

# Draft Genome Sequence of *Anoxybacillus* Strain BCO1, Isolated from a Thermophilic Microbial Mat Colonizing the Outflow of a Bore Well of the Great Artesian Basin of Australia

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***Anoxybacillus* strain BCO1, isolated from a thermophilic (50°C) microbial mat colonizing an outflow of a Great Artesian bore well of Australia, possessed a genome of ~2.8 Mb, with a G+C content of 41.7 mol%, and encoded 3,205 genes.**

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The Great Artesian Basin (GAB) of Australia is the largest fresh and deepest subsurface geothermal water reservoir in the world. The water is used for agriculture and exploited for oil and gas. The aquifer is heated indirectly by the earth's magmatic core up to boiling, and the water chemistry is influenced by the surrounding geologic formation (1), and this variation in temperature and chemistry makes the GAB an ideal ecosystem for investigations of thermophilic *Bacteria* and *Archaea* (2, 3).

*Anoxybacillus* strain BCO1 was isolated from a sample collected from a 50°C microbial mat colonizing a bore well outflow channel (2, 3). The strain was cultured in Medium D (4) under optimal growth conditions (50°C and pH 7.5) to mid-late log growth phase, the cells were centrifuged, and the DNA from the cell pellet was purified (5, 6). The genomic DNA of strain BCO1 consisting of 632,994 reads totaling 112 Mbp (112,602,909 bp) was generated using an Ion Torrent PGM sequencer and a 318 chip at the Australian Genome Research Facility (AGRF) core facility. High-quality filtered data was assembled using GS De Novo Assembler version 2.8; the generated genome of ~2.8 Mbp (34× coverage) consisting of 102 contigs with an average G+C content of 41.7 mol% was analyzed using RAST (7); gene annotation was done using Prokka version 1.10 (8); average nucleotide analysis was done with JSpecies (9); and e-DNA-DNA hybridization (e-DDH) was done using the Genome-to-Genome Distance Calculator (GGDC; <http://ggdc.dsmz.de>) (10).

RAST analysis predicted that the genome sequence comprised 3,205 putative protein-encoding genes, 47 tRNA genes, and 9 rRNA genes (5S rRNA, 16S rRNA, 23S rRNA). Of the 3,205 predicted proteins, 2,539 could be assigned probable biological functions, and the remaining 666 could not be assigned functions or were hypothetical proteins. Genes involved in the anaerobic metabolism of carbohydrates with putative proteins for the production of mixed acid and lactic acid as well as an electron transport chain involved in aerobic growth were identified, providing evidence of the strain's heterotrophic and facultative anaerobic nature.

Strain BCO1 clustered with *A. flavithermus* strain 25, *Anoxybacillus* sp. strains SK3-4 and DT3, and *A. kamachatensis* strain G10 (ANIb value, >94%). e-DDH between strain BCO1 and

*A. flavithermus* strain 25 and *Anoxybacillus* sp. strain SK3-4 was 75%, whereas for *Anoxybacillus* sp. strain DT3 and *A. kamachatensis* strain G10 the values were 46% and 43%, respectively. However, interestingly, genes that encode the respiratory nitrate reductase complex are absent in strain BCO1, which is in common with *A. flavithermus* strain 25 and *Anoxybacillus* sp. strains SK3-4 and DT3 but different from *A. kamachatensis* strain G10, which is reported to possess these genes (11). A more detailed comparative analysis of strain BCO1 with the related four strains will provide further insights into its adaptation and life in the thermophilic microbial mat community of a nonvolcanic thermal ecosystem.

**Nucleotide sequence accession numbers.** The *Anoxybacillus* isolate BCO1 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JRLC000000000](https://www.ncbi.nlm.nih.gov/nuclseq/JRLC000000000). The version described in this paper is version [JRLC010000000](https://www.ncbi.nlm.nih.gov/nuclseq/JRLC010000000).

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