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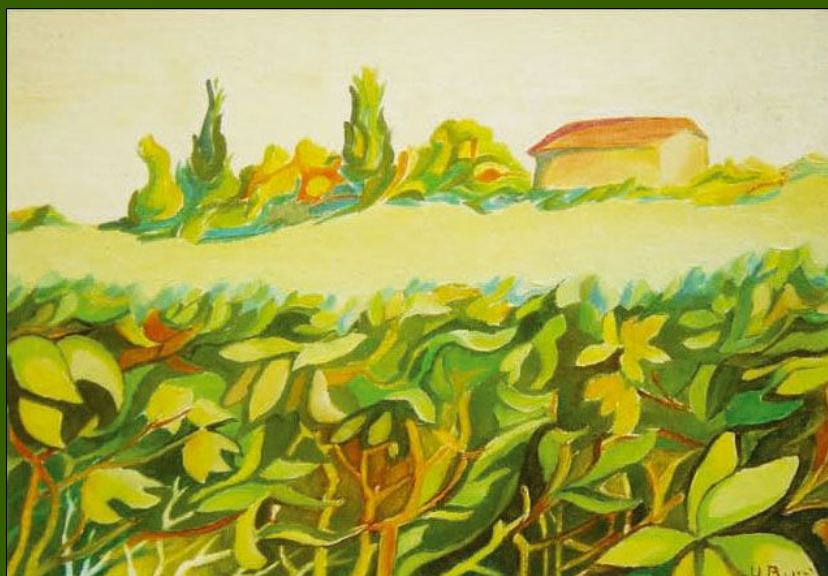


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Comunicazioni Orali - Riassunti



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MOLECULAR AND STATISTICAL TOOLS FOR CONSERVATION AND MANAGEMENT OF GENETIC RESOURCES

Forests are considered the most complex terrestrial ecosystems due to their high level of biodiversity in term of genetic resources, species and habitat (Geburek & Konrad 2008). However, over the past few centuries, the degradation and disappearance of natural forests have caused serious loss of biodiversity (Sodhi et al. 2009). Reduced genetic diversity may lead to a decrease in population's ability to adapt to future changes in biotic and abiotic factors. Thus, evaluation of the genetic diversity and structure of the current populations is an essential prerequisite for management planning and conservation strategies of forest tree species. Tools as molecular markers are being widely used to characterize genetic variation of long-lived species, since they can greatly facilitate the prioritization of conservation strategies (Allendorf et al. 2010). This work aims to evaluate the potential of genetic diversity studies to identify populations and germplasm to be preserved and used in conservation and management programs of genetic resources in forest species. We considered two case studies in which natural populations were genotyped by means of microsatellite markers. In both studies we evaluated the genetic diversity considering different indices such as allelic richness (Ar) private allelic richness (pAr), observed (Ho) and expected (He) heterozygosity. We have also calculated the population inbreeding coefficient (Fis). The population structure was investigated by using SAMOVA 1.0 and STRUCTURE 2.3.3 software. We also combined genetic analysis, spatial statistic tools and GIS technologies. Case Study 1 *Araucaria auracana*. This is an endemic and endangered conifer of South America distributed in Chile and Argentina. We have investigated the structure and genetic diversity of twelve natural populations, nine from the Andes Cordillera and three from the Coast Cordillera. The results indicated high level of genetic diversity in the species with the presence of 4 different gene pools. A significant differentiation between Coastal and Andean populations were found. The current genetic structure of *A. auracana* must be the results of several overlapping factors as exploitation of forest by man and environmental factors associated with Pleistocene glaciations. Case Study 2 *Quercus trojana*. The origin of this species is thought to be in the Balkan Peninsula. In Italy, its current distribution is restricted to the Puglia region and is a remnant of a more wide spread range severely reduced by intensive human exploitation. We have studied the genetic diversity of five populations collected in Alta Murgia National Park and in the surrounding areas. High level of genetic diversity in all populations and the presence of two different gene pools were observed. Based on the values of allelic richness and divergence among populations we indicated three populations to be included in genetic resources conservation programs. Molecular, statistical and spatial analysis proved to be excellent tools to get information on the genetic variability at inter- and intra- population which can be used to indicate measures for gene conservation and management. Conservation strategies are suggested for a set of populations from different gene pools with the necessary genetic variation to face future evolutionary dynamics.

Parole Chiave: Conservation Genetics, *Quercus trojana*, Genetic Resources, Biodiversity

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