



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

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**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  $\geq 1$  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

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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  $\alpha$ -amylases,  $\alpha$ -xylosidases, a chitinase, endo-1,4- $\beta$  xylanases, and a  $\beta$ -mannanase. Like other *Dictyoglomus* spp., the genome has a reverse gyrase. The sporulation gene, *spoVS*, 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. [NIRF0000000](https://doi.org/10.3389/fmicb.2016.01979). The version described in this paper is the first version, NIRF01000000.

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