

MOLECULAR EVIDENCE FOR GLACIAL REFUGIA IN ANTARCTICA

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Background

In the last 1 million years, the Antarctic has undergone more than 10 major glacial cycles (Hays *et al.* 1976). Model reconstructions of past ice-sheet extent suggest that most of the presently ice-free areas would have been completely covered during the last glacial maxima (Huybrechts 2002; DeConto & Pollard 2003). However, recent molecular studies of freshwater and terrestrial communities indicate that several species have survived in isolation for tens of millions of years (Bayly *et al.* 2003; Cromer *et al.* 2006; Stevens *et al.* 2006; Convey *et al.* 2008). This would imply that, unlike the northern hemisphere, where it is thought that biota recolonised ice covered areas from ice free southern latitudes (Hewitt 2000), Antarctic biota survived in a few isolated ice free areas within the continent and subsequently radiated. This *in situ* evolution in refugia means the Antarctic has as a unique collection of endemic fauna and flora (Stevens *et al.* 2006; see Adams *et al.* 2006 for review). However, although this hypothesis has received some support, the patterns in and the processes underlying the past and current distribution and genetic structure of biota in the Antarctic region remain poorly resolved relative to the size of the continent.

Understanding the genetic and phylogeographic structure of the Antarctic biota is important for elucidating biogeography and notably the influence of glacial history and long-term glacial habitat fragmentation, but it is also of conservation significance. Much concern now exists about the potential risks associated with the anthropogenic movement of distinct lineages or species among climatically similar, yet biogeographically distinct areas of Antarctica (Frenot *et al.*, 2005; Hughes & Convey, 2010; Cowan *et al.*, 2011; Lee & Chown, 2011; Terauds *et al.*, 2012). Such intra-regional propagule movements pose a significant potential conservation problem because biota which have already successfully established in, or are indigenous to one region of the Antarctic clearly possess the physiological adaptations and life-cycles that are necessary to survive there and are therefore likely to be able to survive in another region with similar abiotic characteristics.

In this project we used ameronothroid mites as an exemplar group to examine the biogeographic complexity of the Scotia arc and Antarctic Peninsula, seeking to identify possible refugia, and provide a quantitative assessment of likely intra-regional biosecurity risk in the Antarctic by adopting a phylogeographic approach (Avisé, 2000).

Methods

Samples of ameronothroid mites were extracted from ethanol-preserved arthropod collections held by the British Antarctic Survey. The main species which were extracted were *Halozetes belgicae* and *Alaskozetes antarcticus*, but individuals from other groups were taken for use as out groups.

From each individual, total genomic DNA was isolated using a DNeasy Blood & Tissue Kit (QIAGEN, Hilden, Germany) following the manufacturer's recommendations. The widely used mitochondrial cytochrome oxidase subunit I gene (COI) was amplified using primers LCO1490 (5'-GGTCAACAAATCATAAAGATATTGGA-3') and HCO2198 (5'-TAAACTTCAGGGTGACCAAAAATCA-3') (Folmer *et al.*, 1994). Bayesian phylogenetic analysis was performed using BEAST and ARLEQUIN v3.11 was used to investigate the genetic characteristics of populations and to test for the presence of population structure. A fixed rate Bayesian clock implemented in BEAST was used to estimate divergence times.

Main findings

1. Neither *H. belgicae* nor *A. antarcticus* are monophyletic lineages. Instead, both species constitute several divergent lineages that are genetically as distinct as are some species (Salomone *et al.*, 2002; Bock, 2004; Mayer *et al.*, 2007). As is the case with many cryptic species, there are no obvious morphological differences between individuals from different clades, although further detailed studies are required to determine if any subtle morphological differences can be identified.
2. Some sites in the southern Peninsula contained high levels of haplotype and nucleotide diversity in multiple clades for both *A. antarcticus* and *H. belgicae* suggesting that low-lying coastal areas at these two localities have remained ice-free as refugia for a considerable period. The suggestion that sites in this area may have been a glacial refuge for multiple taxa is further supported by the work of Maslen & Convey (2006) that established that areas of south-eastern Alexander Island contain a substantial number of endemic nematode species consistent with refugial origins. Therefore, this area ought to be a priority for further investigations to determine if it provided refugia for other taxa (e.g. tardigrades, rotifers).
3. Within the Antarctic ameronothroid mites, two distinct clades, with specific habitat preferences (marine intertidal vs. terrestrial / supralittoral) exist supporting a model of within habitat speciation, rather than colonization from marine refugia to terrestrial habitats, as previously proposed.
4. Sub-Antarctic South Georgia should be considered distinct from the remainder of the Scotia arc and Antarctic Peninsula. For *H. belgicae* a clear genetic discontinuity exists between these two regions, and biogeographic analysis at higher taxonomic levels also distinguishes this northern tip of the Scotia arc from more southerly sites in the Maritime Antarctic (Pugh & Convey, 2000; Terauds *et al.*, 2012). Consequently, these areas should be considered biogeographically distinct and biosecurity protocols (see http://academic.sun.ac.za/cib/video/Aliens_cleaning_video%202010.wmv) should be implemented for scientists, tourists and other personnel who move between them.

Outputs

Lee, J.E., van Vurren, B.J., Convey, P., Chown, S.L. Genetic structure of microarthropod populations in East and West Antarctica – biosecurity implications. Poster presentation at SCAR OSC 2010

Mortimer E., van Vuuren B.J.V., Lee J.E., Marshall D.J., Convey P. and Chown S.L. Mite dispersal among Southern Ocean Islands and Antarctica before the last glacial maximum. *Proceedings of the Royal Society of London B*, 278, 1247-1255.

van Vurren, B.J., Lee, J.E., Convey, P., Chown, S.L. Conservation Biogeography of the Scotia Arc and Antarctic Peninsula: Mites as exemplars. *In Prep.*

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