## CONSERVATION AND GENETIC DIVERSITY IN JUNIPERUS SPP OF "POLLINO NATIONAL PARK" (BASILICATA, SOUTHERN ITALY)

LAPENNA M.R., IERARDI G., SENESE C., LOGOZZO G., FASCETTI S., SPAGNOLETTI ZEULI P.

Dipartimento di Biologia, Difesa e Biotecnologie Agro-Forestali, Università della Basilicata, Via dell'Ateneo Lucano 10, 85100 Potenza (Italy)

Juniperus nana, Juniperus hemispherica, SSRs, genetic diversity, conservation

The shrub vegetation of high mountains of Pollino National Park, (Lucanian side) is characterised by small procumbent junipers (*Juniperus nana*, *J. hemispherica* - Cupressaceae) forming large carpets in upper level of impassable areas frequently together with other shrubs and Bosnian pine (*Pinus leucodermis* Antoine). They are drought and frost tolerant, although sensitive to fire. Since the Bronze Age to nowadays shrubberies suffered a slow decline and they have survived in refuge sites difficult to reach as rocks, plateaus, ridges of high mountains. In the last decades climatic changes could start a new regressive phase promoting the advance in upper level of mesophilic hardwood forests. Moreover Junipers of upper level are regarded as species critics in taxonomic fields. Both of the Junipers growing in the Pollino areas, for their rarity and vulnerability need to be preserved and propagated. For their longevity and tolerance of environmental stresses they are interesting for nursery purposes too.

Within Terranova del Pollino area (Potenza, Italy) three sites were identified at different altitudes, from 2051 m a.s.l. site in Sic IT9210245 area (Serra di Crispo, Grande Porta di Pollino and Pietra Castello) to 1640 m a.s.l site of 'Piano Jannace'. Ten female individuals from each site were sampled. Genetic diversity between and within sites was studied by means of five nuclear SSR loci. The SSRs were identified among those already developed in different species within the family *Cupressaceae*: 4 specific for *Juniperus communis* and 1 for *Cupressus sempervirens*. 4 out of five microsatellites were polymorphic and over all 37 alleles were identified from 3 to 13 alleles per SSR locus. Variation among sites was also studied.