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**Variable dispersal histories across the Drake Passage: The case of coastal benthic foraminifera**

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**Abstract**

The molecular population structure of eight benthic foraminifera with the same or similar morphotypes in shallow waters of West Antarctica and southern Patagonia was analyzed based on the SSU rDNA. The data suggest recent gene flow across the Drake Passage for the foraminiferal species *Pullenia subcarinata* as well as for a molecular operational taxonomic unit (MOTU) of *Micrometula* but not for the remaining majority of taxa/MOTUs. The molecular population structures of different taxa shown by haplotype networks is highly variable, indicating different dispersal histories. Antarctic species/MOTUs show star-like topologies reflecting post-glacial demographic and/or spatial expansion from limited refugia on the Antarctic continental shelf. Some Patagonian species/MOTUs show reticulate topologies suggesting more steady and prolonged evolution, while others show star-like topologies that could reflect impact of South American glaciations. The time-calibrated Bayesian phylogenetic reconstruction suggests that the isolation between Antarctic and Patagonian species/MOTUs post-dates the Eocene/Oligocene boundary. Large differences in divergence times between the examined foraminifera support the hypothesis that separation of ecosystems on the opposite sides of the Drake Passage was a gradual process that started more than 30 Ma. It seems that the shallow-water monothalamids were the first to be impacted. Among the calcareous forms, the majority of the divergence ages were at 15 Ma or younger, suggesting that the

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