

## GENETIC DIVERSITY EVALUATION OF CALABRIAN PINE (*PINUS LARICIO* POIRET) REVEALED BY MICROSATELLITE ANALYSES: A PRELIMINARY STUDY

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It is generally agreed that genes and genotypes are not distributed at random within a population and that many factors (seed and pollen dispersal, breeding system, genetic drift) strongly influence population genetic structures. Genetic diversity is crucial for population persistence, especially in forest tree species that have become fragmented, bottlenecked or that have rapidly lost genetic variability (Oddou-Muratorio and Klein, 2008).

Calabrian pine (*Pinus laricio* Poiret) is a most divergent and genetically original subspecies of black pine (Gausson and Heywood, 1993), whose natural occurrence is restricted to Calabria and Sicily. In Calabria it grows on the Aspromonte mountain and mainly on the Sila plateau where laricio pine forests cover more than 40,000 ha and characterize the landscape from 900 m up to 1700 m above sea level. Between the endemic populations of the Sila massif, constituting priority habitats under the EU Natura 2000 directive, the “Giant Pines of Sila” Natural Reserve, also known as the “Fallistro Giants”, is a very truly ancient pine forest. The Fallistro Reserve, covering only 5 ha, exceptionally includes about uneven-aged 1500 trees, with more than 40 individuals up to 350 years old (Avolio and Ciancio, 1985). The reserve is left to natural evolution as the local conditions favoring the permanence of *Pinus laricio*, which ages and regenerates abundantly without human interventions.

As far as we know, laricio pine stands located in Fallistro but also in the whole Sila area were never studied at the molecular level. Thus, an in-depth investigation on the genetic diversity and population characteristics within its native range is greatly needed to secure the preservation of *Pinus laricio* diversity but also to enable the development and utilization of appropriate conservation strategies.

Therefore, genetic variability among four geographically distant laricio pine natural populations from the Sila National Park was analyzed using chloroplast SSR markers, originally developed for other *Pinus* species (Vendramin et al, 1996).

Here, we reported that three of the microsatellites tested were polymorphic, showing between 4 and 8 size variants per locus, some of which were found nowhere else or occurred at low frequencies and, thus, represent a group of “rare size variants”. All variants were combined in 101 different haplotypes and 55 of them were found unique (frequency < 1.0%) and uneven distributed among four Sila laricio pine populations. AMOVA analysis revealed a genetic diversity level among populations (6%) quite similar to that previously reported for other black pine species ().

Age effects on the population genetic variability as well as the usefulness of also nuclear microsatellites in monitoring both inter- and intra-population genetic diversity will be provided.

In conclusion, our results allow for the first time to shed light on the evolutionary history and gene pool of Sila laricio pine representing a remarkable, but so far not explored resource, of unquestionable value in forestry.

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