

NUCLEOTIDE DIVERSITY FOR CANDIDATE GENES IN ALEPPO PINE (*PINUS HALEPENSIS* MILL.)

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Survival of tree species is associated to their ability to adapt to new environmental conditions, which depends on the genetic variability of genes involved in the control of adaptive traits, and on their plasticity. Single nucleotide polymorphisms (SNPs) are emerging as an important tool for the assessment of genetic diversity and, if detected in candidate genes, may allow gathering information about adaptive variation. Aleppo pine (*Pinus halepensis*) is an outcrossing highly heterozygous species, with very large effective population sizes. This study presents results on SNP discovery, level of nucleotide polymorphism, haplotype structure and linkage disequilibrium for 254 candidate genes mainly related to drought stress tolerance in natural populations of Aleppo pine. Twenty-six natural populations (a total of 48 individuals) were sampled along a geographical and ecological gradient (Greece, Israel, Algeria, Morocco, Spain and Italy) in order to assess intra- and inter-population nucleotide diversity of these genes. Data from 12000 chromatograms were analyzed and 60% of the genes resulted to be polymorphic.

The main results were:

- The overall nucleotide variation was limited and lower than that observed in most tree species so far studied.
- Tests for genetic differentiation among populations revealed a significantly high F_{st} value for some candidate genes, much higher than those estimated in Aleppo pine for neutral markers (isozymes and chloroplast microsatellites). Moreover, there exists a significant genotypic structure of the populations along the longitudinal gradient. Nucleotide diversity was mainly concentrated in the eastern population
- Tajima's D statistics significantly different from zero (neutral case) are consistent with either simple or more complex signals involving balancing or frequency-dependent selection.
- The extent of linkage disequilibrium within a subset of 10 candidate genes, estimated by r^2 , showed the tendency of a rapid decline within few hundreds of base pairs, as already observed in other conifer species, which are typically outcrossers (e.g., *Picea abies*).

Through the results obtained, we discuss the impact of natural selection and demographic processes, and provide evolutionary and functional hypotheses that potentially explain the variability observed. Possible implications of these results in conservation genetics and association mapping studies are also discussed

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