

Genome Sequence of *Hydrogenophaga* sp. Strain PBC, a 4-Aminobenzenesulfonate-Degrading Bacterium

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***Hydrogenophaga* sp. strain PBC is an effective degrader of 4-aminobenzenesulfonate isolated from textile wastewater. Here we present the assembly and annotation of its genome, which may provide further insights into its metabolic potential. This is the first announcement of the draft genome sequence of a strain from the genus *Hydrogenophaga*.**

4-Aminobenzenesulfonate (4-ABS) is a recalcitrant chemical compound commonly found in textile wastewater as a result of the reductive cleavage of azo dye. The microbial degradation of 4-ABS has been challenging due to the low 4-ABS permeability of the bacterial membrane and also its growth inhibitor property owing to its high homology to *p*-aminobenzoic acid.

Hydrogenophaga intermedia S1 was the first reported bacterial strain with the ability to degrade 4-ABS in coculture with *Agrobacterium radiobacter* S2 (3). Subsequently, three additional bacterial strains with the ability to degrade 4-ABS as a pure culture were isolated from different sites (13–15). *Hydrogenophaga* sp. strain PBC was isolated from textile wastewater and could degrade 4-ABS in coculture with *Ralstonia* sp. strain PBA (5). Interestingly, both *Hydrogenophaga intermedia* S1 and *Hydrogenophaga* sp. PBC strains were auxotrophic for biotin and *p*-aminobenzoic acid, which may explain the roles of their respective helper strains in the biodegradation of 4-ABS. To date, the molecular mechanism of 4-ABS degradation has been studied in great detail in this genus via an approach involving transposon mutagenesis and enzymology (2, 4, 7–9). The recent identification of the genetic components for the oxidation of 4-ABS to 4-sulfocatechol from *Hydrogenophaga* sp. PBC added another crucial piece of the puzzle to the metabolism of 4-ABS (6).

The ability of *Hydrogenophaga* sp. PBC to degrade such a xenobiotic compound is of great value to the field of bioremediation, and thus we sequenced its genome to (i) identify other genes which are indirectly involved in the biodegradation of 4-ABS, (ii) make possible the cloning and characterization of other useful catabolic genes, (iii) aid in future metabolic engineering of this strain, and (iv) provide the first draft genome sequence of a strain from the genus *Hydrogenophaga*.

The genome sequencing of *Hydrogenophaga* sp. PBC was performed using the Illumina Genome Analyzer IIx (100-bp paired-end reads). The reads were trimmed and assembled *de novo* using CLC Genomics Workbench 4.8 (CLC Bio, Denmark). Prodigal 2.50, tRNAscan 1.2, and RNAmmer 1.2 (10–12) were used to predict open reading frames (ORFs), tRNAs, and rRNAs, respectively. Subsequent genome annotation was performed using Blast2GO 2.5.0 (1). The *de novo* assembly results in 94-fold coverage of a 5,144,529-bp draft genome contained in 148 contigs. Contig N50 was approximately 82 kb, and the largest contig assembled was approximately 214 kb. The draft genome has a GC content of 68.44% and contains 4,964 ORFs, 42 tRNAs, and 3 rRNAs.

Hydrogenophaga sp. PBC contains all the genes identified to date to be involved in the biodegradation of 4-ABS. In addition, it contains genes involved in the biodegradation of other aromatic compounds such as terephthalate, phenol, phenoxybenzoate, protocatechuate, and phenylacetate.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project sequence has been deposited at DDBJ/EMBL/GenBank under accession number [AJWL000000000](http://www.ncbi.nlm.nih.gov/nuccore/AJWL000000000). The version described in this paper is the first version, [AJWL010000000](http://www.ncbi.nlm.nih.gov/nuccore/AJWL010000000).

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