GENETIC VARIABILITY OF *QUERCUS PUBESCENS* POPULATIONS FROM NORTH-WESTERN ITALY AND DIFFERENTIATION FROM OTHER OAK SPECIES BELONGING TO *ROBUR* SECTOR

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Pubescent oak (*Quercus pubescens* Willd.) is relatively common in north-western Italy, where it grows mainly in hilly areas and in the basal sector of alpine valleys. The species is phylogenetically related to sessile oak and English oak and gene flow between taxa is possible.

In this work we have analysed morphological and molecular variability to describe the genetic variation and differentiation within and among several natural populations of pubescent oak.

About twenty morphological traits of the leaves and eight microsatellite markers were used to detect genetic variability. The latter were highly polymorphic, displaying a high number of alleles and a wide size range of PCR products. Levels of within and among populations variability were estimated and genetic differentiation was calculated.

Since a mixed stand, where all three species are present, were included in the study, the effect of intraspecific gene flow on the genetic structure of *Q. pubescens, Q. petraea* and *Q. robur* has also been evaluated, and general versus local differentiation has been quantified.

The data obtained are of basic importance for the characterisation of genetic resources and for the adoption of practical and effective measures for *in situ* preservation of biodiversity. Genetic variability is in fact considered the most important factor responsible for adaptive capacity, and therefore for survival under spatial and temporal variation of the environment. We suggest using the results of this work also for the identification of the most valuable stands for production of high quality seeds.