Beech genomes for the future workshop summary

4 April 2025, University of Zurich

As a drought-sensitive species, European beech might be particularly vulnerable to climate change, increasing temperatures and rain-free days in Switzerland and Europe. The drought in 2018 has led to significant dieback in Switzerland, and models estimate large reductions in population growth rate in the coming decades in Europe. However, there is evidence that some beech individuals or populations may be more resistant to drought. Characterizing the genomic variation underlying beech resistance to drier and hotter climates will be key to determine where and under what conditions beech forests will persist in Europe.

For this workshop, we invited researchers who work on beech genomics, including GWAS with natural and experimental populations, experimental approaches involving drought and climate, studies investigating assisted gene flow, and researchers developing strategies to monitor beech genetic diversity. In the drought stress context, we were particularly interested in approaches to find the genetic basis of complex traits such as drought response that are not governed by individual genes and likely to be context dependent. The aim of the workshop was a better overview and understanding of available data and tools, knowledge on pitfalls and challenges, and network of scientists striving to reach similar goals.

Meredith Schuman opened the workshop by highlighting the dire situation of *F. sylvatica* in light of climate-change in Europe, with predicted growth declines across large parts of the continent. Then, Ting Tang, Postdoc at the University of Zurich, presented her recently published work on identifying seed families that are either better for forest mixtures or monocultures. Some seed families prefer a more diverse environment, and others prefer growing in monoculture, suggesting that it might be advisable to use mono-preferring seed families when reforestation is focusing on monocultures, and *vice versa*. Furthermore, she found that genetic identity (seed family) is more strongly related to tree growth in more diverse communities and becomes more important with stand age.

Once we established that intraspecific genetic variation within tree species is key for sustainable forest management, Niels Müller from the Thünen Institute in Germany explained that beech's large distribution range implies a very broad ecological amplitude as this species must deal with many different conditions. He convinced us that in *F. sylvatica*, most of the variation occurs between individuals, not populations. He presented a beech pangenome project leading to the study of structural variants occurring among individuals and showed that large structural variants are present even within an individual. Thus, using a single reference genome is not always appropriate, as doing so may filter out large insertions and deletions including genes that could be potentially adaptive. Finally, he highlighted that engaging in "naïve" assisted gene flow according to the climate of source populations may not be the best strategy, because gene-environment associations are often not very strong in beech. Rather, we might take advantage of the variation within populations to support general adaptive capacity.

Next, Markus Müller from the University of Göttingen presented results of two projects performing genetic association analysis to identify loci potentially adaptive to the environment. In the first project, the group identified potential SNPs associated with several environmental variables and specific leaf area in German stands using different models (Lfmm, TASSEL, pRDA and Bayenv2). For the second project, they studied beech individuals along an elevational gradient in Romania and performed an environmental association study to identify loci potentially involved in drought responses of beech trees. They identified two regions along the beech genome potentially involved in drought adaptation, with one of the regions co-occurring on a chromosome identified in the study of (Lazic et al. 2024).

Interest in the variation expressed among beech saplings from different sources and mother trees.

In the second presentation session, Aksel Pålsson, a postdoctoral researcher at WSL in Birmensdorf, presented ongoing work on the genetic architecture of functional traits in European beech and sessile oak. Using genome-wide association studies (GWAS), he examined how the genetic architecture of these traits differs between the two species and whether allelic effects are associated with climatic distances, providing insights into potential climate adaptation. His findings suggest that oak displays stronger genetic control over these traits and shows evidence of both phenotypic plasticity and climate adaptation, indicating a capacity to respond to climate change. In contrast, beech appears to rely more on phenotypic plasticity, with limited evidence of adaptation, raising concerns about its future persistence. The discussion that followed highlighted the challenges of linking traits directly to fitness, noting that trait–fitness relationships are often context-dependent.

Jaroslaw Burczyk then gave a presentation online from Poland. He introduced beech as a “graceful tree species” and showed work on genetic analyses of both adult and juvenile beech in six sites located in Germany and Poland using nuclear (preferably neutral), chloroplast and mitochondrial DNA. He focused on using complete organellar genomes to assess the history of migration and colonization processes. For specific populations, specific chloroplast and mitochondrial haplotypes were observed arranging the six populations into two distinct groups. However, nuclear data demonstrated a different pattern with three to five genetic ancestral groups. The share of different clusters changed gradually among populations, mostly in the west-east direction. His findings suggest that pollen dispersal is an efficient means of connectivity among populations, and that the current distribution of genetic diversity of beech is based on seed and mostly homogenizing pollen migration (and of course human planting). Interestingly, he found no differences among age groups in terms of chloroplast and mitochondrial haplotypes, and only slight changes in juvenile cohorts in the most northern populations suggesting an increased importance of pollen mediated gene flow from the west.

As the final speaker of the day, Toja Guerra, a research assistant at the University of Zurich, presented her first key lessons learned from a pilot study using Oxford Nanopore sequencing technology for population genomics on pooled samples. In her study, it became evident that achieving equimolar pooling presents significant challenges. ONT requires high-molecular-weight, unfragmented DNA to generate optimal long reads, and differences in DNA quality that are difficult to detect lead to large variation in read numbers. One solution is to sequence more DNA to be sure to obtain sufficient information, but balanced coverage for population genomics is a challenge and costs do not scale. She concluded that although Illumina sequencing is less future-proof, it currently remains the most feasible option in terms of the ratio of expense to reliable information gained for population genomic studies.

Before the lunch break, we used the opportunity to catch some sun and fresh air and visited the beech sapling common garden experiments running at the University of Zurich.

The result of an engaging discussion on genomics tools.

In the afternoon, we made three separate smaller groups to discuss three different topics in more detail and to foster interactions among the workshop participants.

The first group with Kathrin Streit, Lukas Denzler, Julia Born, Sabine Braun, Luca Rohrbach, Ting Tang and Sofia van Moorsel discussed the interest of the forestry sector in the future of beech. Forestry interest in beech is limited due to its low economic value, with some forests even resorting to burning it. Deer also avoid beech, which, however, aids in beech natural regeneration. Ideally, foresters would like rapid ways to assess tree quality, such as identifying a valuable tree in under a minute. There is debate over whether vitality is a reliable predictor, and demand persists for straight-growing trees, shaping both breeding and management priorities. Foresters believe that beech seedlings will manage fine in the near future under climate change. However, beech dominance in a forest does not necessarily equate to high stand-level growth. Therefore, concerns remain about how many seedlings will reach reproductive maturity and successfully reproduce. Beech is highly competitive, but old trees are vulnerable—especially to acute drought stress—and insect outbreaks can further drive high turnover, particularly among older trees. To build heathy forests, Canton Basel has advocated for diversifying with native species, including site-specific tree species mixes.

The second group with Domitille Coq--Etchegaray, Camilla Stefanini, Aurelien Estarague, Cheng Li, Toja Guerra, Markus Müller, Christian Rellstab, Dezanka Lazic, Leo Zeitler, and Jarek Burczyk discussed experimental setups, genome resources, and genomics tools to study the genomic variation of beech forests. They highlighted a gap of studies over the continuum of the life stages of beech trees: most studies use old established common gardens or seedlings growing in experimental conditions to study genetic diversity. For genome resources, the notion of reference bias was discussed in population genomics and how this might include gaps of knowledge regarding specific genetic variants that might be involved in adaptation. They concluded that the beech pangenome project led by the Thunen Institute will tackle the reference bias by creating a beech pangenome allowing to study functions of the “dispensable” (variable) genome across Europe and larger genetic variants such as structural variants. For genomic tools, they highlighted a gap in tools to perform SNPs calling and genotyping from low-coverage Illumina sequencing which allows the sequencing of a large number of individuals to investigate the genetic basis of phenotypic traits at relatively low cost. Regarding cost reductions via pool-seq, some existing methods are limited to animal studies, and their application to plants would require further investigation.

A third group with Lars Opgenoorth, Katrin Heer, Aksel Pålsson, Oliver Gailing, Niels Müller, Lucian Curtu and Merry Schuman discussed what is needed to ensure resilient beech forests in the future. They concluded that to assess the resilience of beech forests requires large-scale, collaborative efforts combining high-resolution genomic and phenotypic data from extensive and ecologically diverse populations. Phenotypic data currently seem to be more limiting than genotypic data. Gaps include limited understanding of plastic traits, epigenetics, and biotic interactions, as well as the need for high-throughput, standardized phenotyping and better trait-fitness linkages supported by tools from remote sensing. Experiments using cloning and other methods to manipulate genotypes in shared environments, across gradients, or with manipulation of environmental factors are needed to understand mechanisms of adaptation and plasticity, and the adaptive value of plasticity. While we have increasing genomic resources, especially short-read data, unlocking meaningful predictions about forest-level resilience will require integrative approaches, improved models, and strategic experimentation—ideally supported by structured trials, pangenomic tools, and comprehensive genotype–phenotype databases.

The workshop then wrapped up with a group photo and an Apéro.

We thank the SwissForestLab for funding the workshop and helping with organization. To all participants, a warm thanks for joining and contributing to engaging discussions.

We hope that this workshop and continuing interactions among all participants will produce new and impactful ideas, initiatives, and projects and look forward to continuing the conversation and the work!

The on-site workshop participants.