Genome Report

Progress in Microbes and Molecular Biology

HH PUBLISHER

Genome sequence of *Novosphingobium malaysiense* strain MUSC 273^T, novel alpha-proteobacterium isolated from intertidal soil

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Abstract : *Novosphingobium malaysiense* strain MUSC 273^T is a recently identified Gram-negative, aerobic alpha-proteobacterium. The strain was isolated from intertidal soil with strong catalase activity. The genome sequence comprises 5,027,021 bp, with 50 tRNA and 3 rRNA genes. Further analysis identified presence of secondary metabolite gene clusters within genome of MUSC 273^T. Knowledge of the genomic features of the strain may allow further biotechnological exploitation, particularly for production of secondary metabolites as well as production of industrially important enzymes.

Keywords: Proteobacteria; antioxidant, mangrove; secondary metabolite

Received: 20th July 2018
Accepted: 5th August 2018
Published Online: 15th August 2018

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Citation: Ser HL, Yin WF, Chan KG, *et al.* Genome sequence of *Novosphingobium malaysiense* strain MUSC 273^T, novel alpha-proteobacterium isolated from intertidal soi. Prog Micobes Mol Biol 2018; 1(1): a0000003.

Short Introduction

Members of the genus *Novosphingobium* can be found in wide range of habitats including soil, deep sea as well as contaminated environments[1-3]. Their ability to degrade mono- and polycyclic aromatic hydrocarbons (PAHs) has attracted much biotechnological interest, notably for biomediation purposes. *Novosphingobium malaysiense* strain MUSC 273^T was isolated as novel species from intertidal soil obtained from Pahang, Malaysia[4]. Based on 16S rRNA gene analysis, the strain displayed highest similarities to *Novosphingobium indicum* H25^T, a type strain which has been shown to be able to degrade PAHs. Furthermore, MUSC 273^T exhibited strong catalase activity, thus was selected for genome sequencing.

Data description

Extraction of genomic DNA was using Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) treatment[5-7]. Genomic DNA quality was checked using NanoDrop spectrophotometer (Thermo Scientific, Waltham, MA, USA) and a Qubit version 2.0 fluorometer (Life Technologies, Carlsbad, CA, USA). Following that, DNA library was prepared with Nextera™ DNA Sample Preparation kit (Nextera, USA). Prior to sequencing, quality of DNA library was examined with Bioanalyzer 2100 high sensitivity DNA kit (Agilent Technologies, Palo Alto, CA). Whole genome shotgun project of MUSC 273^T was carried out using paired sequencing in an Illumina MiSeq platform with MiSeq Reagent Kit 2 (2 × 250 bp; Illumina Inc., Madison, WI, USA), producing 4,376,924 paired-end reads. The assembly of trimmed seqeuence was done with CLC Genomic Workbench version 5.1 (CLC Bio, Denmark), resulting in 85 contigs and an N_{50} contig size of approximately 631,941 bp. The assembled genome size comprised 5,027,021 bp, with an average coverage of 100.0-fold and G + C content of 63.3%. The genome sequence of *Novosphingobium malaysiense* MUSC 273^T has been deposited at DDBJ/EMBL/GenBank under accession of JTDI00000000. The strain was deposited at three

culture collection centers under accession of DSM 27798^T = MCCC 1A00645^T = NBRC 109974^T.

Table 1. General genomic features of N*ovosphingobium malaysiense* strain MUSC 273^T.

	Novosphingobium malaysiense MUSC 273^T
Genome size (bp)	5,027,021
Contigs	85
Contigs N_{50} (bp)	631,941
G + C content %	63.3
Protein coding genes	4,738
tRNA	50
rRNA	3
Putative secondary metabolite gene clusters	9
Homoserine lactone	2
Type 3 polyketides	1
Bacteriocin	1

The assembled genome was annotated using Rapid Annotation using Subsystem Technology (RAST)[8]. Gene prediction was performed using Prodigal version 2.6, while ribos omal RNA (rRNA) and transfer RNA (tRNA) were predicted using RNAmmer and tRNAscan SE version 1.21, respectively[9-11]. The analysis from RAST revealed 4,738 protein-coding genes, along with 50 tRNA and 3 rRNA genes. Out of 4,738 protein-coding genes, 35 genes were identified to encode for enzymes involved in aromatic compounds metabolism. Additionally, the genome also contained 3 genes responsible for production of catalase (E.C. 1.11.1.6) and/or peroxidase (E.C. 1.11.1.7). Presence of these genes may suggest the genomic potential of strain MUSC 273^T, most notably for industrial application and environmental bioremediation purposes. Closer investigation of MUSC 273^T genome with antibiotics & Secondary Metabolite Analysis SHell (antiSMASH) unveiled several clusters of secondary metabolite genes[12]. Total of 9 biosynthetic gene clusters were detected: 2 gene clusters associated with production for homoserine lactone; 1 each for type 3 polyketide and bacteriocin. These results indicate that strain MUSC 273^T may produce natural bioactive compounds (including antibiotics), thus future studies involving characterization of these gene clusters and isolation of the secondary metabolite may assist in the discovery of these valuable compounds.

Acknowledgement

This work was supported by the University of Malaya for High Impact Research Grant (UM-MOHE HIR Nature Microbiome Grant No. H-50001-A000027) awarded to K.-G. C. and External Industry Grant from Biotek Abadi Sdn Bhd (Vote No. GBA-808138 & GBA-808813) awarded to L.-H. L.

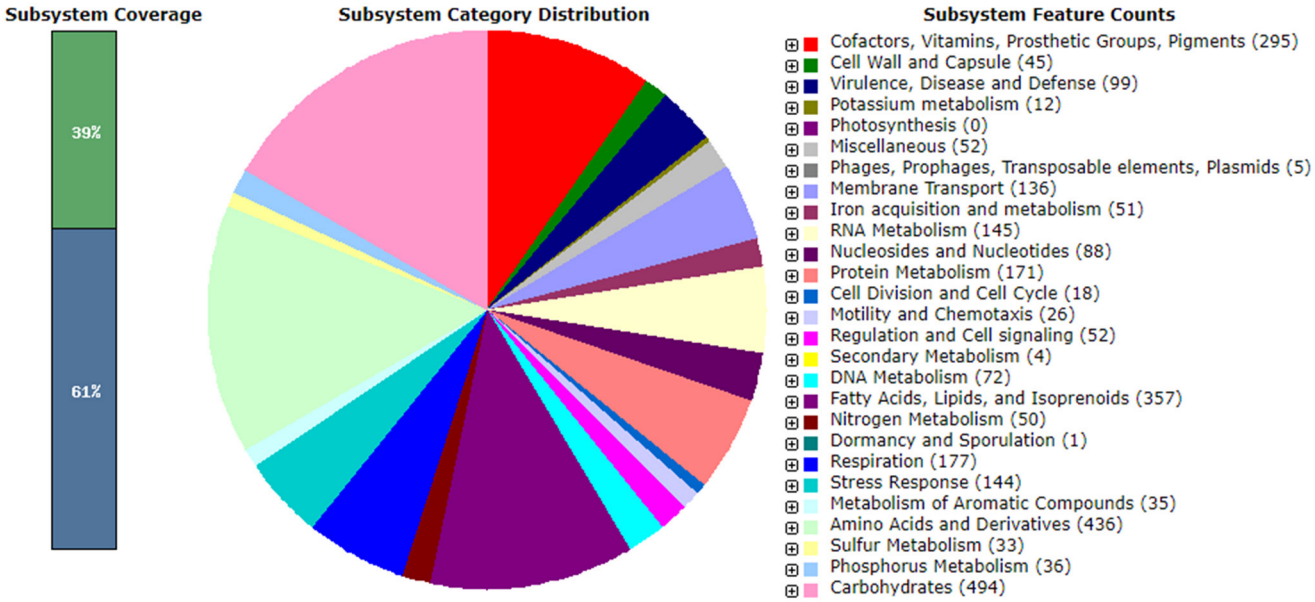

Figure 1. Subsystem category distribution of *Novosphingobium malaysiense* MUSC 273^T (based on RAST annotation server).

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