

Abstract

Introduction and Aim: Understanding the spatial distribution of intraspecific genetic variation in trees is essential for conservation and management of forest genetic resources. In pedunculate oak (*Quercus robur*), an economically and ecologically important European tree, southern and southeastern provenances are considered to be putative reservoirs of local adaptations to warm and dry climates, and yet remain underrepresented in range-wide population genetic studies. Herein, we analyze nuclear and chloroplast population genetic structure of *Q. robur* across Central and Southeastern Europe, including the subspecies *robur* and *pedunculiflora* contact zone, and assess contributions of postglacial recolonization, geographic barriers, fine-scale topography, and human influence to contemporary diversity.

Location: Transect from west-central Europe, north of the Alps to the Black Sea.

Methods: We genotyped 1,500 individuals from 56 populations using 16 nuclear (nSSRs) and 8 chloroplast (cpSSRs) microsatellites. We assessed nuclear genetic structure and diversity with Bayesian and spatial multivariate analyses, quantified differentiation (AMOVA, F_{ST}) and inferred chloroplast lineages/haplotypes differentiation and phylogeographic structure.

Results: nSSRs revealed low but significant among-population differentiation and a coherent pattern with three clusters: west-central Europe, Dinaric Alps - Pannonian Basin, and southeastern Balkans. Genetic diversity increased from west to southeastern Europe. Chloroplast haplotype variation showed pronounced spatial structure congruent with glacial refugia and migration routes. The two subspecies were weakly differentiated and shared chloroplast lineages across the contact zone, indicating substantial gene flow.

Main Conclusions: Postglacial recolonization and landscape features structured genetic variation in *Q. robur*. Southeastern populations retain deep lineage structure and high regional allelic richness with many private haplotypes/alleles, consistent with rear-edge position of postglacial expansion. Elevated diversity in contact zones along the northern Alps indicates admixture among recolonization routes, compatible with cryptic late glacial microrefugia near the Alpine-Carpathian corridor. Integrating nuclear and chloroplast patterns, we recommend safeguarding southeastern gene pools, maintaining connectivity across contact zones, and aligning Genetic Conservation Units with the three major clusters.