Phylogeography of the Giant Trevally (Caranx ignobilis) across the Indo-Pacific

Jessica Glass\textsuperscript{1,2}, Gavin Gouws\textsuperscript{2}, Paul Cowley\textsuperscript{2}, Thomas Near\textsuperscript{1}

\textsuperscript{1}Yale University, Department of Ecology and Evolutionary Biology, New Haven, Connecticut, USA
\textsuperscript{2}South African Institute for Aquatic Biodiversity, Grahamstown, South Africa

Introduction

The giant trevally (Caranx ignobilis; Picea: Carangidae; Fig. 1) is distributed throughout the Indo-Pacific and is a top marine predator associated with coral and rocky reefs. Caranx ignobilis is highly targeted in recreational, commercial, and artisanal fisheries. Despite its economic importance, no examination of its genetic structure has occurred outside of Hawaii, USA. Quantifying genetic diversity, stock structure, and gene flow is useful for developing sustainable management measures. This study contributes by enriching knowledge of the Carangid family and a deeper understanding of the biodiversity of marine fishes in the Indo-Pacific.

Fig. 1. Caranx ignobilis adult and juvenile individuals

Methods

- 123 specimens were analyzed from the Red Sea, Australia, Mozambique and Seychelles (Fig. 2)
- Sequenced a 1045 bp region of the mtDNA gene cytochrome b (cytb)
- Sequences were aligned using the MUSCLE alignment scheme implemented in Geneious

Analyses

- Analyses were conducted in RStudio (v. 0.99.489)
- Diversity and neutrality indices, Fst, and Ψst were calculated using the R package “PopGenome”\textsuperscript{3}
- Pairwise genetic distances were calculated using the TN83 molecular model of evolution in the R package “ape”\textsuperscript{2}
- We tested the significance of pairwise Fst and Ψst values in Arlequin 3.5

Fig. 2. Sampling localities for C. ignobilis specimens

Results

- 61 haplotypes were identified, 24 of which occurred multiple times (Fig 3).
- Both the haplotype network (Fig. 4) and indices of diversity and neutrality (Table 1) provide evidence of population expansion.
- Haplotype and nucleotide diversities were similar across sampling localities (Table 1).
- We observed little geographic structure across Indo-Pacific sampling localities (Table 2).
- Ψst values indicate slight genetic divergence between Red Sea and Australian individuals (Table 2).

Fig. 3. Haplotype Frequencies by Location

Table 1. Summary statistics for each sampling locality.

<table>
<thead>
<tr>
<th></th>
<th>Red Sea</th>
<th>Australia</th>
<th>Mozambique</th>
<th>Seychelles</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. haplotypes</td>
<td>16</td>
<td>25</td>
<td>35</td>
<td>11</td>
<td>61</td>
</tr>
<tr>
<td>Haplotype diversity (H)</td>
<td>0.968</td>
<td>0.969</td>
<td>0.981</td>
<td>0.985</td>
<td>0.978</td>
</tr>
<tr>
<td>Nucleotide diversity (π)</td>
<td>0.009</td>
<td>0.006</td>
<td>0.008</td>
<td>0.007</td>
<td>0.009</td>
</tr>
<tr>
<td>Mean distance (within pops)</td>
<td>0.006</td>
<td>0.008</td>
<td>0.007</td>
<td>0.008</td>
<td>0.008</td>
</tr>
<tr>
<td>Tajima’s D\textsuperscript{1}</td>
<td>-1.150</td>
<td>-0.803</td>
<td>-1.234</td>
<td>-0.622</td>
<td>-1.392</td>
</tr>
<tr>
<td>Fu’s F\textsuperscript{1}</td>
<td>-0.832</td>
<td>-1.771</td>
<td>-2.081</td>
<td>-0.601</td>
<td>-2.483</td>
</tr>
</tbody>
</table>

Table 2. Fst (upper left) and Ψst (lower right) pairwise values. Asterisks (*) indicate p< 0.05.

<table>
<thead>
<tr>
<th></th>
<th>Red Sea</th>
<th>Australia</th>
<th>Mozambique</th>
<th>Seychelles</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fst</td>
<td>-0.0042</td>
<td>0.0098</td>
<td>-0.0041</td>
<td>-0.0241</td>
<td></td>
</tr>
<tr>
<td>Ψst</td>
<td>0.0054</td>
<td>-0.0009</td>
<td>0.0232</td>
<td>-0.0029</td>
<td></td>
</tr>
</tbody>
</table>

Conclusions & Future Research

- Results suggest little geographic structure and ongoing genetic exchange amongst C. ignobilis individuals across Indo-Pacific localities, but some divergence between Red Sea and Australian specimens.
- We noted evidence of population expansion; future analyses will estimate expansion time and direction.

Future research will incorporate finer-scale molecular markers and new localities. The results of this analysis will be examined in the context of tagging and stable isotope studies on C. ignobilis in the western Indian Ocean.

Acknowledgements

This work was funded by the National Science Foundation’s Graduate Research Opportunities Worldwide Program, the U.S. Agency for International Development (USAID) Research and Innovation Fellowship, and the South African Institute for Aquatic Biodiversity.

We thank Philip Hauert, Jude Bisoux, Michelle Heupel, Emmanuel Mburu, Dylan Howell, Hyton Lewis, Rory Scheepers, Bruce Mann, Ryan Daly, Claire Daly, JD Filmalter, and Rhett Bhennett for assistance collecting specimens. We also thank Taryn Bodle and Zandi Adams for assistance in the lab, and Elaine Heemstra for the illustration.

References: