

Seascape genetics of the spiny lobster *Panulirus homarus* in the Western Indian Ocean

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Background

Seascape genetics, where population genetics draws on ecology, oceanography and geography to explain connectivity and spatial genetic structure, was used to examine the fine-scale population genetic structure and phylogeography of the spiny lobster *Panulirus homarus* in the Western Indian Ocean.

Methods

Observed genetic structure based on 21 microsatellite loci was examined in relation to ocean circulation patterns, and to determine the influence of latitude, sea surface temperature (SST) and ocean turbidity on population-level processes. Virtual passive Lagrangian particles advected using satellite-derived ocean surface currents were used to simulate larval dispersal.

Results

At a geospatial level, the genetic clusters recovered corresponded to three putative subspecies, *P. h. rubellus* from the SW Indian Ocean, *P. h. megasculptus* from the NW Indian Ocean, and *P. h. homarus* from the tropical region in-between. In the SW Indian Ocean, the dispersion of particles tracked over a 4-month period provided insight into a steep genetic gradient observed at the Delagoa Bight, which separates *P. h. rubellus* and *P. h. homarus*. South of the contact zone, particles were advected south-westwards by prevailing boundary currents, or were retained in nearshore eddies close to release locations. Some particles released in southeast Madagascar dispersed across the Mozambique Channel, and reached the African shelf. In the NW Indian Ocean, particles were retained within the Arabian Sea.

Conclusion

Complex physical oceanography and biogeographical boundaries could explain genetic diversity among *P. homarus* subspecies, along with isolation by distance. Minimum SST was correlated with genetic variability, suggesting larval tolerance to ambient temperature as a selective factor in dispersal success.