Genome Sequence of *Paracoccus* sp. Strain TRP, a Chlorpyrifos Biodegrader[▽]

Kang Li, Shenghui Wang, Yanhua Shi, Jie Qu, Yi Zhai, Lili Xu, Yongxue Xu, Jinlong Song, Lili Liu, M. Anisur Rahman, and Yanchun Yan*

Graduate School, Chinese Academy of Agricultural Sciences (CAAS), 12 Zhongguancun Nandajie, Beijing 100081, People's Republic of China

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***Paracoccus* sp. strain TRP, isolated from activated sludge, could completely biodegrade chlorpyrifos and 3,5,6-trichloro-2-pyridinol. Here we report the draft genome sequence of *Paracoccus* sp. strain TRP, which could be used to predict genes for xenobiotic biodegradation and metabolism.**

Paracoccus is a metabolically versatile genus with diverse degradative capabilities and potential applications in biotreatment and bioremediation (1). Several strains belonging to the genus *Paracoccus* have been isolated from various contaminated environments (4, 6, 9, 10, 12, 13). *Paracoccus* sp. strain TRP was isolated from activated sludge from the HuaYang pesticide plant in Shandong, China, in our lab. Biodegradation tests showed that it was able to biodegrade not only chlorpyrifos and its metabolite 3,5,6-trichloro-2-pyridinol but also pyridine, methyl parathion, and carbonfuran when provided as the sole source of carbon and energy. It will be potentially useful in the biotreatment of wastewater and bioremediation of contaminated soils (12). The whole genome of *Paracoccus* sp. strain TRP was sequenced to reveal the degradation pathway for chlorpyrifos. As far as we know, this is the first report of the genome of a *Paracoccus* sp. strain that can completely biodegrade chlorpyrifos.

Whole-genome shotgun (WGS) DNA sequencing of *Paracoccus* sp. strain TRP was performed by BGI (formerly the Beijing Genomics Institute) using Solexa paired-end sequencing technology (2, 8, 11). WGS sequence data for 2,027 Mb, giving approximately 500-fold genome coverage, were generated and assembled into 122 contigs, including 3 contigs shorter than 200 bp, using SOAPdenovo v.1.04 (5). Furthermore, the contigs were joined into 110 scaffolds (>1 kb in size) using paired-end information.

The unclosed draft genome sequence analysis of *Paracoccus* sp. strain TRP showed a genome size of 3,915,457 bp with a mean GC content of 62.89%. Annotation of the open reading frames was performed using Glimmer v.3.0 (3) and by comparison with the corresponding data from the COG, KEGG, SwissProt, TrEMBL, and NR databases. We found 3,961 coding sequences (CDSs). There were 3,070 CDSs involving the 21 functional COG groups and 25 CDSs involving the biodegradation and metabolism of xenobiotics, including pentachlorophenol monooxygenase, hydroxyatrazine ethylaminohydrolase,

benzaldehyde dehydrogenase, etc. Genes not yet functionally identified can be identified well upon closure of the genome. In addition, 45 tRNAs were identified by tRNAscan-SE (7) and 5 rRNAs were predicted by rRNA database BLAST. Furthermore, 147 insertion sequence elements, 200 transposases, and 96 tandem repeats were also found.

Gene family analysis of genes from *Paracoccus* sp. strain TRP and the published genome of *Paracoccus denitrificans* Pd1222 (<http://genome.ornl.gov/microbial/pden/>) showed that 39 gene families were constructed (more than 10 genes for each of them). The largest gene family included 181 genes (88 genes from Pd1222 and 93 genes from TRP), and the larger gene family included 59 genes (31 genes from Pd1222 and 28 genes from TRP). All four of the oxidoreductase gene clusters required for the denitrification pathway have been well characterized in both *Paracoccus* strains. Comparative genome analysis of *Paracoccus* sp. strain TRP and *P. denitrificans* Pd1222 will provide further insight into the genomic differences between the members of this genus. Analysis of the genome of *Paracoccus* sp. strain TRP will help us identify diverse biodegradation genes and, further, to elucidate the microbial degradation pathways for chlorpyrifos and other pesticides.

Nucleotide sequence accession number. The WGS project of *Paracoccus* sp. strain TRP has been deposited at DDBJ/EMBL/GenBank under accession number AEPN00000000.

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* Corresponding author. Mailing address: Graduate School, Chinese Academy of Agricultural Sciences (CAAS), 12 Zhongguancun Nandajie, Beijing 100081, People's Republic of China. Phone: 86-10-82109685. Fax: 86-10-82106609. E-mail: yanyanchun@caas.net.cn.

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