

# GENETIC SUBDIVISIONS OF THE RED CORAL (*CORALLIUM RUBRUM*) IN THE MEDITERRANEAN SEA : EVOLUTIONARY HISTORY AND MANAGEMENT IMPLICATIONS

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## Abstract

The genetic structure of the red coral *Corallium rubrum* was analysed in the Western Mediterranean. A clustering analysis identified six genetic groups and evidenced the particular genetic characteristics of Adriatic and North African populations. These data are useful for the management of this harvested species.

**Keywords:** Genetics, Cnidaria, Western Mediterranean

## Introduction:

The management and protection of biodiversity require an analysis of populations structure and connectivity. In the marine environment direct estimation of species dispersal abilities is difficult. Indirect estimates of dispersal can be obtained through genetic data [1]. In the Mediterranean Sea several genetic breaks common to different species have been identified [2] which may define the limits of conservation units [3]. Nevertheless few studies considered samples from Southern Mediterranean (North Africa) whereas a North-South distinction may be observed [4]. The red coral *Corallium rubrum* is an emblematic and harvested species also threatened by climate change [5], [6]. Previous studies indicated genetic differentiation at short distances with several genetic groupings at higher distances [7], [8]; up to now no study included North-African samples.

## Material and Methods:

We applied seven microsatellites loci [8] to 24 populations representing different regions of the Mediterranean distribution area of this species including Adriatic Sea and North Africa (Morocco and Algeria). A bayesian clustering analysis [9] was used for the identification of different genetic clusters. An Analysis of Molecular Variance (AMOVA) allowed to test genetic differentiation between the obtained clusters.

## Discussion:

The clustering analysis are presented in Fig.1 for the retained solutions (K=3 and 6 groups). The clusters correspond to the main geographical subdivisions and are genetically differentiated ( $p < 0.001$ ). Our results confirm the already observed geographical structuring [8] and extend these data with the differentiation of Adriatic samples (a single population analysed before, [7]) and North African samples. Nuclear sequence data suggest a low divergence among these groups [10] and a lack of long term isolation. The North African samples indicate that this area may be a important component of genetic diversity and would deserve more collaborative studies. According to these data the management of this species should take into account these differences at a regional but also a local scale [8].

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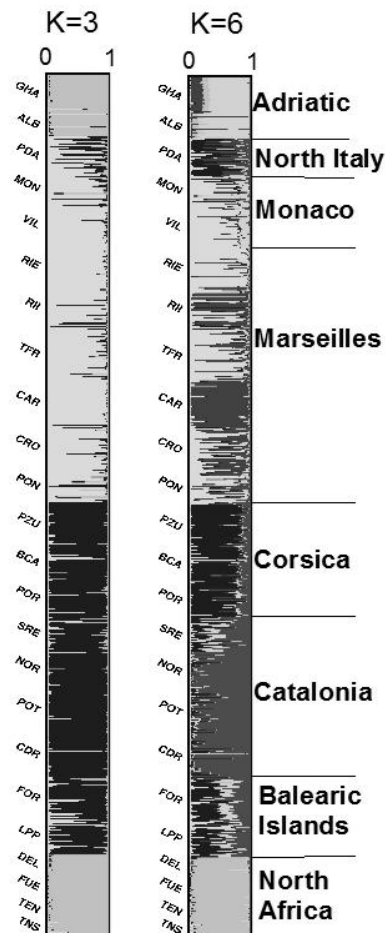


Fig. 1. Clustering analysis: each vertical line corresponds to one individual with colors indicating the assignment score (0 to 1) in each group