

Whole genome sequencing of *Priestia megaterium* isolated from the gut of sea cucumber (*Holothuria leucospilota*)

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ABSTRACT

Priestia megaterium represents a bacterium of interest in a wide application of the field of biotechnology. Often it is sought after for its ability that boasts great rate for biosynthesis production of smaller biological molecules while also representing a suitable host to generate compounds such as cobalamin. The bacterium can also be found in a wide variety of habitats including sea water. Sea cucumbers have begun to be quite popular to a point of extinction in certain species. This interest could be associated to the uniqueness attributed to its gut microbiome or just the organism itself. Nevertheless, the presence of *Priestia megaterium* within the gut of *Holothuria leucospilota* might serve as rationale to the previous statement. Here, we describe a detailed genomic analysis of *Priestia megaterium* isolated from the gut of *Holothuria leucospilota*. Genomic DNA was extracted from nutrient broths which were incubated with pure cultures of *Priestia megaterium* which were previously isolated from the sea cucumber. Whole genome sequencing was carried out using an Oxford Nanopore Technology platform which used a long-read protocol. The study reported a complete genome of *Priestia megaterium* comprising of 5,323,711 bp genome size with a GC content of 37.9 %. Finally, the annotated genome was submitted to the NCBI database. Overall, this study revealed the complete genome of *Priestia megaterium* and would serve to potentially explain its association towards the gut microbiome found within *Holothuria leucospilota*.

KEYWORDS

Gut; *Priestia Megaterium*; Sea cucumber; Whole genome sequencing

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