Background

Sponge taxonomy can be challenging as many groups exhibit extreme morphological plasticity induced by local environmental conditions. Foliose keratozoic sponges of the sub-family Phyllospongiinae (Dictycoceratida, Thorectidae: Strepisporchiaea, Phyllospongia and Carteriospongia) are commonly found in intertidal and subtidal habitats of the Indo-Pacific. Lacking spicules, these sponges can be difficult to differentiate due to the lack of reliable morphological characters for species delineation. We use molecular phylogenies inferred from the nuclear Internal Transcribed Spacer 2 region (ITS2) and morphometrics (19 characters; 52 character states) to identify evolutionarily significant units (ESUs; sensu Moritz) within foliose Phyllospongiina collected from seven geographic locations across tropical eastern and Western Australia (Figure 1). Additionally, we used samples previously described by Bergquist et al. (1988) to compare molecular and morphological data collected in this study.

Morphological plasticity and implications for taxonomy

Morphological and molecular species delineation supported five of the previously known foliose species discussed in detail in Bergquist et al. (1988). However, a taxonomic discrepancy was found with C. foliascens (ESU 1) residing in the Phyllospongia cluster (Cluster I) (Figure 1). High morphological plasticity encountered in C. foliascens (Morph 3, 3.1 and 3.2) supports taxonomic uncertainties between C. foliascens (ESU 1) and P. lamesifera (ESU 2) noted by Bergquist et al. (1988), with morphotypes of the two species exhibiting similar gross morphologies. Morphological plasticities in C. foliascens may reflect influences of environmental parameters (e.g. light and levels of sedimentation). Accordingly, a multifaceted approach is critical for accurate taxonomy of Phyllospongiina and sponges in general.

Phylogeographic relationships

Torres Strait (see on Australia map, Figure 1) served as an intermittent land bridge over periodic glacial cycles in the late Pleistocene up to ~7,000 BP when the sea rose to present day levels (Reeves et al., 2008). Variable levels of genetic diversity (i.e. monomorphic to highly variable geographic populations) found within sampling sites, and the complete segregation of sister sub-clades (1E/1W, 3E/3W, and 4E and 4W) to the east and west coasts of Australia suggests vicariance played a role in shaping Phyllospongiina distribution across Torres Strait (Figure 1). However, the daily drizzle spawing of larvae for several weeks (Whalan et al., 2008; Abdul Wahab et al. 2011) over variable weather and currents may aid range expansion. Genetic mixing via larval migration may contribute to secondary contact and panmixia of reproductively undivided populations in the Holocene (Mirams et al. 2011).

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References

Reeves et al. (2008) Quartenary Int. 183: 3-22
Whalan et al. (2008) MBSP 388: 145-154

Figure 1: Tree representing outgroup rooted Bayesian phylogeny inferred from ITS2 alignment. Three main clusters corresponding to the genera Phyllospongia (I), Carteriospongia (II) and Strepsisporchiaea (III) are highlighted in grey boxes. A total of five distinct clades were recovered, corresponding to species described in Bergquist et al. (1988). Specimens from eastern (E) and Western (W) Australia are highlighted within clades. Morphotypes are represented in coloured boxes corresponding to the assigned clades. Geographical distribution of clades are shown on the map of tropical Australia.

Figure 2: Eight most informative morphological character reconstructions over the ITS2 Bayesian phylogeny. Clades could be separated morphologically based on combinations of these characters. Only sub-clade 1E and 1W were unable to be resolved on the basis of sole morphological characters. ESUs and internal sub-clades (eastern vs western) is possible using several morphological trait combinations.

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A morphological and molecular revision of Phyllospongiinae: how different are similar foliose sponges from the Australian tropics?