

{rokbox title=| Sampling locations of *Galeus melastomus* :: Image:

Authors|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-first-evidence-population-hidalgo-2022-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-first-evidence-population-hidalgo-2022-et-al.jpg{/rokbox}

Simone Di Crescenzo, Alice Ferrari, Claudio Barría, Rita Cannas, Alessia Cariani, Jim Drewery, Lourdes Fernández-Peralta, Daniela Giordano, **Manuel Hidalgo**, Vasiliki Kousteni, Ilaria Anna Maria Marino, Daniela Massi, Teresa Moura, Javier Rey, Paolo Sartor, Umberto Scacco, Fabrizio Serena and Marco Stagioni, 2022.

[First evidence of population genetic structure of the deep-water blackmouth catshark *Galeus melastomus* Rafinesque, 1810.](#)

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Abstract: Among the main measures adopted to reduce anthropogenic impacts on elasmobranch communities, understanding the ecology of deep-sea sharks is of paramount importance, especially for potentially vulnerable species highly represented in the bycatch composition of commercial fisheries such as the blackmouth catshark *Galeus melastomus*. In

the present work, we unravelled the first indication of population genetic structure of *G. melastomus*

by using a novel and effective panel of nuclear, and polymorphic DNA markers and compared our results with previous findings supporting high genetic connectivity at large spatial scales. Given the lack of species-specific nuclear markers, a total of 129 microsatellite loci (Simple Sequence Repeats, SSRs) were cross-amplified on blackmouth catshark specimens collected in eight geographically distant areas in the Mediterranean Sea and North-eastern Atlantic Ocean. A total of 13 SSRs were finally selected for genotyping, based on which the species exhibited signs of weak, but tangible genetic structure. The clearcut evidence of genetic differentiation of

G. melastomus

from Scottish waters from the rest of the population samples was defined, indicating that the species is genetically structured in the Mediterranean Sea and adjacent North-eastern Atlantic. Both individual and frequency-based analyses identified a genetic unit formed by the individuals collected in the Tyrrhenian Sea and the Strait of Sicily, distinguished from the rest of the Mediterranean and Portuguese samples. In addition, Bayesian analyses resolved a certain degree of separation of the easternmost Aegean sample and the admixed nature of the other Mediterranean and the Portuguese samples. Here, our results supported the hypothesis that the interaction between the ecology and biology of the species and abiotic drivers such as water circulations, temperature and bathymetry may affect the dispersion of

G. melastomus

, adding new information to the current knowledge of the connectivity of this deep-water species and providing powerful tools for estimating its response to anthropogenic impacts.

Keywords: conservation, cross-amplification, deep-sea, microsatellite loci, population differentiation, sharks, North-eastern Atlantic Ocean, Mediterranean Sea.