Draft Genome Sequences of Supercritical CO\textsubscript{2}\-Tolerant Bacteria Bacillus subterraneus MITOT1 and Bacillus cereus MIT0214

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<td><a href="http://dx.doi.org/10.1128/genomeA.00140-15">http://dx.doi.org/10.1128/genomeA.00140-15</a></td>
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<tr>
<td>Publisher</td>
<td>American Society for Microbiology</td>
</tr>
<tr>
<td>Version</td>
<td>Final published version</td>
</tr>
<tr>
<td>Accessed</td>
<td>Sun Apr 24 20:15:56 EDT 2016</td>
</tr>
<tr>
<td>Citable Link</td>
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We report draft genome sequences of *Bacillus subterraneus* MITOT1 and *Bacillus cereus* MIT0214 isolated through enrichment of samples from geologic sequestration sites in pressurized bioreactors containing a supercritical (sc) CO₂ headspace. Their genome sequences expand the phylogenetic range of sequenced bacilli and allow characterization of molecular mechanisms of scCO₂ tolerance.

During geologic carbon sequestration (GCS), large quantities of CO₂ are captured, compressed to supercritical (sc) state, and injected underground. Whether microbial activities transform injected CO₂ is not well understood due to toxic effects of scCO₂ (1–5). Samples from GCS sites at Otway Basin, Australia and Frio-2, Texas, were used as inocula for serial enrichment cultures in bioreactors containing scCO₂, yielding strains *Bacillus subterraneus* MITOT1 and *Bacillus cereus* MIT0214, respectively (6). Tolerance of scCO₂ was confirmed by growth of spores in pure cultures and was time and inocula density dependent. To investigate mechanisms of growth under scCO₂, genomic DNA was sequenced.

MITOT1 was sequenced on the Illumina HiSeq 2000 platform (Beijing Genomics Institute). MIT0214 was sequenced on the Illumina GAIIx platform (MIT Biomicrocenter). Paired-end sequencing for strain MIT0214. We thank the MIT Center for Environmental Health Sciences (U.S. National Institute of Environmental Health Sciences (NIEHS) grant P30-ES002109) for Illumina core facility support.

**ACKNOWLEDGMENTS**

Funding for experimental work was provided to J.R.T. by the Department of Energy Office of Fossil Energy under award DE-EE0002128 and by the MIT Energy Initiative. Drilling and coring activities were carried out through the Frio-2 project (U.S. Department of Energy), CO2CRC project (Australian government).

Samodha Fernando and Hector Hernandez assisted with genome sequencing for strain MIT0214. We thank the MIT Center for Environmental Health Sciences (U.S. National Institute of Environmental Health Sciences NIEHS) grant P30-ES002109 for Illumina core facility support.

**REFERENCES**


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