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Population genetic structure and delineation of conservation units in European larch (*Larix decidua* Mill.) across its native range

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Highlights

- Low to moderate genetic differentiation in *Larix decidua* was observed across its native distribution area.
- More significant genetic differences were proven within Alpine larch than in Carpathian larch.
- Three different conservation units were delineated in the Alps and one in the Carpathians.

Abstract

Conservation of the intraspecific genetic diversity of trees is crucial for long-term forest sustainability, especially in the expected scenario of climate change. *Larix decidua* is an excellent example of a very common species for which better knowledge of the population genetic structure is needed. The aim of this study was to examine the molecular genetic variability of *L. decidua* in the Alps and Western Carpathians with adjacent areas using simple sequence repeat (SSR) markers. Low to moderate levels of genetic differentiation were observed among the study populations across the native distribution area of *L. decidua*. Based on AMOVA and PCoA, we revealed a significant correlation between genetic and geographical distances in the whole dataset. The group of analysed populations of Carpathian larch from Eastern Poland, the area of the Jeseníky Mountains in the Czech Republic and the Tatra Region in Slovakia is relatively homogenous with regard to genetics. The F_{ST} values between these populations did not exceed 0.05, indicating low genetic differentiation. In addition, the population from the Eastern Alps could be assigned to this group. A certain level of relationship to Carpathian populations was also observed in the populations from the