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POTENTIAL HAZARD DUE TO BREEDING BETWEEN POPLAR CULTIVATIONS AND WILD RELATIVES IN MEDITERRANEAN ENVIRONMENT

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Most strategies for the genetic improvement and biotechnologies may be applied to the poplars (*Populus* spp.) and their hybrids to increase productivity and adaptability. Due to these facilities, these trees are often used for applications in bioenergy, remediation, and carbon sequestration. However, their weak reproductive barriers and spontaneous hybridization with natural populations may impact the sustainable deployment of new poplar cultivars. Deforestation and intensive management, with plantations of fast-growing tree species, may endanger tree species by the destruction or loss of their habitats, but also by loss of species integrity through hybridization and introgressive gene flow. Consequently, the implementation of conservation strategies requires the monitoring of gene flow in relation to habitat structure. These issues hold true for native poplars, which are considered one of the threatened forest tree species of natural floodplain forests in the temperate zones.

For the purpose to establishing best management approaches for genetic diversity conservation, the objectives of this work were the characterization of spatial genetic structure in poplar stand, and the study of the potential breeding between natural and cultivated populations in the Mediterranean environment.

Two areas were settled within a natural protected area, the Regional Park of Migliarino-San Rossore-Massaciuccoli (Pisa). Area A is a naturally-originated mixed forest stand, and it is close to two poplar plantations. In the Area B, single trees and small groups of *Populus* spp. are scattered in a wetland habitat, along the shores of the Massaciuccoli Lake, near to a poplar plantation. In Area A, poplar naturally-originated were analyzed and assigned, by the sequence analysis, to *P. alba*, and *P. x canescens* hybrid. In the Area B individuals of *P. nigra* are present. The spatial genetic structure showed that four distinct clusters can be identified in the Area A and three clusters in Area B. In the Area A, the high F_{ST} values and the low F_{IS} values suggest the isolation of the subpopulation and the absence of gene flow, due to other tree species acting as barriers. In contrast in the Area B, a moderate gene flow was found among clusters demonstrating the presence of weak barriers. The differences between the spatial genetic structure depended on the environmental features of two habitat. The detection of hybridization (by paternity analysis) between the Area A and the poplar plantation, suggested the occurrence of a possible genetic exchange among a natural stand and the plantation which has to be carefully considered when poplar plantation are made close to natural environment in which parental relatives are present.

Besides, the potential hazard due to hybridization between poplar cultivations and its wild relatives in the surrounding environments of the Regional Park was investigated. Based on the genetic information and using the spatial dataset available for the study area, it seems that gene flow could affect important habitats hosting naturally originated poplar population. The assessment of this potential hazard indicates that some management measures are required to mitigate the risk.