Genome Report

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Draft genome of starch-degrading actinobacterium, *Microbacterium mangrovi* MUSC 115^T isolated from intertidal sediments

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Abstract : *Microbacterium mangrovi* strain MUSC 115^T was isolated from intertidal sediments of Kuantan, Malaysia. Here we describe the draft genome of amylolytic strain MUSC 115^T with total size of 4.4 Mbp from 55 contigs and G + C content of 70.0%. Total of 4,096 coding genes were observed, with 2 putative amylases genes in the draft genome of MUSC 115^T. These genome features of MUSC 115^T can improve our understanding of its starch-degrading mechanism and general physiology of the species, which provide opportunities for biotechnological and industrial exploitation.

Keywords: Rare actinobacteria; mangrove; bioinformatics; genome; *Microbacterium*

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Short Introduction

Members of *Microbacterium* are found in diverse habitats such as soil, plants, water, insects and humans[1-3]. Furthermore, several species of *Microbacterium* are known to degrade heavy metals, crude oil and oligosaccharides[4-6]. The production of active extracellular amylase exhibited by *Microbacterium* species suggest its importance for the starch industry[7,8]. Isolated from intertidal sediments, *Microbacterium mangrovi* strain MUSC 115^T was present as non-spore-forming, Gram-positive bacterium with irregular cocci or rod-shaped. Using polyphasic approach, previous study has identified MUSC 115^T to be a novel species belong to the genus *Microbacterium*[9]. Phylogenetic analyses based on partial 16S rRNA gene sequence showed that MUSC 115^T displayed highest similarity to *M. immunditiarum* SK 18^T (98.1%), followed by *M. ulmi* XIL02^T, *M. arborescens* DSM 20754^T (97.5%), and lower similarities (less than 97.5%) with other *Microbacterium* species. MUSC 115^T displayed significant starch-degrading properties, thus was selected for genome sequencing for its biotechnological potential.

Data description

Genomic DNA of MUSC 115^T was extracted using Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) and subjected to RNase (Qiagen, USA) treatment[10,11,12].The genome of strain MUSC 115^T was sequenced using Illumina MiSeq platform (Institute of Biological Sciences, Faculty of Science, University of Malaya), which generated 4,288,876 paired-end reads. The trimmed sequences were *de novo* assembled with CLC Genomic Workbench version 5.1 (CLC Bio, Denmark), resulting in 55 contigs with N_{50} size of 212,789 bp. The assembled genome size of MUSC 117^T

contains 4,416,601 bp, with an average genome coverage of 103-fold with a G + C content of 70.0 % (Table 1). The genome sequence of *M. mangrovi* MUSC 115^T has been deposited at DDBJ/EMBL/GenBank under accession JTDK00000000. The strain has been deposited at two culture collection centers (=MCCC 1K00252^T = DSM 42140^T).

Table 1. General features of *Microbacterium mangrovi* MUSC 115^T draft genome.

	Microbacterium mangrovi MUSC 115^T
Genome size (bp)	4,416,601
Contigs	55
Contigs N_{50} (bp)	212,789
G + C content %	70.0
Protein coding genes	4,096
tRNA	45
rRNA	3

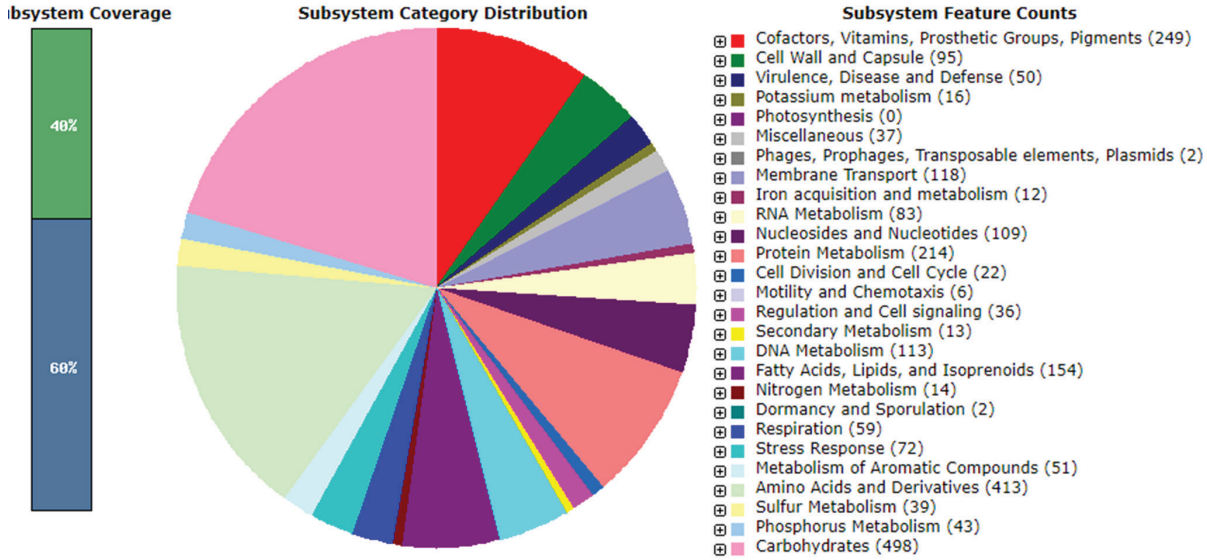

Figure 1. Subsystem category distribution of MUSC 115^T based on RAST server.

The gene prediction was carried out with a prokaryote gene prediction algorithm using Prodigal 2.6, while rRNA and tRNA were predicted with RNAmmer and tRNAscan SE version 1.21, respectively[12-14]. Following that, annotation was performed using Rapid Annotation using Subsystem Technology (RAST)[15]. In the whole genome of MUSC 115^T, total of 4,096 coding genes were detected: 2,948 genes (72.0%) were known to encode functional proteins, 61 genes (1.5%) were predicted to encode hypothetical proteins, and 1,087 genes (26.5%) have no database match. The RAST annotation server has identified majority of the genes (498 genes, 12.2%) were associated with carbohydrate metabolism, among which 86 genes were involved with metabolism of di- and oligosaccharides. Two genes were detected to encode for glucoamylase (EC 3.2.1.3) and alpha-amylase (EC 3.2.1.1) respectively. The presence of these genes may account for its ability to degrade starch.

In conclusion, the draft genome of *Microbacterium mangrovi* MUSC 115^T revealed presence of amylases genes which corresponded to its ability to degrade starch. In order to understand the properties of these amylases produced by strain MUSC 115^T, further studies are required to purify and characterize these enzymes.

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Conflict of Interest

The authors declared that there is no conflict of interest.

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