



Gut microbiome and metabolome of sea cucumber (*Stichopus ocellatus*) as putative markers for monitoring the marine sediment pollution in Pahang, Malaysia

Siew Shing Wei^{a,1}, Choo Mei Yen^{a,1}, Ian P.G. Marshall^b, Hazrulrizawati Abd Hamid^{a,c}, Shamrulazhar Shamzir Kamal^d, Dennis Sandris Nielsen^e, Hajar Fauzan Ahmad^{a,*}

^a Faculty of Industrial Sciences & Technology, Universiti Malaysia Pahang, Lebuhraya Tun Razak, 26300 Gambang, Pahang, Malaysia

^b Center for Electromicrobiology, Department of Biology, Ny Munkegade 116, 8000 Aarhus C, Denmark

^c Centre for Research in Advanced Tropical Bioscience (Biotropic Centre), Lebuhraya Tun Razak, 26300 Gambang, Pahang, Malaysia

^d Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300 Kota Samarahan, Sarawak, Malaysia

^e Department of Food Science, Rolighedsvej 26, 1958 Frederiksberg C, Denmark

ARTICLE INFO

Keywords:

Sediment

Pollution

Microbiome

Antibiotics

Vibrio parahaemolyticus

Stichopus ocellatus

ABSTRACT

Antibiotic contamination in the marine environment forms an emerging threat to marine ecosystems. This study aimed to compare the gut and coelomic microbiota of *Stichopus ocellatus* with sediments between two coastal districts of Pahang, which potentially conferring as putative biomarkers for sediment pollution monitoring. The composition of the bacteria communities was determined using 16S rRNA V3-region gene amplicon sequencing, while hybrid whole-genome sequencing was employed to analyze the genome of *Vibrio parahaemolyticus*. The trace elements and antibiotic compositions were access using high-throughput spectrometry. The alpha- and beta-diversity of bacteria in gut and sediment samples from Kuantan differed substantially within (p -value = 0.017604) and between samples (p -value < 0.007), respectively. *Vibrio* genera predominated in Kuantan samples, while *Flavobacterium* and *Synechococcus* genera predominated in Pekan samples. *Vibrio parahaemolyticus* revealed the presence of *tet(35)* and *bla_{CARB-33}* genes that conceived resistance towards tetracycline and beta-lactam antibiotics, respectively, which were detected in sediment and gut samples.

1. Introduction

Despite the implementation of marine protection regulations, increasing anthropogenic pollution of the marine and coastal environment have been reported globally, posing a threat to marine biodiversity (Häder et al., 2020). Sediment serves as a habitat and provides substrate for multitude of marine life and microorganisms (Hauer et al., 2018). Sediment dynamics driven by the water flow are the major determinants of biotic composition, which can considerably affected by human activities on water (de Jalón et al., 2017). Sediment disturbance can modify habitat composition as a result of changes in sediment supply, affecting the development of benthic organisms and biodiversity of marine habitats (Beldowska et al., 2021). As marine sediment is ultimately related to the extent of associated biological effects in the

surrounding marine environment (Palmer et al., 2022), hence, benthic macroinvertebrate such as sea cucumbers, have been considered as indicators to assess the sediment contamination in marine and aquatic environments (Marrugo-Negrete et al., 2021; Tampo et al., 2021).

Sea cucumbers of the class *Holothuroidea* play an important role as deposit feeders by ingesting the sedimentary organic matter in the ocean to satisfy their nutrient requirements and promote nutrient cycling (Oh et al., 2017). Microbes have been detected in various parts of the body of sea cucumbers, including the gut and coelomic fluid (CF) (Chen et al., 2021; Enomoto et al., 2012). Coupled with the fact that sea cucumbers contain indigenous microorganisms associated with habitats surface sediment and shaped by the food sources from surrounding, the microbial composition in an organisms can reflect the total pollution in benthic environment over a long period of time (Gao et al., 2017; Pagán-

* Corresponding author.

E-mail addresses: ianpgm@bio.au.dk (I.P.G. Marshall), hazrulrizawati@ump.edu.my (H.A. Hamid), skshamrulazhar@unimas.my (S.S. Kamal), dn@food.ku.dk (D.S. Nielsen), fauzanahmad@ump.edu.my (H.F. Ahmad).

¹ These authors contributed equally.