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PRELIMINARY STUDIES ON GENETIC VARIABILITY OF *QUERCUS PUBESCENS* WILD POPULATIONS IN SICILY

A. DE CARLO*, C. VETTORI*, L. SAPORITO**, R. GIANNINI*

*) Istitute of Plant Genetics – CNR, Research Division Florence, Via Madonna del Piano 16, 50019 Sesto Fiorentino (FI), Italy – raffaello.giannini@igv.cnr.it
**) Regione Siciliana, Azienda Regionale Foreste Demaniale, Via della Libertà 97, 90143 Palermo, Italy

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In Sicily the distribution of *Quercus pubescens* Willd. is scattered and covers about 15.000 hectares. The most important populations are located in Madonie (PA), Nebrodi (ME), Iblei (SR), and in Ficuzza Forest (PA). These forests are exsposed to the risk of genetic erosion in consequence of small population size.

Because the presence and maintenance of genetic variation is a prerequisite for their ability to survive in heterogeneous temporal and spatial conditions, and to preserve their adaptability for future generations, in the present work, we have examined the ability of nuclear microsatellites in: i) genotyping the populations; ii) exploring the genetic variability among and within these populations.

Several SSR primer sets, previously developed for *Quercus* spp., are tested for amplification on *Q. pubescens* and 4 SSRs have been selected.

Individuals to be sampled from these populations have been chosen following the morphologycal characters previuosly described for this species by Tutin *et al.* (1993) and Bruschi *et al.* (2000).

Preliminary results indicate that the genetic diversity was found within rather than among populations like observed for others forest populations.

Morever, all populations have been identified by the presence of unique allele; for example, the population of Madonie was characterized by allele 120 (locus 1), by alleles 226, 230 and 222 (locus 2), by allele 228 (locus 3) and by allele 206 (locus 4). The population of Nebrodi was identified by allele 115 (locus 1), allele 218 (locus 2), alleles 208 and 220 (locus 3) and by alleles 228 and 210 (locus 4).