

Neutral and adaptive loci reveal fine-scale population structure in *Eleginops maclovinus* from North Patagonia

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September 6, 2022

Abstract

Patagonia is an understudied area, especially when it comes to population genomic studies with relevance to fishery management. However, the dynamic and heterogeneous landscape in this area can harbor important but cryptic genetic population structure. Once such information is revealed, it can be integrated into the management of infrequently investigated species. *Eleginops maclovinus* is a protandrous hermaphrodite species with economic importance for local communities that is currently managed as a single genetic unit. In this study, we sampled five locations distributed across a salinity cline from Northern Patagonia to investigate the genetic population structure of *E. maclovinus*. We use Restriction-site Associated DNA (RAD) sequencing and outlier tests to obtain neutral and adaptive loci, using FST and GEA approaches. We identified a spatial pattern of structuration with gene flow and spatial selection by environmental association. Neutral and adaptive loci showed two and three genetic groups, respectively. The effective population sizes estimated ranged from 572 (Chepu) to 14,454 (Chaitén) and were influenced more by locality than salinity cline. We found loci putatively associated with salinity suggesting that salinity may act as a selective driver in *E. maclovinus* populations. These results suggest a complex interaction between genetic drift, gene flow, and natural selection in this area. Our findings suggest several units in this area, and the information should be integrated into the management of this species. We discuss the significance of these results for fishery management and suggest future directions to improve our understanding of how *E. maclovinus* is adapted to the dynamic waters of Northern Patagonia.

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Acknowledgments

We thanks to Kristen M. Gruenthal for the RADseq workshop conducted at UWSP, to Valentina Prida and Cristobal Gárce for participate in sampling collection. C.B.C.-A. was supported by ANID FONDECYT initiation grant no. 11180897. C.B.C.-A, D.G-U, J.M.Y were supported by Nucleo Milenio INVASAL funded by ANID – Millennium Science Initiative– NCN16_034. We thanks two anonymous reviewers for providing valuable comments of the manuscript and Susan Cleveland for checking and improving the language or the English style.

Funding

This research and the APC was funded by ANID/CONICYT FONDECYT Iniciación N°11180897”