


Burkholderia cenocepacia Strain CEIB S5-1, a Rhizosphere-Inhabiting Bacterium with Potential in Bioremediation

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***Burkholderia cenocepacia* is considered an opportunistic pathogen from humans and may cause disease in plants. A bioprospection from a plaguicide-contaminated agricultural field in Mexico identified several methyl parathion-degrading bacteria. Here, we report the draft genome sequence of *B. cenocepacia* strain CEIB S5-1, which gave us clues into ecological biodiversity.**

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Burkholderia cenocepacia is an important member of the *B. cenocepacia* complex (BCC), a group of human opportunistic pathogens in patients with cystic fibrosis (1), and it is also widely distributed in the environment, especially in the rhizosphere of crop plants (2). In 2012, Popoca-Ursino (3) reported three new bacterial species of the genus *Burkholderia* isolated from agricultural soil in the state of Morelos, Mexico, and these species have the capability to hydrolyze methyl parathion (MP) and completely degrade *p*-nitrophenol (PNP). From this group, we identified by 16S rRNA phylogenetic analysis *Burkholderia zhejiangensis* strain CEIB S4-3 (4), which completely degraded PNP in 15 h, while *B. cenocepacia* strains CEIB S5-1 and *Burkholderia* sp. S5-2 do the same but in 21 h. These results are relevant, because there are few reports of microorganisms capable of simultaneously hydrolyzing MP and degrading PNP (5–7).

Genomic DNA was obtained using the AxyPrep bacterial genomic DNA miniprep kit (Axygen). The genomic DNA was sequenced in the Genome Analyzer IIX system (Illumina). We obtained a random data set of 26,125,416 paired-end reads, each 72 bases in length. Quality-based trimming was performed with a DynamicTrim (SolexaQA++) perl script, and genome assembly was accomplished using the SPAdes (version 3.1.1) program. The draft genome has 177 contigs, with a calculated 8,055,498 bp of total length and an N_{50} contig size of 170,699 bp. We aligned the draft genome with 41 complete genomes (chromosomes and plasmids) of the *Burkholderia* genus using the NUCmer program. The draft genome of *B. cenocepacia* strain CEIB S5-1 has 92.19, 92.17, 92.12, and 91.82% identity and 6.42, 6.29, 6.69, and 6.15 Mb alignment coverage with the genomes of *B. cenocepacia* HI2424 (3 chromosomes, 1 plasmid, and 7,702,840 bp in length), *B. cenocepacia* AU 1054 (3 chromosomes and 7,279,116 bp in length), *B. cenocepacia* MC0-3 (3 chromosomes and 7,971,389 bp in

length), and *B. cenocepacia* J2315 (3 chromosomes, 1 plasmid, and 8,055,782 bp in length), respectively.

The contigs were analyzed on the RAST server, and 7,390 coding sequences (CDSs) were identified. We also identified the 16S rRNA gene of *B. cenocepacia* strain CEIB S5-1 using the RNAmmer 1.2 server and a comparison with 101 16S rRNA genes of the *Burkholderia* genus and two 16S rRNA genes of the *Ralstonia* genus (outgroup) was made. The sequences were aligned using the MUSCLE server, and a phylogenetic analysis was performed in the MEGA (version 6.1) program with the neighbor-joining algorithm using 1,000 replicates for bootstrapping. Phylogenetic analysis confirms that *B. cenocepacia* strain CEIB S5-1 is closely related to the *B. cenocepacia* species.

The 7,390 predicted CDSs were translated and used for a functional analysis with the Clusters of Orthologous Groups (COG) database. The COG database identified 4,327 proteins (58.55%), 1,507 open reading frames (ORFs) (20.39%) with an identified function and 2,820 ORFs (38.16%) with an uncharacterized function. We are investigating the potential genes involved in PNP and PM degradation.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JTLLT000000000](https://www.ncbi.nlm.nih.gov/nuccore/JTLLT000000000). The version described in this paper is version JTLLT01000000.

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REFERENCES

- Reik R, Spilker T, Lipuma JJ. 2005. Distribution of *Burkholderia cepacia* complex species among isolates recovered from persons with or without

- cystic fibrosis. *J Clin Microbiol* 43:2926–2928. <http://dx.doi.org/10.1128/JCM.43.6.2926-2928.2005>.
2. Bevivino A, Dalmastrì C, Tabacchioni S, Chiarini L, Belli ML, Piana S, Materazzo A, Vandamme P, Manno G. 2002. *Burkholderia cepacia* complex bacteria from clinical and environmental sources in Italy: genomovar status and distribution of traits related to virulence and transmissibility. *J Clin Microbiol* 40:846–851. <http://dx.doi.org/10.1128/JCM.40.3.846-851.2002>.
 3. Popoca-Ursino EC. 2012. Aislamiento de bacterias con capacidad de degradación de plaguicidas organofosforados, evaluación molecular de sus actividades. Tesis de la Maestría en Biotecnología. Centro de Investigación en Biotecnología (CEIB), Universidad Autónoma del Estado de Morelos (UAEM), Toluca, Mexico.
 4. Hernández-Mendoza A, Martínez-Ocampo F, Lozano-Aguirre Beltrán LF, Popoca-Ursino EC, Ortiz-Hernández ML, Sánchez-Salinas E, Dantán-González E. 2014. Draft genome sequence of the organophosphorus compound-degrading *Burkholderia zhejiangensis* strain CEIB S4-3. *Genome Announc* 2(6):e01323-14. <http://dx.doi.org/10.1128/genomeA.01323-14>.
 5. Zhang WM, Zhang JJ, Jiang X, Chao H, Zhou NY. 2015. Transcriptional activation of multiple operons involved in *para*-nitrophenol degradation by *Pseudomonas* sp. strain WBC-3. *Appl Environ Microbiol* 81:220–230. <http://dx.doi.org/10.1128/AEM.02720-14>.
 6. Min J, Zhang JJ, Zhou NY. 2014. The gene cluster for *para*-nitrophenol catabolism is responsible for 2-chloro-4-nitrophenol degradation in *Burkholderia* sp. strain sj98. *Appl Environ Microbiol* 80:6212–6222. <http://dx.doi.org/10.1128/AEM.02093-14>.
 7. Vikram S, Pandey J, Kumar S, Raghava GP. 2013. Genes involved in degradation of *para*-nitrophenol are differentially arranged in form of non-contiguous gene clusters in *Burkholderia* sp. strain sj98. *PLoS One* 8:e84766. <http://dx.doi.org/10.1371/journal.pone.0084766>.