Genome Sequences for Six *Rhodanobacter* Strains, Isolated from Soils and the Terrestrial Subsurface, with Variable Denitrification Capabilities

Joel E. Kostka,a, Stefan J. Green,b Lavanya Rishishwar,a Om Prakash,c Lee S. Katz,d Leonardo Mariño-Ramírez,e,f I. King Jordan,a,f Christine Munk,g Natalia Ivanova,g Natalia Mikhailova,g David B. Watson,h Steven D. Brown,i Anthony V. Palumbo,i and Scott C. Brooksii

School of Biology, Georgia Institute of Technology, Atlanta, Georgia, USAa; DNA Services Facility, Research Resource Center, University of Illinois, Chicago, Illinois, USAii; National Centre for Cell Science, Pune, India; Centers for Disease Control and Prevention, Atlanta, Georgia, USAiii; Pan-American Bioinformatics Institute, Santa Marta, Magdalena, Colombia; United States Department of Energy Joint Genome Institute, Walnut Creek, California, USAiv; Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USAv; and Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USAvi

We report the first genome sequences for six strains of *Rhodanobacter* species isolated from a variety of soil and subsurface environments. Three of these strains are capable of complete denitrification and three others are not. However, all six strains contain most of the genes required for the respiration of nitrate to gaseous nitrogen. The non-denitrifying members of the genus lack only the gene for nitrate reduction, the first step in the full denitrification pathway. The data suggest that the environmental role of bacteria from the genus *Rhodanobacter* should be reevaluated.

The genus *Rhodanobacter* contains 11 described species of Gram-negative, non-spore-forming, rod-shaped bacteria belonging to the family *Xanthomonadaceae* and the class *Gamma-proteobacteria* of the phylum *Proteobacteria*. Described species have been isolated mainly under aerobic conditions from surficial soils (1, 4, 5, 9, 12, 15, 16). Denitrification has not been considered a property of this genus. Recently, two strains of a new species, *Rhodanobacter denitrificans*, were isolated from a contaminated terrestrial subsurface environment and shown to denitrify (7, 13). Furthermore, nitrate-reducing isolates were recently recovered from sewage sludge (17), and we and others determined that *Rhodanobacter thiooxydans* is capable of denitrification (13, 14). In some acidic and nitrate-rich environments, *Rhodanobacter* species dominate bacterial communities (8, 14).

To explore the genetic basis of phenotypes leading to bacterial community dominance in such environments, genome sequences were acquired for three denitrifying strains (R. *denitrificans* 2APBS1 and 116-2 and R. *thiooxydans*) and three strains incapable of denitrification (Rhodanobacter *fulvus*, Rhodanobacter *spathiphylly*, and *Rhodanobacter* sp. 115). A complete R. *denitrificans* 2APBS1T genome sequence was generated using paired-end Illumina and Roche 454 mate-pair sequencing and manual finishing steps, essentially as described previously (3, 6). Four draft genomes (R. *denitrificans* 116-2, R. *thiooxydans*, R. *fulvus*, and R. *spathiphylly*) were generated by de novo assembly of paired-end Illumina sequence data (~5.7 to 9.5 million paired-end reads/genome, yielding ~1.1 to 1.9 Gb of total output/genome) (CLC Genomics Workbench 5.0; CLC bio A/S, Denmark). DNA from each strain was prepared for sequencing using the Nextera library preparation kit (Epicentre, Madison, WI). DNA from *Rhodanobacter* sp. 115 was prepared for sequencing using the Ion Xpress fragment library kit (Life Technologies, Grand Island, NY) and sequenced using a Personal Genome Machine (Ion Torrent, San Francisco, CA), yielding approximately 1.4 Mb of reads (~138 Mb of total output). For *Rhodanobacter* sp. 115, genome assembly was performed as described previously (10) using CG-Pipeline modules (11), yielding 453 contigs and 4.2 Mb of genomic sequence data.

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Address correspondence to Joel E. Kostka, joel.kostka@biology.gatech.edu.

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