

## Summary

Climate change is one of the most serious challenges for contemporary forest management, necessitating the implementation of adaptive management strategies. Such actions should focus on utilizing populations of tree species that are possibly best adapted, thereby supporting the resilience of entire ecosystems under rapidly changing environmental conditions. A key component of these strategies is the identification and conservation of forest tree genetic resources of great ecological, economic and social importance. Maintaining the evolutionary adaptive potential of species largely depends on their existing genetic variability; therefore, preserving the widest possible spectrum of genetic diversity is essential to ensure the continuity of forest ecosystem functioning and the sustainability of forest management. This issue gains particular importance in the light of pessimistic forecasts regarding the future of forests.

This doctoral dissertation comprises three thematically linked scientific articles focused on Scots pine (*Pinus sylvestris* L.) - a key species in the complex forest ecosystems of Eurasia, of great ecological, economic, and social significance, with a long history of both basic and applied research. Over the years, numerous attempts have been made to assess the breeding and genetic value of Scots pine populations, including the long-term provenance trials. These studies formed the basis for identifying the most valuable pine stands and for establishing seed regions. Despite these longstanding efforts, a comprehensive genomic assessment of Poland's most valuable native Scots pine ecotypes is still lacking. Moreover, in light of recent knowledge, the validity of the provenance region delimitation may require substantial revision.

Therefore, the main aim of my research was to investigate the genetic structure, phenotypic variability, and climatic characteristics of the most valuable Polish Scots pine

stands, managed under the strict provenance region system regime. This study investigates 27 Registered Seed Stands (RSS) populations, representing all 24 currently recognized Scots pine seed regions in Poland. Additionally, 31 populations from the species' natural European range, with ten Carpathian sites in Poland, were included as a reference group. A range of methodological approaches was applied, integrating analytical tools and data from population and conservation genetics. Genetic analyses were complemented by measurements of phenotypic traits and characterization of the climatic conditions of the seed stands.

The first article (Lasek et al., 2024; *Evolutionary Applications*, 17: e70038) focuses on characterizing the genetic structure of the current Polish Scots pine seed regions, represented by the most valuable Reserved Seed Stands and selected plus trees. For this purpose, a set of 16 nuclear SSR microsatellite markers, 13 polymorphic mitochondrial DNA markers, and the PiSy50k SNP array were used. High genetic similarity was observed among the studied populations, along with a substantial level of within-population variation. The observed pattern indicates a shared postglacial history of the populations and suggests potential admixture of different gene pools during recolonization. Moreover, the genetic differentiation of the studied stands did not strictly reflect the currently defined provenance regions delimitation in Poland. These results are therefore significant for forest management, contributing to discussions regarding the revision of provenance regions boundaries, particularly in light of the current challenges that Scots pine is facing in Europe.

The second article (Lasek et al., *Forest Ecology and Management*, after revision) examines whether Polish Scots pine stands share a common origin, shaped by postglacial demographic history and admixture of multiple gene pools. Phylogeographic analyses were conducted using an extensive dataset, including over 37,000 genome-wide SNPs

and 12 mitochondrial DNA markers. The primary dataset was expanded with reference populations from across the European range, including the Western Carpathians, and tested 56 sites in total. The analyses demonstrate that historical mixing of European lineages increased the genetic diversity of Polish Scots pine populations, enhancing both their genetic richness and adaptive potential. Compared to European reference populations, Polish RSS stands exhibited high levels of genetic variation and greater within-population haplotype diversity. This approach also allowed the identification of unique evolutionary heritage of Polish highland populations, characterized by distinct genetic composition. The study discusses the implications of these findings for adaptive forestry under climate change, highlighting the importance of Polish populations in European genetic resource management programs.

The third manuscript (Lasek et al., *Forest Ecology and Management*, under review) integrates phenotypic and climatic data from the 27 registered seed stands (RSS), supplemented with genetic information based on thousands of SNP markers and forest productivity modeling under forecasted climate-change scenarios. The results revealed substantial phenotypic variation among the stands, particularly regarding growth traits. Climatic variation alone was insufficient to explain the observed differences in growth performance, and the phenotypic variability could not be explained by neutral genetic structure. Further research is needed to elucidate the genetic basis of the observed phenotypic variation, focusing on identifying genomic signals of local adaptation, as well as progeny trials and assisted migration experiments.

Overall, the results highlight the need to revise management strategies for Scots pine populations, including the principles of provenance regions delineation, and emphasize the necessity of utilizing reproductive material with high genetic diversity. Such an approach is crucial for preserving genetic variation and, consequently, maintaining the

long-term productivity and stability of Scots pine forests under rapidly changing environmental conditions. In the face of ongoing climate change and its already observed negative impacts, strategies aimed at facilitating adaptation, such as assisted migration and assisted gene flow, should be considered.