Genetic structure of *Corallium rubrum* L. 1758 populations from the Tyrrhenian Sea

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At the FAO Technical Consultation on Red Coral of the Mediterranean (AA. VV., 1989) the existence of differences in skeletal structures, colouring and growth rate among red coral colonies were pointed out. Differences in morphological types may be related to environmental gradients or genetically determined. Population genetics studies have been used extensively to reveal the genetic affinities among populations (WARD, 1989). In order to obtain a preliminary characterization of the *Corallium rubrum* genetic structure, two Tyrrhenian populations were analyzed by means of enzyme electrophoresis.

C. rubrum specimens were collected at Calafuria cliff (Leghorn) and Elba Island by SCUBA diving. Each coral colony was considered as an individual, because of its origin from a single planula larva (VIGHI, 1972). Only organic material (polyps and a little coenosarc) was used for the electrophoretical analysis. Electrophoretic techniques have been assayed for 12 enzymes. Migrations were performed on cellulose acetate media (ABBIATI & MALTAGLIATI, in press). Banding patterns enabled the calculation of allelic and genotypic frequencies for thirteen loci. Genetic variability of each population was expressed in terms of polymorphism (0,99% and 0.95% criteria), observed and mean heterozygosity, mean number of alleles.

In both samples the same alleles, showing different frequencies were found. In the Calafuria sample three loci were polymorphic at 0,95 criterion and one at 0.99, while in the Elba sample four loci resulted polymorphic at 0,95 and one at 0,99 criteria, the eight further loci being monomorphic. In the Elba sample polymorphic loci had a more even genetic variability than in the Calafuria one, as shown by Standard Error (SE) values (Tab. 1).

Table 1. Summary in genetic variation of *Corallium rubrum* populations (SE in parentheses).

Population	Mean sample size	Mean number of alleles	% Poly-morphic loci(99)	% Poly-morphic loci(95)	Observed hetero-zygosity	Mean hetero-zygosity
Calafuria	91.1	1.46 (0.18)	30.77	23.08	0.085 (0.041)	0.104 (0.054)
Elba	76.3	1.46 (0.18)	38.46	30.77	0.064 (0.029)	0.073 (0.035)

The mean heterozygosity of both populations agrees with the average invertebrate value (AYALA & KIGER, 1987). A slight difference, not significant by T-test, was observed in the mean heterozygosity values of the two samples.

In literature there are very few data about genetic variability in Anthozoa and most of them concern reef corals. In order to compare our data with those regarding *Pocillopord damicornis* (STODDART, 1984) the mean heterozygosity in polymorphic loci was calculated (Tab.2). Genetic variability of *C. rubrum* resulted lower with respect to the reef coral. An explanation could be differences in the life cycles of the two species. *C. rubrum* eggs develop in the coelenteron and the planulae do not have a large dispersal capability. *P. damicornis* too has brooded planulae, but with over 100 days of planktonic life, sufficient to allow dispersal over large distances (RICHMOND & HUNTER, 1990). Moreover, *P. damicornis* samples analyzed by STODDART came from larger populations then our *C. rubrum* samples; this characteristic is of great importance in maintaining the presence of rare alleles (NEVO *et al.*, 1984).

Table 2. Mean heterozygosity of polymorphic loci in *Corallium rubrum* and in three populations of *Pocillopora damicornis* (STODDART, 1984).

Corallium rubrum		*Pocillopora damicornis*	
Calafuria	0.27	Pocill. Reef	0.35
Elba	0.19	Mary Cove	0.44
		Little Island	0.35

Our data represent a first characterization of *C. rubrum* population genetics. An extension of these studies to further Mediterranean samples is required in order to give a more exhaustive picture of the level of populations structuring.

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Preliminary Observations on benthic communities in a Submarine cave influenced by hydrothermal springs

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Typical submarine caves exhibit very poor and scattered benthic communities (CINELLI *et al.*, 1978; BALDUZZI *et al.*, 1989), with gradual decrease in species numbers and organism cover along the outside-inside gradient (GILI *et al.*, 1986). Absence of light and poor water exchanges are considered as the major reasons for oligotrophy and severe reduction in organism cover and biomass (FICHETZ, 1990).

The Grotta Azzurra marine cave opens in the carbonatic rock of Capo Palinuro (Tyrrhenian Sea). The cave has a volume of about 120000 m^3 and a maximum depth of 33 m (ALVISI *et al.*, in press). A peculiarity of the Grotta Azzurra is the presence of underwater sulphurous springs which form a thermo- and chemocline below the roof of the cave.

Preliminary surveys in the Grotta Azzurra led to the identification of 5 major biological zones (fig.2):

1- immediately outside. Photophilic algal assemblages, dominated by *Dictyota dichotoma*, occur;

2- entrance. Light is severely reduced and crustose coralline species are present;

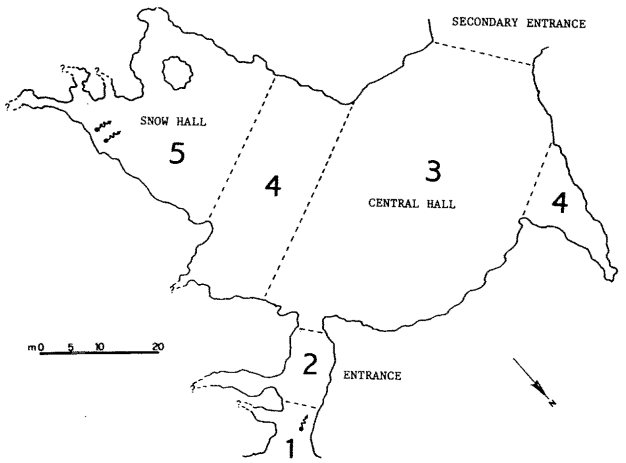
3- central hall. It is virtually dark. Dense faunal assemblages are dominated by passive filter-feeders like *Eunicella cavolinii* and *Eudendrium* sp. This might be explained by efficient water exchanges;

4- completely dark belts. Organism cover is reduced and fauna impoverished as typical of caves with a complete confinement gradient;

5- "Sala della Neve" (Snow Hall). It is the innermost part ot the cave, completely dark and extremely confined in terms of hydrodynamic conditions and trophic alloctonous inputs. Warm sulphur-rich waters accumulate to the vault where a complex of *Beggiatoa*-like filamentous forms and gelatinous colonies develop. White flakes of organic matter detach from the bacterial mats and fall to the bottom. Below, very rich and dense faunal assemblages occur on both the walls (sponges, bivalves, scleractinia) and the sediment floor (sabellid polychaetes, *Pinna nobilis, Antedon mediterranea, Ophioderma longicaudum*). Estimated biovolumes of specimens of the sponge *Geodia cydonium* and of the scleractinian coral *Astroides calycularis* resulted significantly larger for organisms collected here than in other parts of the cave.

These data provide a strong proof of enhanced trophic conditions, in contrast with the cave trophic depletion hypothesis.

Fig. 1. Biological zonation in the Grotta Azzurra: for explanation see text. (Plan of the cave re-drawn from ALVISI *et al.*, in press)



It appears that the unusual launal richness of the Grotta Azzurra is correlated with the presence of sulphide springs. Areas interested by chemosynthesis, in fact, appear to be biologically complex and very productive habitats (TARASOV *et al.*, 1990). Preliminary analysis of stable carbon isotopes by Dr. M.C. Kennicutt of Texas A. & M. University in organisms collected from the Sala della Neve seem to support this hypothesis (SOUTHWARD & SOUTHWARD, 1992). More investigations will be carried out during future research, which will assess organic carbon fluxes in the cave and trophic transfers to the benthos.

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