Summary

Forest ecosystems cover a third of the Earth's land surface and their future is an important factor in climate change. Forest genetic resources entail the capacity of existing genotypes to support forest functions and services. Genetic differences are important as the basis for management decisions: for example, whether to introduce new provenances as opposed to fostering re-generation from local trees. The European beech *Fagus sylvatica* is a widespread forest tree and wood source across Europe and into western Asia, often growing in monodominant or pure stands. A wind-pollinated species, *F. sylvatica* harbors relatively high genetic diversity within versus between populations. Sibling beech trees are reported to be highly plastic, and individuals display increasing variability in performance and survival under global change. For example, neighboring beech trees often show large differences in resistance to extreme drought events and highly variable spring phenology, *i.e.*, the time at which trees unfold their leaves and begin to capture carbon for growth. ***These differences are partly explained by phenotypic plasticity related to competition and microenvironments, but likely also have a genetic basis providing resources for beech forests to adapt. Dissecting such differences requires an individual-based approach: why do individuals differ in their responses to the environment, and which aspects are heritable?*** For forest tree species such as *F. sylvatica*, answering this question requires detailed ecological and genomic information. Although its genome is relatively small (ca. 1 Gbp diploid) and a high-quality reference assembly is available, there is no well-tested database of functionally annotated genome features and so far, no pangenome documenting the species diversity. *F. sylvatica* is an obligate outcrosser with generation times of several decades and is thus not developed as a genetic model. Due to costs of deep sequencing, datasets at the species scale are often taken from small local subsamples or pools using marker-based or reduced representation approaches, without detailed metadata. This hinders our understanding of differences between individuals that are important to predict the future responses of forests to climate change. Advances in genomics and remote sensing open new possibilities for efficient assessment of heritable and functional diversity, especially in non-model species and observational sample sets. Poland and Romania have natural beech populations located in the northeasternmost sites and at hotter margins of their natural distribution, and large tracts of old-growth forests with beech trees approaching their longevity (400-450 yrs) in the Carpathian mountains. Switzerland and Austria monitor forest tree growth, health, traits, and related forest properties including biodiversity measures in stands across the country, and harbor two protected old-growth beech forests on either side of the Alps. The applicants together already have over 1000 georeferenced *F. sylvatica* genomes from across the species range. ***In this project, we propose to (1) describe individual- and population-level genetic variation within and across monitored and old-growth forests in the partner countries in the context of variation across the beech species range, (2) select representative individuals to construct a pangenome, (3) leverage monitoring and remote sensing data to characterize the environment, traits and performance of all sequenced individuals in our database in detail over time, and (4) identify features of the beech genome important for adaptation to variable environments.*** This project will provide essential information for the adaptive management and conservation of beech forests under increasing disturbance and global change.