## Summary

Biodiversity is unevenly distributed across the globe, and areas with exceptional biodiversity are prioritized in conservation efforts. The Caucasus ecoregion is recognised as one of the 36 global biodiversity hotspots, with high biological diversity and endemism. However, this biodiversity faces significant challenges from both global and regional environmental and climatic factors, which pose a significant threat to the survival of the region's biota. Additionally, despite the key evolutionary and biogeographical importance of the region for the origin and formation of the European flora, the Caucasus ecoregion has generally been overlooked in scientific research.

This dissertation presents an analysis of the biogeographic processes, genetic diversity patterns, and demographic history of the Neogene relict tree species, *Castanea sativa* Mill., growing in the natural forest of the Caucasus ecoregion.

*Castanea sativa* Mill., commonly known as the European chestnut or sweet chestnut, is a well-known component of the natural forests of the Mediterranean region and is of great ecological, economic, and cultural importance in the region. The species has deep historical and cultural links with human populations in the Mediterranean, Anatolia, and the Caucasus. However, domestication has led to significant changes in the spatio-temporal aspects of the genetic structure of the species throughout its European range. In contrast, the isolated Caucasian range is thought to be less transformed. However, studies on the genetic diversity and historical biogeography of sweet chestnut in the Caucasian range are lacking. Meanwhile, the species in the Caucasus face multiple threats such as climate change, fragmentation, invasive pests, and overexploitation. Studies of patterns of neutral genetic variation and their underlying determinants, as well as the demographic history of the species across its range, can shed light on the evolutionary history of Neogene relict tree species, a valuable minority in modern floras. In addition, the knowledge gained offers promising opportunities for effective conservation and management, with particular emphasis on the challenges posed by adverse climate change and other forms of human activity.

In the research papers that make up this thesis, a number of methodological approaches have been systematically applied to populations of sweet chestnut. The sampling effort was comprehensive, extending from the westernmost to the easternmost extent of the Caucasian range of sweet chestnut, encompassing a total of 21 populations from Georgia and Azerbaijan,

and a single European stand from Macedonia. Nuclear microsatellite (nSSR) markers were used to assess genetic diversity, population structure, and demographic history. These markers allowed a thorough investigation of the genetic dynamics within the populations and at the landscape level.

The overall aim was to reconstruct the evolutionary history of the species and to understand how this affected the present genetic structure. This was achieved through the rigorous application of Bayesian inference and species distribution modelling. This analytical approach provided insights into the temporal dimensions characterising the divergence between the Caucasian and European populations, as well as intraspecific diversification within the Caucasian range. The ecological and historical drivers of population genetic structure have been identified. Furthermore, the study, which was adept at identifying and delineating impending threats from climate change, included estimating future projections of species range shifts and identifying the least resilient gene pools in response to climate change.

As the scientific evidence shows that genetic diversity is crucial for maintaining the diversity and functioning of ecosystems, the genetically informed conservation strategy was investigated for the Caucasian populations of sweet chestnut. Specifically, niche modelling and genetic characterisation prioritised populations for *in-situ* and *ex-situ* conservation. Furthermore, given the high risk of maladaptation of chestnut populations in the Caucasus as assessed by climate-based projections, an assisted gene flow strategy was evaluated to support the climatic resilience of Caucasian populations.