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DNA BARCODING OF MARINE ORGANISMS FROM TRAWL FISHERY IN HONG KONG

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Effective conservation management can only be formulated and implemented with a thorough understanding on biodiversity in the region of interest. Yet the alpha diversity of many areas remains understudied. In the present study, DNA barcoding was employed to identify marine fish and crustacean species from trawl fishery in Hong Kong waters. A total of 140 fish specimens and 106 crustacean specimens were sampled from 12 collection sites in the eastern, southern and western waters of Hong Kong in 2012. Based on morphology, the fishes are identified into 76 species in 59 genera and 34 families, while the crustaceans belong to 54 species within 34 genera and 18 families. About 90% of the specimens produced satisfactory sequence data of the DNA barcoding gene, mitochondrial cytochrome oxidase c subunit I. The effectiveness of DNA barcoding in species identification, based on 5% sequence divergence as the cut-off value between intraspecific and interspecific variation, was found to be fair since only 67% of the sequences generated can be assigned to a species, using the GenBank and BOLD databases. With the completion of DNA barcoding analysis on about 80% of the specimens, we noted ambiguities in species assignment in about 16% of these specimens between molecular and morphological analyses, thus highlighting the importance of adopting complementary methods for precise species identification. Results from this study lay the foundation for constructing a DNA barcoding database of local marine organisms which would facilitate efficient taxonomic identification for various scientific and educational purposes.