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CONTRASTING MITOCHONDRIAL DNA VARIABILITY BETWEEN MITES AND SPRINGTAILS FROM THE TRANS-ANTARCTIC MOUNTAINS

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We carried out a comparative study using mtDNA (COI) for two free-living, endemic, terrestrial invertebrate taxa—the springtail *Gomphiocephalus hodgsoni* (Hypogastruridae) and the mite *Stereotydeus mollis* (Penthalodidae) collected from sites throughout Victoria Land and the Queen Maud Mountains, Antarctica. Maximum likelihood (ML) analyses revealed low levels of intraspecific sub-structuring for G. hodgsoni (≤2% sequence divergence) with groups mostly corresponding to geographic location. Other well-defined (morphological) species within the Hypogastruridae ranged from 15-22% sequence divergence relative to *G. hodgsoni*. In contrast, ML analyses for *S. mollis* showed considerably higher levels of intraspecific divergence (up to 18% sequence divergence), suggesting the presence of morphologically cryptic species. Other presently described mite species were also readily discernible (14-18% sequence divergence). Within both *G. hodgsoni* and *S. mollis* there were three main groups corresponding to: 1) Taylor Valley; 2) Beaufort Island; and 3) Ross Island together with the adjacent continental sites. We suggest that a common pattern of climatic and geological history – the result of long-term glacial habitat fragmentation – have determined the similar geographic and haplotype distributions found for both species. However, a large variation in substitution rate, around eight times slower for *G. hodgsoni*, compared to *S. mollis*, may be due to their different life history strategies on the Antarctic continent.