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THE ROLE OF A MARINE PROTECTED AREA IN SAFEGUARDING THE GENETIC DIVERSITY OF RARE SPECIES: THE CASE OF *PATELLA FERRUGINEA* GMELIN, 1791 (GASTROPODA: PATELLIDAE)

IL RUOLO DELLE AREE MARINE PROTETTE PER LA SALVAGUARDIA DELLA DIVERSITÀ GENETICA DI SPECIE RARE: IL CASO DI PATELLA FERRUGINA *GMELIN, 1791 (GASTROPODA: PATELLIDAE)*

Abstract - Patella ferruginea *(Gastropoda: Patellidae) is an endangered marine gastropod, distributed on the western Mediterranean coasts, whose range has progressively contracted, due to intense human exploitation. Our attention focused on its genetic structure, in order to gather information about levels of genetic variability of* P. ferruginea *from the Asinara Marine Protected Area and a neighbouring non-protected area.*

Key-words: *endangered species, resource conservation, genetics.*

Introduction - Marine threatened species comprise the giant Mediterranean limpet *Patella ferruginea*, considered the most endangered marine macroinvertebrate in the W-Mediterranean, whose intense human exploitation places its populations under serious risk of extinction. *P. ferruginea*, a protandrous species, shows traits of a k-strategist (see Laborel-Deguen and Laborel, 1991). Such features contribute to confine the habitat of the species, suggesting the presence of small-scale genetic differentiation among limpet populations. This work, performed by ISSRs, would achieve more information about i) the level of gene flow between the population of the Asinara MPA and a close population of a non-protected area, and ii) the efficiency of MPAs in recovering the genetic variability of an endangered species.

Materials and methods - We collected 10 specimens from the non-protected area of Coscia di Donna (CDN) and 30 specimens from three sites (ACS, APS, APB) of the Asinara MPA (N-W Sardinia). Portions of foot muscle were cut employing a non-lethal protocol described in Casu *et al.* (2006). PCR reaction mixture, program of amplification, electrophoresis conditions and gel staining are described in Casu *et al.* (2006). Heterozygosity (H), allelic frequencies, and the coancestry coefficient (FST) values were calculated using the Bayesian method. We further obtained a triangular matrix of interindividual genetic dissimilarity using the 1-relatedness similarity index (Lynch and Milligan, 1994). Subsequently, UPGMA cluster analysis was carried out to construct a dendrogram.

Results - Grouping ACS, APS and APB individuals in the "Asinara Is." population, the values of H calculated for each samples highlight a low level of within-population gene diversity. Differences in band frequencies were significant in all pairwise comparisons between samples from Asinara Is. and CDN by means of

exact tests, whereas comparisons within the three samples from Asinara Is. were not. Interindividual cluster analysis (Fig. 1) sharply distinguished individuals of Asinara Is. from those of CDN, confirming the high genetic differentiation. Otherwise, the dendrogram did not evidence a distinction among individuals from the MPA according to their sampling localities, suggesting that an effective rate of gene flow currently acts within Asinara Is. The value of the coancestry coefficient calculated among the four samples was significantly high (FST=0.234), whilst this estimate reduced of an order of magnitude (FST=0.050) when we take into account individuals from Asinara Is. only. Our data may also suggest a very low connectivity between Asinara Is. and CDN, probably due to the reduction in the number of individuals of *P. ferruginea* populations in other unprotected areas located between them.

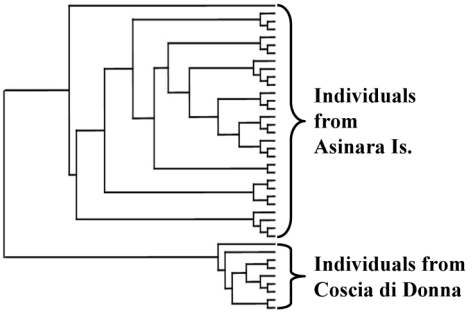

Fig. 1 - UPGMA dendrogram based on the matrix of 1 - relatedness pairwise values among 40 individuals.

Dendrogramma UPGMA costruito sulla matrice di dissimilarità genetica 1 - relatedness tra 40 individui.

Conclusions - The samples from Asinara appear to be well connected, and they can be regarded as a genetically homogeneous unit, or alternatively, as subpopulations with a very recent shared ancestry (Templeton *et al*., 1995). Whereas, the population from CDN, probably due to an intense harvesting, seems to be subjected to the stochastic effect of the genetic drift, which increasingly leads this population to diverge from the neighbouring MPA. The remarkable genetic differentiation highlighted between the sampled areas may represent an hindrance to the recovery of *P. ferruginea* from CDN, bringing the residual population to the risk of extinction; in fact, the population from this non-protected area is more vulnerable to effect of present disturbance, which could remove the population in a single or very few events.

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