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Draft Genome Sequence of Mangrove-Derived *Streptomyces* sp. MUSC 125 with Antioxidant Potential

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INTRODUCTION

Microorganisms remain as one of the most important source of pharmaceutically important drugs (Berdy, 2005; Debbab et al., 2010; Waditee-Sirisattha et al., 2016). Among the bacteria domain, *Streptomyces* genus has received considerable attention by the Scientific community for its seemingly unmatched capability of producing useful bioactive metabolites. The *Streptomyces* genus was initially proposed by Waksman and Henrici (1943); as the largest genus of *Actinobacteria*, it is comprised of over 780 species with validly published names (http://www.bacterio.cict.fr/). These gram-positive bacteria have contributed remarkably in natural product discovery as they synthesize compounds with diverse chemical structures and biological activities such as anticancer, antibacterial, antioxidant, antifungal, and immunosuppresants activities (Berdy, 2005; Gallagher et al., 2010; Manivasagan et al., 2013; Ser et al., 2015a, 2016a).

Over the years, drug screening programs have been focusing on identification of terrestrial microorganisms and investigation of their bioactive potential (Burg et al., 1979; Marcus et al., 1999). However, these efforts have resulted in rediscovery of the known bioactive compounds. Thus, researchers begun to venture into new and/or underexplored areas in the hope of discovering novel, potent bioactive metabolites. The mangrove ecosystem represents one of the world's most dynamic environments that produces commercial forest products, supports coastal fisheries and protects coastlines (Alongi, 2008). Factors such as fluctuations in salinity and tidal gradient are believed to be the driving force for metabolic adaptations, which could in turn lead to production of valuable metabolites. In fact, the growing interest in bioactive potentials of mangrove-derived *Streptomyces* has been demonstrated by the isolation of *Streptomyces pluripotens* (Lee et al., 2014a), *S. fradiae* (Prakash et al., 2015), *S. cheonanensis* (Mangamuri et al., 2016), and *S. malaysiense* (Ser et al., 2016b).

For this study, *Streptomyces* sp. MUSC 125 was initially isolated from mangrove soil in the east coast of Peninsular Malaysia (Lee et al., 2014b). As an attempt to explore the antioxidant capacity of MUSC 125, metal-chelating assay was performed and discovered its potential in quenching ferrous

ions with activity ranging from 10.02 to 51.14% (unpublished data). Thus, the strain was selected for whole genome sequencing to obtain further understanding on its genomic potential.

MATERIALS AND METHODS

Isolation and Culture of Strain MUSC 125

Streptomyces sp. MUSC 125 was isolated from Tanjung Lumpur mangrove forest located in the city of Kuantan, State of Pahang, in December of the year 2012 (Lee et al., 2014b). Purified cultures were maintained on ISP medium 2 slants at room temperature for short-term storage and as glycerol suspensions (20%, v/v) at −80°C for long-term storage.

Genome Sequencing and Bioinformatics Analysis of MUSC 125

The genomic DNA of MUSC 125 was extracted with Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) followed by RNase (Qiagen, USA) treatment (Ser et al., 2015b). Quality of the extracted DNA was examined using NanoDrop spectrophotometer (Thermo Scientific, Waltham, MA, USA) and a Qubit version 2.0 fluorometer (Life Technologies, Carlsbad, CA, USA). Subsequently, DNA library was prepared using Nextera™ DNA Sample Preparation kit (Nextera, USA), while the library quality was validated by Bioanalyzer 2100 high sensitivity DNA kit (Agilent Technologies, Palo Alto, CA) prior to sequencing. The genome of strain MUSC 125 was sequenced on MiSeq platform with MiSeq Reagent Kit 2 (2 × 250 bp; Illumina Inc., Madison, WI, USA). Following that, the paired-end reads were trimmed and *de novo* assembled with CLC Genomics Workbench version 5.1 (CLC bio, Denmark). Gene prediction was performed using Prodigal version 2.6, whereas rRNA and tRNA were predicted using RNAmmer and tRNAscan SE version 1.21 (Lowe and Eddy, 1997; Lagesen et al., 2007; Hyatt et al., 2010). The assembly was uploaded for annotation to Rapid Annotation using Subsystem Technology (RAST) (Aziz et al., 2008).

TABLE 1 | General features of *Streptomyces* sp. MUSC 125 draft genome.

	***Streptomyces* sp. MUSC 125**
Genome size (bp)	7,656,461
G+C content (%)	70.00
Genome coverage	94.0x
Contigs	164
Contigs N_{50} (bp)	139,282
Number of ORFs	5991
tRNA genes	68
rRNA genes (5S, 16S, 23S)	4
Bioproject ID	PRJNA261099
Biosample ID	SAMN03070123
Genome accession	JUIG00000000

RESULTS

Sequencing of MUSC 125 genome using Illumina technology generated a total of 4,518,422 reads. After adapter trimming, the reads were *de novo* assembled into 164 contigs using CLC Genomics workbench. The genome size of MUSC 125 is 7,656,461 bp with G + C content of 70.00% (**Table 1**). The whole genome project of MUSC 125 was deposited at DDBJ/EMBL/GenBank under accession number JUIG00000000 and the version described in this paper is the first version (JUIG01000000). The analyses of the draft genome identified 5991 open reading frames (ORFs), 68 tRNAs, and 4 rRNA (5S, 16S, 23S rRNA). The RAST annotation has assigned these genes into 419 subsystems, with maximum number of genes associated with amino acids and derivatives metabolism (8.84%), followed by carbohydrates (6.93 %) and protein metabolism subsystems (4.73%) (**Figure 1**).

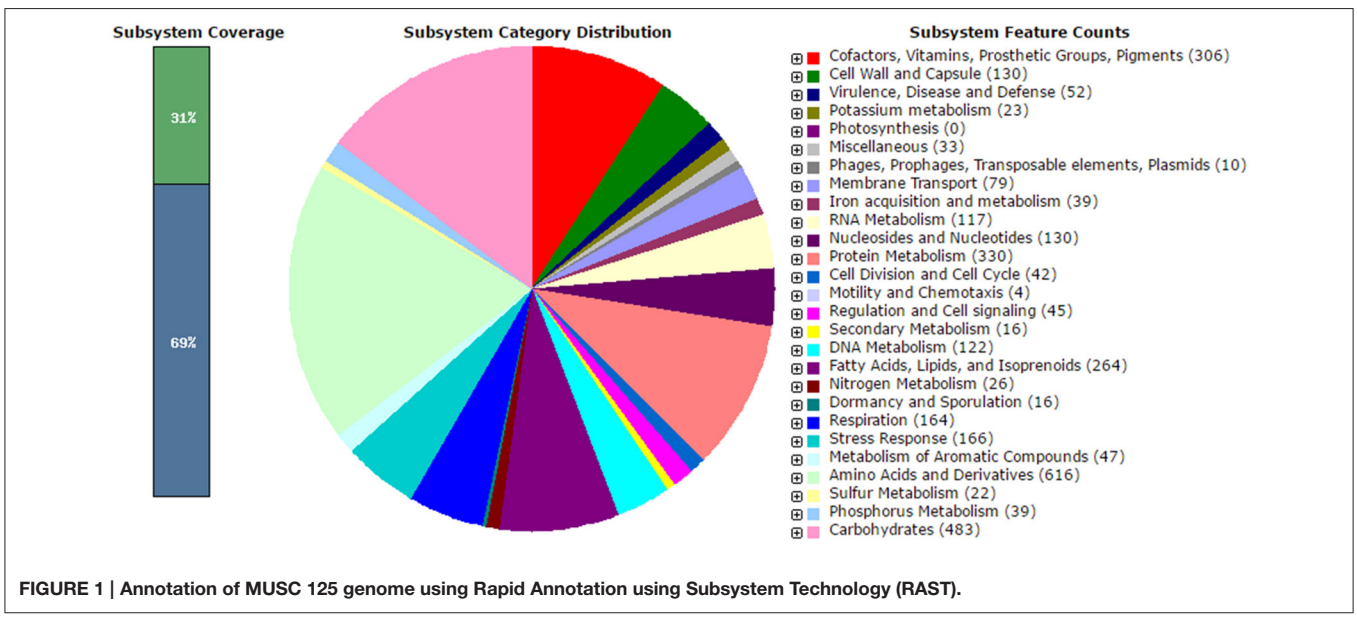

FIGURE 1 | Annotation of MUSC 125 genome using Rapid Annotation using Subsystem Technology (RAST).

Direct Link to Deposited Data and Information to Users

The genome sequence of *Streptomyces* sp. MUSC 125 (Biosample ID: SAMN03070123) can be accessed at NCBI using the accession number JUIG00000000. The genome project data are also available at GenBank under the genome Bioproject ID PRJNA261099. Users can download and use the data freely for research purpose only with acknowledgement to us and citing this paper as reference to the data.

AUTHOR CONTRIBUTIONS

The experiments, data analysis and manuscript writing were performed by H-LS and W-ST, while N-SA, W-FY, K-GC, B-HG, and L-HL. provided vital guidance and technical support. L-HL founded the research project.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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