Workshop – Beech genomes for the future

04 April 2025
University of Zurich - Campus Irchel - Y25 H 92

Zoom Link for online participants

Information
On-site mail contacts: domitille.coqetchegaray@geo.uzh.ch & sofia.vanmoorsel@geo.uzh.ch

UZH Irchel campus is accessible by two bus/tram stations: Milchbuck and Universität Irchel. The building is Y25 - Geographisches Institut Universität Zürich. The building door closest to the seminar room H92 is highlighted by the red star above.

Please be advised that photos may be taken during the event. By attending the "Beech genomes for the future" workshop, you consent to the use of photos in which you appear in social media content published by both the workshop organizational team and official UZH social media channels. Inform us if you don't want to be in photos. (See contact mails above)

Program

8:30 - Registration and welcome coffee

——— Session I (Chair: Meredith Schuman)

9:00-9:10 Welcome
Meredith Schuman (University of Zurich)

9:10-9:30 Identifying seed families with high mixture performance in a subtropical forest biodiversity experiment
Ting Tang (University of Zurich)

9:30-9:50 Genomic variation of European beech reveals signals of local adaptation
Niels Müller (Thünen Institut)

9:50-10:10 Genome-wide association analysis in natural European beech populations
Markus Müller (University of Göttingen)

10:10-10:45 Coffee break

——— Session II (Chair: Sofia van Moorsel)

10:45-11:05 Genetic architecture of climate adaptation in European beech and sessile oak: insights from common garden experiments across Europe
Aksel Pålsson (WSL)

11:05-11:25 Contrasting patterns of genomic diversity at nuclear, mitochondrial, and chloroplast levels in *Fagus sylvatica*
Jaroslaw Burczyk (Kazimierz Wielki University) - online

11:25-11:45 A pilot study for population genomics - feasibility of Oxford Nanopore Technologies
Toja Guerra (University of Zurich)

11:45-12:00 Discussion, global Q&A

12:00-13:00 Stand up lunch

——— Session III (Break-out sessions)

13:00-14:15

1. Interests of the forestry sector in the future of European beech
2. Tools used to study genomic variation and its consequences for beech forests
3. Data needed to test and understand beech forest resilience this century

14:15-14:45 Coffee break

——— Session IV (Break-out sessions summary)

14:45-15:50

15:50-16:00 Closing of the workshop
16:00-17:30 Apero

Notes: Posters will be accessible during coffee, lunch and apero breaks.

Book of Abstracts

Talks

Identifying seed families with high mixture performance in a subtropical forest biodiversity experiment

Ting Tang (University of Zürich)

Afforestation projects using species mixtures are expected to better support ecosystem services than monoculture plantations. While grassland studies have shown natural selection favoring high-performance genotypes in species-rich communities, this hasn't been explored in forests. We used seed-family identity (known maternity) to represent genetic identity and investigated how this affected the biomass accumulation (i.e. growth) of individual trees (n = 13,435) along a species richness gradient (1–16 species) and over stand age (9 years) in a forest biodiversity experiment. We found that among the eight species tested, different seed families responded differently to species richness, some of them growing relatively better in low-diversity plots and others in high-diversity plots. Furthermore, within-species growth variation increased with species richness and stand age, while between-species variation decreased with stand age. These results indicate that seed families within species and their reaction norms along the species richness gradient vary considerably and thus can explain a substantial proportion of the overall variation in tree growth. Our findings suggest that the growth and associated ecosystem services of species-rich mixtures in afforestation projects can be optimized by artificially selecting seed families with high mixture performance in biodiversity experiments.

Genomic variation of European beech reveals signals of local adaptation

Niels Müller (Thünen Institut)

Local adaptation is key for ecotypic differentiation and species evolution. Understanding the underlying genomic patterns can allow the prediction of future maladaptation. Here, we report the whole-genome resequencing of more than 1000 individuals from 100 range-wide populations of European beech (*Fagus sylvatica*). We show that genetic variation closely mirrors geography. Genome-wide analyses for genotype-environment associations (GEAs) identify relatively few potentially adaptive variants after correcting for an overwhelming signal of statistically significant but non-causal GEAs. We characterize the single high confidence genomic region possibly involved in winter temperature adaptation via modulation of spring phenology. Surprisingly, allelic variation at this locus does not result in any apparent fitness differences in a common garden. More generally, reciprocal transplant experiments across large climate distances suggest extensive phenotypic plasticity. In summary, our results emphasize the importance, but also the complexity, of natural genetic variation in forest conservation under climate change.

Genome-wide association analysis in natural European beech populations

Markus Müller (University of Göttingen)

European beech is affected by climate change and a decrease in its growth is predicted for large parts of its distribution range. Therefore, knowledge about the genetic basis of environmental adaptation is of particular importance in this species. We identified genome-wide genetic variation in European beech based on normalized genotyping by sequencing (nGBS) and single primer enrichment technology (SPET). These data were used in genome-wide association analyses (GWAS) in German and Romanian beech populations to identify genetic variation potentially involved in environmental adaptation. Several single nucleotide polymorphisms (SNPs) were significantly associated with environmental variables as well as with drought stress-related traits such as specific leaf area, stomata density or δ13C as measure of intrinsic water use efficiency. We identified a genome region on chromosome 2 to be potentially involved in adaptation. This region is near an adaptation-related region previously identified in an independent range-wide study (Lazic et al. 2024, Nature Communications) showing the importance of complementary research to understand the genetic basis of adaptation in European beech.

Genetic architecture of climate adaptation in European beech and sessile oak: insights from common garden experiments across Europe

Aksel Pålsson (WSL)

Climate change poses a major challenge to plant and animal populations. Their persistence depends on a combination of phenotypic plasticity and evolutionary processes. Despite extensive research on organismal responses to environmental change, it remains largely unclear how long lived and ecologically important tree species will respond to climate change. To address this, we combined growth-related and leaf morphological traits from common garden experiments of sessile oak (*Quercus petraea*) and European beech (*Fagus sylvatica*) established across the species' European ranges with climatic and genomic data. Our goal was to uncover the genetic architecture of key functional traits related to drought responses and growth, and to detect signals of climate adaptation at loci controlling these traits. We first performed genome-wide association (GWA) analyses and subsequently tested the effect of climate transfer distance along temperature and precipitation gradients at candidate loci. Our GWA analyses revealed a polygenic genetic architecture underlying functional traits in both species with oak displaying a higher degree of polygenicity than beech. We found evidence of pleiotropy within functional trait groups. With increasing climatic distance, beech showed limited plastic and adaptive responses at the genomic level. In contrast, oak showed signals of both adaptive plasticity and climate adaptation, particularity at loci associated with short term growth responses to extreme drought. Our findings suggest that, in contrast to oak, beech has limited capacity to respond to climate change. In oak, transplantation from preadapted provenances promoting introgression of adaptive alleles could mitigate future population decline. Our results highlight the complex species- and population-specific responses to climate variation and suggest that oaks may replace European beech as the dominant deciduous tree species across Europe under future climatic conditions.

Contrasting patterns of genomic diversity at nuclear, mitochondrial, and chloroplast levels in *Fagus sylvatica*

Jaroslaw Burczyk (Kazimierz Wielki University)

European beech (*Fagus sylvatica L.*) is one of the most important broadleaved forest tree species in Central Europe; however, its phylogeographic structure, essential for managing forest genetic resources, remains unclear despite several research efforts undertaken. Here, we investigated the genomic diversity of six beech populations (400 individuals, structured in adult, juvenile, and seedling cohorts) in Central Europe based on complete individually assembled mitochondrial and chloroplast genomes, as well as a battery of 1,028,240 nuclear SNPs assessed from whole-genome sequencing experiments. The PCA analyses indicated distinct groups of individuals that corresponded well to their locations. However, nuclear SNPs based on STRUCTURE revealed the three main genetic ancestral clusters (northern, western, and eastern) evident across all populations, generating a reasonable pattern of phylogeographic structure. Genetic differentiation among populations was low Fst=0,0267; however, it was significantly related to physical distance among populations (r=0.8159; p¡0.0002; R2=0.6658). The northernmost population, Świerczyna, demonstrated distinct genetic structure changes across generations. For organellar DNA, we defined 32 and 95 unique assemblies (haplotypes) for mtDNA and cpDNA, respectively, suggesting different rates of evolution of mitochondrial and chloroplast genomes. The spatial distribution of haplotypes among populations was highly unbalanced and slightly different for both types of organellar; however, both types of organellar haplotypes represented two major haplotype groups, unraveling possible migration routes of beech forests. The westernmost population, Boetzingen, exhibited an unusually large diversity of mt- and cpDNA haplotypes (in contrast to relative homogeneity at nSNP), suggesting its artificial establishment.

Genetic adaptation of young beech trees (*Fagus sylvatica*) through weather extremes – Establishing a monitoring method

Toja Guerra (Universität Zürich)

Extreme weather events and their effects on the genetic structure of forest tree populations are a central yet under-researched topic. Preserving genetic diversity is crucial for the sustainability of forests adapting to climate change. Current forest monitoring systems track changes in biodiversity, soil chemistry, nitrogen deposition, ozone, weather, etc. (biotic and abiotic gradients) but rarely consider tree genetic aspects. Genetic monitoring could document changes in the genetic structure of forest stands over time. This is especially relevant for European beech, a key forestry resource that, despite its adaptability, suffered severe losses during the 2018 drought. Beech dieback, coupled with increasing drought periods and the need for resilient forest regeneration motivated this project. The aim is to create a foundational dataset for long-term monitoring and to develop methodologies to study the genetic profiles of beech following extreme weather events, with periodic re-assessments. A central hypothesis is that beech germinating after the 2018 drought exhibit a different genetic composition compared to previous generations, with these changes attributable to drought conditions. The project encompasses ten sites in the Basel and Zürich regions with varying levels of drought (dry, dry and damaged, and moist). Each site involved sampling 20 seedlings that germinated after the 2018 drought and their presumed mother trees (i.e., the tree closest to the seedling) in February 2024. The 400 samples were prepared for DNA extraction for Illumina whole-genome sequencing. Population genetic studies enable detailed analyses of genetic differences among mother trees and seedlings which allow investigating potential adaptation mechanisms in response to the 2018 drought event. The results will form the basis of a genetic long-term monitoring system. This could provide critical insights for sustainable forest management and the adaptation of tree species to future climate changes.

Posters

Genomic signatures of adaptation to drought in European beech and sessile oak: insights from natural populations

Christian Rellstab (WSL)

Because of ongoing climate change, forests are increasingly subject to 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. Here, we investigated the genetic basis 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. 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 over 500 beech and almost 400 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. Our results show highly polygenic and pleiotropic patterns. The genotype–environment associations revealed similar environmental factors driving the genomic signatures of adaptation to drought in the two species, despite different sampling locations. Moreover, we found an enrichment of shared gene families potentially underlying drought-related traits in the phenotype-genotype associations. Overall, our study shows important differences and similarities in adaptive signatures between the two species in relation to drought under climate change.

Leaf spectroscopy reveals drought response variation in *Fagus sylvatica* saplings from across the species' range

Sofia van Moorsel (University of Zurich)

The common European beech (*F. sylvatica*), sensitive to prolonged drought, is expected to shift its distribution with climate change. To persist in novel environments, young trees rely on the capacity to express diverse response phenotypes. Several methods exist to study drought effects on trees and their diverse adaptive mechanisms, but these are usually destructive and challenging for the large sample numbers needed to investigate biological variation. We conducted a common garden experiment outdoors, but under controlled watering conditions, with 180 potted two-year-old saplings from 16 beech provenances across the species' range, representing three distinct genetic clusters. Drought stress was simulated by interrupting irrigation and stomatal conductance and soil moisture were used to assess drought severity. We measured leaf reflectance of visible to short-wave infrared electromagnetic radiation to determine drought induced changes in biochemical and structural traits derived from spectral indices and a model of leaf optical properties. We quantified changes in pigmentation, water balance, nitrogen, lignin, epicuticular wax, and leaf mass per area in drought-treated saplings, revealing differences in likely adaptive responses to drought. *Fagus sylvatica* saplings from the Iberian Peninsula showed signatures of greater drought resistance, i.e., the least drought induced change in spectrally derived traits related to leaf pigments and leaf water content. We demonstrate that high-resolution leaf spectroscopy is an effective and non-destructive tool to assess individual drought responses that can characterize functional intraspecific variation among young beech trees. Next, this approach should be scaled up to canopy-level or airborne spectroscopy to support drought response assessments of forests.