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Genome Sequence of *Rhodobacter sphaeroides* Strain WS8N▽

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***Rhodobacter sphaeroides* is a metabolically diverse photosynthetic alphaproteobacterium found ubiquitously in soil and freshwater habitats. Here we present the annotated genome sequence of *R. sphaeroides* WS8N.**

Rhodobacter sphaeroides can grow using either aerobic or anaerobic respiration and can photosynthesize. *R. sphaeroides* can use a diverse array of different carbon and nitrogen sources and is capable of N_2 fixation when other nitrogen sources are scarce. Organic acids are the preferred carbon sources during heterotrophic growth, while CO_2 is fixed during autotrophic growth. The chemotaxis pathway of *R. sphaeroides* is particularly well studied, as it exhibits striking differences from the more simple pathway used by *Escherichia coli*, most notably by having multiple homologues of the *E. coli* chemosensory proteins, which assemble into two distinct signaling clusters (11, 17) that integrate a multitude of different signals (16) and jointly control flagellar motor rotation (1, 8).

R. sphaeroides WS8 (12), originally designated TS/6, was isolated in Ithaca, NY, by Clayton and Clayton in 1969 (3). *R. sphaeroides* WS8N is a spontaneous nalidixic acid-resistant derivative of WS8 (15). WS8N exhibits enhanced swimming motility and chemotaxis compared to other strains of *R. sphaeroides* such as 2.4.1. For this reason, WS8N is used for the study of chemotaxis signaling (9, 10) and flagellum-based motility (5, 7). WS8N has also been used in studies on bacterial cell biology (13, 14) and plasmid replication (4).

Whole-genome sequencing was performed using Roche 454 GS-FLX pyrosequencing. A combination of reads from shotgun and long-tag paired-end libraries produced approximately 26-fold coverage of the genome. Newbler (454 Life Sciences) was used to assemble the reads *de novo*, yielding 141 large contigs (>500 bp) organized into 16 scaffolds. All but two of the gaps were successfully closed by using Sanger sequencing of uncloned PCR products (Source Bioscience). The 4.42-Mbp genome has a total GC content of 69.1% and comprises two chromosomes (3.14 and 0.97 Mbp) and two large plasmids (200 and 110 kbp). Open reading frames were predicted and annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline.

A total of 4,205 predicted coding sequences were identified. The average length of each coding sequence was 299 amino acids, with a total coding percentage of 88.7%. There are 52 tRNA genes and 9 rRNA genes. The 5S, 16S, and 23S rRNA molecules are encoded once on the large chromosome and twice on the small chromosome. Thirty-three genes encode chemotaxis signaling proteins, i.e., 13 chemoreceptors (9 transmembrane and 4 soluble), 4 CheA proteins, 6 CheY proteins, 4 CheW proteins, 3 CheR proteins, 2 CheB proteins, and 1 CheD protein. All of these are located on the large chromosome, with the exception of six of the chemoreceptor genes and one of the *cheY* genes, which are on the small chromosome.

Comparative genome analysis shows that while the chromosome gene organization of WS8N is similar to that of previously sequenced strains of *R. sphaeroides*, the plasmid composition differs considerably, with ATCC_17029 having one, WS8N and KD131 each having two (6), and 2.4.1 and ATCC_17025 each having five (2).

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AFER00000000. The version described in this paper is the first version, AFER01000000.

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