Forest trees are important drivers of terrestrial biodiversity; however, the predicted global climatic changes and the land use changes in Europe will impact several tree species, resulting in large-scale changes in species' natural ranges, ecosystem functioning, and interactions among species within a few decades. The difficulty in predicting the responses of forest trees to future conditions has led to an increasing interest in research aimed at deciphering the genomic basis of complex traits related to trees' adaptive potential. Indeed, the relationships between genomic and adaptive diversity seem particularly important in keystone forest tree species because such knowledge could readily facilitate the management of forest genetic resources in the face of global climate changes. However, despite several efforts, convincing examples of the relationships between diversity in quantitative and adaptive traits vs. molecular variance at the genomic level are still scarce or missing in forest trees.

Pedunculate (*Quercus robur* L.) and sessile oak (*Q. petraea* (Matt.) Liebl.) are the most important forest tree species in Central Europe, and they are excellent species for studying local adaptation. Oaks often served as model species in forest genetics and genomics and have established reference genomes. In Poland, oaks grow on over 8% (742 836 ha) of the total forested area, and large amounts of seedlings each year are used for reforestation (in 2023: 133 mln seedlings of *Q. robur*, 38 mln seedlings of *Q. petraea*). However, global climate changes are expected to affect European oak forests. Therefore, it is essential to review the decision-making framework for seed sourcing used in reforestation, accounting for possible climate changes.

The main goal of the proposed research is to develop a genetically informed, geographically coherent strategy for conserving and managing forest genetic resources of native oaks in Poland. We intend to identify forest areas that are genetically and evolutionarily distinct and detect geographic regions of greatest or locally-specific genetic diversity. We will investigate the relationships between genomic diversity and environmental variables and use this information to understand the mechanism underlying the spatial patterns of genomic diversity related to adaptation. To ensure achieving these goals, we will introduce two innovations.

The first innovation will be the establishment of the pangenomes of *Q. robur* and *Q. petraea*, which will serve as advanced references for assessing genomic diversity within each species. However, by '*genomic diversity'*, we understand the diversity assessed with all types of available genome-wide polymorphisms, such as SNP (Single Nucleotide Polymorphism), InDels (insertion/deletion polymorphisms), and structural variants, including CNV (Copy Number Variation), PAV (Presence/Absence variation), other SVs (e.g., inversions, translocations, segmental duplications).

The second innovation will be the application of an individual-based sampling (IBS) approach (as an alternative to population-based sampling) combined with the development/update of appropriate statistical methods for assessing the spatial patterns of genomic diversity. Individual-based sampling is a promising approach, particularly for conservation and management efforts, due to the increased coverage of areas believed to improve sample representativeness. It provides a more detailed picture of population structure, better recognition of regions with greater diversity, and allows for prioritizing specific conservation areas. IBS gives a better opportunity for developing sampling designs with increased spatial resolution and coverage of a broad spectrum of environmental variables, and it minimizes bias that might be introduced by specific (outlier) populations sampled.

These two innovations will enable us to thoroughly explore the whole genome sequence (WGS) data of several hundreds of oaks and discover the mechanisms underlying the distribution of genomic diversity across the country. We will verify several vital research hypotheses related to genome organization, genotype x environment associations, phylogeography, and interspecific divergence and hybridization. With this knowledge, we will critically review and update the existing guidelines for managing forest genetic resources, particularly regarding seed-zone delineations and assisted migration of forest reproductive material. The research results will be important for the development of forest tree genomics.