

GUIDELINES ON GENETIC CONNECTIVITY AS A TOOL FOR ASSESSING THE EFFECTIVENESS OF MARINE PROTECTED AREAS

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Abstract

The design and management of Marine Protected Areas (MPAs) and MPA networks should take into account the patterns of spatial distribution and connectivity among populations of the target species. Well-connected and highly diverse populations are more resilient to natural and anthropogenic impacts. In the context of MPA monitoring, genetic analyses are considered a powerful tool for assessing population diversity and connectivity patterns at different spatial scales. Here, two case studies using genetics tools were presented to assess connectivity patterns between protected and unprotected areas in the Mediterranean Sea, providing MPA managers with a set of guidelines to address specific species conservation issues.

Keywords: Genetics, Mediterranean Sea, Marine parks, Conservation

Why and how to monitor genetic connectivity

The design and management of Marine Protected Areas (MPAs) and MPA networks should consider spatial patterns of species distribution and connectivity among populations (1). Connectivity is a fundamental aspect to consider when evaluating the status of existing MPAs and MPA networks, since well-connected and highly diverse populations are more resilient to environmental changes (2). Connectivity patterns can be used as a management tool, providing information on the portion of individuals coming from protected populations retained within MPA borders and the amount of individuals exported from protected populations toward unprotected areas (Fig1).

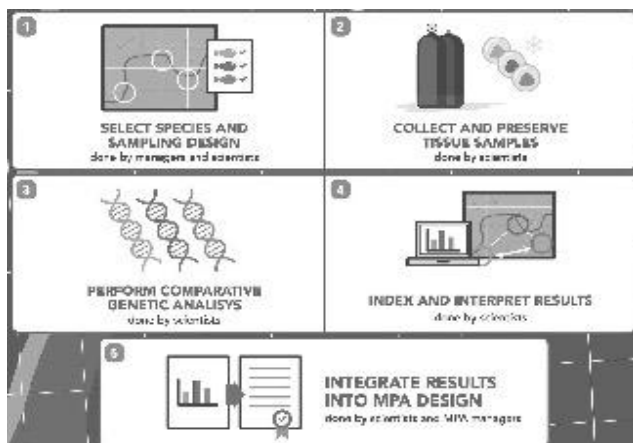


Fig. 1. Schematic standard approach for gathering and integrating genetic data for conservation strategies. Layout and design: La Calle es Tuya, S.C.

In the context of MPA monitoring, genetic tools allow the assessment of connectivity patterns at different temporal and spatial scales, and are possibly non-lethal, allowing their application on endangered species and focal species (3, 4). From this perspective, the number of sampling sites should be defined depending on the geographic extension of the study area. The distance among sites and number of sampling sites would depend on the MPA size, the geomorphological and environmental characteristics and the target species. Specifically, for genetic analyses, at each site, 20-30 individuals per species should be sampled, for instance, within an area of approximately 100 m., separated from 1-10 m apart in the case of sessile individuals or sampling from different shoals in the case of fishes. A small amount of tissue is enough for genetic analysis, which usually can be extracted without harming or killing the individual. Samples should be preserved in 90% ethanol and maintained at 4 °C until processing. Samples could be extracted and sent to a sequence facility. Since connectivity patterns differ among species, several species should be selected to better address MPA management issues, as well as integrating additional information, such as oceanographic and demographic data.

A case study on fishes: the saddled sea bream

The saddled sea bream (*Oblada melanura*) is an economically important species, widely distributed in Mediterranean coastal ecosystems. Although generally protected within Mediterranean MPAs, population genetic patterns of this species are currently unknown in the Western Mediterranean Sea. Genetic structure of the saddled sea bream and the level of genetic connectivity between protected and unprotected populations was investigated. Spatial patterns of population differentiation were assessed at different spatial scales, considering three MPAs of the Western Mediterranean Sea. Values of population differentiation were non-significant, indicating that, at a relatively local spatial scale, protected populations were in general well connected with non-protected ones. At the regional scale, a subtle population structure that reflects the main oceanographic features was present. These results may have important implications for the conservation biology and fisheries management of saddled sea bream like other coastal fish.

A case study on intertidal invertebrates: the limpets

Limpets have a key ecological role in structuring rocky intertidal assemblages. Therefore their conservation is essential to protect these communities. Genetic variability and population connectivity of two widely distributed limpets (*Patella caerulea* and *P. rustica*) were analyzed inside and outside four MPAs in the western Mediterranean Sea using mitochondrial and microsatellite markers. No effect of protection on genetic variability was observed in either species. Mitochondrial marker reveals for both species limited genetic structure among MPAs in the north-Western Mediterranean. Within each location, different patterns of genetic structure and connectivity were observed depending on the species and local hydrodynamic features. These and future genetic connectivity studies will help to MPA managers for the design of MPAs in order to enhance connectivity and genetic diversity that will increase the resilience of marine populations.

References

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