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Abstract

Historical vicariant processes due to glaciations, resulting from the large-scale environmental changes during the Pleistocene (0.012-2.6 million years ago, Mya), have had significant impacts on the geographic distribution of species, especially also in marine systems. The motivation for this study was to provide novel information that would enhance ongoing efforts to understand the patterns of biodiversity on the South African coast and to infer the abiotic processes that played a role in shaping the evolution of taxa confined to this region. The principal objective of this study was to explore the effect of Pleistocene climate changes on South Africa's marine biodiversity using five intertidal gastropods (comprising four rocky shore species *Turbo sarmaticus*, *Oxysteles sinensis*, *Oxysteles tigrina*, *Oxysteles variegata*, and one sandy shore species *Bullia rhodostoma*) as indicator species. Sequence data obtained from partial segments of the mitochondrial cytochrome oxidase c subunit 1 (COI), and the nuclear ribosomal DNA (encompassing part of 5.8S, second Internal Transcribed Spacer and part of 28S, hereinafter called ITS2; or comprising part of the first Internal Transcribed Spacer, 5.8S, second Internal Transcribed Spacer and part of 28S, hereinafter called ITS), were used as genetic markers to construct phylogeographic patterns and to investigate demographic histories of the taxa. Population structure was investigated using haplotype network analyses, pairwise Φ_{ST} statistics, analysis of molecular variance (AMOVA), isolation by distance analyses, Bayesian analysis of population structure (BAPS) and coalescent analysis of gene flow. Demographic history was analysed through Fu's F_s tests, mismatch distributions, and Bayesian skyline plots. Demographic analyses suggest that all five intertidal gastropods studied experienced demographic expansions dating to the late Pleistocene. The sandy shore direct developer *B. rhodostoma* began expansion after the LGM (c. 15 kya) whereas for the four rocky shore broadcast spawners (*T. sarmaticus*, *O. sinensis*, *O. tigrina*, and *O. variegata*) the onset of expansion coincided with or preceded the LGM (c. 25, 60, 50, 40 kya, respectively). Consistent with recent range expansions and gene flow patterns, the population genetic structure in all species was characterised by shallow or a lack of population differentiation. *Oxysteles variegata* was an exception as it showed a deep disjunction, of late Pleistocene origin, between individuals in the west coast Namaqua Bioregion and those in the south coast Agulhas Bioregion. These results provide strong evidence of the vital role that Pleistocene climatic changes and current regimes played in shaping the nature and distribution of biodiversity on the South African coast. In addition, gene flow in all species, except *O. tigrina*, was remarkably asymmetrical with the regions around Cape Infanta and Port Elizabeth acting as source populations. Considering the generally weak population genetic structure and gene flow patterns detected for most gastropod species studied here, it is recommended that *T. sarmaticus*, *O. sinensis*, *O. tigrina* and *B. rhodostoma* be managed as panmictic populations, and that the region encompassing Cape Infanta, and Port Elizabeth should be prioritised for conservation as it appears to harbour source populations. *Oxysteles variegata* was the only species showing distinct population structure and in this instance, species specific conservation efforts should recognize this divergence by treating the two genetic assemblages as distinct management units.