The genetic structure of shared fishery species in the subtropical and warm temperate Western Indian Ocean.

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INTRODUCTION

Southern African marine inshore species are important commercial, recreational and subsistence fisheries in Mozambique and South Africa. However, the stocks of most of these subtropical and warm temperate species have experienced declines in recent history even with species-specific management interventions in these countries. There is also inadequate biological and stock related fisheries data available to effectively manage and rebuild these overexploited stocks (Mann 2013). The aim of this study was therefore to evaluate the genetic diversity and stock structure of three commercially important shared fishery and endemic species: slinger Chrysoblephus puniceus; scotsman Polytegustes praerorbitalis; and catface grouper Epinephelus andersoni (Species details below Mann 2013).

MATERIALS AND METHODS

- DNA samples were collected throughout distribution range (Figure 1). Amplified genes were:
  - E. andersoni: The mitochondrial DNA (mtDNA) cytochrome b and intron 1 of the 57 ribosomal protein (RPS7-1) nuclear gene.
  - P. praerorbitalis: The mtDNA control region and the RPS7-1 gene.
  - C. puniceus: The mtDNA control region and 10 microsatellite loci (Chopelet et al. 2009).

- Several genetic diversity, connectivity and population structure analyses were done: Analysis of molecular variance (AMOVA) and pairwise (FST) and exact tests of population comparisons, and Mantel tests. AMOVA’s were based on (I) oceanographic current dynamics and biogeographic regions and (II) the observed differences from population differentiation.

RESULTS

- DNA sequence analysis revealed significant variation among groups (θST = 0.26, P = 0.05) between five groups: 1. Quissico to Inhaca; 2. Cape Vidal to Port Edward; 3. Port St Johns to Coffee Bay; 4. Mbashe; 5. Port Alfred. The cytochrome b results statistically indicate low haplotype diversity (0.31) and no differentiation (θST = 0.26, P = 0.07) between groups but supports the hypothesis of a recent population bottleneck.

- Table 1: Pairwise values of the relationships between groups (lower diagonal) and the reduced dataset with fish (above diagonal). Significant (P < 0.05) values are highlighted.

DISCUSSION

- E. andersoni population has a complex pattern of genetic diversity. Geographic structuring could be due to low gene flow across barriers such as the Port Alfred and Port St Johns upwelling cells, the Mozambique Channel eddies and biogeographic boundaries (Figure 4). These complex patterns could also reflect the variable movement habits of the species, which though predominantly non-migratory, exhibits pioneering behaviour or range movements, in search of vacant habitats (Maggie 2011). The cytb results however indicate low Hd probably due to an unusually slower mutation than the RPS7-1 region which depicts a more recent picture of diversification and the maternal inheritance of mtDNA.

- The results of RPS7-1 analyses for P. praerorbitalis provide some evidence of weak genetic differentiation between the E. Cape and the Transkei and northern KZN. This structure was strengthened by removing out groups, thus the genetic length at 50% majority, suggesting differentiation in sexually mature males and females and evidence of temporal structuring. The combination of low Hid and low FST observed in the mtDNA dataset is indicative of a recent population bottleneck or founder event. Similarly, the high Hid and low FST observed in the RPS7-1 is also possibly the result of a population bottleneck followed by rapid population growth.

- Although mtDNA and microsatellites indicate a single population of C. puniceus, there was some significant structuring around Gaza, Xai Xai and Inhaca Island (Mozambique) that could be associated with upwelling. Furthermore, migrate-n indicated that ocean circulation may facilitate larval movement or dispersal as net migration rates were influenced by Indian Ocean currents. The uneven spatial and temporal distribution of fishing effort in the past likely ensured that the single mixed transboundary stock of C. puniceus was able to sustain high levels of localised fishing effort.

CONCLUSIONS

These findings raise some important issues on the management of shared fishery resources.

- A need for biology, ecology and life-history data in terms of its spawning habits, larval dispersal (as well as length of the larval phase), larval and adult thermal tolerance limits, and migration habits of species.

- A single stock assessment would likely provide more accurate information on the fishery exploitation in slinger and scotsman.

- The high levels of connectivity among sites suggest that a feasible and efficient management measure to protect these species should include a trans-boundary MPA network in combination with fishery effort reduction in scotsman.

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Figure 1: The broad sampling sites of the three species ranging from Ponta da Barra to Algoa Bay (Picture insets: catface grouper, scotsman and slinger; Maputo, Mozambique sampling and harbour).

Figure 2: Minimum spanning haplotype network of 269 sequences of 12 unique cytochrome b haplotypes of E. andersoni (a); 57 gene intro of P. praerorbitalis (b); and (c) 35 gene intro of C. puniceus (d).}

Figure 3: Principle coordinate analysis (PCA) for all samples. Individual samples are colour coded by sampling site.

Figure 4: Major oceanographic features & barriers influencing the dispersal and genetic structure of the three species among the sampling localities in the region.