

SPATIAL GENETIC STRUCTURE OF *TAXUS BACCATA* L. IN THE WESTERN MEDITERRANEAN BASIN: PAST AND PRESENT LIMITS TO GENE MOVEMENT OVER A BROAD GEOGRAPHIC SCALE

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The knowledge of biodiversity and the implementation of strategic plans for its sustainable use, particularly concerning threatened species and habitats, is one of the main National and International priorities for Research and Development. In this framework, the study of the genetic diversity, and the analysis of the historical, evolutionary and ecological factors and processes that determine its distribution, contributes to the design of sound management policies for its use and conservation.

Long-term management strategies for conservation of yew (*Taxus baccata* L.) populations require the assessment of the distribution of genetic resources at different spatial scales. Therefore, knowledge is needed about the spatial organization of its genetic variation, as well as about gene flow and their relationship with fragmentation and/or isolation in this species. Therefore, we have developed 7 specific microsatellite loci for *Taxus baccata* in order to investigate the genetic structure of this species at different spatial scales: wide-range scale, Mediterranean scale, local scale. Our main objectives are: (i) to know if there are particular areas or geographical regions with different levels of genetic variability and structure; (ii) to assess the role of historical processes in determining such patterns; and (iii) to understand the interaction between the demographic (ecologic) and genetic dynamics under different scenarios of landscape fragmentation.

In this communication we present the results obtained so far for the populations located in the western Mediterranean. We discuss the role of the complex paleogeographic and paleoclimatic history of this region in the current distribution of genetic diversity. Finally, it is expected that these results will help in designing appropriate management strategies for its conservation.