

SSR AND EST-SSR MARKERS TO ASSESS GENETIC DIVERSITY IN EUROPEAN CHESTNUT POPULATIONS

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The genetic diversity is the basis for the adaptability of organisms against environmental changes through natural selection. Populations with low genetic variation are more vulnerable to pollution, to climate changes and habitat alteration due to human activities. In recent years microsatellites have become the most used markers for studying population genetic diversity. These markers, due to their hyper-variability and locus-specific nature are important to measure neutral DNA variation, however they are not useful for measuring the adaptive genetic diversity. Recently, the increased availability of the DNA sequences has given the possibility to develop EST-derived SSR markers, a new type of functional genomic markers. These markers are present in expressed regions of the genome and are more than three times as transferable across species as compared with anonymous SSRs.

Castanea sativa Miller is a widespread species in the Southern Europe. Due to its multipurpose characteristics, man has influenced over many centuries its distribution through propagation and transplanting of plant material and silvicultural practices. Previous studies, aimed to evaluate genetic and adaptive variation of European chestnut were carried out in a large number of populations along its whole distribution area. Genetic variation was estimated by ISSR and isozyme markers (Mattioni et al. 2008) and adaptive variation was estimated for traits related to climate change (water use efficiency, bud burst, bud set, growth) (Lauteri et al. 2004). These previous results showed a high degree of variation within and among populations both at genetic and phenotypic level.

The objective of the present work is to compare the genetic variability and differentiation, based on neutral SSR and EST-SSR markers, of chestnut European populations collected along the Mediterranean distribution range and in areas representative of contrasting climate conditions. Six SSR and 10 EST-SSR, markers developed from oak EST data base within EVOLTREE project, were used to assess genetic diversity in 7 natural chestnut populations from Italy, Spain and Greece. All neutral SSRs tested were polymorphic for all the populations analysed whereas 8, out of the ten EST-SSRs tested, resulted polymorphic. Genomic SSRs, showed higher within population gene diversity and lower among population variation as compared to the EST-SSRs. As shown from AMOVA analysis the proportion of variation within populations were 85% and 71% for genomic microsatellites and for EST-SSRs respectively, while the variation among population was 15% for neutral SSRs and 29% for EST-SSRs. UPGMA and PCA analysis showed slightly different grouping of the populations for the two types of markers. These preliminary results confirm that the

comparison of genomic and EST microsatellite is a useful tool to give a complementary information to understand the genetic and adaptive diversity in chestnut.