CHAPTER SIX

CONCLUSION AND RECOMMENDATION

Sea cucumbers are marine invertebrates that are widely distributed in Malaysia and play important roles not only in the marine ecology, but also in terms of their health benefit for human consumption. In this study, eight specimens of sea cucumbers were collected from two locations in Malaysia seawaters, and identified as two samples of *H. leucospilota* from Pangkor Island, Perak, while those from Manukan Island, Sabah are three samples of *H. atra* and one each of *H. edulis, H. hilla* and *B. vitiensis.* Bacteria were isolated from internal and external body parts of each sea cucumber, and their surrounding sediments and seawaters. Morphological evaluation of the sea cucumber-associated cultivable bacterial community from the sea cucumbers showed variation in their morphology, with Gram-negative rod-shaped bacteria had the highest occurrence, particularly contributed from the two *H. leucospilota* specimens from Pangkor Island, Perak.

Altogether, 58 bacterial samples were successfully identified using 16S rRNA gene sequencing in this study and are distributed among ten genera under four classes, Bacilli (28 genera), Alphaproteobacteria (3 genera), Gammaproteobacteria (26 genera) and Actinobacteria (1 genus). The bacterial group from genera *Bacillus* and *Vibrio* were two of the most frequently occurring bacterial genera associated to the sea cucumbers, with the genus *Vibrio* only found from Pangkor Island, Perak samples while *Bacillus* is the dominant genus in Manukan Island, Sabah samples. The different bacterial composition between samples isolated from sea cucumbers from the two locations demonstrated that there could be geographical variation in the sea cucumbers-associated bacteria.

As an effort to explore the presence of pigmented bacteria with antimicrobial potential from the sea cucumbers, seven bacterial strains belonging to the genera *Staphylococcus*, *Microbacterium, Acinetobacter* and *Pseudomonas* were screened for their pigment production and antimicrobial activity against pathogenic bacteria. Potential phenazine-based compound was detected from *Pseudomonas* sp. PMCC1 extract, while *S. saprophyticus* PMDP, *M. oxydans* PMCT1 and *A. pittii* PMDS1 may produce potential carotenoid pigments. Two pigmented strains of *Pseudomonas* and *Paracoccus* genera demonstrated antibacterial activity against selected human pathogenic bacteria, while genera *Staphylococcus* and *Exiguobacterium* inhibited the growth of *Shigella* sp.. In conclusion, the pigmented bacteria associated with sea cucumbers from Pangkor Island and Manukan Island showed the potential as secondary metabolite producer and some may exhibit antibacterial compounds.

Further studies could integrate community profiling techniques and metagenomic next generation sequencing to comprehensively evaluate the bacterial diversity and produce better conclusive results on the roles of bacterial symbionts. More specimens from various localities in Malaysia is also needed to determine how geography influences the association of bacteria. Information on the prevalence of *Vibrio* spp. with some potential pathogenic strains associated with sea cucumbers from Pangkor Island, Perak may also suggest environmental disturbance at the area during the time of sampling. Hence, proper measures should be considered for protecting the sea cucumbers at the locality and consumers in the future. Other non-pathogenic bacteria isolated from this study can also be further characterised in terms of their potential in numerous applications, and their potential to be used as probiotics to improve sea cucumbers aquaculture in Malaysia. In addition, further characterisation and purification of the pigmented bacteria using nuclear magnetic resonance (NMR) and mass spectrometry will be essential to determine their potential utility in industry.