Genome announcement

Complete genome sequence of Serratia fonticola DSM 4576T, a potential plant growth promoting bacterium

Yan-Lue Lim a, Delicia Yong b, Robson Ee a, Thiba Krishnan a, Kok-Keng Tee b, Wai-Fong Yin a, Kok-Gan Chan a,∗

a Division of Genetics and Molecular Biology, Institute of Biological Sciences, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia
b Department of Medicine, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia

A R T I C L E   I N F O
Article history:
Received 5 September 2015
Accepted 10 September 2015
Available online 12 September 2015

Keywords:
Serratia fonticola
Complete genome sequence
Plant growth promoting bacteria

A B S T R A C T
Here, we present the first complete genome sequence of Serratia fonticola DSM 4576T, a potential plant growth promoting (PGP) bacterium which confers solubilization of inorganic phosphate, indole-3-acetic acid production, hydrogen cyanide production, siderophore production and assimilation of ammonia through the glutamate synthase (GSGOGAT) pathway. This genome sequence is valuable for functional genomics and ecological studies which are related to PGP and biocontrol activities.

© 2015 Elsevier B.V. All rights reserved.

Bacteria with plant growth promoting (PGP) activities are biotechnologically important to enhance crop yields and to sustain a long term ecological balance in the agro-ecosystem (Trivedi et al., 2012). PGP bacteria enhance plant growth and development by facilitating the uptake of nutrients from the environment, producing secondary metabolites (siderophore/phytohormone) to improve yield quantity and quality, protecting plants against infections and aiding in tolerance against abiotic stresses (Zahir et al., 2003). Members of Serratia are well known for their PGP properties, namely Serratia marcescens (Chakraborty et al., 2010; George et al., 2013), Serratia plymuthica (Neupane et al., 2012), Serratia sp. SYS (Koo and Cho, 2009) and Serratia fonticola AU-P3(3) (Devi et al., 2013). In this work, we report for the first time, the complete genome sequence of S. fonticola DSM 4576T.

Genomic DNA was extracted using Masterpure™ DNA Purification Kit (EPICENTRE Inc., Madison, WI, USA) and was converted into 10 kb SMRTbell™ template library according to the manufacturer’s instruction. Using P4C2 sequencing chemistry, DNA sequencing was performed using Pacific Biosciences (PacBio) RSII sequencer in four Single Molecule Real Time (SMRT) cells. The resulting 217.24 fold coverage sequencing reads were then de novo assembled using Hierarchical Genome Assembly Process (HGAP) algorithm version 3. The assembled GC-rich (53.60%) single circular contig of 6,000,511 bp (Table 1) was functionally annotated with NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 2.10, PROKKA pipeline (Seemann, 2014) and Rapid Annotation using Subsystem Technology (RAST) version 2.0 (Aziz et al., 2008). Additionally, a local BLASTP run was carried in search of genes of interest.

Table 1

<table>
<thead>
<tr>
<th>Features</th>
<th>Chromosome</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genomic size (bp)</td>
<td>6,000,511</td>
</tr>
<tr>
<td>GC content (%)</td>
<td>53.60</td>
</tr>
<tr>
<td>ORFs</td>
<td>5336</td>
</tr>
<tr>
<td>Contigs</td>
<td>1</td>
</tr>
<tr>
<td>tRNA genes</td>
<td>22</td>
</tr>
<tr>
<td>rRNA genes</td>
<td>83</td>
</tr>
</tbody>
</table>

Sequence analysis of the genome of S. fonticola DSM 4576T revealed the presence of various genes which are associated to PGP traits. These genes are polyphosphate kinase [EC 2.7.4.1] and phosphate inorganic transporter which are responsible for the solubilization of inorganic phosphate; indole-3-pyruvate decarboxylase [EC 4.1.1.74] which is responsible for phytohormone indole-3-acetic acid production; isochorismate synthase [EC 5.4.4.2] and pyruvate lyase [EC 4.1.3.40] that are needed for the production of salicylic acid that plays a crucial role in response to pathogenic invaders and abiotic stresses (Rivas-San Vicente and Plasencia, 2011); hydrogen cyanide synthases, hcnA, hcnB and hcnC [EC 1.4.99.5], which are needed for hydrogen cyanide (HCN) production; glutamine synthetase genes: glnA [EC 6.3.1.2], glnL
[EC 2.7.13.3] and glnG/ntrC which are involved in the glutamate synthase/glutamine oxoglutarate aminotransferase (GS/GOGAT) pathway. The availability of this complete genome sequence of S. fonticola DSM 45761 provides the basis for biotechnological exploitation of this bacterium for its application in the agriculture.

**Nucleotide sequence accession numbers**

This whole-genome project has been deposited at DDBJ/EMBL/GenBank under the accession number CP011254.1.

**Acknowledgements**

This work received the financial support from the University of Malaya-Ministry of Higher Education High Impact Research Grants (UM-MOHE HIR Grant UM.C/625/1/HIR/MOHE/CHAN/01, no. A000001-50001, UM-MOHE-HIR Grant UM.C/625/1/HIR/MOHE/CHAN/14/1, H-50001-A000027) which was awarded to Kok-Gan Chan.

**References**


