Title: Diversity and identification of soft corals in Mauritius

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Background:

Soft corals have been familiar to science around the globe for centuries, yet only recently scientists have started to recognise soft corals as a key taxa on the reefs. Mauritius has been stated as a resource-rich area with a distinctive coral reef ecosystem where diverse soft corals are abundantly present. Knowledge of soft coral biodiversity and its distribution around the island are very much limited, so this study aimed to elucidate soft coral identification and distribution.

Methods:

Soft corals identified in this study were identified from offshores regions of the island: Albion, Pereybere, Trou aux biches, Ile aux bernache, Blue Bay and Flíc en Flac. A total sample size of 22 individual colonies, distributed among three families; 14 colonies of Alcyoniidae, 4 of Nephtheidae and 4 of Xeniidae was obtained. Out of the 11 genera identified, 4 genera; Sinularia, Sarcophyton, Lobophytum and Capnella were considered the most common at most selected sites. Morphological identification was based on the principle keys such as external form and colouration, type of colony growth, type of polyps and arrangement of sclerites (form and colour) which allowed the identification of the soft corals at genus level. The difficulties encountered with morphological taxonomy can be overcome by the use of molecular characterisation which can facilitate species identification. For the molecular analyses, the specimens were preserved in 95% ethanol prior to DNA extraction and non-coding COI-COII intergenic spacer from the mitochondrial genome was amplified using the primers COI8068F and COI8325R.

Results:

Sequencing allowed identification of some specimens till date: Cladiella krempfi, Klyxum utinomii, Sinulari peculiaris and Sinularia polydactyla with a pairwise sequence divergence ranging from 0 to 0.916 and coinciding with the morphological identification while the other specimens merit more attention.
Conclusion:

Phylogenetic trees constructed from this fragment resolved poorly, especially between species of the same genus. Despite the high variation in this non-coding DNA fragment, its short length limits its application in phylogenetic studies. This is encouraging research on more rapidly evolving DNA fragments in soft corals. More to that, the diversity and abundance of soft corals notably decreased with the increase of human impacts. This was clearly observed on the offshore of Ile aux Bernache where the abundance of soft corals were remarkably high and human activity almost nought.

Keywords: Soft corals, identification, morphological, COI-COII intergenic spacer, phylogenetic