

GENETIC STRUCTURE OF THE RELICT POPULATION OF *TAXUS BACCATA* L. ON THE MONTE GENNARGENTU IN SARDINIA

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ITS, Taxus baccata L., population structure

English yew (*Taxus baccata* L.) is an European gymnosperm with a wide natural range and a discontinuous distribution. *Taxus baccata* L., forms, in fact, small and naturally isolated populations, this being typical of a relict species.

In this work, we studied the genetic structure of the relict population of *Taxus baccata* L. on the Monte Gennargentu (Sardinia). This population is composed by 480 individuals and we analysed, using molecular markers, the genetic intra-population variability and the inheritance in an half-sib progeny.

The molecular marker used was the ITS (Internal Transcribed Spacer) region of the ribosomal DNA, analysed via PCR and cloning.

Sequence analysis showed 4 mutation sites, (transitions C/T). Thanks to the sequences chromatograms, we could see whether the mutation was in homozygosity or in heterozygosity. Having 4 mutation sites, we could obtain the 16 possible combinations of alleles. The population showed only 7 of these combinations (7 alleles). From the combination of these alleles, we found 12 genotypes in the population and just 3 of them in the progeny we analysed.

The analysis considered then, the effective breeding population. The parental population was made up of 74 adult plants with arils, 233 plants, unfertile, defined as little, and 173 adult plants with no arils at the moment of the collection.

Gene and genotype frequencies were calculated for the effective population and the progeny.

Paternity analysis, was also performed to identify the genotypes of the parents which contributed to form the new generation, using the software FaMoz. In our case, we found one maternal genotype associated with 2 possible paternal ones.