Complete Genome Sequence of the Anaerobic Perchlorate-Reducing Bacterium *Azospira suillum* Strain PS

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*Azospira suillum* strain PS (formally *Dechlorosoma suillum* strain PS) is a metabolically versatile betaproteobacterium first identified for its ability to grow by obligate reduction of perchlorate and chlorate [denoted (per)chlorate]. Together with *Dechloromonas* species, these two genera represent the dominant (per)chlorate-reducing bacteria in mesophilic freshwater environments. In addition to (per)chlorate reduction, *A. suillum* is capable of the anaerobic oxidation of humic substances and is the first anaerobic nitrate-dependent Fe(II) oxidizer outside the *Diaphorobacter* and *Acidovorax* genera for which there is a completed genome sequence.

*Azospira suillum* strain PS is a motile Gram-negative facultative anaerobe isolated from animal waste lagoons based on its ability to grow anaerobically by dissipatory (per)chlorate reduction (1). What makes this organism of further biochemical importance are its metabolic capabilities to perform anaerobic oxidation of the quinone moieties of humic acids, as well as anaerobic nitrate-dependent Fe(II) oxidation (6, 7). It was also the first organism shown to be capable of biogenic magnetite and green rust formation through Fe(II) bio-oxidation (6). Strain PS is a member of the *Betaproteobacteria* (1) within the *Rhodocyclaceae* family (12). *Azospira* represents one of the dominant (per)chlorate-reducing genera in the natural environment, and strain PS is a model organism for studying this metabolism (10). The 16S rRNA gene sequence of strain PS has 99% similarity to that of the endophyte *Azospira oryzae* strain N1; however, *A. oryzae* is incapable of dissimilatory (per)chlorate respiration (4).

The completed genome consisted of one contig, 2.5 Mb in length, with an average 65.3% G + C content. A total of 3,443 protein-encoding genes were predicted. Sequencing was performed at the Joint Genome Institute (JGI) using a combination of Illumina GAII and 454 GS-FLX-Titanium to a depth of 30× coverage. Sequence assembly was performed using Newbler v. 2.3 (454 Life Sciences), and genes were called using Prodigal 1.4 (5), GenePRIMP (11), and the JGI’s Integrated Microbial Genomes (IMG) site (8).

Strain PS is only the second (per)chlorate-reducing organism for which there is a completed genome sequence and has provided new insights into the genetics of this metabolism by whole-genome comparisons to *Dechloromonas aromatica* strain RCB (9). Initial analysis of the draft genome indicated that 1,082 of the 3,454 protein-encoding genes had reciprocal best BLAST hits to those of *D. aromatica* strain RCB. The annotation of the genome identified a *cld* gene, and *perABCD* genes clustered together on the chromosome; all five genes are thought to be required for the reduction of perchlorate to chloride (2, 3). Initial comparative genomics used this information to identify a possible (per)chlorate reduction genomic island in four bacterial perchlorate reducers (9). In addition to its ability to oxidize simple organic acids to perchlorate reduction (supported by the genome), this organism has also been demonstrated to be capable of nitrate-dependent oxidation of Fe(II) oxidation and the hydroquinone moieties of humic acids (6, 7, 11, 13), of which the genetic and biochemical mechanism is poorly understood (14).

**Nucleotide sequence accession number.** The genome sequence of *Azospira suillum* strain PS reported in this genome announcement has been deposited in the GenBank database under accession no. CP003153.

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