

European beech (*Fagus sylvatica* L.) is an important forest tree species in Central Europe, both from economic and ecological point of view. However, despite the extensive efforts of the scientific community little is known about genome-wide variation of this species, its distribution among populations and how this variation determines the species' adaptive potential in the face of global climate changes. These limitations were partly due by insufficient genomic resources of beech; nevertheless, recently the teams submitting this project proposal published a high quality reference genome of *Fagus sylvatica*. Joint efforts to investigate genetic diversity and its determinants at genomic level should be beneficial for both countries, but also for entire scientific community and European forestry in general. Studying population genomics of beech populations at north-eastern distribution limits of the species is particularly interesting in the context of its range expansion associated with climate change.

Using the whole genome sequencing (WGS) approach, we will resequence altogether 360 individuals. We will investigate genetic diversity and differentiation among natural populations of *Fagus sylvatica* representing three major refugial lines of this species (reference populations) defined in Central Europe based on our earlier studies facilitated by genomic scans (ddRADseq). Additionally, based on the populations intermediate to the reference populations, we will explore the signatures of admixture between different refugial lineages at genomic level and attempt to identify genomic regions demonstrating admixture asymmetry, supposedly important for adaptation facilitated by lineage admixture. Within the reference populations, we will investigate how the neutral and non-neutral genetic diversity is transferred to younger generations, and will attempt to trace any signatures of selection currently ongoing within the populations located in different parts of the species distribution. These findings will have tremendous importance for understanding the background and underlying mechanisms driving changes in neutral and adaptive genomic regions, which will be relevant for managing of genetic resources of this species in the context of gene conservation but also in silvicultural practices, including tree improvement and assisted migration efforts.

The two research teams submitting this proposal have distinct and complementary areas of scientific excellence. The German team has long lasting interest in genomics, genome evolution, phylogeny, species diversity and systematics. The Polish team has experience on population genetics and genomics of forest trees, gene conservation, mating system and gene flow in plants, particularly in trees. Joint collaboration during this project will be beneficial for both research groups, and will likely lead to long-term cooperation focused on population genomic studies.