JOURNAL OF BACTERIOLOGY, Oct. 2011, p. 5598–5599 Vol. 193, No. 19
0021-9193/11/$12.00 doi:10.1128/JB.05667-11

Genome of a Novel Isolate of *Paracoccus denitrificans* Capable of Degrading *N*,*N*-Dimethylformamide

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Received 27 June 2011/Accepted 8 July 2011

The bacterial genus *Paracoccus* is comprised of metabolically versatile organisms having diverse degradative capabilities and potential industrial and environmental applications for bioremediation in particular. We report a *de novo*-assembled sequence and annotation of the genome of a novel isolate of *Paracoccus denitrificans* originally sourced from coal mine tailings in India. The isolate was capable of utilizing *N*,*N*-dimethylformamide (DMF) as a source of carbon and nitrogen and therefore holds potential for bioremediation and mineralization of industrial pollutants. The genome sequence and biological circuitry revealed thereupon will be invaluable in understanding the metabolic capabilities, functioning, and evolution of this important bacterial organism.

Paracoccus denitrificans is a Gram-negative coccoid bacterium capable of thriving in soil under either aerobic or anaerobic conditions. An important characteristic of this bacterium is its ability to single-handedly convert nitrate to dinitrogen via a process called denitrification (2). *Paracoccus* bacteria have gained significant attention as model organisms due to the overlap with some of the important features specific to mitochondria and that they presumably constitute the ancestors of eukaryotic mitochondria (7, 15). Given this, genomics-enabled insights into the evolution of this taxon are very important.

The Indian isolate of *P. denitrificans* described herein was obtained from coal mine leftovers and was cultured in mineral salts medium (MM1) devoid of any traditional carbon and nitrogen source but fortified with *N*,*N*-dimethylformamide (DMF) (0.5% [vol/vol]). The isolate was previously identified as *Ochrobactrum* species based on partial 16S rRNA gene typing (14); however, the genome sequence provides a clear basis for its identity as *P. denitrificans*.

The genome sequence was determined by Illumina genome analyzer (GA2x, pipeline version l.6) and comprised of sequence traces equivalent to 890 megabytes of data encompassing 72-bp paired-end reads with insert size of 300 bp, and the genome coverage achieved was about 60 times. In addition to the chromosomal complement, our *P. denitrificans* isolate also carried a 60-kb plasmid which has yet to be analyzed with respect to the genes that it carries. The chromosomal sequence was assembled *de novo* into contigs using Velvet (16) assembly tool with a hash length of 39. The draft genome was annotated with the help of the RAST server (1) comparing outputs from GLIMMER (6), GeneMark (3), and EasyGene (11). Artemis (12) was used to obtain the following statistics of the genome. In addition, tRNAscan-SE (13) was used to scan for the total number of tRNAs. The size of the *P. denitrificans* Indian isolate was approximately 3 Mb (2985589 bp) with a G+C content of 65.65% and a coding percentage of 82.4 with 3,744 protein-coding sequences of an average length of 662 bp. The genome revealed 34 tRNA genes (one gene encoding a selenocyteine) and 3 rRNA genes. Analyses for tracing important genes were carried out using the alignment tools Mauve (4, 5), BLAT (9), and Mummer (10). The BioCyc (8) database was used for coordinates of the genes in comparison with the *P. denitrificans* PD1222 genome. Further, NCBI BLAST was used for manual curation. Regions containing genes encoding nitrite transporter, nitrite reductase, nitrate reductase, and ferredoxin were readily located. A few RuBisCO genes along with genes conferring resistance to fosmidomycin, ethidium bromide viologen, tellurium, bicyclomycin, arsenic, and acriflavin were found. In addition, enzymes involved in mineralization of DMF (dimethyl formidase, dimethyl amine dehydrogenase, and monomethyl amine dehydrogenase), cytochrome *c* oxidases, and various proteins related to the cytochrome family were identified.

These observations and the ensuing comparative genomic analyses shall be extremely useful in both furthering fundamental understanding of bioremediation mechanisms encoded by this and other *Paracoccus* species and working toward identification of the scientific basis to weigh the beneficial and harmful effects of such organisms in the environment.

Nucleotide sequence accession number. The genome sequence is deposited in GenBank under accession number CP002897.

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This genome program was supported by the University of Hyderabad through an interim grant to N.A. as a part of the Indo-German International Research Training Group Internationales Graduiertenkolleg (GRK1673)–Functional Molecular Infection Epidemiology (an initiative of the German Research Foundation [DFG] and the University of Hyderabad/University Grants Commission India) of which N.A. is a Speaker. D.S. and T.B.K. acknowledge support from the Department of Biotechnology of the Indian Government for undertaking research on DMF degradation.

We are grateful to M/s Genotypic Technology Pvt. Ltd., Bengaluru, India, for their help with Illumina sequencing. We acknowledge project management/laboratory facility support rendered by Gutti Navamallika.

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