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SHORT COMMUNICATION

Population structure and possible migratory links of common minke whales, *Balaenoptera acutorostrata*, in the Southern Hemisphere

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Abstract Mitochondrial DNA control region sequences were analyzed to investigate population structure and possible migratory links of common minke whales (*Balaenoptera acutorostrata*) in two ocean basins: western South Atlantic (WSA) and western South Pacific (WSP). The results of several different phylogenetic estimations consistently grouped all haplotypes but one ($n = 1$) from these two ocean basins into two separate clades. South and North Atlantic haplotypes were more closely related to each other than either was to haplotypes from the WSP. The interpopulation genetic distance between WSA and WSP whales was similar to that reported between North Pacific and North Atlantic common minke whales (0.0234). The migration rate between the two ocean basins was estimated at near-zero using MDIV. The genetic evidence presented here was consistent with the hypothesis of migratory links among Brazil, Chilean Patagonia and the Antarctic Peninsula, and between low-latitude and Antarctic waters of the WSP. The results suggest multiple populations of common minke whales in the Southern Hemisphere, which may have conservation as well as taxonomic implications. Our single locus results should be corroborated by additional analyses in a larger number of samples and at more genetic markers.

Keywords *Balaenoptera acutorostrata* · Southern Hemisphere · mtDNA · Genetic diversity · Phylogeny

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