

Genome-wide demographic analyses of balaenid whales revealed complex history of gene flow associated with past climate oscillation

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Abstract

The balaenid whale, comprising three species of right whales and the bowhead whale, represents an ancient and highly endangered lineage of marine mammals. To unravel the evolutionary history of balaenid whales with respect to gene flow, a comprehensive analysis based on whole-genome data was conducted for all species within this group. Employing population genomic methodologies, we revealed the polytomic nature of extant right whales, identified passage of historical trans-equatorial migration, and provided estimates to the age of the group. Furthermore, we investigated the impact of glacial cycles on the connectivity of bowhead whale populations. By employing multiple complementary approaches to detect gene flow, we identified and characterized gene flow events from bowhead whales to North Atlantic right whales, offering detailed insights into the process. Lastly, we assessed the phenotypic consequences of interspecies gene flow. The outcomes of our study shed light on the intricate evolutionary history of modern balaenid whales, which have been profoundly shaped by ancient climate events.

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