Inferring evolutionary significant areas from patterns of climatic stability and genetic diversity

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Background:

Global Climate Change (GCC) is one of the greatest threats to biodiversity, and one of the most pressing challenges within conservation science and management. Thus, one of the emerging objectives within conservation practice is to identify and conserve areas of heightened resilience and/or evolutionary potential. However, to effectively conserve resilience and adaptability into the future, it is vital to understand the historical processes that have shaped the patterns seen today. Previous studies assessing the links between past climatic oscillations and contemporary intraspecific genetic variation have found that climatic refugia (i.e. areas that remained habitable through climatic oscillations) are likely to be areas of increased genetic diversity. These areas are likely to have increased resilience with regards to future climatic change, and thus should be prioritized for conservation. However, the influence of climatic refugia on genetic diversity is still largely unexplored within the marine environment, especially within a multi-species context.

Therefore, within this study we explore how paleo-climatic changes since the Last Glacial Maximum (LGM; 21 kya) have influenced the genetic diversity of three southern African rocky shore species, namely the Cape urchin (*Parechinus angulosus*), Granular limpet (*Scutellastra granularis*), and Shore crab (*Cyclgrapsus punctatus*). We then compare areas of past climatic stability to areas of predicted stability from the present until 2100. By combining past and future environmental niche modelling and population genetic analyses, we are able to provide a baseline for both the exposure and sensitivity of rocky shore species to climate change, which will be highly valuable for future conservation prioritizations within the Wester Indian Ocean (WIO) region.

Methods:

To identify climatic refugia we conducted species distribution models (SDMs) to the LGM at 1,000 year intervals, using snapshot simulations of the Hadley Center oceanatmosphere climate model (HADCM3), with mean sea surface temperature and air temperature as predictor variables. SDMs were run with the 'Biomod2' R package, using ensemble approach combining five model types that have been shown to significantly increase model accuracy and performance.

Subsequently, we compared the spatial arrangement of climatic refugia of southern Africa's coastline to the patterns of genetic diversity of three rocky shore invertebrates. Mitochondrial genetic data was obtained for *C. punctatus*, *P. angulosus*, and *S. granualris*, as their distributions span the natural environmental gradient of southern Africa, and they each have existing genetic datasets spanning most of their distribution. Generalized Linear Models (GLMs) were used to assess how well climatic stability and variability explain patterns of haplotype and nucleotide diversity for each species.

Finally, we used the ensemble models to project species distributions into the year 2100, using the HADCM3 model under the intermediate A1B emissions scenario. Patterns past and future climatic stability, and genetic diversity of the three species were then compared to the network of marine protected areas (MPAs) in the region, to identify gaps in the MPA network that should be addressed by future conservation action.

Results:

Preliminary results for *C. puntactus* show that most of the south and eastern coasts of South Africa remained habitable throughout the climatic oscillations since the LGM. Both climate stability, defined as the sum of habitat suitability over time, and climatic variability, defined as the standard deviation in habitat stability over time, were not correlated with either haplotype or nucleotide diversity of *C. punctatus*.

When projecting future climatic stability, we find that the suitable habitat for *C. punctatus* is greatly diminished by 2100, and has largely shifted to the west coast of South Africa. Importantly, the southwestern coast, specifically the Cape Point and De Hoop regions were found to be climatically stable in the past (from the LGM to present), and in the future (from the present to 2100).

These results will be synthesized and presented with those pertaining to *S. granularis* and *P. angulosus*.

Conclusions:

Our study is the first assessment of climatic stability of the southern African coastline and its influence on the genetic diversity of multiple rocky shore species. Our finding of climatic stability showing no significant correlation to patterns of genetic diversity could be owing to the study species having large effective population sizes and dispersal distances, thus making genetic diversity more likely to reflect contemporary environmental pressures rather than climatic changes of the past. The preliminary results suggest that species distributions should not stand alone, but rather, be supplemented by patterns of genetic diversity within conservation planning analyses. Overall, the presented study advances our understanding of climatic stability and species resilience within the WIO region, which also increases our ability to conserve ecosystem persistence and functioning into the future.