ALLOZYMIC GENETIC DIVERGENCE IN THE BIVALVE *MYTILASTER MINIMUS* FROM BRACKISH-WATER AND MARINE HABITATS IN THE WESTERN SARDINIAN COAST (ITALY)

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Abstract

The genetic relationships among 11 samples of the bivalve *Mytilaster minimus* from brackish-water and marine habitats along western Sardinian coast were studied by allozyme electrophoresis. Results obtained for 15 loci showed high levels of both within- and between-population genetic heterogeneity. The positive and significant value of the inbreeding coefficient indicated a general departure from HW equilibrium due to deficiency of heterozygotes. The observed patterns of genetic variability result from the superimposition of two main evolutionary forces: 1) the diverse selective regimes in the different habitat-types and 2) the different history of colonisation and/or geographical distribution.

Keywords: bivalves, brackish water, genetics, Western Mediterranean

Most animal species often show a subdivision into local populations (1). If local populations are exposed to contrasting environmental conditions appreciable populations differentiation may arise determined by genotype-environment interactions (1). Theoretical works provide that populations from unpredictable environment, present a general reduction of genetic variability (2, 3). In order to provide insights on the relationship between genetic structure and habitat type of animal populations we investigated the degree of allozyme genetic divergence between individuals of *Mytilaster minimus* Poli, 1795 (Mollusca, Pelecypoda). *M. minimus* is a small bibalve with maximum shell length of roughly 2 cm, distributed on hard bottoms in lagoons and marine sites of the intertidal belt in the Mediterranean and eastern Atlantic. Life cycle has a planktonic larval stage but larval morphology and life-span are unknown, so that its potential for dispersal cannot reliably be inferred.

Eleven samples (about 40 specimens each) were collected in four different brackish-water basins in western Sardinia (Italy) and in the nearest rocky shore. Whenever possible, more samples were collected within each basin from the inner part of the ponds toward the sea. Five of eleven samples have been collected in the ponds, 3 in the sea and 3 in intermediate sites. Allozyme cellulose acetate electrophoresis, carried out using the procedures outlined in a previous study (4), gave the allele frequencies at 15 presumptive loci. The genetic variability was estimated by the average expected heterozygosity over loci (*H*). The genetic structure of the whole set of populations was analysed by *F*-statistics. Unbiased estimators were obtained by jackknifing across loci and tested for difference from zero by permutation tests. The level of genetic distance between populations was estimated with Nei's (5) unbiased index, *D*. Multidimensional scaling (MDS) was applied to the matrix of genetic distances.

Our results showed a general deviation from Hardy-Weinberg expectations at all loci over all populations ($F_{IS}=0.532$, P< 0.001). Approximately, the observed heterozygosity is one half of the expected one. Deficiency of heterozygote individuals has been commonly observed in allozyme studies on marine and brackish-water bivalves and reflect a trend characteristic to invertebrates with high rate of reproduction and high dispersal capability (6, 7. 8). In the MDS plot the straight line clearly separates the Santa Giusta samples from the others (Fig. 2) while dotted lines separate three groups of samples that are consistent with the gradient pond-sea (Fig. 2). The divergence of Santa Giusta samples from the others could be a consequence of ecological peculiarity of that site and/or depend on the effect of genetic drift after recurrent summer dystrophic crises. The genetic distances found between M. minimus samples are below the values detected for

Figure 1. *Mytilaster minimus.* Location of sampling areas. Within each area samples from brackish-water, marine and intermediate habitats were collected.

congeneric species (for a review see 9). The highly significant value of the coancestry coefficient ($F_{ST}=0.239$, P<0.001) referred to the eleven populations remark their high degree of genetic divergence. The occurrence of genotypes typical of each habitat-type accounts for the observed genetic divergence. Furthermore a number of habitat-private alleles were detected. In addition, in some instances the most frequent allele present in brackish-water samples is the less common in marine samples and *vice versa*. Our results can be explained in terms of adaptation and local selection. The selective forces acting in each habitat-type favour the different genotype and the genetic divergence observed. On the other hand, geographical distance and/or history of colonisation contributed to the present patterns of genotypic variability. Thus the observed pattern results from the superimposition of two main types of forces that influenced population differentiation in a process of local adaptation since the first colonisation events of brackish-water habitats.
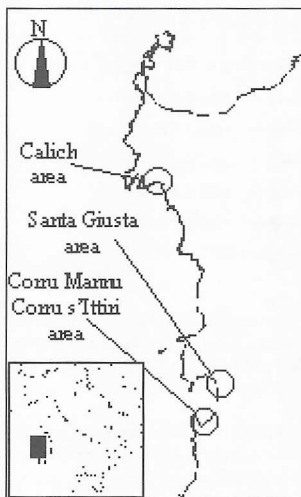

triangles: Corru Mannu - Corru s'Ittiri area
squares: Calich area
circles: Santa Giusta area

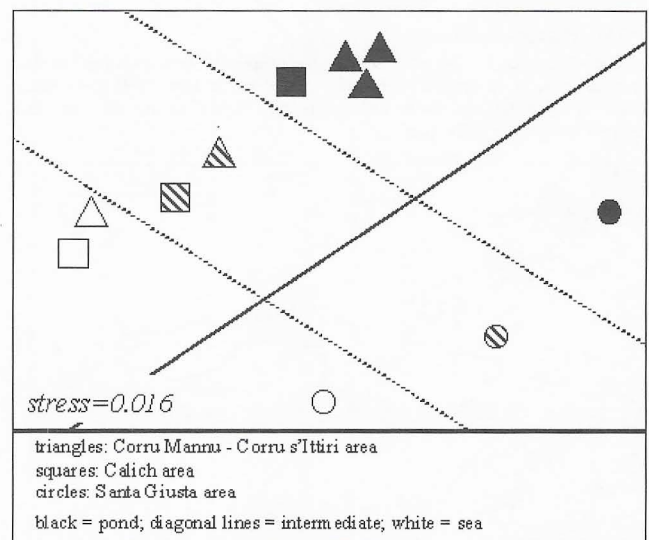black = pond; diagonal lines = intermediate; white = sea

Figure 2. ▯. Multidimensional scaling of Nei's genetic distances. The low value of stress indicates that distances among samples on the plot represent the genetic distances accurately.

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