

# GENETIC STRUCTURE AND DIVERSITY OF THE YELLOW GORGONIAN *EUNICELLA CAVOLINI*: ECOLOGICAL AND EVOLUTIONARY INFERENCES.

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## Abstract

The Mediterranean yellow gorgonian *Eunicella cavolinii* (Cnidaria, Octocorallia) is among sessile species who have suffered mass mortality events following thermal anomalies in the North-Western Mediterranean Sea. We present here the first data on the genetic diversity and structure of this species. The results obtained with four microsatellite markers indicate a strong differentiation between the most distant samples considered here (North Africa, Turkey and France). At a regional scale genetic differences are lower though often significant. No significant differentiation is observed between depths on the same site.

**Keywords:** *Marmara Sea, North-Western Mediterranean, Algerian Basin, Cnidaria, Genetics*

## Introduction

Many marine invertebrates have suffered in recent years, the combined action of anthropogenic pressures and climate change. Thermal anomalies have already affected various sessile species, particularly populations above the thermocline [1]. The impact of such perturbations depends on the diversity of response between individuals and populations, and on dispersal at the metapopulation level.

*Eunicella cavolinii* (Koch1887) is a sessile species that was affected by mortality events during the past two decades, with variable levels of tissue necrosis depending on location, depth and individuals [2]. Its distribution is highly patchy in the Mediterranean Sea, which makes the metapopulation dynamics related to the major role of dispersal and gene flow. Genetic analyzes are a starting point for understanding the genetic structure of the yellow gorgonian and to estimate the spatial connectivity at different scales. This will give us some insights into the potential of recolonization in cases of local extinction. Analyzing levels of gene flow will also help understanding how this species might evolve in contrasted ecological conditions.

## Materials and methods

We performed an analysis of the genetic diversity of this species using four microsatellite loci and 17 shallow samples separated by an interval of a few tens of meters to hundreds of kilometers issued from contrasted environments of the Mediterranean Sea (Fig. 1).



Fig. 1. Map of the 17 samples of *E.cavolinii* (black and white stars). Samples were collected at different locations and depths for the areas indicated by a white star.

## Results

All loci were polymorphic with a total number of alleles ranging from 13, for C20 and C30, to 24, for S14, with a mean value of 17.8 alleles per locus. The observed and unbiased expected heterozygosities varied respectively between 0.30 for SIV (Turkey) and 0.63 for KIA (Algeria) (mean value over populations  $0.48 \pm 0.23$ ), and between 0.38 for SIV and 0.76 for KIA (mean value over populations  $0.55 \pm 0.25$ ). The results indicate similar levels of genetic diversity to those observed in the congeneric species *E. singularis* [3]. This diversity is nevertheless lower than that observed with microsatellites for other Mediterranean octocorals ( $H_{exp} = 0.77$  for the red

coral, *Corallium rubrum* [4], [5] and  $H_{exp} = 0.74$  for the red gorgonian *Paramuricea clavata* [6], [7]). Pairwise differentiation tests between populations showed high values of  $F_{st}$  (Overall  $F_{st} = 0.11$ ), especially between the most distant samples North Africa, Turkey and France. A Principal Coordinates Analysis illustrates the differences between samples and highlights the clear genetic differences between regions (Fig. 2). The non-significant comparisons included mostly samples from sites that were taken at different depths.

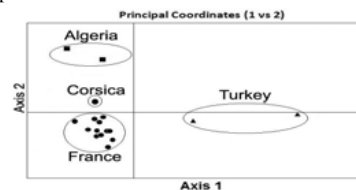


Fig. 2. Principal Coordinates Analysis of the genetic differences between samples.

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