

Comparison of spatial genetic structure and its drivers in Arctic and Antarctic fishes

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Marine populations are genetically structured through historical processes, environmental or physical barriers and life history characteristics. Divergent patterns of demographic history, even among closely-related species sharing climatic changes, raise questions about the influence of species-specific traits on population structure. The Southern Ocean features comparatively high biodiversity, which has been attributed to frequent local extinction-recolonization cycles that have driven benthic, Antarctic organisms into temporary refugia. In contrast, organisms in the Arctic were able to shift latitude in response to changing Pleistocene climate. We therefore hypothesize that Arctic populations were historically less constrained in their distribution than Antarctic fish populations and hence show lower levels of genetic structure.

For assessing the role of lifestyle in influencing demographic history in the Southern Ocean closely related notothenioid fish with benthic (*Trematomus bernacchii*, *T. hansonii*) and semi-pelagic or even cryopelagic (*T. newnesi*) lifestyles were genetically analysed. In the Arctic, polar cod (*Boreogadus saida*), which is often found in association with sea ice, but also throughout the water column to the bottom, can be regarded as semi- or cryopelagic too. The Antarctic species were analysed by six microsatellite and one mitochondrial marker before (Van de Putte et al., 2012) and we extend these analyses with data from nine microsatellite markers in polar cod.

Antarctic species showed significant genetic population structure between High-Antarctic and Peninsular regions and much lower differentiation in pelagic than benthic species. It suggests that the observed patterns are indeed related to ecological traits of Antarctic fish. In the Arctic, we hypothesize genetic structuring inside fjords in Svalbard relative to shelf specimens, which we expect to show low or absent structure as in Antarctic species with a similar lifestyle. Identifying common driving factors for population structure is important in order to enable forecasting, particularly in light of dramatically increasing rates of environmental change. Comparing population genetic patterns and exploring underlying causes from both poles may thus help to shed light on how fish populations survived in the past and may persist in the future.

Reference

- Van de Putte A., Janko K., Kasparova E., Maes G.E., Rock, J., Koubbi P., Volckaert F.A.M., Choleva L., Fraser K.P.P., Smykla J., Van Houdt J.K.J., Marshall C. 2012 Comparative phylogeography of three trematomid fishes reveals contrasting genetic structure patterns in benthic and pelagic species. *Marine Genomics* 8:23-34.