

Complete whole genome sequencing of *Vibrio parahaemolyticus* strain UMP001VA, isolated from sea cucumber *Holothuria leucospilota* from Malaysia harbouring *bla*_{CARB-33} gene

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ABSTRACT

Pathogenic strain of *Vibrio parahaemolyticus* found in marine and coastal ecosystems can cause infections in marine animals. Increasing antibiotic resistance reported in *Vibrio* species may be linked to environmental contamination. Here, we present a 4.99-Mbp complete genome sequence of *V. parahaemolyticus* strain UMP001VA, a Gram-negative bacterium that was isolated from the gut content of a sea cucumber *Holothuria leucospilota* collected from Pulau Rhu, Terengganu, Malaysia. The whole genome sequencing was performed using hybrid *de novo* assembly using Illumina and the Oxford Nanopore Technology platforms. The genome analysis reported a total length of 4,991,208 bp of *V. parahaemolyticus* genome sequences with 45.3 % GC content. The functional annotation of the genome showcased that 56 genes of *V. parahaemolyticus* were associated with virulence, disease, and defence function. Virulence factors found in *H. leucospilota* were related to T3SS1, together with the presence of *bla*_{CARB-33} antibiotic resistance gene conferring ampicillin, piperacillin, and amoxicillin drug resistance were reported. The presence of virulence factors and antibiotic resistance genes reveals the considerable pathogenic potential of *V. parahaemolyticus* in sea cucumbers. Therefore, the whole genome sequencing presented here provides a fundamental genome insight for future assessment of *V. parahaemolyticus* in marine organisms.

KEYWORDS

Antibiotic resistance; *Holothuria leucospilota*; Sea cucumber; *Vibrio parahaemolyticus*

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