Genome Announcement

Genome sequence of Streptomyces mangrovisoli MUSC 149T isolated from intertidal sediments

Hooi-Leng Ser a,b, Wen-Si Tan c, Nurul-Syakima Ab Mutalib d, Wai-Fong Yin c, Kok-Gan Chan c, Bey-Hing Goh a,d,e,* , Learn-Han Lee a,d,e,*

a Monash University Malaysia, School of Pharmacy, Novel Bacteria and Drug Discovery (NBD) Research Group, Selangor Darul Ehsan, Malaysia
b Monash University Malaysia, Jeffrey Cheah School of Medicine and Health Sciences, Biomedical Research Laboratory, Selangor Darul Ehsan, Malaysia
c University of Malaya, Institute of Biological Sciences, Division of Genetics and Molecular Biology, Kuala Lumpur, Malaysia
d University Kebangsaan Malaysia, UKM Medical Centre, UKM Medical Molecular Biology Institute (UMBJ), Kuala Lumpur, Malaysia
e University of Phayao, School of Pharmaceutical Sciences, Center of Health Outcomes Research and Therapeutic Safety (Cohorts), Phayao, Thailand

ABSTRACT

As the largest genus in Actinobacteria family, Streptomyces species have the ability to synthesize numerous compounds of diverse structures with bioactivities. Streptomyces mangrovisoli MUSC 149T was previously isolated as a novel streptomycete from mangrove forest in east coast of Peninsular Malaysia. The high quality draft genome of MUSC 149T comprises 9,165,825 bp with G + C content of 72.5%. Through bioinformatics analysis, 21 gene clusters identified in the genome were associated with the production of bioactive secondary metabolites. The presence of these biosynthetic gene clusters in MUSC 149T suggests the potential exploitation of the strain for production of medically important compounds. © 2017 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/).

Members of Streptomyces genus have received considerable attention and sparked interest among pharmaceutical industry as they are capable of synthesizing compounds of diverse structures with bioactivities including antibiotics, anti-rejection (immunosuppressant), antioxidant and anticancer.1–5 Streptomyces mangrovisoli MUSC 149T was previously isolated as a novel streptomycete with antioxidant potential from mangrove forest in east coast of Peninsular Malaysia6–7 and the strain has been deposited at two culture collection centers (=MCCC 1K00252T = DSM 42140T). Thus, the strain MUSC 149T was selected for genome sequencing as an attempt to identify biosynthetic gene clusters associated with secondary metabolite production.

*Corresponding author at: School of Pharmacy, Monash University Malaysia, 47500 Bandar Sunway, Selangor Darul Ehsan, Malaysia.
E-mails: lee.learn.han@monash.edu, leelearnhan@yahoo.com (L. Lee).
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Table 1 – General features of Streptomyces mangrovisoli MUSC 149T genome.

<table>
<thead>
<tr>
<th>Feature</th>
<th>Streptomyces mangrovisoli MUSC 149T</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome size (bp)</td>
<td>9,165,825</td>
</tr>
<tr>
<td>Contigs</td>
<td>199</td>
</tr>
<tr>
<td>Contigs N50 (bp)</td>
<td>108,867</td>
</tr>
<tr>
<td>G+C content %</td>
<td>72.5</td>
</tr>
<tr>
<td>Protein coding genes</td>
<td>7461</td>
</tr>
<tr>
<td>tRNA</td>
<td>69</td>
</tr>
<tr>
<td>rRNA</td>
<td>4 (55), 1 (165), 1 (235)</td>
</tr>
</tbody>
</table>

content of 72.5%. The whole genome project of MUSC 149T was deposited at DDBJ/EMBL/GenBank under accession number LAVA00000000 and the version described in this paper is the second version (LAVA00000000).

Gene prediction was performed using Prodigal version 2.6, whereas RNA and tRNA were predicted using RNAmer and tRNAscan SE version 1.21.10–12 The assembly was uploaded for annotation to Rapid Annotation using Subsystem Technology (RAST).13 A total of 7461 protein-encoding genes was predicted and assigned to 442 subsystems, along with 69 tRNA and 6 rRNA genes (Fig. 1). Among the subsystems, most of the genes were involved in amino acids and derivatives metabolism (8.97%), followed by carbohydrates metabolism (8.40%) and cofactors, vitamins, prosthetic groups, pigments metabolism subsystems (4.91%).

In order to investigate its bioactive potential, the genome of MUSC 149T was further analyzed using antibiotics & Secondary Metabolite analysis shell (antiSMASH) version 3.0.14 The antiSMASH server revealed 21 gene clusters related to antibiotics and secondary metabolite biosynthesis, with four clusters showed more than 70% similarities to known gene clusters: venezuelin biosynthetic gene cluster (75%), ecode biosynthetic gene cluster (75%), desferrioxamine B biosynthetic gene cluster (83%), and hopen biosynthetic gene cluster (85%). Previously, extract of MUSC 149T was found to possess antioxidant activity; the presence of siderophores biosynthetic gene clusters such as desferrioxamine B has further highlight the antioxidant potential of strain MUSC 149T.

In conclusion, we report the draft genome sequence of S. mangrovisoli MUSC 149T. The availability of its genome sequence has revealed production of potentially medically useful compounds and certainly deserves further detailed study.
Conflicts of interest

The authors declare no conflicts of interest.

Acknowledgments

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References