

POPULATION GENETIC SURVEY OF AN OLD WORLD OAK, *QUERCUS CERRIS*, AS A STARTING POINT FOR THE DEVELOPMENT OF ADAPTIVE OAK MANAGEMENT IN CENTRAL EUROPE

Botond B. Lados, László Nagy, Attila Benke, Csilla É. Molnár,
Zoltán A. Köbölkuti, Attila Borovics, and Klára Cseke

PURPOSE AND SCOPE

Turkey oak (*Quercus cerris*) is a widespread species of cork oak, distributed from Central and southeastern Europe to Asia Minor. The species has long been known for its enormous phenotypic-genotypic variability and extreme adaptability. According to recent results of climate-based modelling of species' future distribution, Turkey oak could be a winner of climate change in Central Europe (Illés and Móricz 2022). For this reason, this species may be a key element in forestry climate adaptation in this region. However, it is necessary to collect detailed information on the species' ecological characteristics, drought adaptation characteristics, and genetic diversity and structure of wild populations throughout its range to develop effective adaptation strategies. In this study, we investigated the genetic diversity and population structure of 32 natural Turkey oak populations throughout the Carpathian Basin and the Balkan Peninsula.

METHODS AND APPROACH

To allow for a detailed survey of genetic diversity and population structure in the study region, we extensively sampled 32 natural populations throughout the Balkans and the Carpathian Basin. As a result, samples of 321 Turkey oak individuals were included in our analyses. Genotyping was carried out by using double digest restriction-site associated DNA sequencing. During single

Botond B. Lados, Research Assistant, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

László Nagy, Senior Research Fellow, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

Attila Benke, Senior Research Fellow, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

Csilla É. Molnár, Institute Engineer, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

Zoltán A. Köbölkuti, Senior Research Fellow, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

Attila Borovics, Head Director, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

Klára Cseke, Senior Research Fellow, University of Sopron, Forest Research Institute, Department of Tree Breeding, Sárvár 9600, Hungary

nucleotide polymorphism calling, we used the Turkey oak genome and the well-annotated genome of cork oak (*Q. suber*) to establish two high-resolution reference-mapped datasets. In our population genetic analyses, we implemented multiple clustering approaches such as fastSTRUCTURE, principal components analysis, and randomized accelerated maximum likelihood to infer population structure.

FINDINGS AND IMPLICATIONS

According to the different clustering approaches, we found strong genetic structures among the investigated Turkey oak populations. Throughout the Balkan Peninsula, populations were separated into three genetic groups (West-Balkan group, Central Balkan group, East-Balkan group), representing the legacy of former glacial refugia. Inside the Carpathian Basin, the West Balkan and Central Balkan groups are mixing, constituting an admixture zone in the central part of Hungary. In addition, we also found an outlier population which constitutes a separate genetic group in the northern part of Romania. This strongly separating group may be the result of a founder event. According to diversity indices, Turkey oak populations have a relatively high level of diversity in the study regions. Based on the more genetically diverse and structured Balkan populations, wild populations of this biogeographical region seem promising for further studies on the species' adaptation to climate change. In addition, the strong genetic structures of natural Turkey oak populations draw attention to the careful implementation of long-distance reproductive material transfers in the practice. Although long-distance movements can increase the local genetic diversity, thus improving adaptability, they can also irreversibly change the locally evolved genetic variation and, by causing introgression, may blur the differences between the naturally differentiated genetic groups.

LITERATURE CITED

Illés, G.; Móricz, N. 2022. Climate envelope analyses suggests significant rearrangements in the distribution ranges of Central European tree species. *Annals of Forest Science*. 79: 35. <https://doi.org/10.1186/s13595-022-01154-8>.

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