

# MICROSATELLITE MARKERS FOR POPULATION GENETIC STUDIES OF THE GIANT RED SHRIMP *ARISTAEOMORPHA FOLIACEA* (CRUSTACEA, DECAPODA)

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## Abstract

Microsatellite markers have been isolated and characterized from the giant red shrimp *Aristaeomorpha foliacea* in order to investigate on the presence of distinct stocks in the Western Mediterranean Sea. Polymorphism of the newly obtained loci was assessed in a restricted sample of 30 specimens, nine loci provided markers with polymorphism (range 2–19 alleles per locus). Six loci, the most polymorphic and easiest to amplify and to score, were tested in a larger sample of 6 populations from the Western Mediterranean Sea. Microsatellite data revealed a substantial genetic homogeneity and no signs of recent bottlenecks, suggesting the existence of a high gene flow that connects all populations.

**Keywords:** Genetics, Crustacea, Western Mediterranean, Deep Waters, Fisheries

## Introduction

The giant red shrimp, *Aristaeomorpha foliacea*, is a cosmopolitan crustacean species, widespread in the eastern and western Atlantic, the western Pacific, the Indian Ocean and the Mediterranean Sea. It is one of the most important exploited crustaceans, having a long traditional and economical significance for the deep fishery of the western and central Mediterranean countries. Despite its commercial importance, little is known about the genetics, population structure, and migration patterns of this species. Since direct tracking movements of individuals is very difficult for marine species, the use of indirect methods, including genetic approaches, for the measurement of connectivity among populations can be very informative. With the aim of studying the population structure and genetic connectivity among giant red shrimp populations from the Western Mediterranean Sea and obtaining new and powerful genetic markers, microsatellites loci were isolated from *Aristaeomorpha foliacea* genome using the FIASCO protocol [1] from a partial genomic library enriched for an AC motif.

## Results

Among 96 recombinant clones obtained, a total of 43 sequences had a microsatellite, 14 of which with flanking region of appropriate length and sufficient quality to allow the design of primers that were used to amplify the genomic DNA of a subsample of 30 specimens from two locations. Four out of 14 microsatellites were immediately discarded because of their low amplification success, while one was found to be monomorphic.

The remaining 9 loci were characterized by a high variability in PIC values (0.36-0.91) and in the number of alleles (range 2 – 19).

In this study only the 6 most polymorphic loci were tested in a larger sample and used to make a preliminary investigation on the genetic structure of Mediterranean giant red shrimps. A total of 115 specimens were analysed from 6 populations: 4 samples were collected off the Sardinian coast (Sant'Antioco, Cagliari, Siniscola, Asinara) and two samples off Sicily (Messina and Sicily Channel). Two loci (Cea17 and Cia82) significantly deviated from HWE and this could be explained by their associated elevated frequencies of null alleles (10% and 19%, respectively) calculated with the algorithm of Dempster [2]. *A. foliacea* populations resulted not genetically differentiated as indicated by the low and not significant pair-wise *F*<sub>st</sub> values calculated with Arlequin 3.1 [3].

Analysis of molecular variance AMOVA clearly showed that genetic variability was largely due to differences among individuals (99.31%) rather than to differences among populations (0.69%).

The absence of population structure was further confirmed by the bayesian clustering method implemented in Structure 2.3 [4] indicating K=1 as the most probable structure.

The PCA performed with Adegenet [5] showed a substantial genetic homogeneity among populations separated by hundreds of kilometres suggesting that western Mediterranean populations could represent a unique panmictic stock (fig 1).

Finally, the bottleneck test [6] and interlocus *g*-tests [7] did not find signs of recent bottlenecks (reduction of population size) or growth (increase of population size after the recovering from a demographic collapse), leading to hypothesize that, up to now, the Western Mediterranean giant red shrimps have experienced a sustainable fishing pressure.

All these results clearly indicate that the microsatellite markers tested here can represent very useful tools for population genetic studies of *A. foliacea*, for instance for monitoring the detrimental genetic effects of any future increasing fishing pressure.

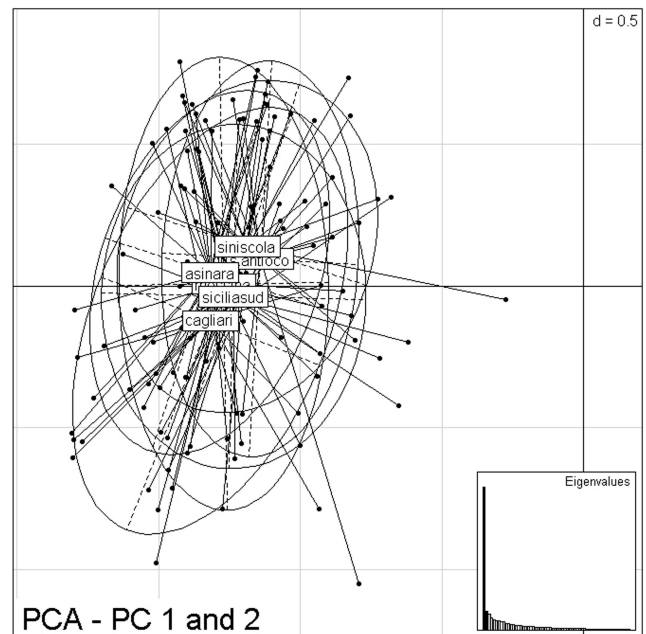


Fig. 1. Typology of giant red shrimp populations obtained by interclass PCA. Eigenvalues corresponding to the represented components are filled in black. Points represent genotypes; samples are labelled inside their 95% inertia ellipses

## References

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