

2014

# Draft Genome Sequence of the Lignin-Degrading Burkholderia sp. Strain LIG30, Isolated from Wet Tropical Forest Soil

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## Recommended Citation

Woo, Hannah L.; Utturkar, Sagar; Klingeman, Dawn; Simmons, Blake A.; DeAngelis, Kristen; Brown, Steven D.; and Hazen, Terry C., "Draft Genome Sequence of the Lignin-Degrading Burkholderia sp. Strain LIG30, Isolated from Wet Tropical Forest Soil" (2014). *Genome Announcements*. 309.  
[10.1128/genomeA.00637-14](https://doi.org/10.1128/genomeA.00637-14)

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# Draft Genome Sequence of the Lignin-Degrading *Burkholderia* sp. Strain LIG30, Isolated from Wet Tropical Forest Soil

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***Burkholderia* species are common soil *Betaproteobacteria* capable of degrading recalcitrant aromatic compounds and xenobiotics. *Burkholderia* sp. strain LIG30 was isolated from wet tropical forest soil and is capable of utilizing lignin as a sole carbon source. Here we report the draft genome sequence of *Burkholderia* sp. strain LIG30.**

Received 4 June 2014 Accepted 6 June 2014 Published 19 June 2014

**Citation** Woo HL, Utturkar S, Klingeman D, Simmons BA, DeAngelis KM, Brown SD, Hazen TC. 2014. Draft genome sequence of the lignin-degrading *Burkholderia* sp. strain LIG30, isolated from wet tropical forest soil. *Genome Announc.* 2(3):e00637-14. doi:10.1128/genomeA.00637-14.

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*Burkholderia* species of *Betaproteobacteria* are ubiquitous in the environment and fulfill many different ecological niches. While some strains, like those of the *Burkholderia cepacia* complex, are pathogenic (1), other members of the genus have beneficial uses as biocontrol or bioremediation agents due to their wide array of secreted extracellular products or robust metabolic capabilities (2, 3). The strain presented here, *Burkholderia* sp. strain LIG30, was recently isolated from the protected Luquillo Experimental Rainforest soil in Puerto Rico using alkali lignin as a sole carbon source (4). Very few bacterial species are known to degrade lignin, and therefore this organism may contain novel lignin-degrading genes.

The genome was sequenced using the Illumina MiSeq platform, which generated 4,002,050 paired-end reads of 300-bp length. Quality-based trimming and genome assembly were performed using the CLC Genomics Workbench, version 7.0, to obtain 140 contigs, with an  $N_{50}$  contig size of 84,253 bp. Genes were identified using the Prodigal algorithm (5) as part of the Oak Ridge National Laboratory genome annotation pipeline. The predicted coding sequences were translated and used to search the NCBI nonredundant database, as well as the UniProt, TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. These data sources were combined to assert a product description for each predicted protein. Noncoding genes and miscellaneous features were predicted using tRNAscan-SE (7), RNAMmer (8), Rfam (9), TMHMM (10), and signalP (11).

The draft genome is 5.5 Mb, with a 66.4% G+C content and 4,996 candidate protein-encoding gene models. Putative functions from COG functional groups were assigned to 73% of the candidate genes; 305 of the assigned genes were associated with secondary metabolite biosynthesis, transport, and catabolism. Based on EC numbers from PRIAM, 2 predicted genes encoded multicopper oxidases and 22 encoded putative peroxidases or catalases that may contribute to the lignin-degrading phenotype

of *Burkholderia* sp. strain LIG30. The 16S rRNA gene, detected using RNAMmer 1.2 (12), has 99.41% identity to those from *B. ambifaria* strain AMMD and 99.34% identity to those from *B. cenocepacia* strain MC0-3 and *B. cenocepacia* strain HI2424 (13).

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JGVW00000000. The version described in this paper is version JGVW01000000.

## ACKNOWLEDGMENTS

Brian H. Davison and Antony V. Palumbo provided guidance.

This work was funded by the Genomic Sciences Program of the Office of Biological and Environmental Research (BER), in the U.S. Department of Energy (DOE), under FWP ERKP752, the Biofuels SFA. The Illumina sequencer and computational infrastructure were provided from the Bioenergy Science Center (BESC), funded under grant ERKP695, which is a DOE Bioenergy Research Center supported by BER. Oak Ridge National Laboratory is managed by UT-Battelle, LLC, for the DOE under contract DE-AC05-00OR22725. The portion of the work conducted by the Joint BioEnergy Institute was supported by the Office of Science, Office of Biological and Environmental Research, of the U.S. Department of Energy under contract no. DE-AC02-05CH11231.

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