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Gene flow in Antarctic fishes: the role of oceanography and life history

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Marine organisms with pelagic larvae are generally assumed to experience high gene flow and low levels of population differentiation. However, variability in life history and environmental characteristics, in particular oceanographic flow fields, can significantly influence dispersal, and their relative effects are frequently unclear. Our research examines the influence of oceanographic and life history variability on gene flow in two species of Antarctic fish: Champsocephalus gunnari and Notothenia rossii. These species are broadly sympatric in their distribution, but differ in aspects of life history that are expected to strongly affect their dispersal capabilities. Our research has used two complementary techniques. Genetic analyses, specifically mtDNA and microsatellite markers, have been used to examine historic and contemporary gene flow and thus describe patterns of population differentiation at the circumpolar scale. These analyses have been compared with predicted larval transport from a global oceanographic model (OCCAM) combined with individual based particle tracking models. In using these complementary techniques, the relative influences of early life history and oceanographic variability can be elucidated. Here we present the key findings of our research, including evidence for inter-specific variation in mitochondrial gene flow at the circumpolar level and a limited degree of genetic structuring within the Scotia Sea.