

Genetic diversity across Marion Island and the sub-Antarctic

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The biogeography of the Antarctic and its surrounding islands is complex and contentious with much of this complexity deriving from the compound history of the South Polar Region. Arguably one of the most important reasons for this situation is the paucity of molecular work for terrestrial species. Recent collaborative efforts within the SCAR Evolution and Biodiversity in Antarctica programme enabled cross-regional sampling across the sub- and maritime Antarctic, and we present here a broad-scale molecular phylogeny for the genus *Halozetes* within the ameronothroid mites. Our study revealed two well-supported monophyletic groups corresponding to intertidal and terrestrial/supralittoral mites, and we argue that niche occupation may be the possible driver of diversification. In contrast to the belief that this group represents an ancient lineage with a Gondwana distribution, our molecular data suggest that *Halozetes* is relatively recent and post dates large scale continental drift. In this respect, biogeography has been largely sculpted by dispersal. Importantly, significant differences were found between our molecular data and current taxonomy, with several of the outgroup taxa nested within the ingroup. In addition, at least one and possibly two *Halozetes* species are paraphyletic, indicating the need for a complete taxonomic revision of this group. At the intraspecific level, arthropod species distributed across Antarctica show strong population subdivisions largely as a result of glaciation^{1,2}. Given that many sub-Antarctic islands have a long history of glaciation and volcanism^{see 3}, genetic substructure can similarly be expected for endemic species occurring on these. Indeed, several Collembola (*Cryptopygus antarcticus* and *Tullbergia bisetosa*)⁴ and mite species (*Eupodes minutes*⁵ and *H. fulvus*) as well as the cushion plant *Azorella selago*⁶ are characterized by significant population subdivision across Marion Island. If vicariance plays a significant role in shaping observed patterns of genetic variation, one would expect species with similar distributions to show similar patterns of population subdivision. This is indeed the case on Marion Island where all endemic populations show phylogeographic patterns that are identical or near identical. Specifically, populations in the vicinity of Kildalkey Bay and Bullard Beach on the eastern side and populations around Swartkops Point on the western side of the island exhibit significant genetic differentiation.

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