



## Genome Announcement

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



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## 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.

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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 (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

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**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.

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