

DNA barcoding of small mesopelagic fish from the Southern Ocean

Heindler Franz Maximilian¹, Christiansen Henrik¹, Dettai Agnes², Collins Martin A.³, Couloux Arnaud⁴, Volckaert Filip A.M.¹ and Van de Putte Anton⁵

¹ Ecology, Evolution and Biodiversity Conservation Section, Katholieke Universiteit Leuven, Charles Deberiotstraat 32 - Box 2439, 3000 Leuven, Belgium
E-mail: franzmaximilian.heindler@kuleuven.be

² Muséum National d'Histoire Naturelle, 57 Rue Cuvier, 75005 Paris, France

³ Government of South Georgia and South Sandwich Islands, Government House, Stanley, Falkland Islands, South Atlantic

⁴ Genoscope - Centre National de Séquençage, 2 Rue Gaston Crémieux, CP 5706, 91057 Evry CEDEX, France

⁵ Directorate Natural Environment, Royal Belgian Institute of Natural Sciences, Gulledele 100, 1200 Brussels, Belgium

Small mesopelagic fish are an important trophic link in the world's oceans as consumers of zooplankton and prey for large fish, marine mammals, and birds. Myctophidae (lanternfishes) predominate in terms of abundance and diversity, and comprise up to 65 % of the entire pelagic deep-sea fish biomass. Their photophore patterns are particularly useful to distinguish species. However, early life stages with less pronounced patterns and individuals damaged during the hauling process often lead to misidentification. DNA barcoding can resolve specimen identification issues and furthermore pinpoint cryptic species, synonymies, or intraspecific phylogeographic patterns. Here, we present a large-scale cytochrome *c* oxidase I gene (COI) data set of 299 previously unpublished Antarctic mesopelagic fishes, with circum-Antarctic sampling range. This data is combined with Rhodopsin (Rho) sequences and publicly available DNA barcodes yielding > 1000 sequences, the largest dataset of Myctophidae sequences as yet. Morphological identifications and sequence clusters were compared. Phylogenetic trees were created using a Maximum Likelihood approach and compared to recent myctophid phylogenies. Intraspecific genetic distances between geographical areas were evaluated, thus creating a comprehensive picture on Myctophids occurring throughout the Southern Ocean. DNA Barcoding proved useful for Antarctic myctophid specimen identification in most cases. We found few hints of cryptic speciation and shallow intraspecific divergences. In general, the spatial phylogeographic structure is low within the Southern Ocean, possibly due to the high abundance of Myctophids and few barriers to gene flow in the well-connected mesopelagic realm. The phylogeny shows that adaptations to (sub-)Antarctic conditions must have occurred several times, yet only few species manage to thrive in cold waters permanently. Understanding the evolution of this ecologically important group in the Southern Ocean is highly topical given rapid environmental changes and potential exploitation.

Keywords: DNA barcoding; COI; Southern Ocean; Myctophidae