CAN WE ESTIMATE MARINE CONNECTIVITY WITH GENETIC APPROACHES? A CASE STUDY ON NORTH WESTERN POPULATIONS OF TWO MEDITERRANEAN GORGONIANS

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Abstract

Genetic studies of octocoral populations in the Mediterranean Sea have revealed a pattern of strong and short distance genetic structure without apparent deep genetic break. In order to better understand such structuring we provide here an analysis of connectivity in the North-Western Mediterranean for two species: the red coral Corallium rubrum, and the red gorgonian Paramuricea clavata. We compare the results obtained by different methods aimed at estimating recent or long term components of gene flow. The results are discussed in the light of the biological characteristics of these species, of their evolutionary history and of the potential limits of the methods used.

Keywords: Genetics, Gulf of Lyon, Cladaria

The management and conservation of natural populations need to take into account gene flow levels as indicators of recolonisation abilities and population connectivity. Population genetic studies of octocorals in the Mediterranean Sea have evidenced unexpected patterns of genetic structuring for species with a larval stage: microsatellite data have shown short to significant genetic differentiation at medium to short distance for the red coral Corallium rubrum, and the red gorgonian Paramuricea clavata ([1], [2], [3], [4], [5], [6]). Significant differences have also been observed between depths in the same site (e.g. between 20 and 40 m for the red coral; [6]). These significant differences have been mainly interpreted as the consequence of reduced mean dispersal abilities. Nevertheless a phylogeographic comparison between the most distant locations did not evidence any deep phylogeographic break for the red coral. This does not support long term isolation even through well-known genetic barriers such as the Almeria – Oran front ([1]). The sampling scheme may also have impacted the observed genetic structure between distant locations ([1]). Moreover FST values and significance do not rely only on dispersal levels but also on effective size and population history (e.g. [7]) and real estimates of dispersal (i.e. not only FST) are still lacking for these species. We analyze here microsatellite data from C. rubrum and P. clavata in order to assess in a comparative way dispersal estimates in the North-Western Mediterranean Sea. The comparison will be done between these two species in the same area in order to look for some potential shared limits to gene flow. We will analyze populations from three distant regions: Marseille, Catalonia and Corsica, with an analysis between regions and between populations inside regions. These regions have been identified as different genetic clusters based on microsatellite data ([6]). This may reflect the impact of several non-exclusive phenomena: hydrographic barriers, lack of suitable habitats between regions, distance effect in a isolation by distance framework. A more precise study of connectivity is then required in this context. A regional analysis of connectivity will also be performed, with a focus on the Marseille area: in this region the populations of these species are separated in two main areas, South and North of the city which might correspond to different genetic groups as well ([6]). A connectivity analysis is interesting here both for understanding population dynamics and evolution but also for management purposes. Finally the question of gene flow between depths in each area will be discussed. It will shed light on the interaction between migration and local selective pressures. A methodological comparison will be done between different approaches for dispersal estimates in order to try to separate the short and long term components of gene flow. The first category of methods used here is assignment approaches which allow the detection of migrant individuals: it then deals with short-term / contemporary connectivity. This is useful in order to evaluate current recolonisation abilities of these species. The second category of methods relies on models dedicated to the estimation of long term migration and effective population sizes. This will give some insights in the evolutionary history of these species and their interaction with environmental heterogeneities and fluctuations.

References