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## PRELIMINARY DATA ON THE GENETIC VARIABILITY OF THE FAN MUSSEL *PINNA NOBILIS* IN THE NORTHERN SARDINIA

### *DATI PRELIMINARI SULLA VARIABILITÀ GENETICA DEL MOLLUSCO BIVALVE PINNA NOBILIS NELLA SARDEGNA SETTENTRIONALE*

**Abstract** - The fan mussel *Pinna nobilis* Linnaeus, 1758 is one of the most endangered Mediterranean bivalve. After a reduction of its distribution as a consequence of anthropic factors, the environmental politics led to a new demographic increasing of individuals in some Mediterranean regions. This work aimed to shed some light on the genetic structure of two new-raised populations in northern Sardinia.

**Key-words:** *Pinna nobilis*, genetics, population dynamics, conservation.

**Introduction** - The fan mussel *Pinna nobilis* Linnaeus, 1758 is the largest endemic Mediterranean bivalve, living in soft-sediment areas and beds of seagrass. Commercial exploitation and habitat pollution strongly affected its populations during the past centuries, leading to a dramatic reduction of the distribution of the species in the last 20-30 years. At present, effort for the protection of *P. nobilis* has led to a great demographic expansion reported in many Mediterranean sites. However, with the exception of the study of Katsares *et al.* (2008), who surveyed four Aegean populations, genetic data are still lacking. In such context, the present study was devoted to improve the knowledge on the genetic variability of Sardinian populations which underwent patterns of demographic regression/expansion.

**Materials and methods** - Forty-nine specimens from two areas of northern Sardinia were analysed: 23 from the Capo Caccia Isola Piana MPA, and 26 from the Tavolara Capo Coda Cavallo MPA. A non lethal sampling strategy was applied, abscising a small portion of mantle tissue from individuals *in situ*. Mitochondrial Cytochrome c Oxidase subunit I gene was amplified using standard PCR and sequencing procedures. Estimates of genetic diversity were obtained using DnaSP (Rozas and Rozas, 1999). Genetic relationships among individuals were inferred using Network ([www.fluxus-engineering.com](http://www.fluxus-engineering.com)). The occurrence of genetic structuring among samples was investigated by Baps (Corander and Tang, 2007). Historical population dynamics were estimated by pairwise differences distribution analysis using DnaSP.

**Results** - Overall, 12 haplotypes were found, four of which were shared between the two areas. Noteworthy, the two most common haplotypes were shared respectively by 14 and 18 individuals, and six were unique. Comparable values of haplotype ( $h \sim 0.8$ ) and nucleotide ( $\pi \sim 0.005$ ) diversity occur at both within and among population levels. Network analysis pointed out a high heterogeneity distributed homogeneously throughout the whole sample, without any evidence of genetic structuring between the two MPAs. The occurrence of different haplogroups could be hypothesised to explain the distribution of the 12 haplotypes in the network. Indeed, Bayesian

analysis evidenced the presence of three groups, being consistent with the network in highlighting the phylogenetic relationships among haplotypes (Fig. 1). The mismatch distribution of pairwise differences showed a starting shape for both the two analysed areas and the whole sample, according with an early population expansion.

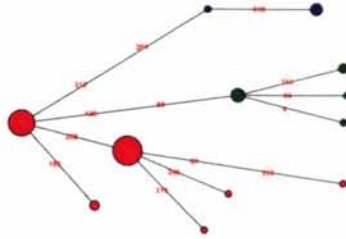


Fig. 1 - Combined Network and Bayesian analysis. Spots on network were coloured according to the distribution of individuals among the three Bayesian groups. Red: group I; green: group II; blue: group III.

*Combinazione tra Network e analisi bayesiana. I cerchi sul network sono colorati secondo l'appartenenza degli individui ai tre gruppi bayesiani. In rosso: gruppo I; in verde: gruppo II; in blu: gruppo III.*

**Conclusions** - The results obtained shed new light on the population dynamics of *P. nobilis* in northern Sardinia. Samples belonging to the MPAs retrieved similar indices of genetic diversity with no occurrence of geographic structuring, which suggest that populations from northern Sardinian represent a panmictic unit. The likely bottleneck which affected such populations seems to have not left signature on their genetic structure, which conversely presents high level of variability. Well-defined phylogenetic relationships characterise the haplotypes distribution, with the occurrence of three distinct haplogroups. This high variability may be explained considering the high rate of mitochondrial evolution found in other bivalves (Hoeh *et al.*, 1996). An alternative explanation lies on the high dispersal capability of the species, which could have contributed to the rapid re-colonisation of northern Sardinia. Similar results were provided by Katsares *et al.* (2008) for Aegean populations, further suggesting the occurrence of high levels of gene flow among populations in some areas of the Mediterranean. In conclusion, Sardinian samples appear to belong to a unique population in early, rapid expansion, promoted by an effective larval dispersal capability.

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