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[Uncovering the Genetic Structure of European Anchovy Populations in Central and Western Mediterranean](#)

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Abstract: Among small pelagic fishes, the European anchovy (*Engraulis encrasicolus*) is a key species within the marine ecosystem of the Mediterranean Sea, exhibiting significant population structure across its geographic range. This study applied state-of-the-art genomic analyses, utilizing 9497 genome-wide SNPs derived from ddRAD sequencing, to investigate population structure, genetic diversity, and genotype-environment associations in anchovy samples collected across 12 locations in the Western and Central Mediterranean as well as nearby Atlantic regions. In order to increase the number of polymorphic loci identified, we first assembled a draft reference genome for the species (1.69 Gb and 79.8% BUSCO completeness), which proved to be a powerful tool for downstream analyses. Two main genetic clusters were delineated: one comprising individuals from the Atlantic and Alboran Sea and the other including those from the Northwestern (particularly Balearic Sea and Gulf of Lion) and Central Mediterranean ($F_{ST} = 0.09$), indicating the Almeria–Oran front as a potential dispersal barrier for gene flow in the species. Seascape genomic analyses identified statistically significant associations between SNPs and environmental variables such as temperature and nutrient availability. Overall, our research highlighted the genetic relationships among anchovies in the studied area, providing essential insights needed for identifying distinct management units and developing conservation strategies, while emphasizing the need to address genetic and environmental dynamics in light of climate change, which may threaten the stability and resilience of anchovy populations and their habitats.

Keywords: ddRAD, *Engraulis encrasicolus*, genome assembly, population genomics, seascape genomics, SNP.