

{rokbox title=|Map of the individual-based sampling design conducted for each species: *Diplodus sargus*, *Palinurus elephas*, *Mullus surmuletus* and *Serranus cabrilla* :: Image: Authors| images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-contrasting-influence-seascape-goñi-2023-thumb-et-al.jpg|} images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-contrasting-influence-seascape-goñi-2023-et-al.jpg{/rokbox}

Laura Benestan, Nicolas Loiseau, Pierre-Edouard Guérin, Angel Pérez-Ruzafa, Aitor Forcada, Esther Arcas, Philippe Lenfant, **Sandra Malloí**, **Raquel Goñi**, Laure Velez, David Mouillot, Oscar Puebla, Stéphanie Manel, 2023.

[Contrasting influence of seascape, space and marine reserves on genomic variation in multiple species.](#)

Ecography. Volume 2023. Issue 1. January 2023. <https://doi.org/10.1111/ecog.06127>

Abstract: Marine reserves are being established worldwide to conserve and manage marine resources, and are also often assumed to conserve the evolutionary potential of marine populations. However, comparisons of genomic patterns inside and outside marine reserves in multiple species are scarce. Here, we aim to fill this gap by 1) comparing genomic variation in protected versus unprotected areas in a network of eight reserves in the Mediterranean Sea, and 2) disentangling the effect of seascape, space and marine reserves on this genomic variation in 1297 individuals from four species genotyped at more than 10 000 SNPs each. We report homogeneous patterns of local genetic diversity within and outside reserves in three of the four species (the white seabream *Diplodus sargus*, the striped red mullet *Mullus surmuletus*

and the European spiny lobster

Palinurus elephas

). Surprisingly, the comber *Serranus cabrilla* shows lower genetic diversity in protected areas, highlighting an apparent conservation paradox that may be due to increased predation by protected fishes in the reserves. Multivariate analyses reveal that seascape factors (salinity, temperature and chlorophyll) and space exert a significant influence on genomic variation in some cases, while protection status has no detectable effect. Nevertheless, four marine reserves (Cabo de Palos, Cerbère-Banyuls, Cap de Creus and Illes Columbretes) harbor singular genetic variation in one or two species. This pattern, observed in the four species, suggests that reserves contribute to preserve genetic variation locally. Our study illustrates that we can document key aspects of the genetic variation of marine species and their interaction with seascape factors, space and protection status in multiple species. It stresses the need for a multi-species approach to inform marine conservation planning, opening up new perspectives at the community level.

Keywords:genetic diversity,no-take marine protected areas,seascape genomics.