Genome Announcement

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

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**ABSTRACT**

Streptomycetes remain 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.

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

Genomic DNA extraction of MUSC 26T was carried out with Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) before RNase (Qiagen, USA) treatment.6,9 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 Bioanalyzer 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 × 250bp; 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 N50 size of 45,324 bp (Table 1). The assembled genome size of MUSC 26T 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 26T was deposited at DDBJ/EMBL/GenBank under accession number MLCF00000000 and the version described in this paper is the first version (MLCF01000000).

The genomic potential of MUSC 26T was further explored with antibiotics & Secondary Metabolite analysis shell (antiSMASH), Predict Informatics for Secondary Metabolites (PRISM) and BAGEL3.14-17 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 26T 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**

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**References**


**Table 1 – General features of Streptomyces gilvogriseus MUSC 26T genome.**

<table>
<thead>
<tr>
<th>Feature</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome size (bp)</td>
<td>5,213,277</td>
</tr>
<tr>
<td>Contigs</td>
<td>206</td>
</tr>
<tr>
<td>Contigs N50 (bp)</td>
<td>45,324</td>
</tr>
<tr>
<td>G + C content (%)</td>
<td>73.0</td>
</tr>
<tr>
<td>Protein coding genes</td>
<td>4337</td>
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<tr>
<td>tRNA</td>
<td>53</td>
</tr>
<tr>
<td>rRNA</td>
<td>1 (5S), 3 (16S), 1 (23S)</td>
</tr>
</tbody>
</table>

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*MG,*, *ML,*, *MC,*, *MM,* and *MG*: indicate the low, medium, middle, and high scores, respectively.


