



# Draft Genome Sequence of *Leifsonia poae* Strain BS71, Isolated from a Drought Microcosm

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**ABSTRACT** We report the draft genome sequence of *Leifsonia poae* strain BS71. This bacterium was isolated from a low soil moisture content model soil microcosm inoculated with forest soil that had been subject to chronic warming.

Climate change is expected to increase drought conditions globally (1). To examine climate effects on soils, a field warming experiment was established in the Harvard Research Forest (HRF), a temperate forest ecosystem in Petersham, MA (42.54°N, −72.18°W) (2). In October 2017, mineral horizon soil was collected from heated plots. A microcosm was generated by inoculating a 0.8-μm filtered soil slurry into an artificial soil microcosm at 30% water content and incubating it for 4 months at 15°C, feeding it weekly with cellobiose and NH<sub>4</sub>NO<sub>3</sub>, as described previously (3). These conditions were hypothesized to enrich for bacteria capable of growing in low soil moisture. Strain BS71 was isolated from the microcosm on a 1% glucose/0.4% potato infusion (Sigma-Aldrich, St. Louis, MO) agar plate, pH 6, under aerobic conditions for 8 days at 25°C in the dark. BS71 was identified as *Leifsonia poae* by analyzing the 16S rRNA PCR product produced with the 27F/1492R primer pair (4) using IDTAXA (5).

BS71 DNA was prepared for sequencing by growing a single colony on 10% tryptic soy agar at 25°C for 7 days in the dark, scraping the biomass, and extracting the DNA using the Qiagen genomic DNA protocol (Valencia, CA). Whole-genome sequencing was completed at the University of Massachusetts Medical School (UMMS) sequencing center. The DNA was sheared using a Bioruptor device (Diagenode, NJ) to a mean size of 20 kb. A PacBio SMRTbell library kit was used to construct a library, which was sequenced on the PacBio RS II platform. The 150,292 raw reads, generated from a single cell, were filtered using the SMRT portal P-filter module (minimum subread length, 50 nucleotides; minimum polymerase quality, 75; and minimum polymerase read length, 50 nucleotides), and the resultant 69,059 filtered reads had a read *N*<sub>50</sub> value of 7,302 bases.

The genome was assembled using *sprai* v0.9.9.23 (<https://anaconda.org/bioconda/sprai>) and *Canu* v1.5 (6). The final draft assembly contained 5 contigs (contig *N*<sub>50</sub>, 3.98 Mb) and was estimated to be 98.99% complete and 0.063% contaminated using CheckM v1.0.18 (7) in KBase (8). Gene annotations were completed within JGI's Integrated Microbial Genomes (IMG) MGAP v4.16.5 (9) with the gene calling program Prodigal v2.6.3 (10, 11). Default parameters were used for all software except where noted. The genome is 4,144,138 bp (coverage, 94.3×), with a GC content of 67.84%, and is predicted to encode 3,961 proteins, a single rRNA operon, and 45 tRNA genes.

A manually curated list of drought-associated genes was compared between BS71 and the 20 *Leifsonia* genomes with the greatest 16S rRNA gene homology within IMG's database. A greater number of beta-glucosidase (EC 3.2.1.21) annotated genes were present in BS71 (24 genes), compared to 10 or fewer such annotated genes in the other *Leifsonia* (Table 1). Beta-glucosidase enzymes are diverse and play an important

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**TABLE 1** Protein-protein BLAST results for beta-glucosidase (EC 3.2.1.21) annotated genes

GeneID	Taxon identified by BLASTp highest score	Identity (%)	No. of amino acids	IMG annotation description
2806535936	<i>Humibacter</i> sp. strain WJ7-1	71	846	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806536034	<i>Streptacidiphilus fuscans</i>	63	401	Family 1 glycosyl hydrolase
2806536039	<i>Leifsonia shinshuensis</i>	70	96	Family 1 glycosyl hydrolase
2806536324	<i>Microbacterium azadirachtae</i>	60	788	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806536495	<i>Leifsonia shinshuensis</i>	84	599	Glycoside hydrolase family 3 protein
2806536706	<i>Leifsonia</i> sp. strain NCR5	81	831	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806536737	<i>Frondihabitsans</i> sp. strain 762G35	73	776	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806536747	<i>Leifsonia</i> sp. strain Root227	94	391	Family 1 glycosyl hydrolase
2806536801	<i>Leifsonia</i> sp. strain NCR5	82	617	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806537199	<i>Leifsonia</i> sp. strain PS1209	79	501	Beta-glucosidase
2806537254	<i>Plantibacter flavus</i>	65	592	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806537278	<i>Microbacterium</i> sp. strain Root61	91	761	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806538045	<i>Rathayibacter</i> sp. strain AY1A3	67	805	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806538050	<i>Nonomuraea</i> sp. strain 160415	61	403	Family 1 glycosyl hydrolase
2806538065	<i>Thermocatellispora tengchongensis</i>	70	746	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806538066	<i>Microbacteriaceae bacterium</i>	78	389	Glycosyl hydrolase family protein
2806538078	<i>Thermocatellispora tengchongensis</i>	64	797	Beta-glucosidase
2806538079	Unclassified <i>Leifsonia</i>	77	609	MULTISPECIES: glycoside hydrolase family 3 C-terminal domain-containing protein
2806538223	<i>Plantibacter</i> sp. strain YR521	69	781	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806535250	<i>Actinoplanes</i> sp. strain OR16	68	578	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806535263	<i>Streptomyces</i> sp. strain yr375	83	409	Family 1 glycosyl hydrolase
2806535267	<i>Leifsonia</i> sp. Root227	88	751	ABC transporter substrate-binding protein
2806535268	<i>Leifsonia</i> sp. Root227	86	786	Glycoside hydrolase family 3 C-terminal domain-containing protein
2806534677	<i>Mycobacterium</i> sp.	63	747	Glycoside hydrolase family 3 C-terminal domain-containing protein

role in biomass conversion of recalcitrant carbon (12). The presumptive BS71 drought tolerance is also supported by the annotation of two distinct aquaporin genes and genes for the production and transport of osmoprotectants. This genome supports the hypothesis that the drought conditions characteristic of climate change may select for bacteria with drought-associated traits.

**Data availability.** The 16S PCR product sequence accession number is [OL515151](#). The raw whole-genome sequence reads are available in GenBank under the BioProject accession number [PRJNA745001](#). The Sequence Read Archive (SRA) accession number is [SRR15142240](#), and the nucleotide sequence accession number is [JAIHLP000000000](#). The annotation reported in this study is available at the Joint Genome Institute as the *Leifsonia poae* BS71 first assembly ([https://img.jgi.doe.gov/cgi-bin/m/main.cgi?section=TaxonDetail&page=taxonDetail&taxon\\_oid=2806310494](https://img.jgi.doe.gov/cgi-bin/m/main.cgi?section=TaxonDetail&page=taxonDetail&taxon_oid=2806310494)).

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