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Species diversity and potential growth rates of common scorpaenids found in coastal Singapore shores

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In our preliminary results, five CCA species exhibited high genetic variation compared to one other species, *Pneophyllum conicum*. 18S rDNA sequence divergences of *P. conicum* from Japan (n=1) and Hawaii (n=5) ranged 0.1-0.6%. In contrast to *P. conicum*, sequence divergences of *Lithophyllum kotschyianum* from Japan (n=1), Hawaii (n=2) and Fiji (n=1) were 0.6-2.0%; *Hydrolithon onkodes* from Japan (n=1) and Australia (n=1), 3.7 %; *H. reinboldii* from Japan (n=1) and Hawaii (n=4), 0.1-3.2%; *Neogoniolithon brassica-florida* from Japan (n=1), Australia (n=1) and Hawaii (n=2), 0.1-3.7%; and *Mesophyllum erubescens* from Japan (n=1) and Hawaii (n=2), 1.1%.

What causes such different levels of genetic variation? First, the true species diversity is likely to be underestimated because of the limited number of the morphological characters. In recent taxonomic studies of CCA, species circumscriptions focus on reproductive structures rather than gross morphology and vegetative structures. For example, *N. brassica-florida* was synonymized with several previously described species that are now considered to be growth forms of *N. brassica-florida*. However, this species may include some genetically and morphologically different species. Secondly, the lower levels of genetic variation in *P. conicum* may be caused by a reduced mutation rate, although it seems unlikely that such a large difference in mutation rate exists between algae occupying similar ecological niches within the same order. Thirdly, *P. conicum* from Japan and Hawaii is apparently genetically conspecific. To confirm whether species examined consist of either several cryptic species or even different species, further morphological and molecular studies of several specimens of each species need to be conducted.

Poster -2

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The ecology of scorpaenids is poorly studied. Present information stems primarily from venom studies and a few taxonomic descriptions which have dealt with the toxicity and biochemistry of stonefish. In general, little much has been done with regards to studying the general biology and ecology of stonefish and other scorpaenids. In determining the growth rates of common scorpaenids found in Singapore, a two month sampling census at 24 sites around coastal Singapore indicated that there are eight species of scorpionfish found locally thus far. The most common species included long spine scorpionfish, *Paracentropogon longispinnus*, the stargazer waspfish, *Trachycephalus uranoscopus* and estuarine stonefish, *Synanceja horrida* respectively. The largest scorpaenid found in Singapore was *S. horrida* while the smallest was *P. longispinnus*. Otoliths extracted from these three common species indicate that the relative growth rates could potentially be determined using otolith weight in relation to body size for *P. longispinnus*, *T. uranoscopus* and *S. horrida*. However, validation of age using electron microscopy of otoliths for these species will be required to confirm this finding.

Poster -3

The union of Barcoding and Taxonomy: A case study in the commercially valuable blue swimming crab, *Portunus pelagicus* species complex

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Whilst DNA barcoding has been shown to uncover hidden pockets of biodiversity in different animal groups, species discovery via barcoding should nevertheless be carried out in tandem with careful