

Connectivity the Southern Ocean: population genomics of icefish

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The teleost fauna of the Southern Ocean is dominated both in terms of abundance and biomass by icefish of the suborder Notothenioidei. These fish are a rare example of a marine adaptive radiation with more than 120 extant species. Their diversification concurred with key adaptations to a cold, stable environment. Rapid environmental changes and increasing anthropogenic pressures, however, may affect their diversity and call for sound management and conservation measures. Characterizing genetic structuring in time and space is an important prerequisite to define targets for such measures. The oceanographic system of the Southern Ocean is dominated by the Antarctic Circumpolar Current that is connected to local gyres and fronts. While this current in conjunction with long pelagic larval phases may act as homogenizing force between populations, other factors such as habitat discontinuity or local adaptation can increase genetic differentiation. Current reduced genome representation approaches such as restriction-site associated DNA (RAD) sequencing enable characterization of markers on a genome wide level even in non-model species. We use these techniques to infer large and fine scale patterns of contemporary population structure in icefish and relate observed signals in genomic variability to potential driving forces of connectivity, such as ocean current systems.

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