**The role of Scarus ghobban and Diadema Savignyi as potential vectors of coral pathogens on the reefs of SW Madagascar**

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**Introduction**

Although there are over 160 species of known corallivorous organisms (Rotjan and Lewis 2008), very little information is available on their role as vectors of potential coral pathogens. It was suggested that both marine vertebrates and invertebrates have the ability to transmit coral pathogens (e.g. Sussman et al. 2003, Aebly and Santavy 2006), though in some cases the mode of transmission remains unclear. In this study we investigated the role of two potential vectors of coral bacterial pathogens, the parrotfish Scarus ghobban (Fig. 1A) and the sea urchin Diadema savignyi (Fig. 1B), on the reefs of SW Madagascar (Toliara). This was achieved by comparing the composition of the bacterial communities associated with the jaws of these organisms to those found on healthy and diseased corals (Echinopora hirsutissima), and present in the overlying water column.

**Material and methods**

**Sampling (sterile swabs; 5 replicates / sample type)**

- Jaws of *S. ghobban*
- Aristotle’s lantern of *D. savignyi*
- Tissues of healthy *Echinopora hirsutissima*
- Tissues of diseased *E. hirsutissima*
- Water in vicinity of sampled *E. hirsutissima*

**Bacterial cultures**

**DNA extraction and amplification of 16S rDNA gene**

**Sequencing**

**DGGE – band extraction and re-amplification**

DGGE gels were analysed using ANOSIM in PRIMER 6.0. The presence of potential bacterial pathogens on the jaws of *S. ghobban* and *D. savignyi* was evaluated through comparison with the bacterial population of healthy and diseased (apparently affected by white syndrome) colonies of the coral *E. hirsutissima*, and through comparison with known bacterial sequences on BLAST (NCBI).

**Reference list**


**Acknowledgements**

Special thanks to everyone from BioMar I also thank the HSM having hosted and supported the field work for this study.

**Results and discussion**

Sequences obtained from bacterial cultures and extracted DGGE bands of all sample types revealed bacteria from a variety of phyla. This double methodology (culture dependent and independent) approach limits the influence of bias associated with bacterial culture and PCR on the results. The bacterial communities of all sample types appeared to be dominated by Bacillales, α- and γ-proteobacteria (Table 1), which supports results obtained by Frias-Lopez et al. (2002; for coral samples only). Though these data provide interesting insight into the bacteria associated with *S. ghobban* and *D. savignyi* jaws (bacteria associated with seawater and hermatypic corals having been described in previous studies (e.g. Rohwer et al. 2002, Frias-Lopez et al. 2002)), this is by no means an extensive characterisation of the bacterial communities associated with these sample types.

Interestingly, several potential pathogens (known coral pathogens and bacteria associated with diseased coral tissues) were identified within the bacterial communities of all samples (predominantly in diseased *E. hirsutissima* and *S. ghobban* jaw samples (Table 2)). This suggests that, since *D. savignyi* and *S. ghobban* carry potential pathogens on their oral appendages, they could theoretically transfer these between coral hosts. However, some of these potential pathogens were also found within seawater and healthy *E. hirsutissima* samples (Table 2). This highlights the ubiquitous character of many coral pathogens and suggests that some of them could be present within the coral’s normal bacterial community, and upregulated by certain factors (e.g. physical/environmental stress). As a result, the bacterial community of the coral host could shift to being dominated by diseased-associated bacteria (Mao-Jones et al. 2010). In theory, bite mark lesions resulting from the action of corallivorous organisms could therefore be sufficient to trigger such shifts, potentially resulting in disease development.

**Table 2. Potential pathogens (known coral pathogens and bacteria associated with diseased coral tissues) identified among the various sample types.**

<table>
<thead>
<tr>
<th>Phylum</th>
<th>Class</th>
<th>Order</th>
<th>Family</th>
<th>Genera</th>
<th>Species</th>
</tr>
</thead>
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<td>Bacillales</td>
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<td>Bacillales</td>
<td>Bacillales</td>
<td>Bacillus</td>
<td><em>B. brevis</em></td>
</tr>
<tr>
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<td>Alpha-proteobacteria</td>
<td>Alpha-proteobacteria</td>
<td>Alpha-proteobacteria</td>
<td>Alpha-proteobacteria</td>
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<tr>
<td></td>
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<td>Gamma-proteobacteria</td>
<td>Gamma-proteobacteria</td>
<td>Gamma-proteobacteria</td>
<td><em>G. elongata</em></td>
</tr>
<tr>
<td></td>
<td>Epsilon-proteobacteria</td>
<td>Epsilon-proteobacteria</td>
<td>Epsilon-proteobacteria</td>
<td>Epsilon-proteobacteria</td>
<td><em>E. hirschii</em></td>
</tr>
</tbody>
</table>

**Figure 1. A - Bluebarred parrotfish (Scarus ghobban), B - sea urchin Diadema savignyi**