

Isolation and Genome Sequencing of *Bacillus Megaterium* Found from the Gut Sea Cucumber (*Holothuria Leucospilota*)

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Abstract

Bacillus megaterium is a bacterium that is widely used in the application of biotechnology. Often its popularity is due to its ability to represent a suitable host to generate compounds such as cobalamin and perform biosynthesis production of smaller biological molecules. The bacterium can also be found in a wide variety of habitats including sea water. The interest towards sea cucumbers have skyrocketed to a point of extinction in certain species. This popularity could be due to the uniqueness associated to the gut microbiome observed within sea cucumber or just the organism itself. However, the presence of *B.megaterium* within the gut of *Holothuria leucospilota* could prove an answer to the previous statement. In this study, isolation of an unknown bacterium (which was *B.Megaterium*), identification and genomic analysis of the bacterium which was obtained from the gut of *H.leucospilota* was carried out. DNA was extracted using commercial kits, and later quantified using a NanoDrop Biophotometer. The V3-V4 region of the 16s RNA was used as specific primers for PCR amplification. Quality of DNA and PCR results were verified using agarose gel electrophoresis. Identification was carried out by performing sanger sequencing towards the PCR products obtained. The study identified and reported a complete genome of *B.megaterium* comprising of 5,323,711 bp genome size with a GC content of 37.9%. The annotated genome was submitted to the NCBI database. Overall, this study revealed the complete genome of *B.megaterium* and would serve to potentially explain its association towards the gut microbiome found within *H.leucospilota*.

Keywords: *Bacillus megaterium*; *Holothuria leucospilota*; Gut; Sea cucumber; Genome sequencing.