

{rokbox title=| Bathymetric maps of western Europe and the Mediterranean showing the locations of sampling sites for lobsters *Homarus gammarus* (left) and crawfish *Palinurus elephas* (right) :: Image:

Authors|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-shared-distinct-patterns-diaz-2023-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-shared-distinct-patterns-diaz-2023-et-al.jpg{/rokbox}

Charlie D. Ellis, Kirsty L. MacLeod, Tom L. Jenkins, Lénia D. Rato, Youenn Jézéquel, Mišo Pavičić, **David Díaz**, Jamie R. Stevens, 2023. [Shared and distinct patterns of genetic structure in two sympatric large decapods.](#)

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Abstract:

Aim Comparing genetic structure in species with shared spatial ranges and ecological niches can help identify how dissimilar aspects of biology can shape differences in population connectivity. Similarly, where species are widely distributed across heterogeneous environments and major topographic barriers, knowledge of the structuring of populations can help reveal the impacts of factors which limit dispersal and/or drive divergence, aiding conservation management.

Location European seas of the northeast Atlantic and Mediterranean.

Taxa European clawed lobster (*Homarus gammarus*) and European crawfish (*Palinurus elephas*), two sympatric, heavily fished decapods with extensive dispersal potential.

Methods By RAD-sequencing 214 *H. gammarus* from 32 locations and 349 *P. elephas* from 15 locations, we isolated 6340 and 7681 SNP loci, respectively. Using these data to characterise contemporary population structuring, we investigate potential spatial and environmental drivers of genomic heterogeneity.

Results We found higher levels of differentiation among clawed lobsters than crawfish, both globally and within basins, and demonstrate where known hydrographic and topographic barriers generate shared patterns of divergence, such as a genetic break between the Atlantic and Mediterranean basins. Genetic structure not common to both species is principally apparent in the Atlantic portions of their range, where clawed lobster exhibits a genetic cline and increased differentiation towards range margins, while crawfish appear effectively panmictic throughout this region.

Main Conclusions We attribute the comparative lack of crawfish population structuring to their greater dispersal tendencies via a longer pelagic larval duration and sporadic adult movements. In contrast, genetic connectivity in clawed lobster is relatively restricted, with the correlation of site of origin and temperature to geographical heterogeneity at many divergent loci indicative of both neutral and adaptive processes. Our results help inform how contemporary management can account for likely demographic connectivity and marry the

conservation of genomic variation with sustainable fisheries in these ecologically and economically important crustaceans.

Keywords: crustacea, fisheries, genetic, structure, lobster, marine, connectivity, phylogeography, RA D-seq, spiny lobster.