

Summary

Context

The high degree of endemism and special cold adaptations make Antarctic organisms highly vulnerable to global change. Given the current fast warming and loss of ice sheets, protection of the unique Antarctic biodiversity becomes a most urgent issue. The delimitation of Marine Protected Areas (MPAs) is one of the most important tools to protect marine habitats. Nine MPA domains have been suggested by the Convention on the Conservation of Antarctic Marine Living Resources (CCAMLR) in the Southern Ocean (SO) but only two have been realized so far and four more are in the planning stage. The COPE project provides data on genetic connectivity of endemic *Charcotia* amphipods and *Trematomus* fishes to optimize the delimitation of MPAs in the Southern Ocean and identify regions of particular concern.

Objectives

The COPE project has five major objectives:

1. Delimitate genetic species of selected amphipod and fish morphospecies for subsequent population genetic analyses and the identification of cryptic diversity.
2. Obtain genomic data on neutral genetic variability, connectivity and population structure of two key taxa of the SO, scavenging *Charcotia* amphipods and *Trematomus* fish at a circum-Antarctic scale.
3. Use outlier analyses from genomic data to test for local adaptation to abiotic factors that characterize the seascape.
4. Compare patterns of genetic connectivity in both taxa groups to their life histories including dispersal capacities and seascapes.
5. Model the distribution of *Charcotia* and *Trematomus* species in the SO from existing occurrence data and environmental data layers.

Conclusions

The COPE project successfully achieved its objectives. Most analyses were based on existing collections in the two partner institutions because of reduced ship time linked to the COVID-19 pandemic. We recommend the extension of databases and datasets with abiotic and biodiversity information to further develop the scarce biological knowledge, and, for example, to feed into Species Distribution Models and dispersal models linked to hydrodynamic models. We made several important contributions to the field: we detected additional cryptic diversity in both target taxa, contributing to realistic estimates of endemic diversity in Antarctic marine ecosystems. Reconstructions of the realized ecological niche in amphipod sister species revealed pronounced inter- and intraspecific differences, illustrating trophic plasticity of scavenging Antarctic amphipods. The project provided the first estimates of genome sizes for 16 Antarctic amphipod species, confirming large differences and the presence of giant genomes in amphipods. This database forms an important base for genomic research. The most relevant and

novel results are estimates of genetic population differentiation and structuring in two amphipod and six *Trematomus* species at various geographic scales in the Southern Ocean. The genome-wide data revealed various patterns, even among closely related species. We found evidence for the absence of population structure within the Eastern Weddell Sea in three *Trematomus* fish species. In contrast, we observed patterns of geographic isolation in two other *Trematomus* species and the amphipod *Charcotia obesa*. There is also evidence for population differentiation at small scales, for example along the Western Antarctic Peninsula or within the Eastern Weddell Sea. Observed patterns of putatively adaptive genetic variation suggest that chromosomal rearrangements might play a key role in adaptation of *Trematomus* fishes. Putatively adaptive patterns observed in *Charcotia obesa* resulted from two geographically close locations in the Western Antarctic Peninsula. These locations fall within the same bioregion, which suggests that the adaptation is driven by local conditions. Some patterns of genetic connectivity are new and surprising, as for example the connection between one side of the Filchner Trough and the western Weddell Sea, which might be linked to oceanic currents. The connectivity results are highly relevant for the delimitation of MPAs in the Southern Ocean; they identify the Filchner Trough as potential stepping stone region, requiring special protection. Our results also emphasize the need of networks of connected MPAs to accommodate large scale differences but also the incorporation of adjacent bioregions in MPAs to protect local genetic differentiation. We plan to draft a science communication paper for the next meeting of the Working Group on Ecosystem Monitoring and Management (WG-EMM) in preparation of the 2025 CCAMLR meeting to be sure that our results are valorised for science policy and the conservation of the Southern Ocean.

Keywords

Amphipoda, connectivity, cryptic diversity, fish, genomics, hydrodynamics, Notothenioidei, population structure, population differentiation, RAD sequencing, seascape, Southern Ocean, species distribution models.