# Draft genome sequence of Microbacterium sp. TNHR37B isolated from a heated aquifer bore well of the Great Artesian Basin, Australia

AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

# Draft Genome Sequence of *Microbacterium* sp. TNHR37B Isolated from a Heated Aquifer Bore Well of the Great Artesian Basin, Australia

**Joseph Adelskov,[a] Bharat K. C. Patel[b]**

School of Natural Sciences, Griffith University, Brisbane, Queensland, Australia[a]; School of Earth, Environment and Biological Sciences, Queensland University of Technology, Brisbane, Queensland, Australia[b]

**ABSTRACT** *Microbacterium* sp. strain TNHR37B was isolated from a geothermal bore well sample (50°C) collected from a region of coal seam gas extraction activities. The 3.5-Mb genome with a G+C content of 69.9% contained unique genes, and a low similarity value for average nucleotide identity using BLAST was observed with the available 73 *Microbacterium* sp. genomes.

**Received** 3 March 2017 **Accepted** 7 March 2017 **Published** 27 April 2017

**Citation** Adelskov J, Patel BKC. 2017. Draft genome sequence of *Microbacterium* sp. TNHR37B isolated from a heated aquifer bore well of the Great Artesian Basin, Australia. Genome Announc 5:e00251-17. https://doi.org/10.1128/genomeA.00251-17.



Address correspondence to Bharat K. C. Patel, bharatgu19@gmail.com.

*Microbacterium* sp. strain TNHR37B was isolated on media D (1) enriched with natural gas from a sample collected from a high-temperature bore well (50°C) located in Surat basin near the town of Bundi, Queensland, Australia. Routine cultivation was in aerobic TYEG medium, which contained mineral salts (2) and 0.2% each of tryptone, yeast extract, and glucose. BLAST analysis of the 16S rRNA gene sequence of strain TNHR37B (815 bp) revealed that it was closely related to *Microbacterium lacticum* strain DSM 20427 (98% similarity). The genus *Microbacterium*, originally proposed by Orla-Jensen (3) is a member of the family *Microbacteriaceae*, phylum *Actinobacteria*, and currently comprises 96 species (http://www.bacterio.net). Here, we report the draft genome sequence of *Microbacterium* sp. strain TNHR37B.

TNHR37B was grown to late log phase in aerobic TYEG medium, and high-molecular-weight DNA was extracted using a modification of Marmur's method (4). A TruSeq library, constructed from the DNA and sequenced on an Illumina MiSeq platform at the Australian Genome Research Facility (AGRF), produced 1,245,912 paired-end reads of 250-bp length but was reduced to 1,201,672 reads after quality filtering (total 60,083,600 bp). *De novo* genome assembly using SPAdes version 3.5.0 (5) produced a draft assembly consisting of four large contigs ($N_{50}$ = 1,357,620 bp; mean coverage of 159×) with a genome size of 3,518,558 bp and a G+C content of 69.9%. Annotation of the draft genome sequence using Prokka version 1.12b (6) identified 3,276 open reading frames consisting of 54 RNA genes and 3,222 protein-coding sequences.

Comparative analysis of the genome sequence of *Microbacterium* sp. strain TNHR37B using average nucleotide identity (100-bp fragment, BLAST method; ANIb) revealed that the *Microbacterium* sp. AO20al1 genome (ANIb identity of 92.19%) was the most similar and that the additional 73 *Microbacterium* sp. genomes that were available in GenBank at the time of analysis shared a much lower ANIb identity (between 83.55 and 86%). These ANIb values are well below the proposed bacterial species demarcation threshold of 95 to 96% and correspond to a 16S rRNA gene similarity value of 98.65% (7). The RAST annotation pipeline (8) revealed that *Microbacterium* sp. TNHR37B contained genes related to one-carbon metabolism, fermentation, metabolism of aromatic compounds, osmotic stress, heat shock, and detoxification. as well as genes involved in the metabolism and utilization of mannose, fructose, L-rhamnose, L-fucose, xylose,

L-arabinose, D-ribose, mannitol, glycogen, glycerol, lactate, and chitin. Further comparative analysis of the draft genome with the four closest *Microbacterium* sp. genomes, including strain AO20a11, identified 278 genes unique to strain TNHR37B. These unique genes were annotated as metallo-beta-lactamase, alpha-galactosidase (three genes), putative aminoglycoside nucleotidyltransferase, phosphoesterase, chromate transport protein, o-methyltransferase, predicted glycoside hydrolase, aminoglycoside phosphotransferase, coenzyme F420-dependent oxidoreductase, UDP-glucose dehydrogenase, FAD-dependent oxidoreductase, cellobiose phosphotransferase, and putative integral and ABC membrane transporter proteins. The uniqueness of these genes to the *Microbacterium* genus was confirmed by PSI-BLAST against the NCBI NR database.

**Accession number(s).** This whole-genome shotgun project was deposited in DDBJ/ENA/GenBank under the accession number LQGV00000000. The version described in this paper is the first version, LQGV01000000.

## ACKNOWLEDGMENTS

An Australian Postgraduate Award (APA) scholarship to J.A. and the IT infrastructure for genomics provided by the National eResearch Collaboration Tools and Resources (NeCTAR) Project to B.K.C.P. are gratefully acknowledged.

## REFERENCES

1. Brock TD, Freeze H. 1969. *Thermus aquaticus* gen. n. and sp. n., a nonsporulating extreme thermophile. J Bacteriol 98:289–297.
2. Ogg CD, Patel BKC. 2009. *Caloramator australicus* sp. nov., a thermophilic, anaerobic bacterium from the Great Artesian Basin of Australia. Int J Syst Evol Microbiol 59:95–101. https://doi.org/10.1099/ijs.0.000802-0.
3. Takeuchi M, Hatano K. 1998. Union of the genera *Microbacterium* Orla-Jensen and *Aureobacterium* Collins et al. in a redefined genus *Microbacterium*. Int J Syst Bacteriol 48:739–747. https://doi.org/10.1099/00207713-48-3-739.
4. Marmur J. 1961. A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J Mol Biol 3:208–218. https://doi.org/10.1016/S0022-2836(61)80047-8.
5. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
6. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.
7. Kim M, Oh HS, Park SC, Chun J. 2014. Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. Int J Syst Evol Microbiol 64:346–351. https://doi.org/10.1099/ijs.0.059774-0.
8. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics 9:75. https://doi.org/10.1186/1471-2164-9-75.