

{rokbox title=|Geographical distribution of sampling sites :: Image:

Authors|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-sardines-junction-seascape-albo-2023-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-sardines-junction-seascape-albo-2023-et-al.jpg{/rokbox}

Aglaia Antoniou, Tereza Manousaki, Francisco Ramírez, Alessia Cariani, Rita Cannas, Panagiotis Kasapidis, Antonios Magoulas, **Marta Albo-Puigserver**, Elena Lloret-Lloret, Jose Maria Bellido, Maria Grazia Pennino, Maria Cristina Follesa, Antonio Esteban, Claire Saraux, Mario Sbrana, Maria Teresa Spedicato, Marta Coll, Costas S. Tsigenopoulos, 2023.

Sardines at a junction: Seascape genomics reveals ecological and oceanographic drivers of variation in the NW Mediterranean Sea.

Molecular Ecology: Volume 32. Issue 7. <https://doi.org/10.1111/mec.16840>

Abstract: By evaluating genetic variation across the entire genome, one can address existing questions in a novel way while raising new ones. The latter includes how different local environments influence adaptive and neutral genomic variation within and among populations, providing insights into local adaptation of natural populations and their responses to global change. Here, under a seascape genomic approach, ddRAD data of 4609 single nucleotide polymorphisms (SNPs) from 398 sardines (*Sardina pilchardus*) collected in 11 Mediterranean and one Atlantic site were generated. These were used along with oceanographic and ecological information to detect signals of adaptive divergence with gene flow across environmental gradients. The studied sardines constitute two clusters ($F_{ST} = 0.07$), a pattern attributed to outlier loci, highlighting putative local adaptation. The trend in the number of days with sea surface temperature above 19°C, a critical threshold for successful sardine spawning, was crucial at all levels of population structuring with implications on the species' key biological processes. Outliers link candidate SNPs to the region's environmental heterogeneity. Our findings provide evidence for a dynamic equilibrium in which population structure is maintained by physical and ecological factors under the opposing influences of migration and selection. This dynamic in a natural system warrants continuous monitoring under a seascape genomic approach that might benefit from a temporal and more detailed spatial dimension. Our results may contribute to complementary studies aimed at providing deeper insights into the mechanistic processes underlying population structuring. Those are key to understanding and predicting future changes and responses of this highly exploited species in the face of climate change.

Keywords: climate change, ddRAD, outliers, population genomics, SNPs.