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NEW RESULTS ON THE GENETIC DIFFERENTIATION BETWEEN POPULATIONS OF SCOTS PINE (*PINUS SYLVESTRIS* L.) FROM SEVERAL GEOGRAPHIC REGIONS OF ITS NATURAL RANGE

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Scots pine (*Pinus sylvestris* L.) occupies a larger natural range than any other species from the whole *Pinaceae* family, extending from Europe to the Far East (Manchuria) through Siberia. Because of such a wide geographic spreading, with very different environmental conditions, and because of the long evolutionary history of this pine, a large intraspecific variation is expected to occur. The aim of this research is to study the genetic diversity and the differentiation between populations representative of the Italian and of the remaining Eurasian natural range of Scots pine; in the case in point, eight Italian populations, 22 populations from the rest of Europe (nine of which are French) and one from Asia (Turkey), for a total of 31 populations, were studied by using isozymes as genetic markers, analysed through horizontal starch gel electrophoresis. The obtained results confirm the previously observed sharp differentiation of an Italian population, located in the Emilian Apennine: it is a relict and isolated remnant from glacial migrations, and it is even less similar to the studied Italian Alpine populations than the remaining foreign populations, which tend to group together with them. These new observations supply further evidence of the status of important genetic resource for this small and autochthonous stand, whose differentiation could depend both on its origin from a different glacial refugium and on a different evolutionary history, and whose 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. On the basis of the obtained values of genetic distance, the seven Italian populations from the Alps tend to group together and appear rather differentiated from the remaining ones, suggesting both a different postglacial origin and a relative genetic isolation due to the Alpine barrier, but their cluster is close to a group of French populations, suggesting a common origin and a subsequent differentiation. Other French populations are scattered along the dendrogram. Some hypotheses on the postglacial recolonization routes followed by this species are also discussed. The results of this research are increasing the available knowledge on Scots pine, making it possible the drafting of more accurate programmes of genetic resource conservation.