<table>
<thead>
<tr>
<th>Title</th>
<th>Draft genome sequence of Thauera sp. strain SWB20, isolated from a Singapore wastewater treatment facility using gel microdroplets</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Dichosa, Armand E. K.; Davenport, Karen W.; Li, Po-E.; Sanaa A. Ahmed; Daligault, Hajnalka; Gleasner, Cheryl D.; Kunde, Yuliya; McMurry, Kim; Lo, Chien-Chi; Reitenga, Krista G.; Daughton, Ashlynn R.; Shen, Xiaohong; Frietze, Seth; Wang, Dongping; Johnson, Shannon L.; Drautz-Moses, Daniela Isabel; Schuster, Stephan; Chain, Patrick S.; Han, Cliff</td>
</tr>
<tr>
<td>Date</td>
<td>2015</td>
</tr>
<tr>
<td>URL</td>
<td><a href="http://hdl.handle.net/10220/50058">http://hdl.handle.net/10220/50058</a></td>
</tr>
<tr>
<td>Rights</td>
<td>© 2015 Dichosa et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.</td>
</tr>
</tbody>
</table>
Draft Genome Sequence of *Thauera* sp. Strain SWB20, Isolated from a Singapore Wastewater Treatment Facility Using Gel Microdroplets


Bioscience Division, Los Alamos National Laboratory, Los Alamos, New Mexico, USA; Singapore Centre on Environmental Life Sciences Engineering, Nanyang Technological University, Singapore

* Present address: Krista G. Reitenga, University of Maryland School of Medicine, Baltimore, Maryland, USA; Ashlynn R. Daughton, Defense Systems and Analysis, Los Alamos National Laboratory, Los Alamos, New Mexico, USA; Xiaohong Shen, Beacon Analytical System, Inc., Saco, Maine, USA; Seth Frietze, College of Natural and Health Sciences, University of Northern Colorado, Greeley, Colorado, USA.

We report here the genome sequence of *Thauera* sp. strain SWB20, isolated from a Singaporean wastewater treatment facility using gel microdroplets (GMDs) and single-cell genomics (SCG). This approach provided a single clonal microcolony that was sufficient to obtain a 4.9-Mbp genome assembly of an ecologically relevant *Thauera* species.

Species of the betaproteobacterial *Thauera* genus have been characterized as being able to aerobically (1–3) or anaerobically (4–7) degrade aromatic compounds under denitrifying conditions, as well as to oxidize organic acids and alcohols (8). Due to the potential of *Thauera* species in bioremediation applications and for their ability to produce exopolysaccharides (9), much interest has been focused on assembling and annotating the genomes of these ecologically relevant bacterial species. Interestingly, all the currently available *Thauera* sp. genomes were obtained from isolates from sludge/wastewater treatment facilities (9,10).

Recently, our team utilized the combined technologies of gel microdroplets (GMDs) and single-cell genomics (SCG) to obtain several near-complete genomes of novel bacterial species inhabiting the human oral and gut microbiomes (11,12). We applied this approach to coculture a complex sewage wastewater microbial community to attempt the recovery of as many diverse bacterial representatives as possible. We flow-sorted 176 GMDs and then subjected each to whole-genome amplification and bacterial 16S rRNA sequencing (11). We found that SWB20 clustered with MZ1T and S2, while MZ1T and S2 are more closely related (data not presented). Our SNP analysis yielded a core genome size of 1,064,233 bp across all seven *Thauera* strains. Both the close phylogeny and very low SNP differences compared to MZ1T and S2 suggest that SWB20 may be a unique *T. aminoaromatica* strain. Compared to the remaining *Thauera* sp. genomes, SWB20 averaged ~10% SNP composition (data not shown).

Nucleotide sequence accession numbers. The draft genome sequence of *Thauera* sp. strain SWB20 has been deposited as a whole-genome shotgun project at DDBJ/EMBL/GenBank under the accession no. JTDM00000000 (BioProject ID PRJNA267225). The version described in this paper is version JTDM01000000.
ACKNOWLEDGMENTS

We thank Steve Turner of Pacific Biosciences for supplying the PacBio sequencing materials. This genome-sequencing project was partially supported by the Los Alamos National Laboratory through the Laboratory Directed Research and Development Fund, grant 20100034DR. It was released under grant LA-UR-14-23425.

REFERENCES


