

# Genomic study shows differences between populations of black sea urchin in the Mediterranean

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These results indicate that salinity, and not so much temperature, affect the populational structure, and suggest that this species could be favoured in a situation of global warming. Credit: Creu Palacín, UNIVERSITY OF BARCELONA-IRBio

Global environmental changes such as those caused by climate warming can have a deep impact on the ecosystems. In this context, it is vital to gather biological and ecological information of the main species to predict and mitigate the potential effects of these changes in the distribution, abundance and interaction of these species.

The study, led by Marta Pascual, lecturer at the Faculty of Biology and member of the Biodiversity Research Institute (IBRio) of the Universidad de Barcelona, and Xavier Turon, CSIC research lecturer at the Centre for Advanced Studies of Blanes (CEAB-CSIC), has analyzed the genetic structure of a key [species](#) in the shallow littoral ecosystems in the Mediterranean: the black sea urchin (*Arbacia lixula*).

The results, published in the journal *Frontiers in Marine Science*, confirm that the global warming could have a light impact on this species, since its population receive a higher impact due to salinity than temperature. According to the researchers, this discovery sheds light on the potential effects of climate change in a key ecological species, and it indicates the vulnerability of the urchin species *Paracentrotus lividus*.

"In the Mediterranean, there are mainly two species of sea urchins in the littoral area: the edible species *Paracentrotus lividus* and the black sea urchin, *Arbacia lixula*, which we do not eat. These are bioengineer species, since they can shape the ecosystems where they live due to their diets," says Creu Palacin, member of the Department of Evolutionary Biology, Ecology and Environmental Sciences and the IRBio.

Populational structure studies enable researchers to determine the level of connectivity between populations and, therefore, the dispersive ability of the species in the studied area. Also, they allow them to establish what environmental variables have a higher influence in this structuration and involve a major challenge of adaptation. "Studying these adaptation and connectivity processes provides us with an idea of how these species can

respond to environmental changes," notes Carlos Carreras, first author of the article and member of the Department of Genetics, Microbiology and Statistics, and also member of the IRBio.



Researchers have analysed the genetic structure of a key species in the shallow littoral ecosystems in the Mediterranean: the black sea urchin (*Arbacia lixula*). Credit: Creu Palacín, UNIVERSITY OF BARCELONA - IRBio

## **From Tarifa to Dalyan**

The researchers carried out genomic analyses of 240 subjects of eleven

populations of sampled black sea urchins in the Mediterranean coast, from Tarifa to Dalyan (Turkey). They used the genotyping-by-sequencing (GBS), a technique that allows researchers to analyze a representative part of the genome of each individual, characterize its genotype and compare it to that of other subjects using different genetic markers. "Genomic tools are necessary to detect the genetic differentiation in these cases and to identify those environmental variables with a higher influence in the genetic structuration," notes Marta Pascual.

The results indicate there are genetic differences among the populations of the western Mediterranean and the eastern Mediterranean, and that the structuration is mainly determined by the variability of salinity between these two areas, while temperature seems to play a secondary role. "Moreover, note the researchers, the populations are generally well-connected—except for those between eastern and western Mediterranean areas, which could favor changes in their distribution if the environmental conditions require so."

## **The potential movement of the common urchin**

These data contrast with the results obtained in a previous study by the same research group on the distribution of the *P. lividus* urchin, the other most abundant species in the littoral area of the Mediterranean. These species present a more marked structuration, and also, the differences of the populations are determined by the salinity and the temperature. "This means that the black sea urchin could live better in a global warming scenario, and therefore, could move the *P. lividus* urchin due to a major connectivity among populations. These changes of species could have a great impact on the affected ecosystems due to urchin's role as engineers," notes Xavier Turon.

## Next objective: Genome sequencing

The next step in this research line is to know in depth about the genomic regions that have been detected for both species in this study. With this aim, the UB researchers have developed a project led by the lecturer of the Faculty of Biology Cinta Pergueroles, as part of the call of the Catalan Earth Biogenome project of the Institute for Catalan Studies for the sequencing of the *Arbacia lixula* genome. "The model genomes are a fundamental tool, since they allow us to locate the regions that we identify as affected by the environmental variables we analyzed, as well as the genes we can find," conclude the researchers.

**More information:** Carlos Carreras et al, The Two Sides of the Mediterranean: Population Genomics of the Black Sea Urchin *Arbacia lixula* (Linnaeus, 1758) in a Warming Sea, *Frontiers in Marine Science* (2021). [DOI: 10.3389/fmars.2021.739008](https://doi.org/10.3389/fmars.2021.739008)

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