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16S rRNA GENE SEQUENCING FOR PHYLOGENETIC ANALYSIS OF MALAYSIAN SEA ANEMONES

Farah Hanis Zulkipli ^{1,*}, Ridzwan Hashim ¹, Norafiza Zainuddin ¹, Kamarul Rahim
Kamaruddin ² and Aileen Tan Shau Hwai ³

¹ Department of Biomedical Science, Kulliyah of Allied Health Science, International Islamic University Malaysia, Kuantan, Pahang, Malaysia

² Department of Biotechnology, Kulliyah of Science, International Islamic University Malaysia, Kuantan, Pahang, Malaysia

³ School of Biological Sciences, Universiti Sains Malaysia, Malaysia

*Corresponding author: farahzulkipli@gmail.com

Sea anemones (Phylum Cnidaria: Class Anthozoa) comprises approximately a thousand species. A number of ten species are known to be the hosts to anemone fishes. Out of that, six species can be found in Malaysian coastal waters. Producer of biologically active polypeptides and protein, source of a compound for vertebrate heart stimulant, indicator animal for ultraviolet radiation in marine environment, medications that prevent patients from rejecting newly transplant organs, and source of food in some areas of North America and Asia are among its potentials and uses. The ethnic groups of Bajau and Suluk in Sabah, Malaysia consume it as their native food. In terms of genetic data, only one chromosomal 18S rRNA gene sequence of *Heteractis magnifica* from Malaysian coastal water is available in the GenBank, National Center for Biotechnology Information (NCBI), U.S. National Library of Medicine (GenBank accession no.: AY372260, deposited in 2003) to date. Due to lack of genetic study of sea anemone in Malaysia, this study was performed to generate the genetic profiles of Malaysian sea anemones and then to determine the phylogenetic relationship between the present species using 16s ribosomal RNA (rRNA) genes of mitochondrial DNA. Generally, this study has significantly contributed to the availability of more genetic data of Malaysian sea anemones. For future genetic studies, we suggest incorporating more specimens of Malaysia sea anemones from broader geographical locations of Malaysia, and the use of complete mtDNA genes along with morphological approaches for better species identification as these could provide better insights.

Keywords: genetic profile, Malaysia, 16s rRNA gene, sea anemone