Genome Announcement

Genome sequence of Streptomyces gilvigriseus MUSC 26T isolated from mangrove forest

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A R T I C L E   I N F O

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

A B S T R A C T

Streptomycetes remain as one of the important sources for bioactive products. Isolated from the mangrove forest, Streptomyces gilvigriseus MUSC 26\textsuperscript{T} was previously characterised as a novel streptomycete. The high quality draft genome of MUSC 26\textsuperscript{T} 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\textsuperscript{T}. 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.\textsuperscript{1–5} As a novel streptomycete isolated from mangrove forest, Streptomyces gilvigriseus MUSC 26\textsuperscript{T} has been deposited in two culture collection centres (=MCCC 1K00252\textsuperscript{T} = DSM 42140\textsuperscript{T}). The methanolic extract of MUSC 26\textsuperscript{T} was prepared as previously described and it has demonstrated significant neuroprotective activity.

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https://doi.org/10.1016/j.bjm.2017.04.012
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against free radical-induced damage in SHSY-5Y neuronal cells (data not shown). Thus, the strain MUSC 267 was selected for genome sequencing as an attempt to identify biosynthetic gene clusters associated with secondary metabolites production.

Genomic DNA extraction of MUSC 267 was carried out with Masterpure™ DNA purification kit (Epicentre, Illumina Inc., Madison, WI, USA) before RNase (Qiagen, USA) treatment. 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 Bioanlyser 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 N50 size of 45,324 bp (Table 1). The assembled genome size of MUSC 267 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 267 was deposited at DDBJ/EMBL/GenBank under accession number MLCF0000000 and the version described in this paper is the first version (MLCF0100000).

Table 1 – General features of Streptomyces glycofusus MUSC 267 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>
</tr>
<tr>
<td>tRNA</td>
<td>53</td>
</tr>
<tr>
<td>rRNA</td>
<td>1 (5S), 3 (16S), 1 (23S)</td>
</tr>
</tbody>
</table>

Gene prediction was performed using Prodigal version 2.6, whereas tRNA and rRNA were predicted using RNAmmer and trNAscan SE version 1.21. The assembly was uploaded for annotation to Rapid Annotation using Subsystem Technology (RAST). 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 267 was further explored with antibiotics & Secondary Metabolite analysis shell (antiSMASH), Prediction Informatics for Secondary Metabolites (PRISM) and BAGEL3. The antiSMASH server detected two gene clusters associated with siderophores production; one of which showed 40% similarities to desferroxamine 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 267 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. A00001-50001) and PPP Grant (PG090-2015B) awarded to K.-G.C.

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