



## Genome Announcement

# Genome sequence of *Streptomyces gilvigriseus* MUSC 26<sup>T</sup> isolated from mangrove forest

Hooi-Leng Ser<sup>a,b,c</sup>, Wen-Si Tan<sup>d</sup>, Nurul-Syakima Ab Mutalib<sup>e</sup>, Wai-Fong Yin<sup>d</sup>, Kok-Gan Chan<sup>d,f</sup>, Bey-Hing Goh<sup>a,c,g,h</sup>, Learn-Han Lee<sup>a,b,c,g,h,\*</sup>

<sup>a</sup> Monash University Malaysia, School of Pharmacy, Novel Bacteria and Drug Discovery Research Group (NBDD), Selangor Darul Ehsan, Malaysia

<sup>b</sup> Monash University Malaysia, Jeffrey Cheah School of Medicine and Health Sciences, Biomedical Research Laboratory, Selangor Darul Ehsan, Malaysia

<sup>c</sup> Monash University Malaysia, School of Pharmacy, Biofunctional Molecule Exploratory Research Group (BMEX), Bandar Sunway, Malaysia

<sup>d</sup> University of Malaya, Faculty of Science, Institute of Biological Sciences, Division of Genetics and Molecular Biology, Malaysia

<sup>e</sup> Universiti Kebangsaan Malaysia, UKM Medical Centre, UKM Medical Molecular Biology Institute (UMBI), Kuala Lumpur, Malaysia

<sup>f</sup> Vice Chancellor Office, Jiangsu University, Zhenjiang 212013, PR China

<sup>g</sup> University of Phayao, School of Pharmaceutical Sciences, Center of Health Outcomes Research and Therapeutic Safety (Cohorts), Phayao, Thailand

<sup>h</sup> Monash University Malaysia, Global Asia in the 21st Century (GA21) Platform, Health and Well-being Cluster, Implementation and Clinical Outcomes (PICO), Asian Centre for Evidence Synthesis in Population, Bandar Sunway, Malaysia

## ARTICLE INFO

## Article history:

Received 10 February 2017

Accepted 3 April 2017

Available online 2 February 2018

Associate Editor: Rodrigo Galhardo

## Keywords:

Genome sequence

*Streptomyces gilvigriseus*

Mangrove

AntiSMASH

Neuroprotective

## ABSTRACT

Streptomycetes remain as one of the important sources for bioactive products. Isolated from the mangrove forest, *Streptomyces gilvigriseus* MUSC 26<sup>T</sup> was previously characterised as a novel streptomycete. The high quality draft genome of MUSC 26<sup>T</sup> contained 5,213,277 bp with G+C content of 73.0%. Through genome mining, several gene clusters associated with secondary metabolites production were revealed in the genome of MUSC 26<sup>T</sup>. These findings call for further investigations into the potential exploitation of the strain for production of pharmaceutically important compounds.

© 2018 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

The members of *Streptomyces* are of great importance for bioactive products; these organisms are capable of producing a range of structurally diverse compounds with various bioactivities including antibiotics, anti-rejection (immunosuppressant), antioxidant and anticancer.<sup>1–5</sup> As a novel

streptomycete isolated from mangrove forest, *Streptomyces gilvigriseus* MUSC 26<sup>T</sup> has been deposited in two culture collection centres (=MCCC 1K00252<sup>T</sup> = DSM 42140<sup>T</sup>). The methanolic extract of MUSC 26<sup>T</sup> was prepared as previously described and it has demonstrated significant neuroprotective activity

\* Corresponding authors at: School of Pharmacy, Monash University Malaysia, 47500 Bandar Sunway, Selangor Darul Ehsan, Malaysia. E-mails: [lee.learn.han@monash.edu](mailto:lee.learn.han@monash.edu), [leelearnhan@yahoo.com](mailto:leelearnhan@yahoo.com) (L. Lee).

<https://doi.org/10.1016/j.bjm.2017.04.012>

1517-8382/© 2018 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

**Table 1 – General features of *Streptomyces gilvigriseus* MUSC 26<sup>T</sup> genome.**

	<i>Streptomyces gilvigriseus</i> MUSC 26 <sup>T</sup>
Genome size (bp)	5,213,277
Contigs	206
Contigs N <sub>50</sub> (bp)	45,324
G + C content (%)	73.0
Protein coding genes	4337
tRNA	53
rRNA	1 (5S), 3 (16S), 1 (23S)

against free radical-induced damage in SHSY-5Y neuronal cells (data not shown).<sup>4,6,7</sup> Thus, the strain MUSC 26<sup>T</sup> was selected for genome sequencing as an attempt to identify biosynthetic gene clusters associated with secondary metabolites production.

Genomic DNA extraction of MUSC 26<sup>T</sup> was carried out with Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) before RNase (Qiagen, USA) treatment.<sup>8,9</sup> DNA quality was accessed using NanoDrop spectrophotometer (Thermo Scientific, Waltham, MA, USA) and a Qubit version 2.0 fluorometer (Life Technologies, Carlsbad, CA, USA). Construction of DNA library was performed using Nextera™ DNA Sample Preparation kit (Nextera, USA) and the library quality was validated by Bioanalyser 2100 high sensitivity DNA kit (Agilent Technologies, Palo Alto, CA) prior to performing paired-end sequencing on MiSeq platform with MiSeq Reagent Kit 2 (2 × 250 bp; Illumina Inc., Madison, WI, USA). The paired-end reads were trimmed and *de novo* assembled with CLC Genomics Workbench version 7 (CLC bio, Denmark). The analysis generated 206 contigs with N<sub>50</sub> size of 45,324 bp (Table 1). The assembled genome size of MUSC 26<sup>T</sup> contained 5,213,277 bp, with an average coverage of 40.0-fold and G+C content of 73.0%. The whole genome project of MUSC 26<sup>T</sup> was deposited at DDBJ/EMBL/GenBank under accession number MLCF00000000 and the version described in this paper is the first version (MLCF01000000).

Gene prediction was performed using Prodigal version 2.6, whereas rRNA and tRNA were predicted using RNAmmer and tRNAscan SE version 1.21.<sup>10–12</sup> The assembly was uploaded for annotation to Rapid Annotation using Subsystem Technology (RAST).<sup>13</sup> A total of 4337 protein-encoding genes was predicted and assigned to 363 subsystems, along with 53 tRNA and 5 rRNA genes. Among the subsystems, most of the genes were involved in carbohydrates metabolism (7.39%), followed by amino acids and derivatives metabolism (5.90%) and protein metabolism subsystems (5.81%).

The genomic potential of MUSC 26<sup>T</sup> was further explored with antibiotics & Secondary Metabolite analysis shell (antiSMASH), PRediction Informatics for Secondary Metabolomes (PRISM) and BAGEL3.<sup>14–17</sup> The antiSMASH server detected two gene clusters associated with siderophores production; one of which showed 40% similarities to desferrioxamine B biosynthetic gene cluster. The presence of these biosynthetic gene clusters suggest possible production of compounds responsible for the neuroprotective activity. Apart from siderophores, PRISM and BAGEL3 detected two gene clusters associated with class I lantipeptide and one gene cluster associated with lasso peptide and bacteriocin, respectively. Overall, these findings

highlighted the genomic potential of MUSC 26<sup>T</sup> and prompted further comprehensive studies to allow utilisation of the strain for production of pharmaceutically important compounds.

## Conflicts of interest

The authors declare no conflicts of interest.

## Acknowledgments

This work was supported by PVC Award Grant (Project Q7 No. PVC-ECR-2016), External Industry Grant (Biotek Abadi Vote No. GBA-808813), MOSTI eScience funds (Project No. 06-02-10-SF0300) awarded to L.-H.L. and MOSTI eScience funds (Project No. 02-02-10-SF0215) awarded to B.-H.G., and a University of Malaya for High Impact Research Grant (UM-MOHE HIR Nature Microbiome Grant No. H-50001-A000027 and No. A000001-50001) and PPP Grant (PG090-2015B) awarded to K.-G.C.

## REFERENCES

- Berdy J. Bioactive microbial metabolites. *J Antibiotics*. 2005;58:1–26.
- Solecka J, Zajko J, Postek M, Rajnisz A. Biologically active secondary metabolites from Actinomycetes. *Open Life Sci*. 2012;7(3):373–390.
- Tan LTH, Ser HL, Yin WF, Chan KG, Lee LH, Goh BH. Investigation of antioxidative and anticancer potentials of *Streptomyces* sp. MUM256 isolated from Malaysia mangrove soil. *Front Microbiol*. 2015;6:1316.
- Ser HL, Tan LTH, Palanisamy UD, et al. *Streptomyces antioxidans* sp. nov., a novel mangrove soil actinobacterium with antioxidative and neuroprotective potentials. *Front Microbiol*. 2016;7:899.
- Ser HL, Palanisamy UD, Yin WF, Chan KG, Goh BH, Lee LH. *Streptomyces malaysiense* sp. nov.: a novel Malaysian mangrove soil actinobacterium with antioxidative activity and cytotoxic potential against human cancer cell lines. *Sci Rep*. 2016;6:24247.
- Lee LH, Zainal N, Azman AS, et al. Diversity and antimicrobial activities of actinobacteria isolated from tropical mangrove sediments in Malaysia. *Sci World J*. 2014;698178:1–14.
- Ser HL, Zainal N, Palanisamy UD, et al. *Streptomyces gilvigriseus* sp. nov., a novel actinobacterium isolated from mangrove forest soil. *Antonie van Leeuwenhoek*. 2015;107:1369–1378.
- Ser HL, Tan WS, Ab Mutalib NS, et al. Genome sequence of *Streptomyces pluripotens* MUSC 135T exhibiting antibacterial and antioxidant activity. *Mar Gen*. 2015;24:281–283.
- Ser HL, Tan WS, Ab Mutalib NS, et al. Draft genome sequence of mangrove-derived *Streptomyces* sp. MUSC 125 with antioxidant potential. *Front Microbiol*. 2016;7:1470.
- Lowe TM, Eddy SR. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res*. 1997;25:955–964.
- Lagesen K, Hallin P, Rodland EA, et al. consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res*. 2007;35:3100–3108.
- Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinf*. 2010;11:119.

13. Aziz RK, Bartels D, Best AA, et al. The RAST Server: rapid annotations using subsystems technology. *BMC Gen.* 2008;9:75.
14. Weber T, Blin K, Duddela S, et al. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res.* 2015;43:W237–W243.
15. Skinnider MA, Dejong CA, Rees PN, et al. Genomes to natural products prediction informatics for secondary metabolomes (PRISM). *Nucleic Acids Res.* 2015;43:9645–9662.
16. Skinnider MA, Johnston CW, Edgar RE, et al. Genomic charting of ribosomally synthesized natural product chemical space facilitates targeted mining. *PNAS.* 2016;113:E6343–E6351.
17. Van Heel AJ, de Jong A, Montalban-Lopez M, Kok J, Kuipers OP. BAGEL3: automated identification of genes encoding bacteriocins and (non-) bactericidal posttranslationally modified peptides. *Nucleic Acids Res.* 2013;41:W448–W453.