Journal of Bacteriology

Genome Sequence of the Nitroaromatic Compound-Degrading Bacterium Burkholderia sp. Strain SJ98

Shailesh Kumar, Surendra Vikram and Gajendra Pal Singh Raghava

J. Bacteriol. 2012, 194(12):3286. DOI: 10.1128/JB.00497-12.

JB Journals.ASM.org

Genome Sequence of the Nitroaromatic Compound-Degrading Bacterium *Burkholderia* sp. Strain SJ98

Shailesh Kumar, Surendra Vikram, and Gajendra Pal Singh Raghava

Bioinformatics Centre, Institute of Microbial Technology, Council of Scientific and Industrial Research, Chandigarh, India

We report the 7.85-Mb genome sequence of *Burkholderia* sp. strain SJ98, isolated from agricultural fields of Assam, India. The draft genome of this strain will be helpful in studying the genetic pathways involved in the degradation of aromatic compounds.

Burkholderia sp. strain SJ98 was isolated from a pesticide-contaminated soil sample from agricultural fields in Assam, India, by using an enrichment technique developed by Samanta et al. (6). *Burkholderia* sp. SJ98 is known to degrade a number of aromatic compounds, e.g., *p*-nitrophenol, *o*-nitrobenzoate, *p*-nitrobenzoate, and 4-nitrocatechol (4), 2-chloro-4-nitrophenol (5), and 3-methyl-4-nitrophenol (2). As *Burkholderia* sp. SJ98 is a potential candidate for the biodegradation of these aromatic compounds, whole-genome sequencing of the strain was carried out to explore the genetic organization and genes involved in the degradation of nitroaromatic compounds.

The genome of *Burkholderia* sp. SJ98 was sequenced by one standard (single-end) and one paired-end run of 454 GS FLX technology (Roche). Totals of 739,460 high-quality single-end reads and 539,992 high-quality paired-end reads in an 8-kb insert library were obtained. All the data provide 64.4× coverage of the *Burkholderia* sp. SJ98 genome.

Roche's 454 reads were assembled into 17 scaffolds of 7.89 Mb (with 0.74% N bases, where N is unknown) and 79 large contigs of 7.85 Mb by a Newbler 2.5.3 assembler. *N*50 lengths for scaffolds and contigs were 1.32 Mb and 464.6 kb, respectively.

All 79 large contigs were used for gene prediction and annotation by RNAmmer 1.2 (3) and the RAST (Rapid Annotation using Subsystem Technology) system (1). We further manually annotated some genes.

The genome of *Burkholderia* sp. SJ98 is 7,850,519 bp long and assembled into 79 large contigs with a G+C content of 62.70%. Of 7,418 genes predicted, 7,364 were protein-encoding genes and 54 were RNA genes. Comparison of genome sequences available from the RAST server shows that *Burkholderia xenovorans* LB400 (score, 542), *Burkholderia* sp. strain Ch1-1 (score, 505), and *Burkholderia mallei* ATCC 23344 (score, 503) are the closest neighbors of strain SJ98.

Strain SJ98 contains genes for urea decomposition, aromatic amino acid degradation, chorismate synthesis, the Entner-Doudoroff pathway, the serine-glyoxylate cycle and folate biosynthesis, salicylate and gentisate catabolism, benzoate degradation, the chloroaromatic degradation pathway, aromatic amino acid catabolism, gentisate degradation, *p*-hydroxybenzoate degradation, salicylate ester degradation, and quinate degradation, the same as *B. xenovorans* strain LB400. But strain SJ98 does not have genes for a putrescine utilization pathway, a 4-hydroxyphenlylacetic acid catabolic pathway, *p*-cymene degradation, and nitrogen fixation, which are present in the LB400 strain. Strain SJ98 contains genes for aromatic amino acid transport protein AroP, L-lysine permease, proline uptake and utilization, soluble methane monooxygenase (sMMO), and phenol hydroxylase, which are absent in strain LB400. In the SJ98 genome, we found genes for nitrobenzoate nitroreductase, phenyl acetate coenzyme A (CoA) oxygenase, benzoate formate decarboxylase, and salicylate hydroxylase, involved in biodegradation of nitroaromatic compounds.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AJHK00000000. The version described in this paper is the first version, AJHK01000000. Genome assembly and annotation data files can be downloaded from the genomics web portal of the Bioinformatics Centre of the Institute of Microbial Technology at http://crdd.osdd.net/raghava/genomesrs/.

ACKNOWLEDGMENTS

This work was funded by the Institute of Microbial Technology Council of Scientific and Industrial Research (IMTECH-CSIR). S.K. and S.V. are supported by a research fellowship from the Council of Scientific and Industrial Research.

REFERENCES

1. **Aziz RK, et al.** 2008. The RAST Server: rapid annotations using subsystems technology. BMC Genomics **9**:75.
2. **Bhushan B, Samanta SK, Chauhan A, Chakraborti AK, Jain RK.** 2000. Chemotaxis and biodegradation of 3-methyl-4-nitrophenol by Ralstonia sp. SJ98. Biochem. Biophys. Res. Commun. **275**:129–133.
3. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
4. **Pandey G, Chauhan A, Samanta SK, Jain RK.** 2002. Chemotaxis of a Ralstonia sp. SJ98 toward co-metabolizable nitroaromatic compounds. Biochem. Biophys. Res. Commun. **299**:404–409.
5. **Pandey J, et al.** 2011. Reductive dehalogenation mediated initiation of aerobic degradation of 2-chloro-4-nitrophenol (2C4NP) by Burkholderia sp. strain SJ98. Appl. Microbiol. Biotechnol. **92**:597–607.
6. **Samanta SK, Bhushan B, Chauhan A, Jain RK.** 2000. Chemotaxis of a Ralstonia sp. SJ98 toward different nitroaromatic compounds and their degradation. Biochem. Biophys. Res. Commun. **269**:117–123.

Received 28 March 2012 Accepted 29 March 2012

Address correspondence to Gajendra Pal Singh Raghava, raghava@imtech.res.in.

S.K. and S.V. have contributed equally to the study.

doi:10.1128/JB.00497-12