

High-throughput amplicon sequencing of gut microbiome sea cucumber in Pahang, Malaysia

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ABSTRACT

Sea cucumbers are soft-bodied marine organisms found in the benthic environment which are known as trepang, gamat or timun laut by locals. Sea cucumbers are commercially exploited for their body extracts due to their therapeutic properties and as culinary demands. Moreover, sea cucumbers are host to complex community of microbes. However, less efforts were documented on the identification of these microbial communities using high-throughput sequencing approach. The purpose of this study is to identify the gut microbiome of the sea cucumber from *Stichopus ocellatus* species. For this study, the sea cucumbers were collected from a coastal area in Pahang, Malaysia. The gut contents were sampled and processed fresh upon collection and maintained on ice prior delivery to the storage facility. The DNA was extracted prior two steps Polymerase Chain Reaction (PCR) for amplicon library preparation by targeting the V4 region of 16S rRNA. The prepared libraries were sequenced using the Illumina iSeq 100 system. The raw data were analysed using QIIME2 and other bioinformatics software. Here, we observed that the gut of *Stichopus ocellatus* is home for the genera of *Vibrio*, *Tropicibacter*, *Desulfopila* and *Halioglobus*. Remarkably, the bacteria from the genus *Vibrio* are the most abundant bacteria colonising the gut microenvironment. This study suggests baseline microbial community that inhibit the gut of sea cucumber that may confer biotechnological important bacteria for pharmaceutical applications and drug development.

KEYWORDS

Libraries; Ecology; Polymerase chain reactions; Microorganisms; Amplicons; Bacteria; Bioinformatics; Therapeutics

ACKNOWLEDGEMENT

The authors are thankful to the grant given by the Ministry of Higher Education of Malaysia and the University Malaysia Pahang. They also thank the divers from INOCEM Research Station, IIUM for their kind and brave efforts during the sample collection of sea cucumbers. This research is supported by research grants awarded by Ministry of Higher Education (Grant no: FRGS/1/2019/WAB13/UMP/03/1) and by Universiti Malaysia Pahang, Malaysia under UMP Fundamental Research Grant (Grant no: RDU190364 and PGRS2003107). Last but not least, we would sincerely thank Kurita Water and Environment Foundation (KWEF) who also funded this work (Grant no: UIC201511).