

Marked phylogeographic structure of Gentoo penguin reveals an ongoing diversification process along the Southern Ocean

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Abstract

Two main hypotheses have been debated about the biogeography of the Southern Ocean: (1) the Antarctic Polar Front (APF), acting as a barrier between Antarctic and sub-Antarctic provinces, and (2) the Antarctic Circumpolar Current (ACC), promoting gene flow among sub-Antarctic areas. The Gentoo penguin is distributed throughout these two provinces, separated by the APF. We analyzed mtDNA (HVR1) and 12 microsatellite loci of 264 Gentoo penguins, *Pygoscelis papua*, from 12 colonies spanning from the Western Antarctic Peninsula and the South Shetland Islands (WAP) to the sub-Antarctic Islands (SAI). While low genetic structure was detected among WAP colonies (mtDNA F_{ST} = 0.037–0.133; microsatellite F_{ST} = 0.009–0.063), high differentiation was found between all SAI and WAP populations (mtDNA F_{ST} = 0.678–0.930; microsatellite F_{ST} = 0.110–0.290). These results suggest that contemporary dispersal around the Southern Ocean is very limited or absent. As predicted, the APF appears to be a significant biogeographical boundary for Gentoo penguin populations; however, the ACC does not promote connectivity in this species. Our data suggest demographic expansion in the WAP during the last glacial maximum (LGM, about 20 kya), but stability in SAI. Phylogenetic analyses showed a deep divergence between populations from the WAP and those from the SAI. Therefore, taxonomy should be further revised. The Crozet Islands resulted as a basal clade (3.57 Mya), followed by the Kerguelen Islands (2.32 Mya) as well as a more recent divergence between the Falkland/Malvinas Islands and the WAP (1.27 Mya). Historical isolation, local adaptation, and past climate scenarios of those Evolutionarily Significant Units may have led to different potentials to respond to climate changes..

Keywords

Climate change, Demographic history, Polar region, Population structure, Seabirds.