Draft Genome Sequence of a Dictyoglomus sp. from an Enrichment Culture of a New Zealand Geothermal Spring

Anna-Louise Reysenbach  
*Portland State University*, reysenbacha@pdx.edu

John A. Donaho  
*Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA*

John F. Kelley  
*Portland State University*

Emily St. John  
*Portland State University*

Christina Turner  
*Portland State University*

Follow this and additional works at: https://pdxscholar.library.pdx.edu/bio_fac

Part of the Biology Commons, and the Genetics and Genomics Commons

Let us know how access to this document benefits you.

**Citation Details**


This Article is brought to you for free and open access. It has been accepted for inclusion in Biology Faculty Publications and Presentations by an authorized administrator of PDXScholar. Please contact us if we can make this document more accessible: pdxscholar@pdx.edu.
Authors
Anna-Louise Reysenbach, John A. Donaho, John F. Kelley, Emily St. John, Christina Turner, Mircea Podar, and Matthew B. Stott

This article is available at PDXScholar: https://pdxscholar.library.pdx.edu/bio_fac/207
Draft Genome Sequence of a *Dictyoglomus* sp. from an Enrichment Culture of a New Zealand Geothermal Spring

Anna-Louise Reysenbach, John A. Donaho, John F. Kelley, Emily St. John, Christina Turner, Mircea Podar, Matthew B. Stott

*Biology Department, Portland State University, Portland, Oregon, USA*

*Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA*

*School of Biological Sciences, University of Canterbury, Christchurch, New Zealand*

**ABSTRACT** A draft genome of a novel *Dictyoglomus* sp., NZ13-RE01, was obtained from a New Zealand hot spring enrichment culture. The 1,927,012-bp genome is similar in both size and G+C content to other *Dictyoglomus* spp. Like its relatives, *Dictyoglomus* sp. NZ13-RE01 encodes many genes involved in complex carbohydrate metabolism.

*Dictyoglomus* spp. form a distinct bacterial phylum, with only two described species with genome sequences, *D. turgidum* (1) and *D. thermophilum* (2, 3). *Dictyoglomus* spp. have been detected in thermophilic environments, such as terrestrial hot springs (2, 4–8) and paper pulp factory effluent (9), and they have an unusual morphology consisting of large spherical bodies assembled from bundles of filamentous cells (2, 5, 9). *Dictyoglomus* spp. are of industrial interest due to their capability to ferment a wide range of complex carbohydrates, including starch, cellulose, xylan, and pectin (2, 8, 10, 11). Due to the low number of representative genomes, their phylogenetic placement within the domain *Bacteria* is not certain as *Dictyoglomus* spp. are, although they appear to be affiliated most closely with a cluster containing *Coprothermobacter*, *Synergistes*, *Acetothermia*, and *Thermotogales* (1, 12, 13).

We obtained a genome of a novel *Dictyoglomus* sp., NZ13-RE01, from a New Zealand hot spring enrichment culture (Hell’s Gate, Tikitere, New Zealand, 38°03’47”S, 176°21’39”E, pH 6.0, 74°C). Enrichments were incubated at 80°C for 4 days in a modified anaerobic DSMZ medium (no. 88) containing yeast extract (0.5 g/liter) and tryptone (0.5 g/liter). Spherical bodies were apparent in the enrichment cultures by phase-contrast microscopy. DNA was extracted using the Qiagen DNeasy blood and tissue kit. Metagenome Nextera DNA libraries were sequenced on the Illumina MiSeq platform. Adapters and low-quality reads were trimmed using Trimmomatic (14), reads were assembled with IDBA-UD version 1.1.0 (15, 16), and contigs ≥1 kb were binned using MaxBin version 1.4.5 (17). To optimize the assembly, the reads were mapped back to the *Dictyoglomus* sp. NZ13-RE01 draft genome using Bowtie2 version 2.2.5 (18) and SAMtools version 1.2 (19, 20) and reassembled with IDBA-UD. The genome was further curated using emergent self-organizing maps (21). Open reading frames were annotated using the Rapid Annotations using Subsystems Technology (RAST) server (22–24), the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (25), the Clusters of Orthologous Groups of proteins (COG) database (26), and the dbCAN database (27). tRNAs were predicted with tRNAscan-SE version 2.0 (28).

Based on CheckM (29) analysis, the *Dictyoglomus* sp. NZ13-RE01 genome is about 100% complete with no contamination. The 1,927,012-bp genome consists of 34 contigs, with a 33% G+C content, 1,870 predicted protein-coding genes, and 48 tRNAs. The *Dictyoglomus* sp. NZ13-RE01 genome has an average nucleotide identity (ANI) score of 74% and an average amino acid identity (AAI) score of 65% compared to the

Received 3 February 2018  Accepted 13 February 2018  Published 15 March 2018


Copyright © 2018 Reysenbach et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Anna-Louise Reysenbach, reysenbacha@pdx.edu.
genomes of both *D. turgidum* and *D. thermophilum* (30, 31). Further, Circos synteny plots (32) show that the *Dictyoglomus* sp. NZ13-RE01 genome does not share the highly syntenic genome arrangement found between *D. turgidum* and *D. thermophilum* (1). Considering the dissimilarity in genome nucleotide and amino acid sequences, and the low synteny in genome arrangement between NZ13-RE01 and either of the described *Dictyoglomus* spp., it is likely that NZ13-RE01 represents a new species within the genus *Dictyoglomus*.

The *Dictyoglomus* sp. NZ13-RE01 genome encodes an extensive suite of carbohydrate metabolism genes (63 glycosyl hydrolases, 10 carbohydrate esterases, and 28 glycosyltransferases), including α-amylases, α-xylodidas, a chitinase, endo-1,4-β-xylanases, and a β-mannanase. Like other *Dictyoglomus* spp., the genome has a reverse gyrase. The sporulation gene, spoIVS, was also present and has been proposed to play a role in morphological changes in *Dictyoglomus* spp. (1).

**Accession number(s).** The nucleotide genome sequence reported here has been deposited in DDBJ/ENA/GenBank under the accession no. NIRF00000000. The version described in this paper is the first version, NIRF01000000.

**ACKNOWLEDGMENTS**

We thank Yitali Liu for assistance with the enrichment cultures and Kristen Brileya and Jennifer Meneghin for assistance in the initial stages of the project. We thank Haley Nasman for her assistance in metagenomic analysis. We also thank the Tikitere Trust (Whakapoungakau 24) for its continued support and for sampling access in the Hell’s Gate geothermal area.

This work was funded by the National Science Foundation (grant no. DEB 1134877 to A.-L.R. and M.P.) and by the Geothermal Resources of New Zealand research program at GNS Science (to M.B.S.).

**REFERENCES**


