associations, *Picea glauca*, dendrophenotype, drought adaptation, treeline

Session 4:
Innovative methods and approaches

Poster Session A: Wednesday 15 September 13:00–15:50

Posters

Maghuly, Fatemeh:
Proteomic profiles of middle and late stage of *Jatropha curcas* seed reveal key pathways operating maturation process

Ulaszewski, Bartosz:
Complete chloroplast genomes of *Fagus sylvatica* L. reveal sequence conservation in the inverted repeat and the presence of allelic variation in NUPTs.

Kesälahti, Robert Sebastian:
Optimising exome capture of *Pinus sylvestris* using species-specific repetitive DNA blocker

Booker, Tom R.:
Methods for identifying the genetic basis of local adaptation and assessing convergent evolution

Proteomic profiles of middle and late stage of *Jatropha curcas* seed reveal key pathways operating maturation process

Contribution ID: 122

Maghuly, Fatemeh

The seeds play a fundamental role in the plants' life cycle, plant survival, and human use. Thus, targeting proteins to discover novel enzymes underlying seed maturation is the most promising breeding strategy. In the current study, we mapped the protein patterns of *Jatropha curcas* seeds from six different maturation stages on an open-pollinated plant under field conditions. Using emerging proteomic-profiling techniques (Micro LC-QTOF-MS) allowed us to explore 51,974 spectra, identifying 23,988 peptides and 6,188 proteins (1% false-discovery rate, FDR), out of which 254 proteins were shared among six different stages. In fact, 4,595 non-redundant proteins with a minimum of two peptides (1% FDR) were confirmed from six maturation stages, higher than those detected by two-dimensional gel electrophoresis. From non-redundant proteins, 3,850 were annotated as *J. curcas*. However, similar to 2D gel electrophoresis, the number of identified proteins was reduced during seed maturation: The maximum number of proteins in stage II (1,249) and the minimum number in stage VI (413). Principal coordinate analysis (PCoA) plots show clear separation from different maturation stages. Moreover, *in silico* functional annotations allocated the largest portion of the identified proteins 484 (41%) to the "post-translational modification, protein turnover, and chaperones". The second-largest class with 156 proteins (13%) were of the "unknown function" group, followed by "energy production and conversion" (11%), "translational and ribosomal structure and biogenesis" (9.2%) as well as "carbohydrate transport and metabolism" (9%). Although the successful applications and annotations hamper *Jatropha* because of the high abundance of unknown protein functions, the proteins with unknown function may be unique in *J. curcas* seed as novel transcripts. The integration of obtained data builds an expanded coverage of proteins seeds in *J. curcas*. It provides an authentic perspective on the contribution of dynamic regulation of protein expression and turnover during seed maturation.

Keywords: proteomic profiling, seed maturation process

Complete chloroplast genomes of *Fagus sylvatica* L. reveal sequence conservation in the inverted repeat and the presence of allelic variation in NUPTs

Contribution ID: 126

Ulaszewski, Bartosz; Meger, Joanna; Mishra, Bagdevi; Thines, Marco; Burczyk, Jaroslaw

Growing amounts of genomic data and more efficient assembly tools advance organelle genomics at an unprecedented scale. Genomic resources are increasingly used for phylogenetic analyses of many plant species, but are less frequently used to investigate within-species variability and phylogeography. In this study, we investigated genetic diversity of *Fagus sylvatica*, an important broadleaved tree species of European forests, based on complete chloroplast genomes of 18 individuals sampled widely across the species distribution. Our results confirm the hypothesis of a low cpDNA diversity in European beech. The chloroplast genome size was remarkably stable (158,428±37 bp). The polymorphic markers, 12 microsatellites (SSR), four SNPs and one indel, were found only in the single-copy regions, while inverted repeat regions were monomorphic both in terms of length and sequence, suggesting highly efficient suppression of mutation. The within-individual analysis of polymorphisms showed a large number of markers (>9000) which were proportionally present in gene and non-gene areas. However, an investigation of the frequency of alternate alleles revealed that the source of this diversity originated likely from nuclear-encoded plastome remnants (NUPTs). Phylogeographic and Mantel correlation analysis based on the complete chloroplast genomes exhibited clustering of individuals according to geographic distance in the first distance class, suggesting that the novel markers and in particular the cpSSRs could provide a more detailed picture of beech population structure in Central Europe.

Keywords: complete chloroplast genome, genoimc markers, heteroplasmy, population genomics, European beech

Optimising exome capture of *Pinus sylvestris* using species-specific repetitive DNA blocker

Contribution ID: 149

<u>Kesälahti, Robert Sebastian</u>; Cervantes, Sandra; Kujala, Sonja T; Kumpula, Timo A; Mattila, Tiina M; Niskanen, Alina K; Savolainen, Outi; Pyhäjärvi, Tanja

Conifer genomes are among the largest of all known species and are highly enriched in repetitive DNA sequences. Special approaches are required to obtain genomic data in a cost-efficient manner from such genomes. Exome capture has proven to be a powerful tool for producing large amounts of sequence data from targeted genes. As a part of the protocol, various blockers are used to prevent non-target DNA from binding to exome capture baits. In human applications, DNA fragments generated from repetitive DNA sequences (c0t-1 DNA) are used as blockers. However, c0t-1 DNA generated from the target species itself has not been used in exome captures with conifers before. We designed a bait set for *Pinus sylvestris* based on a gene-level supertranscript assembly and a set of candidate genes. The set consists of 18,184 regions. We tested the performance of the set by performing six exome captures with three different treatments: commercial developer reagent, and 30,000 ng or 60,000 ng species-specific c0t-1 DNA. We used the treatments to determine the optimal amount of c0t-1 DNA. Our bait set performed well: the mean coverage of target region varied between 89.3–90.8% among treatments and almost all targeted regions were covered. We discovered 409,034 high-quality SNPs (SNP quality > 30, read depth > 30 and mapping quality > 50) across all the treatments. Treatments with commercial developer reagent had the largest number of missing SNPs (mean 12,213), compared to on average 352 missing SNPs in the 60,000 ng c0t-1 DNA treatment. Differences between the treatments in the amount of missing data were observed in both on-target and off-target-regions.Our results demonstrate that exome captures can be (i) used to easily obtain genomic data from areas of interest from large and complex genomes, and (ii) improved by the use of species-specific c0t-1 DNA.

Keywords: exome capture, conifers, *Pinus sylvestris*, c0t-1 DNA

Methods for identifying the genetic basis of local adaptation and assessing convergent evolution

Contribution ID: 152

Booker, Tom R.; Singh, Pooja; Yeaman, Sam; Whitlock, Michael C.

Studying local adaptation can provide a window into the process of evolution, yielding insights about the nature of evolvability and constraints to diversification. A potentially powerful method to identify locally adaptive genetic variation is the genotype–environment association (GEA) study. In GEA studies, the correlation between allele frequency and environmental variables that are presumed to reflect selection gradients are examined for many markers across the genome. Alleles that have strong evidence for correlation with environmental variables, or that are outliers in the genome-wide distribution of correlations, are taken as evidence for loci involved in local adaptation. Typically, each marker is considered independent of all others. However, closely linked sites can have highly correlated genealogical histories and may therefore carry similar information about a particular region's involvement in local adaptation. In this presentation, we outline the Weighted-Z Analysis (WZA), a method we have developed to perform GEA using analysis windows to take advantage of information carried by closely linked sites. By analysing simulations modelling local adaptation, we find that the WZA outperforms commonly used GEA approaches in a variety of settings. Finally, we develop a novel method to identify convergent evolution among multiple species using an approach based on order statistics. We validate these methods using simulated data. This presentation is complementary to the oral presentation entitled “Convergence in local adaptation to climate in conifers across North America and Europe”.

Keywords: population genomics, landscape genomics, genotype–environment association, convergent evolution

Session 1: Climate change genomics

Tuesday 14 September 16:20–18:55

Chair: Dr. Pascal Milesi, Uppsala University, SciLife Laboratory, Sweden

Oral Presentations

16:20	**Keynote:** **Kelly, John:** Measuring the genome-wide response to natural selection in natural plant populations
17:05	**Sekely, Jill Terese:** Disentangling local adaptation drivers in the Andean *Nothofagus pumilio*
17:25	**Coq--Etchegaray, Domitille:** Genome-wide association study of leaf specialized metabolites in sessile oak (*Quercus petraea*) provenances
17.45	***Short Break***
17:55	**Singh, Pooja:** Convergence in local adaptation to climate in conifers across North America and Europe in the integration of genomic and transcriptomic data for phenotype prediction
18.15	**David-Schwartz, Rakefet:** Hybridization and adaptation to environmental drought in *Pinus*
18.35	**Lind, Brandon:** How off are genetic offset predictions? Lessons from common gardens and three clades of conifers

Keynote
Measuring the genome-wide response to natural selection in natural plant populations

Contribution ID: 168

Kelly, John

Evolution by natural selection occurs when the frequencies of genetic variants change because individuals differ in Darwinian fitness components such as survival or reproductive success. Differential fitness has been demonstrated in field studies of many organisms, but it remains unclear how well we can quantitatively predict allele frequency changes from fitness measurements. Here, we characterize natural selection on millions of Single Nucleotide Polymorphisms (SNPs) across the genome of the annual plant *Mimulus guttatus*. We use fitness estimates to calibrate population genetic models that effectively predict allele frequency changes into the next generation. Despite the challenges of measuring selection in the wild, we find a strong correlation between predicted and observed allele frequency changes, which suggests that population genetic models have a much greater role to play in forward-time prediction of evolutionary change. Finally, we discuss how the combination of different genomic methods can address questions about how populations respond to environmental change.

Keywords: genomics, *Mimulus*, global change, adaptation

Disentangling local adaptation drivers in the Andean *Nothofagus pumilio*

Contribution ID: 127

<u>Sekely, Jill Terese</u>; Arana, María Verónica; Marchelli, Paula; Mattera, María Gabriela; Pastorino, Mario; Soliani, Carolina; Heer, Katrin; Opgenoorth, Lars

Disentangling the effects of individual environmental factors is important for determining the driving factors of local adaptation. However, natural forests inhabit landscapes with overlapping and interacting environmental gradients, which makes this endeavor notoriously difficult *in situ*. The cold-adapted *Nothofagus pumilio* forests present an ideal study system because they stretch over a 2000-kilometer range, from the high-altitude subtropics (35°S) to sea level at the southernmost tip of Tierra del Fuego (56°S). This species inhabits the southern Andes mountains, which run almost perfectly North to South and contain clear precipitation, day-length, and temperature gradients, which are three of the most biologically important environmental gradients. To assess *in situ* adaptation, we sampled 500 *N. pumilio* adults along these gradients using a paired-site sampling design. A pair contained two sites that were close enough to share an evolutionary history but far enough apart in elevation to experience different temperature conditions. Using a set of ~50,000 SNPs from candidate genes and the CHELSA dataset of global climate parameters, we performed an association genetic analysis to discover genes that may be under selection. We investigated population structure (e.g. ADMIXTURE), possible SNP outliers (pcadapt, outFLANK), and gene–environment associations (LFMM2). These results will fuel further downstream analyses of local adaptation including phenotype–environment associations and demographic history inference.

Keywords: local adaptation, genotype-environment associations*, in situ*

Genome-wide association study of leaf specialized metabolites in sessile oak (*Quercus petraea*) provenances

Contribution ID: 142

Coq--Etchegaray, Domitille; Bernillon, Stéphane; Le Provost, Grégoire; Lalanne, Céline; Moing, Annick; Plomion, Christophe; Brachi, Benjamin

European white oaks are long-lived species and are one of the most important foundation species in European temperate forests. In the context of global climate change, droughts, heat waves and emerging biotic enemies such as insects and pathogens are putting populations and ecosystems at risk. Specialized metabolites play a key role in tree defenses against natural enemies and protection against abiotic stresses such as UV exposure and drought. Here, we used high-throughput MS-based metabolomics to explore the natural variation of over 100 leaf specialized metabolites in 25 sessile oaks from nine provenances, all growing in a common garden in France. Among the metabolites analyzed, which included mostly hydrolysable tannins and flavonoïds, very few displayed differentiation among provenances, of which 22 displayed clear bimodal distributions with phenotypic classes present at balanced frequencies in all provenances. To investigate the genetic bases of leaf specialized metabolites, we performed whole-genome low-coverage (~10X) sequencing of all individuals phenotyped in order to perform genome-wide association mapping. We identified over 1.6 million genome-wide SNPs, which revealed little genetic differentiation among provenances. Linkage disequilibrium (r^2) decayed below 0.2 over 2 kb, suggesting that our genome-wide SNPs were sufficient to capture most genetic variation. We performed a genome-wide association analysis for the leaf specialized metabolites, identified candidate genes and checked for signatures of selection along the genome. Our results suggest that (i) oak provenances display extensive variation for leaf specialized metabolites, (ii) this variation is to a great extent genetically determined, and (iii) variation of individual metabolites is governed by few major loci.

Convergence in local adaptation to climate in conifers across North America and Europe

Contribution ID: 160

Singh, Pooja; Booker, Tom R; Lind, Brandon; Lu, Mengmeng; Aitken, Sally; Whitlock, Michael C; Yeaman, Sam

Instances of convergent evolution can shed light on the evolutionary constraints shaping adaptation. Conifers are an excellent model to test hypotheses related to convergent evolution, because they exhibit pronounced adaptation to local environments. We analysed landscape genomic datasets from eight species of conifers sampled from two continents and representing 150 million years of evolution. Genotype environmental association (GEA) analyses were first conducted on each species separately using the Weighted-Z Analysis (WZA) method. We then identified genes involved in local adaptation to variation in temperature, moisture, and elevation. We established orthology among genes as the unit of convergence across all species. Using these orthologous groups, we apply novel methods to assess the extent of convergent evolution between pairs of taxa and to identify genes that are locally adaptive in multiple species. Using our results, we examine whether there is a phylogenetic signal in patterns of convergence and if repeated evolution occurs at the gene or biological pathway level. Our findings have important implications for informing assisted gene flow practices and conservation management as the climate changes. The methods we use are detailed in the poster presentation entitled “Methods for identifying the genetic basis of local adaptation and assessing convergent evolution (Booker TR et al.).”

Keywords: local adaptation, population genomics, convergence, climate change, conservation

Hybridization and adaptation to environmental drought in *Pinus*

Contribution ID: 134

Houminer, Naomi; Riov, Joseph; Osem, Yagil; Ashkenazi, Mor; Moshe, Yosi; Rozen, Ada; Sherman, Amir; Moshelion, Menachem; David-Schwartz, Rakefet

Increased genetic diversity through hybridization is one of the major genetic strategies to cope with the rapid climate change in forests. Interspecific hybridization provides novel genetic variants that enable tree populations to survive and thrive in changing climates. The extent of hybridization in planted mixed-forests and the fitness of hybrids over either parent species are poorly understood. We evaluated hybridization between the closely related species *Pinus brutia* and *Pinus halepensis* in mixed forests at four sites with different annual precipitation ranging from 650 to 430 mm. Hybridization was analyzed at three developmental stages: seeds, young seedlings, and surviving seedlings following several months of environmental drought. Seeds from *P. brutia* trees were 4.9 ± 2.4% hybrids, while populations of young seedlings and of seedlings that survived the dry summer consisted of 10.7 ± 1.6 and 20.7 ± 6.2% hybrids, respectively. Some of the hybrids demonstrated varying degrees of admixture as a result of subsequent crosses within the population. This increasing rate of *P. brutia* x *P. halepensis* hybridization along the developmental stages suggests an advantage of hybrids over either parent species in adaptation to drought. The physiological basis for drought resistance was an earlier reduction in stomatal conductance in hybrids, at 44% relative water content (RWC) instead of 36 and 32% in *P. halepensis* and *P. brutia,* respectively. Our phenological, genetic, and physiological results suggest a program to develop valuable resources of increased genetic diversity and adaptation through natural hybrids of *Pinus*.

Keywords: drought, adaptation, hybrids, pines

How off are genetic offset predictions? Lessons from common gardens and three clades of conifers

Contribution ID: 158

Lind, Brandon; Candido-Ribeiro, Rafael; Singh, Pooja; Lu, Mengmeng; Obreht Vidakovic, Dragana; Booker, Tom R; Whitlock, Michael C; Isabel, Nathalie; Yeaman, Sam; Aitken, Sally

Understanding how species will respond to climate change is paramount for maintaining conservation and management priorities throughout the next century. However, while increasing in recent popularity, the methods often used to predict population vulnerability to future climate change remain largely unvalidated and there is need for further exploration into (hyper)parameterization, training, and inference. Here, we use sets of range-wide genetic data from jack pine (*Pinus banksiana*) and two varieties of Douglas-fir (*Pseudotsuga menziesii*) to train distinct models of multiple genetic offset methods, and then fit these models to the climate of common gardens where an independent sample of individuals from these same populations was grown and phenotyped. We quantify the performance of these offset methods using the relationship of predicted offset with 1) two year-old seedling phenotypes in a single common garden of Douglas-fir (increment growth, shoot biomass), and 2) 52-year percent mortality and growth in jack pine from two long-term provenance trials. Additionally, we explore the use of climatic and geographic distances as the sole measure of genetic offset and compare these results with those from genomic modelling. We propose best practices for using offset predictions, and discuss some of the nuances that could increase or decrease the predictive accuracy of these offset methods.

Keywords: genetic offset, climate change, common gardens, genomics

Session 1:
Climate change genomics

Poster Session A: Wednesday 15 September 13:00–15:50

Posters

Meger, Joanna:
Genomic signatures of natural selection at phenology-related genes in a widely distributed tree species *Fagus sylvatica* L.

Rellstab, Christian:
Range-wide signatures of genetic adaptation to drought in two widespread European tree species

Roskilly, Beth:
Rangewide patterns of climate adaptation in western larch

Wehenkel, Christian:
Genome-wide scans for detecting adaptation to local environment in *Populus tremuloides*, a keystone North American tree species

Genomic signatures of natural selection at phenology-related genes in a widely distributed tree species *Fagus sylvatica* L.

Contribution ID: 128

Meger, Joanna; Ulaszewski, Bartosz; Burczyk, Jarosław

The diversity of phenology-related genes is expected to contribute to local adaptation in widely distributed plant species growing in climatically variable geographic areas, such as forest trees. European beech (*Fagus sylvatica* L.) is a widespread and one of the most important broadleaved tree species in Europe; however, its potential for adaptation to climate changes is controversially discussed, and little is known about the molecular basis of climate change-relevant traits like bud burst. We explored single nucleotide polymorphisms (SNPs) at candidate genes related to bud burst in beech individuals sampled across 47 populations in Europe. The SNP diversity was monitored for 380 candidate genes using the sequence capture approach, providing 2,909 SNP unlinked loci. We used two complementary analytical methods to find loci significantly associated with geographic, climate (expressed as principal components) or phenotypic (spring and autumn phenology, height, survival) variables. Redundancy analysis (RDA) was used to detect candidate markers across two spatial scales (entire study area and within sub-regions). We revealed 201 candidate SNPs at the broadest scale, 53.2% of which were associated with phenotypic variables. Additive polygenic scores, which provide a measure of the cumulative signal across significant candidate SNPs, were correlated with the climate variable (principal component, PC1) related to temperature and precipitation availability and spring phenology, suggesting that in beech selection favors genotypes with earlier bud burst under warmer and wetter habitats within its range. Moreover, different genotype−environment associations were identified within Southeastern Europe, compared to the entire geographic range of European beech, implying that selection pressures may differ across spatial scales. This study indicates that environmental conditions may play important roles as drivers of genetic diversity of phenology-related genes that could influence local adaptation in European beech.

Keywords: genotype–environment association, local adaptation, sequence capture, candidate genes, bud-burst phenology

Range-wide signatures of genetic adaptation to drought in two widespread European tree species

Contribution ID: 143

Dauphin, Benjamin; Lesur, Isabelle; Martínez-Sancho, Elisabet; Opgenoorth, Lars; Reutimann, Oliver; Heer, Katrin; Scotti, Ivan; Plomion, Christophe; Gugerli, Felix; Fonti, Patrick; González-Martínez, Santiago; Rellstab, Christian

As a consequence of ongoing climate change, forests are increasingly subject to ever more frequent and long-lasting temperature- and drought-induced stress. More extreme environmental conditions have led to increased mortality, as observed in Europe after the recent unprecedented droughts. Given their long generation time, it is hard to assess how forest tree species cope with rapidly changing conditions. We investigated the genetic bases of drought resistance in European beech (*Fagus sylvatica*) and sessile oak (*Quercus petraea*), two ecologically and economically important European forest tree species. To do this, we collected environmental, genomic, and tree-ring data from 19 and 22 populations across the European continent, sampled in environmentally contrasting pairs if possible. Using climatic, topographic, and edaphic descriptors, we generated drought-related indices to model environmental constraints at high spatial resolution, describing past and present habitat conditions of 510 beech and 386 oak individuals. We performed genotype–environment association analyses to identify loci potentially under selection. In addition, we used individual tree-ring width series to generate phenotypic traits to test for genotype–phenotype associations, e.g., related to resilience to extreme drought events. We discuss the differences and similarities in adaptive signatures between species in relation to drought under climate change.

Keywords: drought, fagaceae, adaptation, genomics, dendrochronology

Rangewide patterns of climate adaptation in western larch

Contribution ID: 151

Roskilly, Beth; Lind, Brandon; Lu, Mengmeng; Yeaman, Sam; Aitken, Sally

Shifting climates are disrupting historical patterns of local adaptation in tree populations, introducing a pressing need to understand the risks posed by climate change and mitigation strategies such as assisted gene flow. Climate niche modeling projects that areas of future suitable climate for western larch (*Larix occidentalis* Nutt.) will stretch far north and west of its contemporary distribution, making it a desirable candidate for assisted migration trials. It was the first conifer species approved to be operationally planted north of its native range in British Columbia, and these plantings have demonstrated its reforestation potential on many sites throughout the province. Previous common garden studies indicate weak geographic clines for growth and other adaptive traits compared to co-occurring evergreen species, suggesting western larch populations may possess high phenotypic plasticity and standing genetic variation. However, no studies have leveraged a combination of phenotype- and genotype-environment associations to test population differentiation and patterns of local adaptation to climate across the extent of its current natural distribution. We assessed phenotypic data on seedling growth, phenology, cold hardiness of 52 natural populations and 28 selectively-bred families in a common garden experiment at the University of British Columbia (UBC) campus in Vancouver, British Columbia, in 2020. We are implementing moderate and severe drought treatments in 2021 to assess traits related to drought tolerance, population-level plasticity (GxE), and correlations of phenotypic traits among treatments. We have also generated exome-capture sequence data for pooled samples from 45 populations for genotype–environment association analyses to identify the strength of and climatic drivers of local adaptation. We are using this information to assess vulnerabilities related to climate change and inform strategies for matching seed sources with emerging climates.

Keywords: landscape genomics; assisted migration; climate change

Genome-wide scans for detecting adaptation to local environment in *Populus tremuloides*, a keystone North American tree species

Contribution ID: 165

Simental Rodriguez, Sergio Leonel; Hernández-Díaz, José Ciro; Hernández-Velasco, Javier; Porth, Ilga; Goessen, Roos; González-Elizondo, M. Socorro; Fladung, Matthias; Groppe, Kathrin; Jaramillo-Correa, Juan P.; Olivas-García, Jesús Miguel; Gernandt, David S.; Martínez-Ávalos, José Guadalupe; Carrillo-Parra, Artemio; Lopez-Sanchez, Carlos Antonio; Mendoza-Maya, Eduardo; Sáenz-Romero, Cuauhtémoc; Blanco-García, Arnulfo; Wehenkel, Christian

Provenance region is an area within which trees can be moved with little risk of maladaptation, because of the low environmental variation. Since trees may become maladapted under climate change, understanding current patterns of adaptive variation in species has become crucial to enlighten and guide climate resilient afforestation. *Populus tremuloides* is the most broadly distributed forest tree in North America, distributed over a 6,000 km North–South gradient. In a genome-wide association study (GWAS), we located, delimited and mapped Mexican *P. tremuloides* Michx. provenances for recent climatic conditions and a projection for 2030 (Representative Concentration Pathway of ~4.5 Wm^{-2}). We expect to observe: (i) associations between origins and local climate, soil, geographical and topographical factors, and (ii) a latitudinal change of origins, along with a contraction of species distribution for the period 2030. After sequencing, 1.5 million unfiltered SNPs from 96 populations of *P. tremuloides* across its entire distribution in Mexico were detected. After filtering with MAC = 2, MAF = 0.025, 0.05 and 0.2 and MAS = 2 and max-missing 0.85 and 20% missing data using VCFtools and R, we found 13,340 filtered SNPs and 32 adaptive SNPs. Several SNP outliers were significantly associated with climate and soil variables (up to R^2 =0.44). According to the scenario for 2030, the estimated distribution for *P. tremuloides* populations and provenances changed in size and position. Our provenance modeling could help to understand local adaptation in *P. tremuloides*.

Keywords: SNP, genome, outliers, provenance

Session 3:
Demography and post-glacial recolonization

Wednesday 15 September 16:20–18:55

Chair: Prof. Dr. Tanja Pyhäjärvi, University of Helsinki, Finland

Oral Presentations

16:20 **Keynote:**
Johri, Parul:
The role of non-adaptive evolutionary processes in shaping genomic variation

17:05 **Ojeda, Dario:**
The impact of rainforest area reduction in the Guineo-Congolian region on the tempo of diversification and habitat shifts in the Berlinia clade (Leguminosae)

17:25 **Giles Pérez, Gustavo Ibrahim:**
Unravelling the mechanisms driving pre-zygotic isolation in a fir species-complex from central Mexico

17.45 ***Short Break***

17:55 **Kastally, Chedly:**
Genomic assessment of Scots pine expansion in Europe

18.15 **Cannon, Charles:**
Old and ancient trees are life history ‘lottery’ winners and act as evolutionary buffers against long-term environmental change

18.35 **Gugerli, Felix:**
Highlights from two decades of Swiss stone pine (*Pinus cembra*) research on the distribution of genetic diversity in response to multi-facetted evolutionary forces

Keynote

The role of non-adaptive evolutionary processes in shaping genomic variation

Contribution ID: 169

Johri, Parul

The question of the relative evolutionary roles of adaptive and nonadaptive processes has been a central debate in population genetics for nearly a century. While advances have been made in the theoretical development of the underlying evolutionary models, as well as in statistical methods for estimating their parameters from large-scale genomic data, a framework for an appropriate null model is still lacking. We propose that an appropriate null model should jointly account for the evolutionary processes known to be in constant operation in natural populations — genetic drift (as modulated by the demographic history of the population) and selection against deleterious mutations. We show how not accounting for such constantly operating processes affects inference in population genetics. Specifically, we show how segregating deleterious mutations affect patterns of variation at “neutral” sites near functional genomic components and bias the inference of demography as well as positive selection from population genomic data. We demonstrate a potential solution to this fundamental problem — a novel statistical framework for jointly inferring the contribution of the relevant selective and demographic parameters, accounting for effects of selection on linked sites. Our approach represents an appropriate null model for inference in population genetics at large, which is necessary to accurately assess the role of adaptive processes in shaping genomic variation and is especially relevant for species whose genomes have a high density of selected sites.

The impact of rainforest area reduction in the Guineo-Congolian region on the tempo of diversification and habitat shifts in the Berlinia clade (Leguminosae)

Contribution ID: 157

de la Estrella, Manuel; Cervantes, Sandra; Janssens, Steven; Forest, Felix; Hardy, Olivier; Ojeda, Dario

The Guineo-Congolian region in Africa constitutes the second largest area of tropical rainforest (TRF) in the world. It covered an estimated 15–22 million km^2 during the late Miocene (55–11 Ma) and it has since experienced a declining trend, currently reaching 3.4 million km^2, associated with increasing aridification and the replacement of TRF by savanna habitats. In this study we examine whether rainforest area contraction led to a decrease in net diversification rates linked to increasing extinction, or if it is associated with increasing opportunities for allopatric or ecological speciation during periods of forest fragmentation. We used a target enrichment approach combined with a complete data set representing all genera within the Berlinia clade. We combined phylogenomic, dating estimates, habitat reconstruction and diversification rate analyses to infer the effect of change in rainforest area coverage at three taxonomic levels: among genera, within genera (*Anthonotha* and *Englerodendron*) and across the widely distributed *A. macrophylla*. We recovered fully resolved and well-supported relationships among all genera and among species within the two genera. Most genera (87.5%) diverged before the Pleistocene, but *Anthonotha* and *Englerodendron* diversified recently, during the most recent cycles of forest contraction and expansion of the Pleistocene. We found three major clusters within *A. macrophyla* with Upper Guinea as the likely origin of the species. Our results suggest that the Berlinia clade displays an overall trend of accumulation of species over evolutionary time, suggesting the reduction in TRF area has not decreased net diversification rates. Most habitat shifts to savanna occurred in the Miocene, with no major habitat shifts during the most recent phases of forest expansion–contraction in the Pleistocene. Shifts in habitat from lowland forest to savanna did not trigger diversification rates, but habitat fragmentation might have increased diversification rates through allopatric speciation

Keywords: climate change, phylogeography, Africa, phylogenomics, habitat shifts

Unravelling the mechanisms driving pre-zygotic isolation in a fir species-complex from central Mexico

Contribution ID: 109

Giles Pérez, Gustavo Ibrahim; Aguirre Planter, Erika; Eguiarte Fruns, Luis Enrique; Jaramillo Correa, Juan Pablo

Secondary contact after allopatric speciation often leads to interspecific gene flow and the establishment of stable hybrid zones. However, when species have evolved partial reproductive isolation while in allopatry, and hybrids have low overall fitness, secondary contact may lead to ‘reinforcing’ such mating barriers (and thus speciation). In plants, self-fertilization and disjunct breeding phenologies may decrease interspecific mating, and are thought to play a key role during reinforcement. However, other processes may also lead to developing prezygotic barriers without the need of reinforcement, such as local adaptation and/or founder effect-related genetic drift (e.g., during the colonization of new environments). We aimed testing how mating barriers developed in a fast diverging conifer species-pair, *Abies flinckii* and *A. religiosa*, distributed in sky-islands in central Mexico. They form two sympatric zones where interspecific mating seems rare because of disjunct reproductive phenologies. By analyzing 1,147 SNPs genotyped across 23 populations, we compared several demographic scenarios, all based on the well-known geological history of central Mexico. Coalescent simulations supported a rapid species divergence (~ 1.2 Ma), followed by early asymmetric gene flow (mostly from *A. flinckii* into *A. religiosa*), exclusively in the most ancient of the contact zones. The colonization model was not supported. Our results point to early reinforcement as the most likely mechanism for preventing hybridization and originating the observed inbreeding and differentiation patterns within and between species. This study suggests that a wider spectrum of evolutionary processes than previously thought underlie speciation in conifers; these may help explaining how the large species diversity observed in the (sub)tropics originated.

Keywords: disjunct reproductive phenology, geographic isolation, phylogeography, speciation

Genomic assessment of Scots pine expansion in Europe

Contribution ID: 147

Kastally, Chedly; Tyrmi, Jakko; Urpilainen, Santtu; Bastien, Catherine; Cervera, María Teresa; Vendramin, Giovanni G.; Savolainen, Outi; Pyhäjärvi, Tanja

Pinus sylvestris (Scots pine) is the most widespread conifer species in Europe, extending latitudinally from southern Spain to northern Finland, and spanning Eurasia longitudinally. During the Last Glacial Maximum, however, *P. sylvestris* distribution in Europe was contained in glacial refugia present in southern Europe, south of the Pyrenees and the Alps, and, in Central Europe, on the western side of the Carpathians. These glacial refugia have played a key role during the following northward expansion of *P. sylvestris*. Yet, due to the challenging size of its genome, our knowledge of the genetic diversity of *P. sylvestris* in Europe is still limited, notably in those glacial refugia, potentially limiting our understanding of the recent history of this species. To address this issue and to improve our understanding of how glacial refugia might have shaped the current genetic diversity of *P. sylvestris* since the last glacial maximum (LGM), we collected genomic data for 20 populations sampled across Europe along the latitude: from the main glacial refugia in the South to the northernmost parts of its range. We characterized its genetic diversity across Europe using 32,000 SNPs, identifying patterns consistent with previous findings. We further explored multiple hypotheses relative to the northward expansion of the species that could explain the current patterns of genetic diversity by estimating the relative contribution to the genetic diversity of the northern populations of Scots pine from southern European populations. A better assessment of the distribution of the genetic diversity of *P. sylvestris*, and of its evolutionary history in Europe will provide a valuable resource for improving conservation plans of this species.

Keywords: glacial refugia, scots pine, range expansion, population genetics

Old and ancient trees are life history ‘lottery’ winners and act as evolutionary buffers against long-term environmental change

Contribution ID: 107

Cannon, Charles; Piovesan, Gianluca; Munne, Sergi

In natural communities, trees can live for many centuries with sustained fecundity and death is primarily a stochastic process. We use a neutral stochastic death model to examine the demographic patterns that emerge over 15,000 years, across a range of population sizes and empirically observed mortality rates. We found a small proportion of trees (~1% of population at 1.5% mortality) are life-history ‘lottery’ winners, achieving ages 10-20 greater than median age. This maximum age increases with larger populations and lower mortality rates. Additionally, roughly one quarter of trees (~24%) achieve ages that are 3-4 times greater than median age. We objectively identify three age classes (young, old, and ancients) and illustrate the unique diversity contributed by each, given millennial, complex environmental cycles. Ancient trees radically change the variance in generation time and fitness, bridging infrequent environmental cycles, while old trees stabilize population level variation across environmental cycles. These life-history ‘lottery’ winners only exist in old-growth forests, are vital to long-term forest dynamics, and can provide invaluable insight into environmental history and individual longevity. Protecting these ancient trees and the old-growth forests that contain them, even the smallest fragments, should be among our highest conservation priorities.

Highlights from two decades of Swiss stone pine (*Pinus cembra*) research on the distribution of genetic diversity in response to multi-facetted evolutionary forces

Contribution ID: 140

Gugerli, Felix; Dauphin, Benjamin; Brodbeck, Sabine; Rellstab, Christian

Swiss stone pine, *Pinus cembra*, is a foundation species of the alpine timberline ecotone in the central European Alps and shows scattered occurrence in the Carpathian Mountains. As a closed-cone pine, its seeds are primarily dispersed by the spotted nutcracker, which is therefore a key factor for migration, e.g., affecting post-glacial re-colonization and shaping small-scale patterns of genetic diversity. Despite wide-ranging pollen flow, *P. cembra* displays a distinct spatial genetic structure across its range based on nuclear microsatellites. Genetic diversity at these markers is distributed unevenly, with high values associated to putative glacial refugia and areas of contact zones between genetic lineages. At the regional scale in Switzerland, central populations are more diverse than peripheral ones at the level of neutral exome variation, while heterozygosity at putatively adaptive loci was found to decrease with increasing habitat suitability. These findings highlight how demography- and selection-related evolutionary processes differently shape patterns of genetic diversity. Our recent study comparing adult and juvenile cohorts in Swiss stands of *P. cembra* revealed very low historical changes in allele frequencies at neutral and temperature-/precipitation-associated loci. Extrapolating these genotype–environment associations into the expectedly warmer and drier future suggested high genomic vulnerability of this species to global warming, even under a climate change scenario including mitigation measures. Nevertheless, alleles putatively beneficial for warm and dry conditions were already present in high-elevation juvenile cohorts near the colonization front. Hence, an upward shift through the establishment of bird-dispersed seeds seems a plausible strategy to respond to increasing pressure from lower elevation by competitors like Norway spruce invading stone pine habitat. Transferring our findings on past, current and future microevolutionary trends to stakeholders may help mitigating negative trends in this species, which is highly valued for its key role in ecosystem functions, its timber, and the emblematic appearance.

Keywords: genetic diversity, genetic structure, genomic vulnerability, *Pinus cembra*, postglacial re-colonization

Session 3:
Demography and post-glacial recolonization

Poster Session B: Thursday 16 September 13:00–15:50

Posters

Danusevicius, Darius:
Prospects of ancient DNA genotyping: an example with 11000 years old pines from the bottom of the Baltic sea

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

Degen, Bernd:
Targeted sequencing reveals large scale genetic structure of pedunculate oak at both nuclear and plastid genome in Europe

Bruxaux, Jade:
Large distribution but low differentiation: how can we explain the Scots pines paradox?

Niskanen, Alina K:
Fine-scale genetic structure in the Scots pine

Leunda, Maria:
Ancient DNA can provide insights into past and future genetic diversity of forests

Coşgun, Sevil:
Exploring cryptic Mediterranean *Abies alba* stands to check a genetic climate impact hypothesis and vegetation model projections

Prospects of ancient DNA genotyping: an example with 11,000 years old pines from the bottom of the Baltic sea

Contribution ID: 104

Danusevicius, Darius; Buchovska, Jurata

Salty sea water or peat well conserves fossil wood. Can we extract high-quality DNA from such samples and use it for evolutionary studies? Such old samples dating to the end of Pleistocene would reveal valuable data on species, origins of migration, and mutation models of our DNA markers. We need to put this question broader and maybe establish a common database or DNA bank of such samples. We discuss these prospects by presenting a DNA genotyping study of 11,000 year-old individuals of Scots pine found at the bottom of the Baltic sea. We extracted high-quality DNA from these samples and amplified PCR fragments at the mitochondrial DNA *nad*7.1 locus and 11 nuclear microsatellite loci. We also revealed some genetic associations between the ancient Scots pine trees and the present-day southern Lithuanian populations (assignment probability 0.37–0.55) and several wetlands in Lithuania. Our study shows that salty sea water efficiently preserves ancient DNA in wood at the quality levels suitable for genetic testing of trees dated back as far as 11,000 years before present.

Keywords: aDNA, postglacial migration, evolutionarily history

Detecting genomic signatures of ecological speciation and parallel evolution in oaks

Contribution ID: 117

Lazic, Desanka; Hipp, Andrew L.; Carlson, John E.; Gailing, Oliver

The role of adaptive divergence in speciation is widely accepted; however, underlying genetic mechanisms that are leading to reproductive isolation are still unknown. Due to ongoing gene flow among species with different ecological preferences, oaks arose as a model organism for studying species coherence in the face of gene flow. Because of their wide distribution and overlapping ranges of differently adapted species, oaks are suitable for studies focusing on the genes that play a potential role in adaptive isolation as well as species maintenance despite high interspecific gene flow. In our study we generated new whole-genome sequence data for species pairs of the white oak (*Quercus petraea*, *Q. robur*) and the red oak group (*Q. rubra*, *Q. elipsoidalis*) in order to analyze the genomic architecture of reproductive isolation and adaptive divergence across taxonomic sections. We sampled eight population pairs of white oaks in Germany and genotyped them with 21 nSSR markers in order to identify species in neighboring populations and to select individuals for whole-genome resequencing. Individuals from four selected population pairs of red oaks and white oaks have been resequenced. Data processing is currently being done. Using this generated data, we will be able to study the genomic distribution of loci that differentiate these species in the face of introgression. Specifically, we will perform outlier screens in white oaks and red oaks to test for parallel species divergence by natural selection. This study will give us a better insight into the genetic basis for the maintenance of species integrity in oaks in the face of interspecific gene flow, and the role of genes that distinguish the species today in initial lineage divergence.

Keywords: *Quercus*, speciation, adaptive divergence, reproductive isolation

Targeted sequencing reveals large scale genetic structure of pedunculate oak at both nuclear and plastid genome in Europe

Contribution ID: 132

Degen, Bernd; Yanbaev, Yulai; Mader, Malte; Ianbaev, Ruslan; Blanc-Jolivet, Celine

So far, most large-scale genetic inventories of pedunculate oak were focused on the plastid genome which showed the impact of post-glacial re-colonisation and manmade seed transfer. But what was the impact of pollen-mediated gene flow on the large-scale genetic structure? To answer this question, we did a genetic inventory on 1970 trees from 197 locations in 13 European countries. All samples were screened with a targeted sequencing approach on a set of 381 polymorphic loci (356 nuclear SNPs, 3 nuclear indels, 17 chloroplast SNPs and five mitochondrial SNPs). We identified 13 plastidial haplotypes, which showed a strong spatial pattern with a highly significant autocorrelation up to a range of 1250 km. Significant spatial genetic structure up to 1250 km was also observed at the nuclear loci, whereas Bayesian clustering analysis revealed alternative sub-division into two to seven gene pools. The genetic diversity was negatively correlated with longitude, showing higher values in the West and centre and lower values at the northern, eastern and south-eastern edges of the natural distribution range. We discuss the implications of different population genetic and demographic factors as well as hybridisation on the observed large-scale genetic structure of both nuclear and plastid genomes.

Keywords: *Quercus robur*, gene flow, spatial genetic structure, large-scale genetic inventory, post-glacial recolonisation

Large distribution but low differentiation: how can we explain the Scots pines paradox?

Contribution ID: 137

Bruxaux, Jade; Zhao, Wei; Hall, David; Konrad, Heino; Semerikov, Vladimir; Wang, Xiao-Ru

Scots pine (*Pinus sylvestris*) has the second largest distribution among conifers in the northern hemisphere, ranging from Spain to China, and from Turkey to northern Scandinavia. As expected with such large distribution and climate range, it exhibits phenotypic differences, with more than 150 morphological varieties described, and distinct local adaptation to climate gradients. Yet, the differentiation between populations is small at the nuclear level, even when including distant populations from Spain and central Russia (F_{ST} = 0–0.1). For comparison, Norway spruce (*Picea abies*) exhibits a significantly higher differentiation (F_{ST} = 0.15–0.22) despite a smaller distribution. One possible reason behind this low differentiation is a fast recolonization from a limited number of individuals and refugia during the last glacial maximum, circa 17,000 years ago, maintained by long-distance gene flow thanks to wind pollination. To evaluate this hypothesis, we sampled 2,896 trees from 210 populations covering the whole range of the species distribution, including the eastern part of Russia, Mongolia, and China, which were never studied before, and sequenced them using genotyping-by-sequencing (GBS). After filtering, we confirm the low genetic differentiation between populations at this larger scale, with a continuous isolation-by-distance pattern between Spain and Scandinavia on one side, and between Scandinavia and China on the other side. This dataset will then be used to propose a demographic history of the species and evaluate the relevance of the different refugia hypotheses.

Fine-scale genetic structure in the Scots pine

Contribution ID: 145

Niskanen, Alina K; Kujala, Sonja T; Kärkkäinen, Katri; Savolainen, Outi; Pyhäjärvi, Tanja

Knowledge of fine-scale genetic structure, the distribution of genetic diversity in a short distance, is important in evolutionary research and practical applications such as conservation and breeding programs. In trees, spatial aggregation of related individuals is often caused by limited seed and/or pollen dispersal. Seed dispersal ability limits the speed a tree species can spread to new areas. Gene dispersal distances can be inferred from fine-scale genetic structure. Estimates of dispersal distances are useful both in studying post-glacial recolonization and the adaptation to the ongoing climate change. We studied the fine-scale genetic structure of Scots pine (*Pinus sylvestris*) in two sampling sites located 20 km apart within Punkaharju Intensive Study Site (ISS) in Southeast Finland. We genotyped 468 adult trees on 150,000 SNPs using a custom made Affymetrix array and used a pruned set of 28,378 SNPs in the spatial analyses. We found that pairwise relatedness decreased when distance increased. Second degree relatives (r = 0.177–0.354, e.g., half-siblings), the closest relationship we detected, and unrelated individuals (r < 0.044) had median distances of 55 (range 17–407 m) and 327 meters (range 10–1164 m), respectively. Despite the clustering of related individuals, the sampling sites were not differentiated (F_{ST} = 0.0005). Utilizing the regression slope of relatedness on spatial distance, we estimated neighborhood sizes (Nb = 2700–3700) and gene dispersal distances (σ_g = 66–77 m) for both sampling sites. Despite low genetic differentiation of Scots pine populations in intermediate and long distances, related individuals are aggregated within a forest batch. This result can be directly utilized to define proper sampling distances for evolutionary studies and to avoid inbreeding in breeding programs.

Keywords: dispersal, genetic structure, genomics, *Pinus sylvestris*, relatedness

Ancient DNA can provide insights into past and future genetic diversity of forests

Contribution ID: 159

Leunda, Maria; Sperisen, Christoph; Höhn, Laura; Aregger, Sina; Bilat, Julia; Dziomber, Laura; Gugerli, Felix; Alvarez, Nadir; Schwörer, Christoph

Climate change directly affects plant populations by, among other impacts, shifting their range of distribution. Such range shifts are predicted to lead to a decrease in genetic diversity due to genetic drift along the colonization front. However, high levels of genetic diversity are a prerequisite for population persistence. Genetic studies that investigated the impact of climate change on genetic diversity of trees are scarce and limited to a few hundreds of years, therefore being unable to resolve the impacts of climate change over many generations. Natural archives, such as lake sediments, can conserve plant remains for millennia and have been regularly used in paleoecology to reconstruct vegetation dynamics based on pollen and plant macrofossil analysis. Recent advances in molecular techniques allow the analysis of ancient DNA (aDNA) still present in macrofossils, providing insights into demographic processes and their genetic consequences across several hundreds to thousands of years. In this study, we aim to investigate the impact of the Younger Dryas – Early Holocene transition (ca. 11,700 cal yr BP) on conifer populations and their genetic trajectories in the Southern Swiss Alps. This climatic transition is considered a close analogue to the current climate warming regarding the rate and amplitude of temperature change (2-4°C within < 100 years). To do so, we analyze two sites at different elevations: the mire Gola di Lago (972 m a.s.l.) and Lago del Starlarèsc (1975 m a.s.l.). We combine pollen, plant macrofossil, and microcharcoal analysis as proxy for vegetation dynamics, with aDNA analysis from selected needles as indicators of past demogenetic changes. This work will provide valuable information on the understanding of genetic changes in tree populations under climate change conditions and will help developing guidelines for managing mountain forests under climate change.

Keywords: paleogenetics, population dynamics, lake sediments, plant macrofossils, southern Alps

Exploring cryptic Mediterranean *Abies alba* stands to check a genetic climate impact hypothesis and vegetation model projections

Contribution ID: 162

Coşgun, Sevil; Schwörer, Christoph; Cherubini, Paolo; Conedera, Marco; Gobet, Erika; Gugerli, Felix; Sperisen, Christoph; Alvarez, Nadir; Tinner, Willy

As the world is facing unprecedented global change effects, drastic changes in floral and faunal systems seem highly likely. Paleoecology provides the opportunity to obtain detailed information about ecological properties and processes such as the climatic niche or natural ranges of species in dynamic equilibrium with climate. For instance, *Abies alba* is commonly known to grow in cool and moist areas of Central Europe; however, recent progress in paleoecological, ecophysiological, and dynamic modeling research suggests an ability to also grow well under warmer climates with moderate summer droughts and low disturbance. Besides, the recent discovery of individual cryptic stands of *A. alba* under warm and summer-dry conditions close to the Mediterranean Sea indicates that *A. alba* possesses adaptations to cope with the Mediterranean climate and suggests a strong future potential of *A. alba* in Europe under global warming. However, such considerations are so far hampered by our poor knowledge of the mesomediterranean and submediterranean *A. alba* ecotypes that were mostly extirpated during the Late Holocene. To fill this gap, the genetic variation of *A. alba* related to microclimatic conditions will be investigated within large altitudinal and latitudinal gradients in Ticino and Italy. Single-nucleotide polymorphism (SNP) genotyping will be employed to estimate potential source populations and to identify their divergence according to different climatic conditions. In addition, paleogenomic studies using hybridization capture of target DNA will provide genetic information on the ecotypes that have been eradicated by land use and may have possessed genetic adaptations to a warmer climate. Ultimately, we aim to generate deeper knowledge about the ecology of *A. alba* to simulate the behavior of the species under future climate change.

Keywords: global change, climate impacts, vegetation changes, *Abies alba*

Session 2:
Genomics of interactions

Thursday 15 September 16:20–18:55

Chair: Dr. Martina Peter, WSL Birmensdorf, Switzerland

Oral Presentations

16:20 **Keynote:**
Kohler, Annegret:
The evolution of mycorrhizal genomes and transcriptomes

17:05 **Dauphin, Benjamin:**
Genomic determinants of ectomycorrhiza formation in a basidiomycete with poplar

17:25 **Tiret, Mathieu:**
Implementing group selection in forest tree breeding

17.45 ***Short Break***

17:55 **Gaudet, Muriel:**
Genomic insight into the variable resistance of *Castanea sativa* Mill. to *Dryocosmus kuriphilus* Yasumatsu

18.15 **Prospero, Simone:**
Temporal changes in pathogen diversity in a perennial plant–pathogen–hyperparasite system

18.35 **Heinzelmann, Renate:**
Genome-wide analyses of climate change and anthropogenic impacts on the *Dothistroma* needle blight pathogen of pines

Keynote
The evolution of mycorrhizal genomes and transcriptomes

Contribution ID: 141

<u>Kohler, Annegret</u>; Kiss, Eniko; Miyauchi, Shingo; Morin, Emmanuelle; Nagy, Laszlo G; Grigoriev, Igor V; Martin, Francis; Mycorrhizal Genome Initiative

Mycorrhizal fungi coevolved with their hosts since the emergence of land plants, and the combination of calibrated phylogenies with the growing number of fungal genomes allows new insights into the evolutionary history of mycorrhizal symbiosis. The comparison of 135 genomes from mycorrhizal fungi with wood or litter decomposers confirmed the general trend within ectomycorrhizal (ECM) fungal genomes to reduce genes coding for plant cell wall degrading enzymes (PCWDEs). However, since ECM fungi evolved from diverse ancestors like white-rot fungi or litter-decaying fungi, there is a wide diversity in the remaining decomposing ability of ectomycorrhizal symbionts, and the expression of the remaining genes coding for PCWDEs has to be carefully controlled during root colonization. Do mycorrhiza-induced transcripts originate from conserved genes or are they species-specific? For *Laccaria bicolor* we had shown that both conserved and clade-specific genes are important to establish symbiosis with the roots of the host tree *Populus*. Using a phylostratigraphy approach, we compared the "symbiosis-toolbox" of ten ectomycorrhizal interactions. In Ascomycota and Basidiomycota, an average of 74 and 67% of ectomycorrhiza-induced genes predated the evolution of ectomycorrhizal symbiosis, respectively. Approximately 6 and 18% of ectomycorrhiza-induced genes were already present in the most recent common ancestors of Ascomycota and Basidiomycota. These findings suggest that the origin of most genes induced during ectomycorrhiza development and functioning predates the emergence of symbiosis in the studied fungal lineages, implying that these genes have been co-opted for ectomycorrhiza development during evolution from saprotrophic ancestors. The set of conserved ectomycorrhiza-induced genes showed only little overlap among the analyzed species, suggesting that independently evolved ectomycorrhizal lineages recruited different ancestral gene families with similar functions but no orthology for symbiosis, in addition to a likewise unique set of novel genes, including effector-like small-secreted proteins, that evolved after the origins of symbiosis.

Keywords: ectomycorrhiza, genomics, tree-microbe interaction, evolution, transcriptomics

Genomic determinants of ectomycorrhiza formation in a basidiomycete with poplar

Contribution ID: 124

Dauphin, Benjamin; de Freitas Pereira, Maíra; Cardoso Anastacio, Thalita; Fauchery, Laure; Guinet, Frédéric; Dutra Costa, Maurício; Martin, Francis; Peter, Martina; Kohler, Annegret

Forest ecosystems are made up of a wide diversity of organisms that interact at all levels of biological organisation, from genes to communities. In resource-limited environments, trees have associated with mycorrhizal fungi to facilitate the uptake and exchange of nutrients and water as well as carbon elements produced by photosynthetic activities. As such, the emergence of these symbiotic interactions was a major evolutionary innovation for plants and fungi. However, although a large number of fungal genomes have recently been sequenced, the molecular mechanisms underlying ectomycorrhizal traits remain poorly understood. Here, we investigate the basidiomycete *Pisolithus microcarpus*, an ectomycorrhizal fungus, native to the southern hemisphere, which has the ability to form such relationships with eucalyptus and acacias trees as well as non-host trees under experimental conditions (e.g. poplar). Using a unique collection of 41 monokaryons, the parental dikaryon and five dikaryons formed by spontaneous crosses between monokaryons, six ectomycorrhizal traits were measured including mycorrhization rate over a four-week period, which revealed a wide phenotypic variation in the proportion of poplar roots colonised by the different monokaryons, ranging from incompatible to fully compatible strains. Although originating from the same fruitbody, ectomycorrhizal traits of poplar plants inoculated with these strains exhibited contrasting responses, suggesting a genetic role underlying the signalling pathway and development of these symbiotic organs. Hence, we used whole-genome sequencing data to search for genetic variants and gene networks in *P. microcarpus* that are putatively involved in key ectomycorrhizal traits. We will test genotype-phenotype associations using linear mixed models that provide insights into the effect size of specific variants. In parallel, we performed gene expression analysis to compare functional responses between compatible and incompatible strains. By combining genomic and transcriptomic approaches, we aim to provide a comprehensive understanding of the genetic component determining these symbiotic relationships under controlled experimental conditions.

Keywords: ectomycorrhizal fungi, experimental evolution, genome-wide association study, genomics, symbiosis

Implementing group selection in forest tree breeding

Contribution ID: 105

Tiret, Mathieu; Lascoux, Martin; Sanchez, Leopoldo

Classic breeding programs, either phenotype, pedigree or genomic based, generally focus on individuals (i.e. individual breeding values). However, intraspecific competition between selected candidates impacts economic performance of forest tree stands. Competition analyses with the dataset of *Eucalyptus globulus* showed that trees surrounded by relatives were up to 15% taller than when surrounded by less close relatives. We implemented a program to optimize stand performances by managing neighbouring in plantations, based on interaction level inferred either at an individual or at a genetic level. What would genomic selection be if neighbouring information was used as a feedback to genetic evaluation? We address the main technical issues and what could be expected in a long run when implementing "group selection" in the particular case of a *Populus nigra* breeding program.

Keywords: group performance, genomic selection, populus nigra, long term breeding, group selection

Genomic insight into the variable resistance of *Castanea sativa* Mill. to *Dryocosmus kuriphilus* Yasumatsu

Contribution ID: 136

Gaudet, Muriel; Beritognolo, Isacco; Cherubini, Marcello; Ciolfi, Marco; Mattioni, Claudia; Pollegioni, Paola; Villani, Fiorella

The insect *Dryocosmus kuriphilus* (Asian chestnut galls wasp) was accidentally introduced from China to Italy in 2002 and has become one the most damaging pests of *Castanea sativa* (sweet chestnut). The insect infests chestnut buds, inducing formation of galls, with strong impact on plant growth and nut production. The current control strategy for *D. kuriphilus* relies essentially on the introduction and massive release of the parasitoid *Torymus sinensis* as biocontrol agent. On the contrary, little effort has been made to improve the resistance of the host plant. The main objective of this study was to search genetic sources of resistance within the germplasm of *C. sativa*. A comparative field trial at IRET-CNR, including provenances from Spain, Italy and Greece, was screened for severity of infestation by *D. kuriphilus*. Two independent studies identified a Greek provenance (Hortiatis) that expressed the lowest susceptibility and the highest proportion of immune plants. The phenotypic data suggest that this provenance could bring specific genetic factors of resistance to *D. kuriphilus*. In order to test this hypothesis, a genome-wide association study was set up by comparing susceptible and resistant plants of Hortiatis provenance by a Pool-Seq experiment. The experimental design included susceptible and resistant plants from the same provenance to reduce the risk of spurious association due to population structure. DNA pools of the two groups (25 plants each) were sequenced with 50x coverage. Sequence reads were aligned to the reference genome of *C. mollissima,* and the two pools were compared to identify SNPs associated to resistance. Several significant SNPs were identified on five contigs belonging to chromosome K of the reference genome. This genomic region is screened to identify candidate genes and polymorphisms linked to resistance mechanisms, which could be used in breeding programmes, after validation in unrelated independent plants.

Keywords: sweet chestnut, Asian chestnut gall wasp, Pool-Seq, resistance

Temporal changes in pathogen diversity in a perennial plant–pathogen–hyperparasite system

Contribution ID: 166

Prospero, Simone; **Lea, Stauber; Daniel, Croll**

The evolution of pathosystems is driven by selection in both hosts and pathogens, shaping the genetic diversity in populations. Similarly, hyperparasites can affect co-evolutionary trajectories by influencing the stability of both pathogen and host populations. However, how pathogens of perennial hosts evolve in the presence of a hyperparasite has rarely been studied. Here, we investigated temporal changes in genetic diversity of the invasive chestnut blight pathogen *Cryphonectria parasitica* in presence of its parasitic mycovirus *Cryphonectria* hypovirus 1 (CHV1). The virus reduces fungal virulence and represents an effective natural biocontrol agent against chestnut blight in Europe. We analyzed genome-wide diversity and CHV1 prevalence in *C. parasitica* populations in southern Switzerland that were sampled twice at a time interval of about 30 years. Overall, we found that both pathogen population structure and CHV1 prevalence were retained over time. We did not detect a significant impact of CHV1 infection on fungal genetic diversity. Rather, our results indicate that the fungal populations are largely shaped by mating among dominant, closely related genotypes and genetic drift, which is likely a direct consequence of the relatively recent introduction of the pathogen into Europe. Our study highlights that in a novel pathogen–hyperparasite system on a perennial host, both pathogen population structure and hyperparasite prevalence can be retained over several decades in southern Switzerland. Vegetative incompatibility loci associated with asymmetric CHV1 transmission may contribute to additional stabilization of genetic diversity.

Keywords: biological invasion, evolutionary dynamics, vegetative incompatibility, inbreeding, biological control

Genome-wide analyses of climate change and anthropogenic impacts on the *Dothistroma* needle blight pathogen of pines

Contribution ID: 167

<u>Heinzelmann, Renate</u>; Capron, Arnaud; Wong, Barbara; Feau, Nicolas; Hamlin, Richard

The ascomycete fungi *Dothistroma septosporum* and *Dothistroma pini* are the causal agents of *Dothistroma* needle blight (DNB). The disease has a cosmopolitan distribution and primarily affects pine species (*Pinus* spp.). Since the late 1990s, the impact of DNB in the northern hemisphere has dramatically increased. Severe outbreaks of DNB result in early defoliation, growth loss and eventual tree mortality. In western North America, *D. septosporum* is found along a wide climatic gradient ranging from California to south-eastern Alaska. Its host range includes several native pine species like lodgepole pine (*Pinus contorta* var. *latifolia*), shore pine (*Pinus contorta* var. *contorta*), Jack pine (*Pinus banksiana*), ponderosa pine (*Pinus ponderosa*) and knobcone pine (*Pinus attenuata*). By sequencing the genomes of >200 *D. septosporum* isolates from western North America and ~150 isolates from a worldwide collection, we aim to elucidate the population structure of *D. septosporum* in western North America as well as its relatedness to other populations worldwide. Furthermore, we are investigating climate adaptation of local populations by phenotyping a subset of approx. 150 North American isolates for growth rate on agar medium at different temperatures. In an inoculation experiment with lodgepole pine seedlings we are investigating virulence of local populations. First analyzes indicate the presence of several geographically confined and genetically distinct *D. septosporum* populations in western North America. However, we also find genotype groups with a wide geographic distribution and in some areas different genetic groups seem to coexist. Finally, we will try to understand how local adaptation of populations, recent changes in climate and impacts of humans have shaped the genetic structure of the current *D. septosporum* populations in western North America, by conducting analyzes including genomic and climatic data, as well as results from our experimental studies.

Keywords: genomics, population genetics, local adaptation, fungal pathogens, forest pathology

Session 5:
Conservation strategies

Friday 17 September 13:00–15:50

Chair: Dr. Marjana Westergren, Slovenian Forestry Institute, Ljubljana, Slovenia

Oral Presentations

13:15 **Keynote:**
Aleksic, Jelena M.:
Tailoring conservation to suit Serbian spruce

14:00 **Fussi, Barbara:**
Genetic markers support the selection of conservation units and seed stands for rare tree species – white elm, field maple, yew and service tree

14:20 **Arenas Jiménez, Sebastian:**
Contribution of regional and local soil variation to genetic differentiation in a Mexican fir

14:40 ***Short Break***

14:50 **Jiménez Ramírez, Azucena:**
Spatial versus temporal genetic variation in early fitness traits of *Pinus sylvestris* from contrasting edaphic environments

15:10 **Semizer-Cuming, Devrim:**
In the search for climate resilient oaks (*Quercus* spp.) to better conserve forests

15:30 **Rudow, Andreas:**
Swiss genetic conservation units project – a pragmatic approach towards a long-term perspective of the conservation of forest genetic resources

Keynote
Tailoring conservation to suit Serbian spruce

Contribution ID: 130

Aleksic, Jelena M.; Vendramin, Giovanni G.; Piotti, Andrea

Mediterranean forest tree species are particularly sensitive to the global climate warming, and two Mediterranean conifers, Sicilian fir and Serbian spruce, stand out as currently the most threatened ones due to their extremely narrow distribution range. Both species are IUCN-red listed and protected by the law. Conservation of Serbian spruce *(Picea omorica)* was initiated in 1955, when a rigid conservation strategy was applied, without any intervention allowed in c. 30 remnant populations scattered within an area of c. 200 km^2 in the Western Balkans. Such a strategy, implemented without any genetic knowledge on the species, remained to the present days, and the only advancement regarding Serbian spruce conservation over the past 15 years refers to the inclusion of seven populations (four natural populations and three planted stands) into the pan-European network of genetic conservation units (GCUs) for the dynamic conservation of forest genetic resources. In the meanwhile, a drought-induced physiological weakening of Serbian spruce trees followed by infestation of *Armillaria ostoyae* and, in turn, a rapid dieback of trees has been observed, suggesting that Serbian spruce is losing the race against climate warming. However, at the same time, genetic knowledge on the species improved significantly. Whole-population genetic characterizations provided in-depth understanding of within-population genetic patterns and genetic changes in natural regeneration following disturbances. Therefore, the conditions for genetically-informed conservation and, eventually, species genetic rescue have been met, and a ten-year program, worth 10 million EUR and comprising ten work packages, has been formulated and will be presented.

Keywords: *Picea omorika*, conservation genetics, Balkans, long-term refugia, spatial genetic structure

Genetic markers support the selection of conservation units and seed stands for rare tree species – white elm, field maple, yew and service tree

Contribution ID: 116

<u>Fussi, Barbara;</u> Kavaliauskas, Darius; Rau, Bernhard; Seho, Muhidin

Rare tree species are among the possible alternative tree species that have a positive distribution potential under the expected climatic conditions. To ensure future conservation and use, different populations were phenotypically assessed and genetically characterized. A total of 20 populations of *Acer campestre*, 18 *Ulmus laevi*s, 19 *Taxus baccata* and six *Sorbus domestica* populations were genotyped in Bavaria. The genetic differentiation observed varied depending on the tree species. In the field maple, the genetic differentiation among populations was low and no geographical pattern in Bavaria was found. The recolonization of the tree species after the last Ice Age indicates a mixture of different lines in southern Germany. In the white elm, the genetic differentiation among populations was strong. On the basis of the results, two main clusters can be delineated based on the catchment areas of the two main river systems of “Main” and “Danube”. For yew in Bavaria, three groups were found, which, however, do not show a spatial genetic structure. Due to the small-scale distribution of the service tree in northern Bavaria, no genetic difference could be found between the populations. Using genetic parameters, seed harvest and conservation units are suggested for the four tree species. The genetic diversity of seed stands should be as high as possible to ensure a high degree of adaptability of the forest reproductive material. By harvesting seeds from many trees with sufficient distance between them, the genetic diversity of the forest reproductive material (FRM) can be increased. For the future use of the rare tree species in forest conversion measures, seed orchards should increasingly be built up. Plus trees were selected for all four tree species to complement or build new seed orchards. The seed stands proposed for the four tree species are gradually included in the Bavarian register for seed harvesting stands.

Keywords: rare tree species, seed stands, provenance regions, conservation units

Contribution of regional and local soil variation to genetic differentiation in a Mexican fir

Contribution ID: 123

Arenas Jiménez, Sebastian; Giles-Pérez, Gustavo; Cruz-Nicolás, Jorge; Reyes-Galindo, Veronica; Mastretta-Yanes, Alicia; Aguirre-Planter, Erika; Eguiarte, Luis; Jaramillo-Correa, Juan Pablo

Local adaptation is a critical evolutionary process that allows plants to grow better in their native environment than immigrants; thus increasing population differentiation across a species' range. Detecting the molecular bases and selective drivers of local adaptation is still a difficult task, particularly for non-model sessile species with long generation times, like forest trees. This is further complicated by the contrasting spatial and temporal scales at which selective forces may operate, which raises the question of whether similar candidate genes can be detected when studying species at rage-wide and local levels. We aimed answering this question using landscape genomic approaches for understanding how edaphic variation could account for population structure at two geographic scales in sacred fir (*Abies religiosa*), an endemic conifer from central Mexico. We looked for genotype–soil associations at both the range-wide (102 individuals from 18 populations) and local scales (87 trees in one test-trial stand). At the range-wide level, we observed three distinct genetic clusters, distributed from east to west along the Transverse Volcanic Belt. After controlling for such neutral genetic structure, we only found seven SNPs associated with soil composition. At the within-population level, we detected two weakly differentiated genetic groups and no genotype–soil associations. The polygenic models constructed suggests that soil-driven selective forces are possibly more important at large geographic scales, which is likely related to high dispersal capabilities of this species. Soil variation (and its associated genes) should, thus, be taken into account when planning conservation and assisted migration programs.

Keywords: genotyping-by-sequencing, landscape genomics, local adaptation, natural selection, *Abies religiosa*

Spatial versus temporal genetic variation in early fitness traits of *Pinus sylvestris* from contrasting edaphic environments

Contribution ID: 120

Grivet, Delphine; Jiménez Ramírez, Azucena; Robledo Arnuncio, Juan José

Studies of local adaptation in forest tree populations frequently reveal adaptive genetic divergence over broad spatial scales, yet population adaptation to the environment might occur more locally. Evidence of adaptive differentiation over small scales is scant in forest trees, and it is unclear to what extent the higher levels of gene flow expected over short distances may enable adaptation to local conditions. We investigate here evidence of local adaptation to contrasting local soil types (siliceous versus calcareous-dolomitic) in two large natural Scots pine (*Pinus sylvestris*) populations in the central Iberian Peninsula (Spain), which grow six kilometers apart from each other and show substantial quantitative trait divergence. We conducted a greenhouse experiment using 4,842 open-pollinated seeds from 81 mother trees originating from the two populations, and from different altitudes and seed-crop years within each population. Seeds were sown in the two types of natural local substrate, and we monitored seedling emergence, early survival and growth for two years. We did not find evidence of adaptation, as seedlings originating from each soil type did not exhibit higher survival or growth when growing on their corresponding soil type. However, we found strong evidence of environmental maternal effects on early seedling fitness, with both seedling emergence and survival strongly positively associated with seed mass, and with higher phenotypic variation among seedlings from different seed-crop years than among seedlings from different populations or altitudes within seed-crop years.

Keywords: local adaptation, genetic variation, early fitness, maternal effects, gene flow

In the search for climate resilient oaks (*Quercus* spp.) to better conserve forests

Contribution ID: 118

<u>Semizer-Cuming, Devrim</u>; Neophytou, Charalambos; Fussi, Barbara; Rellstab, Christian; Mück, Isabel; Schlosser, Franziska; Seegmüller, Stefan; Michiels, Hans-Gerd

Understanding the interactions between species and their environments has utmost importance to mitigate climate change and adapt forest conservation and management strategies. Relict oak (*Quercus* spp.) stands on extremely dry sites – e.g. scree or rocky slopes – in Central Europe are mostly far too unproductive and therefore not interesting for forestry. As they have not undergone intensive forest management, they are presumably autochthonous and have likely experienced habitat continuity since the early Holocene. This suggests that oak populations on relict sites have most probably adapted to pronounced drought conditions over many generations and, thus, harbor valuable genetic resources for adaptation to ongoing climate change. Here we study oak stands on 52 dry and 11 moist sites located in southern Germany and Alsace using a multifaceted approach to: (i) confirm the relictness of the stands by examining indicator species (beetles, mosses and lichens), (ii) characterize their refugial origin and autochthony using nuclear and chloroplast markers and compare it with the existing data on managed oak forests, (iii) study adaptive genetic variation based on targeted Pool-Seq and genotype–environment association methods, (iv) examine drought-stress physiology in mature trees and their progenies, and (v) provide a basis for a progeny trial to examine the genetic determination of stand growth characteristics. Low chloroplast haplotype diversity and indicator beetle species support the hypothesis of autochthony and relictness. Pooled allele frequency validation between 20 individuals and their pool revealed a high correlation ($R^2 = 0.93$), confirming the suitability of our Pool-Seq approach. Preliminary processing of the sequencing reads resulted in 2.8 million SNPs. Stress-related substances, particularly ascorbate and vescalagine-castalagine correlated positively with stand aridity. The holistic approach applied in the project is expected to improve the conservation management of genetic resources in oaks and to help establishing climate-resilient oak forests.

Keywords: adaptation, climate change, drought, relict oaks, resilience

Swiss genetic conservation units project – a pragmatic approach towards a long-term perspective of the conservation of forest genetic resources

Contribution ID: 129

Rudow, Andreas

In Switzerland, endemic species of the Alpine region occur, and particular site–factor combinations as well as the topographically conditioned spatial isolation can lead to strong genetic differentiation on rather short distance. In the application-oriented project "Genetic Conservation Units Switzerland", a methodology was developed and tested to identify target populations of selected tree species and for subsequently evaluating and establishing suitable genetic conservation units. One main goal was to create synergies between the existing network of forest reserves and the conservation of forest genetic resources, also respecting the federal authorities' demands. The results show that the chosen approach is successful: Existing forest reserves cover a considerable part of the relevant target populations of seven pilot tree species. A multi-stage procedure allows to involve the cantons in the evaluation of dedicated forest reserves to be selected as genetic conservation units and to clearly promote their acceptance. This approach lays the foundation for systematic long-term monitoring of forest genetic resources in Switzerland and for the respective cooperation at the pan-European level.

Keywords: application-oriented project, forest genetic resources, genetic conservation units, long-term monitoring, Switzerland

Session 5:
Conservation strategies

Poster Session A: Wednesday 15 September 13:00–15:50

Posters

Geue, Julia C.:
Landscape genomics of Norway spruce (*Picea abies* [L.] Karst): a range-wide investigation of local adaptation

Belton, Samuel Patrick:
GeneNet: Mapping the genetics of Ireland’s native forests in a European context

Ribeiro-Barros, Ana I.:
Biodiversity dynamics in the Miombo-Mopane woodlands: the case of the Niassa Special Reserve and Limpopo National Park, Mozambique

Rathore, Dheeraj Singh:
Studying the genetic diversity and resilience of four commercially important broadleaved tree species in Ireland

Landscape genomics of Norway spruce (*Picea abies* [L.] Karst): a range-wide investigation of local adaptation

Contribution ID: 131

<u>Geue, Julia C.</u>; Sullivan, Alexis R.; Wang, Xiao-Ru

Human impacts on the environment are severe and affect ecosystems around the globe. Changing environmental conditions modify natural selection pressures, forcing populations to either shift their distributional range or respond plastically or adaptively to novel conditions. Forest tree species with long generation times, such as Norway spruce (*Picea abies* [L.] Karst) may be particularly vulnerable to rapid environmental changes, because range shifts take a long time, and plastic responses are probably limited. Hence, they most likely need to adapt genetically to the new conditions, which largely depend on standing genetic variation within populations. Thus, it is critical to map standing adaptive genetic variation in order to understand how species are adapted to their current environment and how they will be affected by future changes. Landscape genomic approaches have greatly facilitated our ability to map this genetic variation and help identify adaptations to local environmental conditions. To identify major patterns of adaptive variation in Norway spruce, we exploit a large dataset of single nucleotide polymorphisms (SNPs) obtained through genotyping-by-sequencing from 1,446 individuals across 153 sites across the species' range. Using gene–environment association (GEA) studies, we identify loci whose allele frequencies are correlated to the environment, suggesting that they represent adaptations to local conditions. The identification of the environmental correlates also provides key insights into the underlying selective pressures. An improved understanding of the processes driving adaptive variation of Norway spruce, and how they may be affected by human activities, is crucial to inform conservation management strategies. At-risk populations as well as viable populations can be identified and changes in distribution due to climate change can be predicted, which can eventually benefit future forest management.

Keywords: landscape genomics, local adaptation, isolation by environment, Norway spruce, standing genetic variation

GeneNet: Mapping the genetics of Ireland’s native forests in a European context

Contribution ID: 144

<u>Belton, Samuel Patrick</u>; Fox, Erica; Connolly, John; Cubry, Philippe; Kelleher, Colin

Of Europe’s 265 native tree species, 42% are at a high risk of extinction. The severity of this risk partly depends on the abundance of its forest genetic resources (FGR). If the abundance of FGR for a given species is low, its adaptive potential against future environmental challenges will also be low. Mapping Europe’s FGR is therefore critical for understanding which populations must be prioritised in future conservation efforts. GeneNet, which is funded by the Irish Department for Agriculture, Food and the Marine, is a two-year collaborative project between the National Botanic Gardens and Trinity College Dublin. The project sets out to map Ireland’s native FGR for the purpose of updating the European FGR database, EUFGIS. This database was initiated by the European Forest Genetic Resources Programme (EUFORGEN), an EU-wide network that promotes and shares information on FGR conservation. EUFGIS maps locations known as “conservation units” which are likely to possess important FGR. Preliminarily, Ireland has 17, although none of these have been characterised genetically. The two main aims of GeneNet are to: update the Irish EUFGIS section with a more detailed geographical information system (GIS) using the most recent Irish woodland surveys and forestry databases, and genetically characterise the 17 initial conservation units along with a further 25 units. Genetic characterisation will involve haplotyping seven high-priority species, including black alder, ash, downy birch, silver birch, sessile oak, common oak and Scots pine. Haplotyping will mainly be achieved using established chloroplast DNA and microsatellite markers which have been used to characterise other European populations. Currently, molecular analysis is underway on over 600 individual trees sampled across 20 ancient woodland sites. The results of GeneNet will be used to resolve broad phylogeographic patterns across Europe and elucidate the contribution of Ireland’s native trees to the overall FGR of Europe.

Keywords: phylogeography, native Irish trees, haplotyping, conservation

Biodiversity dynamics in the Miombo-Mopane woodlands: the case of the Niassa Special Reserve and Limpopo National Park, Mozambique

Contribution ID: 150

Maquia, Ivete; Fareleira, Paula; Videira e Castro, Isabel; Soares, Ricardo; Arthur Ribeiro Brito, Denise; Marques, Isabel; Ribeiro, Natasha S.; Ribeiro-Barros, Ana I.

The Miombo-Mopane Woodlands are the most predominant type of vegetation in Southern Africa, belonging to one of the five largest wilderness areas of biodiversity, with economic, ecological and ethnobotanical relevance. Together, these ecosystems occupy ca 2.5 million km^2, 90% of which are considered intact and 36% integrated in conservation areas. These ecosystems host ca. 4,600 endemic vascular plants, mostly tree legumes, belonging to the Leguminosae family. In this poster, we will address the dynamics of biodiversity, with particular emphasis on the soil, in two of the most important conservation areas: The Niassa Special Reserve (NSR; Miombo) and the Limpopo National Park (LNP; Mopane), both located in Mozambique. NSR represents one of the most pristine and least disturbed areas of Africa’s deciduous Miombo Woodlands and LNP belongs to the Great Limpopo Transfrontier Park (GLTP), a transboundary community-based initiative for biodiversity conservation, peace and socio-economic empowerment.

Keywords: Miombo, Mopane, biodiversity, rhizosphere

Studying the genetic diversity and resilience of four commercially important broadleaved tree species in Ireland

Contribution ID: 155

Rathore, Dheeraj Singh; Gorriz, Miguel Nemesio; Hodkinson, Trevor R.; Barth, Susanne; Byrne, Stephen; Kelleher, Colin

Utilisation of genetic diversity of tree species through breeding and propagation programmes will enable forests to maintain their functionality, contribute positively to productivity and increase forest resilience to changing climate and potential biotic threats. Ireland has *in-situ* and *ex-situ* conservation gene banks of commercially important broadleaved tree species such as alder, ash, birch, and sycamore. However, the genetic diversity of these tree species in the Irish gene banks remains understudied. Therefore, current work will evaluate genetic diversity of alder, birch, and sycamore tree species in Irish gene banks, and study susceptibility of ash and alder to ash dieback and *Phytophthora*, respectively. We will characterise genetic relationships within and among the tree populations, and assess their resilience to exiting diseases in Ireland for ash and alder. Findings from this project will deliver greater understanding of the extent and nature of genetic diversity and resilience in gene bank collections; thereby enhancing the role of these resources in improvement programmes of these broadleaved tree species in Ireland.

Keywords: forest genomics, disease resistance, tree improvement, DNA fingerprinting, bioinformatics

Session 6:
Towards climate-smart forests

Friday 17 September 16:20–18:55

Chair: Dr. Charalambos Neophytou, BOKU, Vienna, Austria

Oral Presentations

16:20 **Keynote:**
González-Martínez, Santiago C.:
Using genomics to improve predictions of population responses of forest trees in the face of climate change

17:05 **Candido Ribeiro, Rafael:**
Adaptive genetic variation associated with drought hardiness in coastal and interior Douglas-fir and its interplay with cold hardiness

17:25 **Lachmuth, Susanne:**
Using standardized genomic offsets to inform climate-smart seed transfer in North American red spruce conservation

17.45 ***Short Break***

17:55 **Olsson, Sanna:**
Diagnostic genetic markers to ascertain the origin of forest reproductive material: a case study with *Pinus pinaster*

18.15 **Reutimann, Oliver:**
Abiotic factors predict taxonomic composition and genetic admixture in closely located populations of hybridizing oak (*Quercus* spp.) species

18.35 **Curtu, Alexandru-Lucian:**
Conservation of genetic resources of oak species more adapted to a drier and hotter climate – *Quercus pedunculiflora* in Romania

Keynote
Using genomics to improve predictions of population responses of forest trees in the face of climate change

Contribution ID: 170

González-Martínez, Santiago C.

Predicting future population responses of forest trees is challenging, as it involves extrapolating information from a moderate number of provenances tested in only a few common gardens (environments) to the full distribution range of a species. Nevertheless, accurate predictions of future tree population responses to climate change are necessary to adequately manage and use forest genetic resources. In this talk, I will review recent papers and provide insights on the use of genomics to improve the power of predictive models. I will also present a case study in maritime pine where multiple models were tested for accuracy of predictions. In particular, I will focus on methods combining information from common gardens via genotype-phenotype association (i.e. polygenic scores and/or counts of positive-effect alleles, PEAs, as identified by genome-wide association studies, GWAS) and extensive genotyping of natural populations. Models combining population demographic history, provenance climate-of-origin, and positive-effect height-associated alleles may explain as much variance as models relying directly on the common garden design, at least for highly-structured species such as maritime pine, and provide better predictions outside the range of the provenances tested in common gardens. In addition, local or regional PEAs improved the models with respect to full-distribution ones, indicating that alleles involved in adaptation may be geographically restricted. While complex genetic architecture may prevent us to identify molecular variation underlying adaptive traits, it may also help to improve the accuracy of genomic predictions, in particular for highly polygenic traits as those related to growth or some functional traits. Future challenges and common flaws of this approach will also be highlighted.

Keywords: local adaptation, phenotypic prediction, GWAS, maritime pine, climate change

Adaptive genetic variation associated with drought hardiness in coastal and interior Douglas-fir and its interplay with cold hardiness

Contribution ID: 164

Candido Ribeiro, Rafael; Lind, Brandon; Lu, Mengmeng; Singh, Pooja; Obreht Vidakovic, Dragana; Yeaman, Sam; Aitken, Sally

To investigate the extent of drought hardiness across the range of Douglas-fir (*Pseudotsuga menziesii*, including both the interior and coastal var. *glauca* and *menziesii*), we conducted a common garden experiment with seedlings from 74 natural provenances where we monitored chlorophyll fluorescence, visual damage and height over time on plants submitted to a drought-to-death treatment during the summer. Strong differences were observed between the two varieties despite a weak signal of local adaptation to drought within each variety due to large within-provenances variation. In a subsequent study, we conducted a case-control genome-wide association study with 20 of the same provenances (80 seedlings/provenance) to identify putative adaptive genetic variants associated with drought hardiness. Associations were tested between drought hardiness and allele counts for over 1.5 million SNPs in pooled extremes (ten cases and ten controls per provenance). Considering a *p*-value threshold of 0.05 (after correction for false discovery rate), we successfully identified 1,274 SNPs significantly associated with drought hardiness in the interior variety and 907 in the coastal variety. Next, we will annotate the genes identified in this analysis, and examine the distribution of these putatively adaptive alleles across 74 natural and 14 seed-orchard populations to explore potential differences in genetic architectures between varieties and regions. We will also explore the interplay between candidate genes identified in this study and candidate genes found to be associated with cold hardiness in a third experiment. Predictions of genomic vulnerability under climate change scenarios will be performed for SNPs highly associated with drought hardiness. Results from this study, part of the CoAdapTree project, will be used to inform breeding programs and assisted gene flow strategies for reforestation of coastal and interior Douglas-fir in the face of climate change.

Keywords: case-control GWAS, local adaptation, drought hardiness, cold hardiness, climate change

Using standardized genomic offsets to inform climate-smart seed transfer in North American red spruce conservation

Contribution ID: 163

Lachmuth, Susanne; Capblancq, Thibaut; Prakash, Anoob; Keller, Stephen R.; Fitzpatrick, Matthew C.

Genomic offsets quantify the disruption of existing genotype-environment associations under environmental change and have gained attention in conservation science by providing an evolutionary perspective often absent from management planning. We combined genomic offsets derived from gradient forest modeling of genomic turnover along climatic gradients and niche modeling to inform conservation of red spruce (*Picea rubens*), a cold-adapted tree species endemic to eastern North America. We show how genomic offsets can be standardized by re-expressing them as *z*-scores such that they quantify the deviation from contemporary genomic turn-over across the landscape. We evaluated the predictive power of the genomic offsets using growth data from three common gardens before predicting disruption of genotype-climate associations across the current range under end of 21st century climate. To inform climate-smart seed transfer programs, we constrained the acceptable genomic offset between potential seed donor populations under current and recipient planting sites under future climate relative to contemporary genomic turnover (threshold *z*-score). We explored variation in donor and recipient importance of each grid cell across the landscape by considering all cells with contemporary spruce populations as potential donors for seed transfer to potential recipient habitat of varying size and climatic range and summed acceptable matches for each donor and recipient grid cell. Recipient importance represents the sum of donor cells from which suitable seeds could be transferred and can be interpreted as a habitat suitability metric that accounts for intra-specific variation in climate adaptation, which we compared to ecological niche modelling-based projections of climate suitability. Our approach extends previous applications of the genomic offset concept as it constrains donor-recipient matches relative to the contemporary genomic turnover across a species range in a standardized manner and allows the selection of seed sources and planting sites that maximize the representation of the adaptive genomic variation existing in a species.

Keywords: assisted migration, environmental niche model, genomic offset, gradient forest, *Picea rubens*

Diagnostic genetic markers to ascertain the origin of forest reproductive material: a case study with *Pinus pinaster*

Contribution ID: 135

Olsson, Sanna; Westergren, Marjana; Grivet, Delphine; González-Martínez, Santiago C.; Alía Miranda, Ricardo; Robledo-Arnuncio, Juan J.

Comparative studies of forest tree provenances have demonstrated their performance differences (e.g. growth and productivity) in multiple environments. This information is central to delineate seed (planting) and breeding zones, as well as to predict expected stand performance in the face of climate change. Under EU regulation of forest reproductive material (FRM; fruits, seeds, plants and plant tissue), the region of provenance is the basic unit for marketing and is defined by specific ecological conditions as well as phenotypic and genetic characteristics. Genetic markers can assist in discrimination for marketing control of FRM and, thus, inform seed transfer guidelines. In our study, we used a genomic dataset (6,100 SNPs, 665 samples from 16 provenances / 34 populations) of *Pinus pinaster*, representative of most of its distribution range, to discriminate among gene pools, provenances and populations, and to assign individuals to these categories. We use three methods to evaluate the reliability of large datasets for genetic discrimination and assignment: 1) Rubias, an R package for performing genetic stock identification and associated tasks, 2) a supervised machine-learning genetic-assignment framework implemented in assignPOP, and 3) the network-based genetic-assignment tool BONE. We evaluated the pros and cons of each method and assessed their suitability and limitations to discriminate among candidate gene pools, provenances and populations. Using simulations, we tested their ability to identify the true source (gene pool, provenance or population) of target samples consisting of either one individual or a group of individuals (e.g. a seedlot). We tested several scenarios of pure and mixed seedlots, focusing on a few practical cases of what foresters might be facing. According to our results, the three programs provide similar results, with some exceptions. The identified markers that can best discriminate among gene pools, provenances or populations are proposed to be used as diagnostic tools for FRM identification.

Keywords: forest reproductive material, provenance regions, genetic assignment, mixture analysis, genetic stock identification

Abiotic factors predict taxonomic composition and genetic admixture in closely located populations of hybridizing oak (*Quercus* spp.) species

Contribution ID: 148

Reutimann, Oliver; Dauphin, Benjamin; Baltensweiler, Andri; Guichoux, Erwan; Gugerli, Felix; Kremer, Antoine; Rellstab, Christian

A central interest in evolutionary ecology is to identify which environmental factors determine the spatial distribution of species. Ecological niche models have given insights into ecological and evolutionary processes that shape the distribution of species on large spatial scale. Much less is known about what influences the spatial distribution of hybridizing species and their admixed individuals at small (local to regional) spatial scale. Hybridizing white oak species (*Quercus* spp.) represent an ideal study system to elucidate which environmental factors determine their relative abundance and admixture levels in admixed forest stands. Here, we used species-diagnostic SNP markers and high-resolution topographic and soil data to identify the environmental factors associated with taxonomic composition of individuals and populations in 15 mixed stands of *Q. petraea* and *Q. pubescens* in the Valais, an inner-Alpine valley in Switzerland. At the individual level, generalized linear models (GLMs) applied with a stepwise procedure for model selection explained a small part of variation ($R^2 = 0.35$), most likely because taxonomic variation within sites was much higher than environmental variation. At the population level, GLMs often explained a large part of variation ($R^2 = 0.54–0.70$) of the taxonomic indicators. Mean taxonomic composition of the sites depended mainly on altitude and geographic position. Interestingly, the more variation we found in predictors related to topographic position, the higher the genetic admixture in a population. Taxonomic variation within sites was driven by variation in variables related to solar radiation. Our results show that a multitude of topographic and edaphic factors shape the taxonomic and admixture landscape of these two hybridizing oak species at local scale, and that regional heterogeneity of these factors promote taxonomic diversity and admixture. Overall, our study stresses the prospects of studying high-resolution environmental factors for understanding and predicting taxonomic composition in response to changing climatic conditions.

Keywords: white oaks, admixture, taxonomic composition, abiotic factors

Conservation of genetic resources of oak species more adapted to a drier and hotter climate – Quercus pedunculiflora in Romania

Contribution ID: 121

Curtu, Alexandru-Lucian; **Șofletea, Neculae; Finkeldey, Reiner; Gailing, Oliver; Apostol, Ecaterina; Budeanu, Marius; Ciocirlan, Elena**

Introduction of new forest tree species and provenances that are more suited to a drier and hotter climate is an actual topic in many European countries. Here, we focus on marginal populations of pedunculate oak known as *Quercus robur* ssp. *pedunculiflora* or *Q. pedunculiflora* that are located at the hot margins of the species distribution in south-eastern Romania. We found evidence of genetic differentiation between the marginal populations (*Q. pedunculiflora*) and core populations of *Q. robur* by sampling pairs of populations and using both genomic and EST-SSR markers. The vast majority of oak individuals (92%) could be assigned according to their origin (marginal/core population). The highest degree of admixture was found in an isolated, mixed oak forest on sand dunes in the Danube Delta. Our results suggest that *Q. pedunculiflora* genetic resources may harbor genetic variants better adapted to xeric conditions. The conservation strategy of *Q. pedunculiflora* considered both *in-situ* and *ex-situ* approaches. A network of *in-situ* gene conservation units has been established across its natural distribution range in Romania. Further conservation efforts should be devoted to preserve the unique natural population from the Danube Delta. For breeding and conservation purposes, a clonal seed orchard of *Q. pedunculiflora* has recently been established in the eastern part of the *Q. pedunculiflora* distribution range.

Keywords: genetic resources, oak species, climate change, local adaptation, gene conservation

Session 6: Towards climate-smart forests

Poster Session B: Thursday 16 September 13:00–15:50

Posters

Segun Bolarinwa, Michael:
Importance of forests in combating climate change

Jiménez Ramírez, Azucena:
Measuring recent effective gene flow among large populations in *Pinus sylvestris*: local pollen shedding does not preclude substantial long-distance pollen immigration

Liepe, Katharina Julie:
European hornbeam – not only a servant, but rather future candidate to add value

Jansen, Simon:
Is the grass always greener on the other side? Identifying seed sources for oak forests in a changing climate

Kastally, Chedly:
Studying the impacts of tree improvement on adaptation at the phenotypic and genomic level on Scots pine

Kurz, Mirjam:
Tracing the origin of Oriental beech plantations across Western Europe and reporting hybridization with European beech

Importance of forests in combating climate change

Contribution ID: 106

Segun Bolarinwa, Michael

In many rural areas of Nigeria, citizens still make use of firewood sourced from indiscriminate felling of trees to cook, which releases enormous amounts of carbon monoxide into the atmosphere that further deplete the ozone layer that cause climate change. Climate change has lead to significant increases in temperature combined with a decrease in rainfall, leading to increased water stress for vegetation and a greater frequency and severity of droughts. A warmer and drier climate affects the productivity of forests and provokes natural disturbances such as wildfire and pest outbreaks. The solution is reforestation and afforestation demonstrating the importance of forests to ecological stability. Also, there is an urgent need to develop an adaptive sustainable forest management (ASFM) strategy which supports the entire spectrum of benefits that forests provide, including the supply of wood as only one of many ecosystem services. Transition to ASFM supposed substantial changes in all forestry operations including reforestation, afforestation, thinning, forest protection, and regulation of final felling, as well as a new understanding of the role of forests in the sustainability of agro-forestry landscapes. Existing forests should be conserved and special measures of protection put in place where they are threatened. In light of expected increase of water stress, special attention should be paid to the selection and use of drought-resistant species and provenances as well as to the creation of seed banks for the conservation of the gene pool of native trees and shrubs. Monitoring and early warning systems are also needed for assessing feedback of forests to environmental change and extreme climate disaster, the occurrence of invasive species and pest outbreaks because forests help to prevent soil degradation and increases biodiversity. I look forward to the actualization of the United Nations Sustainable Development Goals (SDGs) 7 and 13: Clean Energy and Climate Action, respectively.

CANCELLED

Keywords: ozone layer, climate change, reforestation, conservation, biodiversity

Measuring recent effective gene flow among large populations in *Pinus sylvestris*: local pollen shedding does not preclude substantial long-distance pollen immigration

Contribution ID: 119

Grivet, Delphine; Jiménez Ramírez, Azucena; Robledo Arnuncio, Juan José

There is a generally poor understanding of the interaction between gene flow and local adaptation in forests. Estimating recent gene flow among genetically differentiated tree populations would help to shed light on this matter. We estimate here recent gene flow among two large native Scots pine (*Pinus sylvestris*) populations in the central Iberian Peninsula (Spain) using an original Bayesian approach based on uniparentally inherited markers. These populations grow on contrasting edaphic conditions six kilometers apart from each other, well within the range of pollen transport distances for this species, but they intriguingly show substantial genetic divergence in quantitative traits. We found substantial and asymmetric gene flow rates (8 and 21%) among the two natural populations and even greater recent gene flow immigration (42–64%) from nearby plantations into the two natural populations. Our results suggest that local pollen shedding within large tree populations does not preclude long-distance pollen immigration from large external sources. Overall, we believe that a combination of hypotheses might explain the apparent joint of gene flow and strong adaptive genetic differentiation: divergent selection, decreasing migrant fitness with age and environmental maternal effects.

Keywords: pollen dispersal, migration rate, Bayesian inference, chloroplast microsatellites, local adaptation

European hornbeam—not only a servant, but rather future candidate to add value

Contribution ID: 125

Liepe, Katharina Julie; Liesebach, Mirko

The drought years of 2018 to 2020 forced some of our native tree species to reach their border. Conifer stands with Norway spruce and Scots pine experienced high damages due to the lack of precipitation, high temperatures and biotic agents. Common beech, the species often held high as alternative had vast loses in vitality across Germany. Therefore, alternatives to the common species portfolio are strongly required. Species of little scientific knowledge get into focus for the reconstruction of forests, but also for the reforestation of devastated areas. One of these candidates is European hornbeam (*Carpinus betulus*), which is supposed to be highly drought-tolerant. From a silvicultural perspective, it has only small economic value till now and is used mainly to promote a positive stem form of oaks. Ecologically, hornbeam has highly valuable characteristics: it is shade tolerant, suitable in admixture with other broadleaves as well as conifer species, it has a deep root system, and its litter is easily decomposed, which improves soil conditions. An increasing proportion of hornbeam in our forest stands requires promotion and active planning. Current stands are often too small and spatially disjunct to realize notable increases through natural regeneration. Therefore, the here presented project, to be launched in October 2021, focuses on genetic and phenotypic variation of European hornbeam and the identification of highly valuable and adaptive basic material in a new provenance trial. Using reproductive material from these selected stands promotes the establishment of stands, which are biologically stable, rich in structure and beneficial from an economic point of view. We like to strongly encourage you to join the discussion and share your expertise about valuable seed sources of European hornbeam to become part of our provenance selection.

Keywords: *Carpinus betulus*, climate change, provenenance trial, seed source selection

Is the grass always greener on the other side? Identifying seed sources for oak forests in a changing climate

Contribution ID: 139

Jansen, Simon; Acar, Pelin; Aravanopoulos, Filippos; Çiftçi, Asiye; Değirmenci, Funda Özdemir; Duyar, Kürşad; İdman, Özlem Mavi; Kansu, Çiğdem; Kaya, Zeki; Kleinschmit, Jörg; Leigh, Deborah M.; Lyrou, Fani G.; Rellstab, Christian; Semizer-Cuming, Devrim; Tourvas, Nikolaos; Neophytou, Charalambos

Given the pace of climate change, it is likely that local gene pools of forest trees will not be able to adapt in sufficiently short time to the changing environmental conditions. Hence, the transfer of forest reproductive material (FRM) from preadapted seed provenances has been suggested as a promising tool to ensure forest stability. However, local guidelines for the use of FRM are still predominantly focused on regional and static seed sources. The new BiodivERsA project ACORN will develop innovative concepts of seed transfer guidelines for the three closely related white oak species *Quercus robur*, *Q. petraea*, and *Q. pubescens*. By using genetic and genomic tools in combination with common garden experiments, the project will identify drought-adapted oak populations at both regional and continental scales. Following this concept, two study areas within the natural distribution range of all three white oak species (Central Europe and Eastern Mediterranean) will be used to test whether (1) certain genes and genomic regions show an association with drought-related environmental parameters, (2) there is a common signature of drought adaptation among populations, and (3) there are genotype x phenotype associations at traits involved in drought response. These results will then be used to develop comprehensive FRM transfer strategies robust to the demands of climate change and adaptive species management. As the marketing and use of FRM is regulated by European and international legislation, the project will involve applied research institutes that formulate FRM guidelines, stakeholders, and policy makers from all cooperating countries. This will help to ensure considering all practical and policy-related aspects and, finally, to increase the resilience of our future forests.

Keywords: forest reproductive material, seed transfer guidelines, genetic adaptation

Studying the impacts of tree improvement on adaptation at the phenotypic and genomic level on Scots pine

Contribution ID: 153

Kastally, Chedly; Kujala, Sonja T.; Pyhäjärvi, Tanja; Kärkkäinen, Katri; Savolainen, Outi

Previous work has thoroughly examined the relationships of climatic factors and transfer effects on survival and growth in Scots pine by using provenance and progeny trial data. This provides good guidance for the choice of regeneration materials for current and future climates. The guidelines are also relevant, to some extent, for genetically improved trees. Tree improvement emphasizes growth and survival. To understand the effects of early stage breeding and selection on adaptation in Scots pine, we compare adaptive traits in seedlings in natural populations, plustrees, and an early breeding generation. We also compare the genetic composition of the different populations across the genome, using the Axiom PiSy50k genotyping array. Further, we explore potential effects of different management and selection strategies on the genetic diversity and adaptation of Scots pine in Finland.

Keywords: conservation, PiSy50k, Scots pine, tree improvement, selective breeding

Tracing the origin of Oriental beech plantations across Western Europe and reporting hybridization with European beech

Contribution ID: 156

Kurz, Mirjam; Brang, Peter; Rezzonico, Fabio; Smits, Theo; Kohler, Martin; Bauhus, Jürgen; Kölz, Adrian; Zhelev, Peter; Sevik, Hakan; Hansen, Ole K.; Gömöry, Dusan; Paule, Ladislav; Csilléry, Katalin; Sperisen, Christoph

With climate change, forest management is increasingly faced with the challenge of maintaining the ecosystem services forests provide. Oriental beech (*Fagus orientalis*) has been proposed for assisted migration (AM) – the translocation of populations within or outside of their natural range – to replace drought-sensitive European beech (*F. sylvatica*) at critical sites. We present a database of eight Oriental beech plantations in Germany, France and Switzerland in the proximity of natural European beech stands that can be used as natural laboratories for studying the benefits and drawbacks of AM. One of the most critical questions for AM is whether the introduced and local beech populations hybridize with one another, which may lead to hybrid vigor or outbreeding depression. Oriental beech has a vast distribution range from Iran to the Balkans, thus the origin of the plantations could play an important role in this outcome. Using 16 SSR loci, we identified five highly diverged genetic clusters that correspond to populations from different mountain ranges and different degrees of divergence from European beech (F_{ST} from 0.13 to 0.25). Then, we identified the genetic origin of each European plantation. Further, in two plantations of Caucasus origin, we found evidence for extensive hybridization between the two beech subspecies with 10 and 30% of the seedlings having a hybrid status. Finally, we also observed the spring phenology in two plantations and found evidence for an earlier bud break in Oriental beech, suggesting that gene flow between the two subspecies could be asymmetric. Our database and results showcase the evaluation of the potential risks of AM with oriental beech and call for future studies that compare the drought tolerance of the two subspecies and their hybrids.

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Area Map

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2	Lecture room: Engler-Flurysaal
3	Canteen