

{rokbox title=|Median-joining network of Control Region (CR) haplotypes shown by P. bogaraveo :: Image: Authors| thumb=|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-high-conectivity-deep-hidalgo-2025-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-high-conectivity-deep-hidalgo-2025-et-al.jpg{/rokbox}

Martina Spiga, Giusy Catalano, Federica Piattoni, Alice Ferrari, Carolina Johnstone, Kenza Mokhtar-Jamaï, Montse Pérez, Fabio Fiorentino, **Manuel Hidalgo** and Alessia Cariani, 2025. [High Connectivity in the Deep-Water Pagellus bogaraveo: Phylogeographic Assessment Across Mediterranean and Atlantic Waters](https://doi.org/10.3390/fishes10100527) .Fishes.2025. 10(10). 527. <https://doi.org/10.3390/fishes10100527>

Abstract: The Blackspot Seabream, *Pagellus bogaraveo*, is a commercially valuable species widely distributed in the northeastern Atlantic and Mediterranean. Its biology makes it vulnerable to overfishing, but its population structure and ontogenetic migration strategy remain unclear. Building on previous work based on microsatellite markers, we expanded the investigation by analysing the mitochondrial Control Region (CR) to complement nuclear data. We analysed 199 specimens from 13 sites and combined the new CR sequences with 129 published records to achieve the broadest coverage in terms of biogeographic and genetic data. We calculated genetic diversity and performed AMOVA, pairwise Φ_{ST} comparisons, and multivariate analyses. Eighty-eight haplotypes were identified, showing high haplotype diversity ($H_d = 0.767\text{--}0.945$) and moderate nucleotide diversity ($\pi = 0.0026\text{--}0.0054$). Most genetic variation occurred within populations, and overall analyses indicated genetic homogeneity. However, pairwise analysis and AMOVA confirmed significant differentiation of the Azores population. These results confirm extensive genetic connectivity throughout the Atlantic–Mediterranean range of *P. bogaraveo*, likely due to a combination of large larval dispersal and a common spawning migration strategy, but identify the Azores as a genetically distinct unit. This highlights the need to consider both large-scale connectivity and local divergence in fisheries management.

Keywords: control region, mtDNA, genetic population structure, blackspot seabream.