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Connectivity in Southern ocean fish: A tale of five fish

A.P. Van de Putte¹, K. Janko², G.E. Maes¹, J.K.J. Van Houdt¹, E. Kasparov², M.A. Collins³ et al

¹K.U. Leuven, Belgium, ²Laboratory of Fish Genetics, Czech Republic, ³British Antarctic Survey, United Kingdom

Marine species show a suite of characteristics, such as great dispersal capabilities and large population sizes which promote gene flow in an environment that lacks obvious physical boundaries. The Southern Ocean is characterized by large and small scale circulation patterns that respectively promote circum-antarctic dispersal or local retention. Schematically, genetic differentiation can result from historical patterns maintained over geological time or from present-day isolation attributable to biological characteristics of the species.

We used a comparative approach to population genetic analysis based on microsatellite markers and mitochondrial DNA sequences to determine the impact of reproductive strategy and habitat on the genetic structure of individuals sampled around the Antarctic continent. Five species were selected to test the impact of habitat and reproductive strategy on genetic structure on a present day and a historical scale. These include four coastal species, *Trematomus newnesi*, *Trematomus hansonii*, *Trematomus nicolai*, *Trematomus bernacchii* and one oceanic species *Electrona antarctica*.

The benthic *T. bernacchii* displayed the strongest population structure combined with limited genetic diversity, while the mesopelagic *E. antarctica* displayed no genetic structure at all and a high genetic diversity. This indicates that there is indeed an effect of habitat and reproductive strategy on the genetic structure on the historical and present day genetic structure of Southern Ocean fish. Within a historical context these results indicate that species with a more benthic habitat and limited or no pelagic phase were more affected by reduction in suitable habitat due to ice sheet expansions as was shown by a previous study. On a contemporary scale dispersal appears to be promoted by a longer pelagic larval phase and pelagic habit as adult.

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