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

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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_E* 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.

KEYWORDS

Antibiotics; Microbiome; Pollution; Sediment; Stichopus ocellatus; Vibrio parahaemolyticus

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