

GENETIC DIFFERENTIATION BETWEEN POPULATIONS OF SCOTS PINE (*PINUS SYLVESTRIS* L.) FROM ITALY AND OTHER EUROPEAN COUNTRIES

S. PUGLISI*, A. LOPS**, G. RAINALDI**

*) Institute of Plant Genetics - CNR, Via Amendola 165/A, 70126 Bari, Italy

***) Department of Biochemistry and Molecular Biology, University of Bari, Via Orabona 4, 70126 Bari, Italy

population genetics, Pinus sylvestris, genetic diversity, genetic differentiation, natural range

The aim of this research is to study the differentiation between eight Italian populations of Scots pine (*Pinus sylvestris* L.) - already surveyed in a previous investigation, and which are representative of the Italian natural range - and some populations representative of other countries of the boundless natural range of this species. The used technique is isozyme analysis carried out by means of horizontal starch gel electrophoresis. Some preliminary results are shown here, regarding a group of European countries. The obtained values of genetic distance show that the previously observed strong differentiation of a relict and isolated Italian population (a remnant from glacial migrations), located in the Emilian Apennine, has been confirmed: as a matter of fact, it is even less similar to the other studied Italian populations (from the Alps) than some foreign populations which tend to group together with them. These results confirm that this small and autochthonous stand is an important genetic resource: its differentiation reveals a different evolutionary history or a different origin (glacial refugium), and its values of genetic diversity parameters are similar to those found in the other Italian populations, in spite of its geographic isolation from the main range of this species. As far as they are concerned, the seven Italian populations from the Alps appear rather differentiated from the remnant, suggesting that the Alpine barrier caused a genetic isolation strong enough to condition their evolutionary pathway. These results cast new light over the available knowledge on this species, since until now Italian populations have been never compared to other European ones, and make it possible the drafting of more accurate programmes of genetic resource conservation. On the basis of the obtained results, some hypotheses on the postglacial recolonization routes followed by this species are discussed.