

## The Genome Sequence of the Obligately Chemolithoautotrophic, Facultatively Anaerobic Bacterium *Thiobacillus denitrificans*

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Received 1 September 2005/Accepted 30 November 2005

**The complete genome sequence of *Thiobacillus denitrificans* ATCC 25259 is the first to become available for an obligately chemolithoautotrophic, sulfur-compound-oxidizing,  $\beta$ -proteobacterium. Analysis of the 2,909,809-bp genome will facilitate our molecular and biochemical understanding of the unusual metabolic repertoire of this bacterium, including its ability to couple denitrification to sulfur-compound oxidation, to catalyze anaerobic, nitrate-dependent oxidation of Fe(II) and U(IV), and to oxidize mineral electron donors. Notable genomic features include (i) genes encoding *c*-type cytochromes totaling 1 to 2 percent of the genome, which is a proportion greater than for almost all bacterial and archaeal species sequenced to date, (ii) genes encoding two [NiFe]hydrogenases, which is particularly significant because no information on hydrogenases has previously been reported for *T. denitrificans* and hydrogen oxidation appears to be critical for anaerobic U(IV) oxidation by this species, (iii) a diverse complement of more than 50 genes associated with sulfur-compound oxidation (including *sox* genes, *dsr* genes, and genes associated with the AMP-dependent oxidation of sulfite to sulfate), some of which occur in multiple (up to eight) copies, (iv) a relatively large number of genes associated with inorganic ion transport and heavy metal resistance, and (v) a paucity of genes encoding organic-compound transporters, commensurate with obligate chemolithoautotrophy. Ultimately, the genome sequence of *T. denitrificans* will enable elucidation of the mechanisms of aerobic and anaerobic sulfur-compound oxidation by  $\beta$ -proteobacteria and will help reveal the molecular basis of this organism's role in major biogeochemical cycles (i.e., those involving sulfur, nitrogen, and carbon) and groundwater restoration.**

*Thiobacillus denitrificans*, first isolated by Beijerinck over a century ago (4), was one of the first nonfilamentous bacteria ever described to be capable of growth on inorganic sulfur compounds as sole energy sources (47, 49). Characterized by its ability to conserve energy from the oxidation of inorganic sulfur compounds under either aerobic or denitrifying conditions, *T. denitrificans* is the best studied of the very few obligate chemolithoautotrophic species known to couple denitrification to sulfur-compound oxidation (*Thiomicrospira denitrificans* and *Thioalkalivibrio thiocyanodenitrificans* also have this ability [76, 85]). Despite many years of work on the biochemistry of inorganic sulfur-compound oxidation by *Thiobacillus thioparus* and *T. denitrificans*, the mechanisms of oxidation and how they are coupled to energy conservation are still not well understood in these  $\beta$ -proteobacteria, relative to the advances made with facultatively chemolithotrophic  $\alpha$ -proteobacterial genera, such as *Paracoccus* and *Starkeya* (28, 39, 45, 50). The availability of the complete genome sequence should enable elucidation of the sulfur-oxidation pathway(s) and lead to specifically focused biochemical investigations to resolve these knowledge gaps.

Recent studies have revealed that, in addition to sulfur-compound oxidation, *T. denitrificans* has broader oxidative capabilities that may not contribute to energy conservation, including anaerobic, nitrate-dependent oxidation of certain

metals, such as iron (78). The metabolic repertoire of this widely distributed bacterium can influence the carbon, nitrogen, sulfur, and iron cycles in many soil, aquifer, and sediment environments and is particularly relevant to in situ bioremediation of contaminated groundwater. Environmentally relevant capabilities of *T. denitrificans* include intrinsic biodegradation of nitrate, one of the most problematic groundwater contaminants worldwide, by anaerobic, nitrate-dependent oxidation of minerals such as FeS and pyrite (FeS<sub>2</sub>) (see, e.g., references 6, 56, and 78). *T. denitrificans* is the first and only autotrophic bacterium reported to carry out anaerobic (nitrate-dependent) oxidation of U(IV) oxide minerals (5), which could partially counteract efforts to remediate uranium-contaminated aquifers by in situ reductive immobilization [i.e., microbially mediated conversion of relatively soluble U(VI) species to poorly soluble U(IV) minerals]. The intriguing mechanism by which this species can oxidize mineral electron donors that cannot be taken into the cell is currently unknown, but its elucidation will be facilitated by the availability of the genome.

In this article, we present the complete genome sequence of *T. denitrificans* strain ATCC 25259, the first obligately chemolithoautotrophic, sulfur-oxidizing,  $\beta$ -proteobacterium to be sequenced. We describe some general features of the *T. denitrificans* genome, including recent gene acquisition, as well as genetic components involved in sulfur-compound oxidation, hydrogen metabolism, aerobic respiration, denitrification, autotrophy, central carbon metabolism, and heavy metal resistance.

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## MATERIALS AND METHODS

**Organism source.** *T. denitrificans* strain ATCC 25259 was obtained from the American Type Culture Collection (ATCC). This strain was originally isolated by B. F. Taylor in the 1960s (83, 84) and was deposited with the ATCC in 1969, where it was freeze-dried for storage and distribution. For this study, unless noted otherwise, *T. denitrificans* was grown with thiosulfate under denitrifying conditions, as described elsewhere (5).

**Sequencing, coding sequence prediction, and annotation.** Genomic DNA was isolated from *T. denitrificans* and the complete genome was sequenced as described previously (15). Briefly, small-insert (2- to 3-kb), medium-insert (6.5- to 8.5-kb), and large-insert (35- to 45-kb) libraries were generated by random mechanical shearing of genomic DNA. In the initial random sequencing phase, approximately ninefold sequence coverage was achieved. The sequences from all libraries were assembled together and viewed using the Phred/Phrap/Consed suite (P. Green, University of Washington) (22, 23, 31). Physical gaps were closed by PCR and sequencing. Open reading frames likely to encode proteins (coding sequences [CDS]) were identified and annotated by automated and manual curation as previously described (15).

**Comparative genomics.** The Integrated Microbial Genomes system of the Joint Genome Institute (<http://img.jgi.doe.gov/>) was used for identification of orthologs and to identify CDS unique to *T. denitrificans* on the basis of BLASTP results; the cutoff values applied were  $E < 10^{-5}$  and 30% identity and  $E < 10^{-2}$  and 20% identity, respectively.

**Generation of phylogenetic trees and other analyses.** Phylogenetic trees were generated by identifying potential homologs of translated *T. denitrificans* CDS by use of BLASTP (1) searches against the nonredundant (nr) GenBank database from the National Center for Biotechnology Information. Typically, trees included the top 50 BLASTP matches. However, sequences were excluded when their BLASTP E values fell below a cutoff of  $10^{-5}$ . For the phylogenetic tree results presented in this article, the lowest ranking sequences shared 24 to 54% identity and 43 to 71% similarity with the query sequences. Sequences were aligned and alignments refined using ClustalX version 1.8 (38) and manual adjustments. Phylogenetic trees were generated by using the *protdist* program and the *neighbor* program of the PHYLIP package (24, 25) to calculate distances (using the Jones-Taylor-Thorton matrix) and for clustering (neighbor-joining method), respectively. Membrane-spanning domains of proteins were identified using TmHMM (52, 75). The SignalP program (7) was used to identify putative signal peptides.

**RT quantitative PCR analysis.** For 18 selected genes, mRNA levels under exposure conditions of interest were determined by reverse transcription-quantitative PCR (RT-qPCR) analysis. The target genes included Tbd0210, Tbd0561, Tbd0562, Tbd0822, Tbd0823, Tbd0872, Tbd0873, Tbd0874, Tbd1365, Tbd1408, Tbd1926, Tbd2282, Tbd2283, Tbd2326, Tbd2327, Tbd2480, Tbd2488, and Tbd2658. Cultures of *T. denitrificans* were grown anaerobically with thiosulfate and nitrate and were then anaerobically harvested by centrifugation and washed using techniques and conditions described elsewhere (5). Washed cells (~6.5 mg protein) were resuspended in stoppered serum bottles under strictly anaerobic conditions in 5 or 10 ml of bicarbonate-buffered medium. Cells were resuspended with either thiosulfate (20 mM) and nitrate (20 mM) or FeCO<sub>3</sub> (3.5 mmol/liter) and nitrate (3.5 mM). Chemical analyses (ion chromatography, spectrophotometric determination of ferrozine-iron complexes) of the resuspended cultures were performed to confirm that nitrate reduction and either thiosulfate or Fe(II) oxidation were occurring when the cultures were harvested for RNA. RNA extraction was carried out using a MasterPure Complete DNA and RNA Purification Kit (EpiCentre) and a modified protocol. Total RNA was reverse transcribed and amplified using a QuantiTect SYBR Green RT-PCR kit (QIAGEN) with gene-specific primers. Each gene-specific PCR was performed in triplicate using 25- $\mu$ l reactions containing ~20 ng of template on a Prism 7000 cycler (ABI). Calibration curve determinations were performed with genomic DNA serially diluted over a range of 4 to 5 orders of magnitude. The PCR conditions were optimized to be performed as follows for all transcripts: 30 to 35 cycles at 50°C for 30 min; 95°C for 15 min; 94°C for 15 s; 58°C for 30 s; 72°C for 30 s.

**Nucleotide sequence accession number.** The annotated genome sequence has been deposited in the GenBank/EMBL sequence database under accession no. CP000116.

## RESULTS AND DISCUSSION

**General genome features.** The genome of *T. denitrificans* strain ATCC 25259 consists of a single circular chromosome 2,909,809 bp in length with an average G+C content of 66.1%

(Fig. 1 and Table 1). GC skew analysis does not reveal the origin of replication. Nucleotide position 1 of the chromosome is assigned to the predicted origin of replication, flanked on one side by the *dnaA* (Tbd0001), *dnaN* (Tbd0002), and *gyrB* (Tbd0003) genes and on the other by *rpmH* (Tbd2827) and *mpA* (Tbd2826). Two copies of the 16S rRNA operon are located in regions of the genome separated by more than 1,380 kb. Few other repeated sequences were discovered in the genome, with the exception of a duplicated IS4-like insertion sequence. Thus, the numbers of repeated elements, insertion sequence elements, and transposons are low compared with those typically found in bacterial genomes sequenced to date.

A total of 2,827 protein-encoding genes were identified, with an average length of 952 bp and accounting for 92.5% of the sequence. Among the predicted genes, 2,183 (77.2%) have been assigned a putative function, with the remainder designated as encoding a protein with unknown function, a conserved hypothetical protein, or a hypothetical protein. Of these, 89 predicted genes had no match in comparisons performed using BLAST versus the nr database with an E value cutoff of  $10^{-6}$  or better. When distributed into biological role categories based on the COG database (82), the largest number of predicted proteins fell into the categories of energy production (6.6%), cell envelope biogenesis (6.0%), and inorganic ion transport (5.7%).

When searches using the KEGG database of complete genomes were performed, more than half (1,624) of the predicted proteins revealed top BLAST hits to one of the 12  $\beta$ -proteobacteria available in this database, including *Azoarcus* sp. strain EbN1 (626 hits), the obligate chemolithoautotrophic bacterium *Nitrosomonas europaea* (346 hits), *Chromobacterium violaceum* (236 hits), *Ralstonia solanacearum* GMI1000 (189 hits), *Burkholderia pseudomallei* (118 hits), and *Bordetella bronchiseptica* (61 hits). Aside from  $\beta$ -proteobacteria, the organisms most frequently associated with the top BLAST hits were *Methylococcus capsulatus* (107 hits), *Pseudomonas aeruginosa* (75 hits), an environmentally versatile  $\gamma$ -proteobacterium, *Pseudomonas putida* (42 hits), and *Geobacter sulfurreducens* (42 hits), a  $\delta$ -proteobacterium best known for its versatility in dissimilatory metal reduction.

**Recent gene acquisition.** There is ample evidence of horizontal transfer in the *T. denitrificans* genome, inferred from local base composition to have been imported from an evolutionarily distant source. At least 13 regions, up to 25 kb in size, have been identified (on the basis of anomalies in observed G+C content and trinucleotide signature [40]) as likely recent integration events into the *T. denitrificans* genome that have not had time to drift toward the genome average (Table 2). Almost all of these putative regions of horizontal gene transfer carry phage integrases or other phage remnants, and a few of these regions are also flanked by tRNA genes, which are used as integration sites for many bacteriophages. Most of these regions are found to harbor many hypothetical or conserved hypothetical genes, and several carry restriction modification systems, which are known to be associated with mobile elements and indeed act as selfish mobile genetic elements themselves (51), whereas another region carries a cluster of genes encoding part of a type IV pilus. Although these likely recent insertions in the *T. denitrificans* chromosome are consistent with the concept of a fluid genome, it remains to be shown

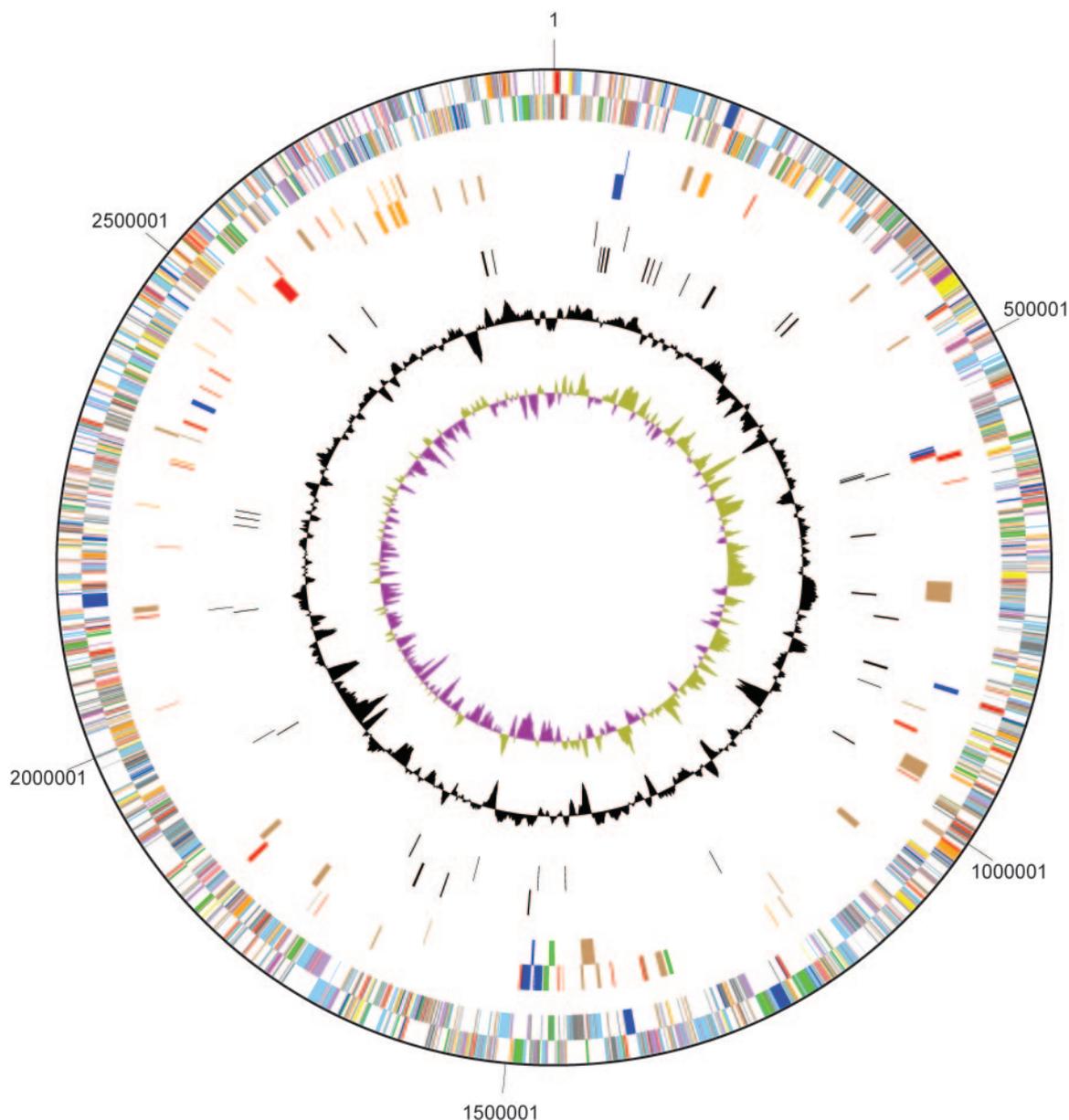


FIG. 1. Schematic circular diagram of the *T. denitrificans* ATCC 25259 genome. Outer circle, predicted coding regions on the forward strand, color-coded by role categories (dark gray, hypothetical proteins; light gray, conserved hypothetical and unknown function; brown, general function; red, DNA replication and repair; green, energy metabolism; blue, carbon and carbohydrate metabolism; cyan, lipid metabolism; magenta, transcription; yellow, translation; orange, amino acid metabolism; pink, metabolism of cofactors and vitamins; light red, purine and pyrimidine metabolism; lavender, signal transduction; sky blue, cellular processes; pale green, structural RNAs); second circle, predicted coding regions on the reverse strand, color coded as for the outer circle; third and fourth circles, coding regions (on forward and reverse strands) predicted to be involved in denitrification (blue), sulfur-compound oxidation (red), hydrogen oxidation (green), autotrophic carbon assimilation (orange), and metal ion transport-resistance (brown); fifth and sixth circles, coding regions found to have a CXXCH heme-binding motif and therefore potentially encoding *c*-type cytochromes; seventh circle, deviation from the average G+C; eighth circle, GC skew (olive, positive; purple, negative).

what role these regions may play in the metabolic or defense repertoire of *T. denitrificans*.

**Taxonomy of *T. denitrificans* strain ATCC 25259.** Following the reclassification of numerous  $\alpha$ -,  $\beta$ -, and  $\gamma$ -proteobacterial species previously classified as *Thiobacillus* spp., only three  $\beta$ -proteobacteria are now securely placed in that genus: *T. thioparus*, *T. denitrificans*, and *T. aquaesulis* (47, 49). Of these,

the last is a moderate thermophile and only *T. denitrificans* is capable of strictly chemolithotrophic anaerobic growth with denitrification using inorganic sulfur-compound oxidation as the sole source of energy (46, 49). Apart from this feature, *T. denitrificans* and *T. thioparus* are physiologically very similar mesophilic obligate chemolithoautotrophs. The G+C content of different strains ranges between 62 and 67% for *T. thioparus*

TABLE 1. General features of the *T. denitrificans* strain ATCC 25259 genome

Characteristic	Value
Chromosome size (bp)	2,909,809
G+C ratio (%)	66.07
Coding density (%)	92.5
No. of predicted protein coding genes	2,827
Average CDS length (bp)	952
No. of predicted proteins unique to <i>T. denitrificans</i> (%)	89 (3.1)
No. of rRNA operons	2
No. of tRNA genes	43
No. of other small RNAs	3
No. of predicted proteins with putative function (%)	2,183 (77.2)
No. of predicted proteins with unknown function (%)	644 (22.8)
Protein categories (%)	
Energy production	6.6
Inorganic ion transport	5.7
Cell envelope biogenesis	6.0
BLASTP comparison against the KEGG completed microbial genomes database (no. of top KEGG hits)	
β-Proteobacteria	1,624
γ-Proteobacteria	455
α-Proteobacteria	119
δ-Proteobacteria	92
Archaea	22

and 63 and 68% for *T. denitrificans* (46, 79, 88). DNA hybridization distinguished the two species, which show only 22 to 29% cross-hybridization (46). Comparison of 16S rRNA gene sequences in the GenBank nr database shows that identities between different strains of *T. thioparus* range between 95.2 and 99.6% and that the type strains of *T. thioparus* (ATCC 8158) and *T. denitrificans* (NCIMB 9548) show 96.3% identity to each other (D. P. Kelly, unpublished data). Consequently, the ability to denitrify is a key physiological criterion in distinguishing between the species, given the similarity of their 16S rRNA gene sequences. *T. denitrificans* strain ATCC 25259 was originally isolated from Texas soil (84; ATCC catalog) and has

been shown to have physiological properties characteristic of this species. *T. denitrificans* ATCC 25259 shows 97.6% identity (with respect to 16S rRNA genes) to the type strain *T. denitrificans* NCIMB 9548.

**Sulfur-compound oxidation.** A number of enzymes involved in inorganic sulfur-compound oxidation and energy conservation have previously been studied in *T. denitrificans* and the closely related β-proteobacterium *T. thioparus*; some of these enzymes have been purified and characterized biochemically. The *T. denitrificans* enzymes include APS (adenylylsulfate) reductase, an AMP-independent sulfite oxidase, a siroheme sulfite reductase, and APS:phosphate adenylyltransferase (or APAT) (2, 12, 13, 29, 69–71). Biochemical studies, as well as the high growth yields and the entry into the electron transport chain of electrons from sulfur-compound oxidation at the level of quinone-cytochrome *b*, indicate highly efficient energy-conserving mechanisms of sulfur-compound oxidation in *T. denitrificans* (42–45). The mechanisms of inorganic-sulfur oxidation by *T. denitrificans*, which oxidizes polythionates as well as thiosulfate, sulfide, and, for some strains, thiocyanate, appear more similar to those of γ-proteobacteria such as *Halothiobacillus* spp. than to the well-defined thiosulfate-oxidizing, multienzyme system of α-proteobacterial chemolithotrophs (45, 50, 68).

As would be expected from previous biochemical work with *T. denitrificans*, its genome contains a diverse complement of genes encoding enzymes that catalyze inorganic sulfur-compound oxidation and energy conservation (by both substrate-level and electron transport-linked phosphorylation). The importance of sulfur-compound oxidation to *T. denitrificans* is underscored by the occurrence of multiple oxidation pathways for certain sulfur compounds and multiple copies of a number of genes associated with sulfur-compound oxidation (see overview in Fig. 2). The unusual ability of this bacterium to oxidize

TABLE 2. Regions with uncharacteristic G+C content and Karlin signatures<sup>a</sup>

Location in genome (nt) <sup>b</sup>	% G+C	CDS	BLAST hits
394058–402433	58.87	Tbd0363–Tbd0373	Phage integrase, regulatory protein, hypothetical proteins
979890–1004773	57.39	Tbd0925–Tbd0943	Methylase, transposase, regulatory protein, helicase (Snf2/Rad54 family), type III restriction-modification system (methylase, restriction enzyme), phage integrases, and several hypothetical proteins
1264595–1271704	56.99	Tbd1207–Tbd1215	Phage integrase, conserved imported protein, and hypothetical proteins
1395068–1400129	52.43	Tbd1314–Tbd1318	Phage integrase and hypothetical and conserved hypothetical proteins
1424272–1431083	60.88	Tbd1342–Tbd1354	Mostly hypothetical proteins and a conserved imported protein
1575347–1583813	57.71	Tbd1487–Tbd1492	Type II/III restriction-modification system (helicase, methylase), conserved hypothetical and hypothetical proteins
1767440–1787406 <sup>c</sup>	60.46	Tbd1679–Tbd1695	Phage integrase, conjugal transfer region (TraWBAY), a number of hypothetical proteins, and imported AAA superfamily ATPase and conserved hypothetical protein
1955614–1961331	61.96	Tbd1861–Tbd1865	Type IV pilus proteins (PilE/WXV and FimT)
2052544–2061073	59.64	Tbd1958–Tbd1969	Transposases, conserved imported hypothetical proteins, and hypothetical proteins
2089032–2093604 <sup>c</sup>	57.82	Tbd2000–Tbd2005	Phage integrase, plasmid recombination protein, and several hypothetical proteins
2160137–2166983 <sup>c</sup>	62.36	Tbd2066–Tbd2073	Phage integrase, phage replication protein, DNA helicase, and several hypothetical proteins
2750091–2764591	57.46	Tbd2675–Tbd2685	Phage integrase, prophage regulatory protein, type I restriction-modification system (HsdMS, HsdR)
2900270–2905890	61.02	Tbd2817–Tbd2823	Phage integrase, phage primase and phage regulatory protein

<sup>a</sup> All regions are also supported by Karlin signature difference.

<sup>b</sup> nt, nucleotide.

<sup>c</sup> Flanked by a tRNA gene.

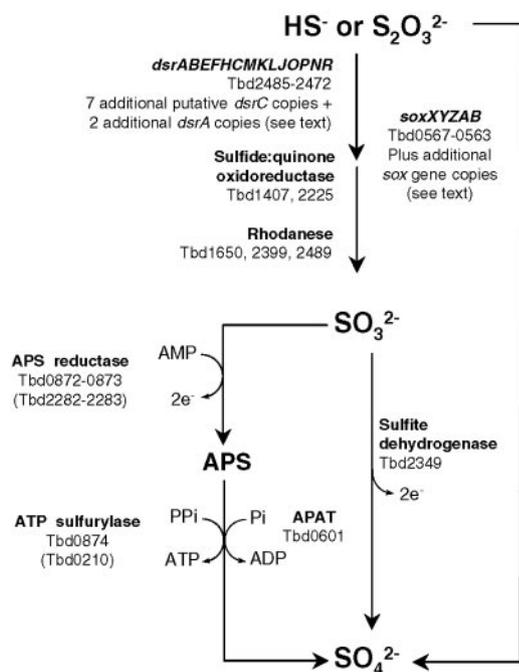


FIG. 2. Schematic overview of key genes/enzymes putatively associated with sulfur-compound oxidation in *T. denitrificans*. Genes in parenthesis have been shown to be lesser expressed paralogs (this study). The biochemical roles of a number of gene products represented in this figure have not been experimentally demonstrated in *T. denitrificans* and are uncertain. Sulfide:quinone oxidoreductase is not proposed to catalyze the direct oxidation of sulfide to sulfite but rather may participate in an indirect pathway (20). The arrow between thio-sulfate and sulfate (right side) represents the possibility that SoxB catalyzes a sulfate thiohydrolase reaction (28) in *T. denitrificans*. APAT, APS:phosphate adenyltransferase.

inorganic sulfur compounds under both aerobic and denitrifying conditions raises the question of whether different sulfur-oxidizing enzymes are involved under aerobic versus anaerobic conditions. Although such questions cannot be resolved by genome analysis alone, they can be addressed by transcriptional studies using whole-genome oligonucleotide microarrays, which are now enabled by the availability of the *T. denitrificans* genome. Included among the genes that are likely to be critical to sulfur-compound oxidation by *T. denitrificans* are *sox* (sulfur-oxidation) genes, *dsr* (dissimilatory sulfite reductase) genes, and genes associated with the AMP-dependent oxidation of sulfite to sulfate (Fig. 2). These genes serve as the focus of this section.

Little molecular genetic work on the sulfur-oxidation (*sox*) systems of *T. denitrificans* has been conducted to date. The model for genes encoding sulfur-oxidation enzymes has been derived primarily from three  $\alpha$ -proteobacteria: *Paracoccus pantotrophus*, *Starkeya novella*, and *Pseudaminobacter salicylatoxidans*. In *T. denitrificans*, genes showing various levels of sequence identity to *sox* genes of these  $\alpha$ -proteobacteria have been detected, but gene clusters of the length found in facultatively chemolithotrophic, aerobic, thiosulfate-oxidizing bacteria do not occur. Thus, extensive *sox* clusters have been observed in *P. pantotrophus*, *S. novella*, and *P. salicylatoxidans*: *soxRSVWXYZABCDEFGHIJ*, *soxFDCBZYAXWV*, and *soxGTRS-*

*VWXYZABCD*, respectively (GenBank X79242, AF139113, and AJ404005) (27, 28, 91). In contrast, the largest cluster in *T. denitrificans* consists of *soxXYZAB* (Tbd0567–Tbd0563), using the *P. pantotrophus* naming scheme. Comparison of deduced SoxX, -Y, -Z, -A, and -B sequences of *T. denitrificans* to those of *P. pantotrophus*, *Chlorobium tepidum*, *P. salicylatoxidans*, and *S. novella* revealed sequence identity in the range of 28 to 55%. This indicated that while the genes encoding these Sox functions had been putatively identified, they differed significantly from those of the reference organisms. Interestingly, the translated *soxXYZA* genes showed higher identities to those of the green sulfur bacterium *C. tepidum* (42 to 55%) than to those of *Paracoccus*, *Starkeya*, and *Pseudaminobacter* spp. (28 to 38%). Additional copies of *soxA* were identified outside of the *soxXYZAB* cluster in *T. denitrificans* (Tbd0917–Tbd0918). A noteworthy difference between SoxA encoded in the *T. denitrificans* genome and those of *P. pantotrophus* and *P. salicylatoxidans* is that the latter are diheme cytochromes (28) whereas SoxA copies in *T. denitrificans* (Tbd0564 and, putatively, Tbd0918) are monoheme cytochromes.

For *soxB*, the *T. denitrificans* sequence can be compared to that of another  $\beta$ -proteobacterium as well as to those of  $\alpha$ -proteobacteria, because the sequence from *T. thioparus* is available (GenBank AJ294326; partial sequence, 344 translated amino acids) (59). In fact, of the *sox* genes, only *soxB* has thus far been the subject of intercomparison across the  $\alpha$ -,  $\beta$ -, and  $\gamma$ -proteobacterial groups (59); this comparison revealed a distant phylogenetic relationship of the *soxB* sequence of *T. thioparus* to those of  $\alpha$ - and  $\gamma$ -proteobacteria. Consistent with phylogenetic relationships based on 16S rRNA, the predicted SoxB sequence of *T. denitrificans* (Tbd0563) is much more similar to that of *T. thioparus* (88% identity) than to those of *P. pantotrophus*, *S. novella*, and *P. salicylatoxidans* (48 to 50% identity). The encoded SoxB sequences for *T. thioparus* and *P. pantotrophus* (GenBank CAC82470 and CAA55824) showed 50% identity to each other.

Other *sox* genes found in the contiguous cluster of *P. pantotrophus* were remote from each other in the *T. denitrificans* genome. These included tentatively identified copies of *soxH* (Tbd1041, Tbd1103), *soxE* (Tbd2027, Tbd2034), *soxF* (Tbd2035), and *soxW* (Tbd2117). Tbd2349 corresponded to the *soxC* (sulfite dehydrogenase) of *P. salicylatoxidans* and *P. pantotrophus* and the *sorA* of *S. novella*; thus, the encoded protein may be a sulfite dehydrogenase, catalyzing AMP-independent oxidation of sulfite to sulfate. BLAST probing of the genome with the nucleotide and deduced amino acid sequences of the *soxD* of *P. pantotrophus* and *S. novella* produced no hits, so a gene corresponding to the  $\alpha$ -proteobacterial *soxD* appeared to be absent. As the proteins encoded by *soxCD* in *Paracoccus* spp. are believed to catalyze the oxidation of sulfane-sulfur to the oxidation level of sulfite (28), an alternative system is likely present in *T. denitrificans*.

Coding functions have been ascribed to many of the  $\alpha$ -proteobacterial *sox* genes discussed above (27, 28, 63–65, 67, 68). *soxX* and *soxA* encode SoxXA, a heterodimeric *c*-type cytochrome. *soxY* and *soxZ* encode SoxYZ, the “thiosulfate-binding” enzyme A of *P. pantotrophus*. *soxC* and *soxD* encode the molybdo-protein SoxC and diheme *c*-type cytochrome SoxD of an  $\alpha_2\beta_2$ -heterodimeric “sulfur dehydrogenase”; SoxCD has also been shown to function as a sulfite dehydrogenase. *soxB* encodes SoxB, a sulfur-thiol esterase, identified in *P. pantotrophus* as

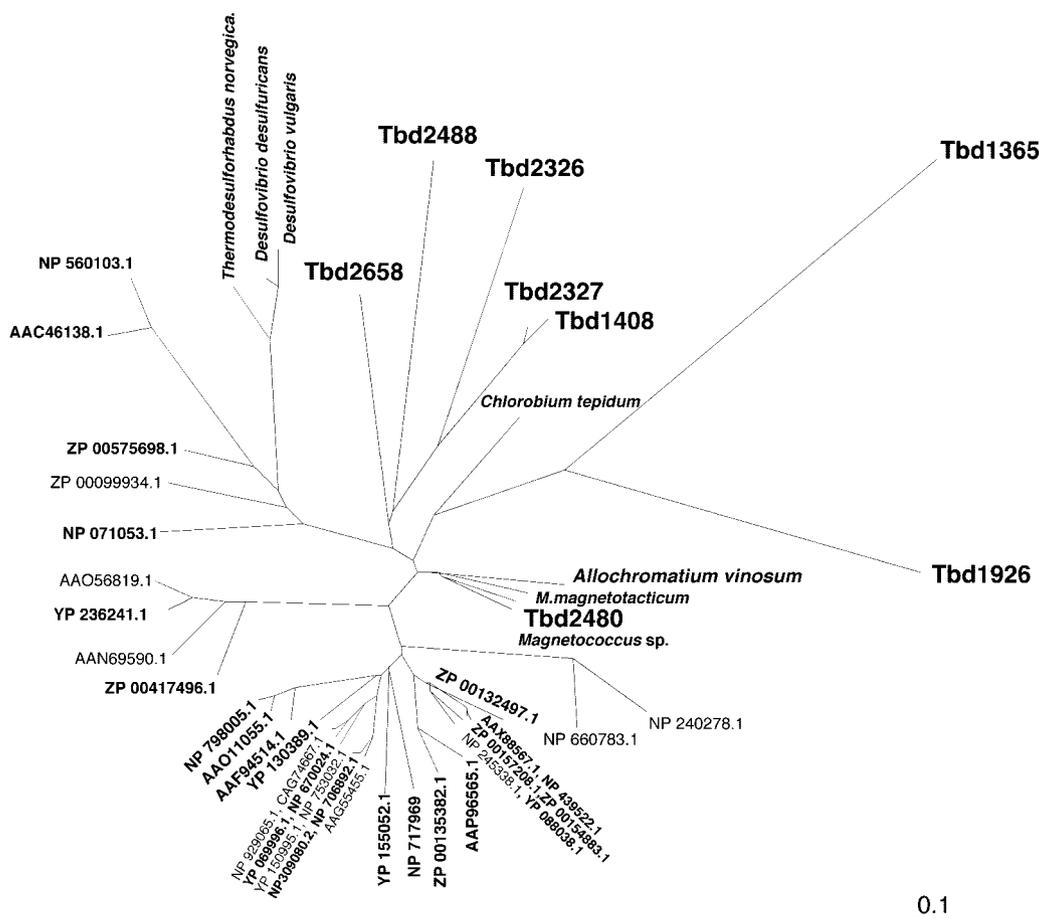


FIG. 3. Phylogenetic relationships among the eight putative DsrC proteins encoded in *T. denitrificans* ATCC 25259 and the top BLASTP matches from the GenBank nr database for Tbd2480. Of the proteins represented in this figure that are not from *T. denitrificans*, more than 70% are known or predicted to be DsrC or more broadly related to sulfite reductases (indicated in boldface type). For limbs that show species names rather than GenBank accession numbers, the corresponding accession numbers are as follows: *A. vinosum* (AAC35399.1), *M. magnetotacticum* (ZP 00052645.1), *Magnetococcus* sp. (ZP 00287929.1), *C. tepidum* (NP 663123.1), *T. norvegica* (CAC36215.1), *D. desulfuricans* (ZP 00130056.2), and *D. vulgaris* (YP 011988).

enzyme B, a protein with a dinuclear manganese center that catalyzes thiosulfate cleavage and sulfate production. *soxE* encodes a *c*-type cytochrome. *soxF* encodes a sulfide dehydrogenase/ flavocytochrome-*c* oxidoreductase protein. *soxRS* are reported to have a regulatory function. *soxGH* are currently of uncertain function. Finally, the SoxFGH proteins (which are all periplasmic) were reportedly not required for lithotrophic growth of *P. pantotrophus* on thiosulfate, although they were induced by thiosulfate. The proteins SoxXA, SoxYZ, SoxB, and SoxCD can be reconstituted into a system catalyzing thiosulfate-, sulfite-, sulfur-, and hydrogen sulfide-dependent cytochrome *c* reduction in *P. pantotrophus* and *P. versutus*, although this multienzyme system may not operate in the facultative chemolithotroph *S. novella*. The *soxB* gene has also been identified in *T. thioparus*, some  $\gamma$ -proteobacteria (including *Halotheiobacillus* and *Thiomicrospira* spp.), and some phototrophic sulfur bacteria (59).

In *T. denitrificans*, central roles for the putative SoxXA, SoxB, and SoxYZ gene products are suggested by the clustering of the genes encoding them, but the low polypeptide sequence identity of these to the corresponding sequences in *P.*

*pantotrophus* could mean that their biochemical functions might differ considerably from those of *P. pantotrophus*. The thiosulfate-oxidizing multienzyme system of *P. pantotrophus* (and of other  $\alpha$ -proteobacteria) is located in the periplasm, but there is considerable evidence from studies of *T. denitrificans* (and other obligately chemolithotrophic sulfur oxidizers) that at least some reactions of thiosulfate, sulfite, and sulfide oxidation require membrane-associated processes (43). Deduction of the functions of the putative *T. denitrificans* *sox* genes solely by reference to the roles of the *sox* complexes in *Paracoccus* species must clearly be done with caution, because even if they were acquired primordially by lateral gene transfer (59), they could encode significantly modified enzyme functions in extant  $\alpha$ - and  $\beta$ -proteobacteria.

In a few bacteria that oxidize inorganic sulfur compounds, namely *T. denitrificans*, *Allochrochromatium vinosum*, and *C. tepidum*, a siroheme-containing sulfite reductase has been proposed to catalyze the oxidation of certain inorganic sulfur species (e.g., hydrogen sulfide or sulfane-sulfur derived from thiosulfate) to sulfite (20, 71, 86). Thus, dissimilatory sulfite reductase, which is encoded by *dsr* genes and named for its

catalytic role in sulfate-reducing bacteria and archaea, is apparently used in the reverse direction for dissimilatory oxidation of sulfur compounds. Siroheme-containing sulfite reductase (with an  $\alpha_2\beta_2$  structure encoded by *dsrAB*) was previously purified from *T. denitrificans* strain DSM 807 (86). A gene cluster (*dsrABEFHCKMLJOPNR*; Tbd2485–Tbd2472) occurs in *T. denitrificans* ATCC 25259 that is very similar in terms of gene sequence and organization to a *dsr* cluster in *A. vinosum* that was studied by Dahl et al. (17). A notable difference in gene organization is that *dsrS* in *T. denitrificans* (Tbd2558) is not part of the *dsr* cluster, as it is in *A. vinosum*, and that a *cysG* (siroheme synthase)-like gene is located adjacent to *dsrR* in *T. denitrificans* (Tbd2471). For the translations of most of these *dsr* genes, the degree of identity with the corresponding *A. vinosum* sequences is >55%. This is the only major cluster of *dsr* genes in the finished *T. denitrificans* sequence, which contrasts with the claim by Dahl et al. (17) that there are two *dsr* gene clusters (on the basis of their examination of shotgun clone sequences in GenBank).

A noteworthy finding with regard to *dsr* genes in *T. denitrificans* was that two genes, *dsrC* and *dsrA*, are replicated multiple times in the genome, typically with no more than one or two adjacent genes that are putatively associated with sulfur-compound oxidation. Eight putative copies of *dsrC* were identified (Fig. 3): Tbd2480 (located in the large *dsr* gene cluster), Tbd2488 (located next to Tbd2489, which encodes a rhodanese-related sulfurtransferase), Tbd2658, Tbd2326 and Tbd2327 (which are adjacent to each other), Tbd1365 (located near a *dsrA* copy, Tbd1369), Tbd1408 (located next to Tbd1407, which encodes sulfide:quinone oxidoreductase), and Tbd1926. The degree of sequence identity among the corresponding predicted DsrC copies ranges from 26 to 88%. DsrC is a soluble, cytoplasmic protein whose function is not currently known (62). A cysteine residue at the C terminus of DsrC that is highly conserved in a range of bacteria including *A. vinosum* and various sulfate-reducing bacteria (62) is present in only two of the eight copies encoded in the *T. denitrificans* genome, including the copy located in the *dsr* cluster (Tbd2480) and Tbd2658. In fact, overall, the translated DsrC from Tbd2480 was more similar to DsrC in *A. vinosum* than to the other seven copies in *T. denitrificans* (Fig. 3). Inasmuch as Tbd2480 is the *dsrC* copy in *T. denitrificans* most likely to code for functional DsrC, it is noteworthy that, like *dsrC* in *A. vinosum* (17, 62) and unlike all other *dsrC* copies in *T. denitrificans*, Tbd2480 appears to be constitutively expressed [as indicated by RT-qPCR results for *T. denitrificans* carrying out thiosulfate or Fe(II) oxidation under denitrifying conditions; Table 3]. As shown in Table 3, Tbd2480 is relatively highly expressed when oxidizing either thiosulfate or Fe(II), whereas none of the other seven putative *dsrC* copies is highly expressed under both conditions.

Three putative copies of *dsrA* were identified in the *T. denitrificans* genome: Tbd2485 (located in the large *dsr* gene cluster), Tbd1309, and Tbd1369 (located near a *dsrC* copy). The degree of sequence identity among the corresponding predicted DsrA copies was high (from 78 to 83%). As *dsrA* encodes the  $\alpha$  subunits of the  $\alpha_2\beta_2$ -structured siroheme sulfite reductase, it is curious that two copies of *dsrA* in the *T. denitrificans* genome are not located near copies of *dsrB*, which encodes the  $\beta$  subunits; indeed, only one *dsrB* copy was identified in the genome (Tbd2484). Thus, the nature of

TABLE 3. Differential transcription of selected genes in *T. denitrificans* that occur in multiple copies

Genes compared	Thiosulfate-induced transcription (fold difference) <sup>a</sup>	FeCO <sub>3</sub> -induced transcription (fold difference) <sup>b</sup>
<i>dsrC</i> (putative)		
Tbd2480/Tbd2480 <sup>c</sup>	1 <sup>d</sup>	0.38
Tbd2488/Tbd2480 <sup>c</sup>	1.4	0.025
Tbd2658/Tbd2480 <sup>c</sup>	0.069	0.006
Tbd2326/Tbd2480 <sup>c</sup>	0.015	0.002
Tbd2327/Tbd2480 <sup>c</sup>	0.009	0.002
Tbd1365/Tbd2480 <sup>c</sup>	0.039	0.009
Tbd1408/Tbd2480 <sup>c</sup>	0.82	0.031
Tbd1926/Tbd2480 <sup>c</sup>	0.001	0.002
APS reductase		
$\alpha$ subunit		
Tbd0872/Tbd2282	80	NA <sup>e</sup>
$\beta$ subunit		
Tbd0873/Tbd2283	740	NA
ATP sulfurylase		
Tbd0874/Tbd0210	5	NA
Nitric oxide reductase		
<i>norC</i>		
Tbd0562/Tbd0822	63	NA
<i>norB</i>		
Tbd0561/Tbd0823	61	NA

<sup>a</sup> Cells harvested for RNA while carrying out thiosulfate oxidation and denitrification (see Materials and Methods).

<sup>b</sup> Cells harvested for RNA while carrying out oxidation of Fe(II) (in FeCO<sub>3</sub>) and denitrification (see Materials and Methods).

<sup>c</sup> Comparison made to the number of transcripts for Tbd2480 under thiosulfate-induced conditions. The transcript copy number for Tbd2480 under these conditions was relatively high (in the copy number range of Tbd0562 and Tbd0561, which encode subunits of nitric oxide reductase, a key enzyme involved in denitrification).

<sup>d</sup> By definition.

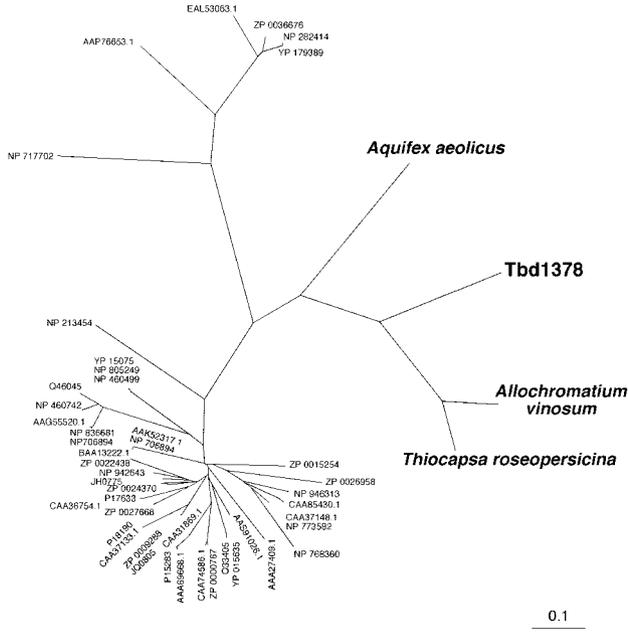
<sup>e</sup> NA, not analyzed.

*dsr* gene duplication in *T. denitrificans* differs from that observed in *C. tepidum*, whose genome includes two copies of the *dsrCABL* cluster (17, 20).

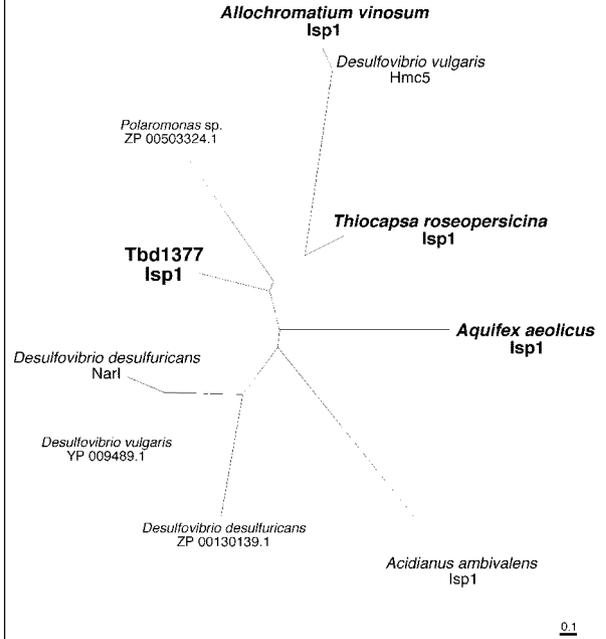
*T. denitrificans* ATCC 25259 contains genes encoding all the enzymes necessary to catalyze the AMP-dependent oxidation of sulfite to sulfate (Fig. 2). All but one of these enzymes is used in the reverse direction by sulfate-reducing bacteria for the activation of sulfate to APS and the subsequent AMP-yielding reduction of APS to sulfite. APS reductase, an  $\alpha\beta$ -heterodimeric iron-sulfur flavoenzyme, is encoded by Tbd0872–Tbd0873 and catalyzes the AMP-dependent oxidation of sulfite to APS. Another pair of genes, Tbd2282–Tbd2283, also putatively encodes APS reductase, but RT-qPCR results suggest that the Tbd0872–Tbd0873 genes are much more highly expressed during thiosulfate oxidation (Table 3). ATP sulfurylase, which catalyzes an ATP-yielding substrate level phosphorylation that converts APS to sulfate, is encoded by Tbd0874 and also by Tbd0210 (with the former being more highly expressed; Table 3). APAT, which is encoded by Tbd0601 and catalyzes an alternative substrate-level phosphorylation that converts APS to sulfate (yielding ADP rather than ATP), is not reversible (although it was formerly misnamed ADP sulfurylase) (13).

The *T. denitrificans* genome includes other genes that are

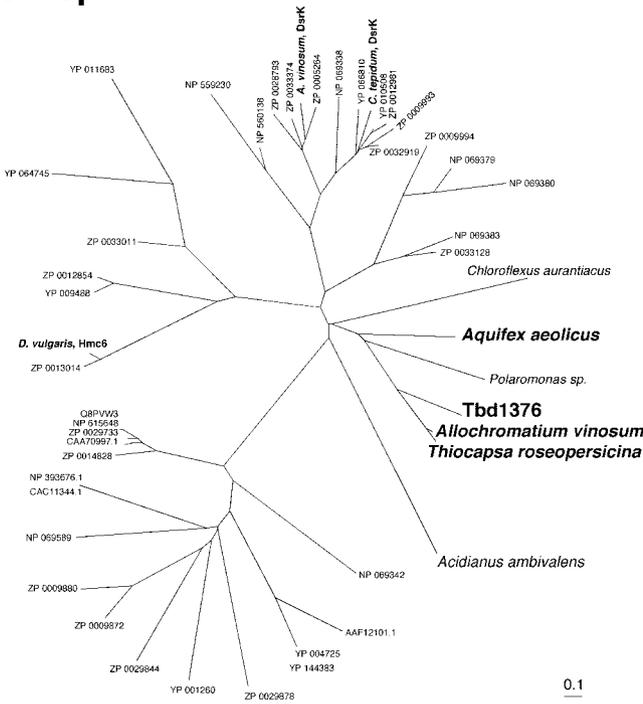
### A. HynS



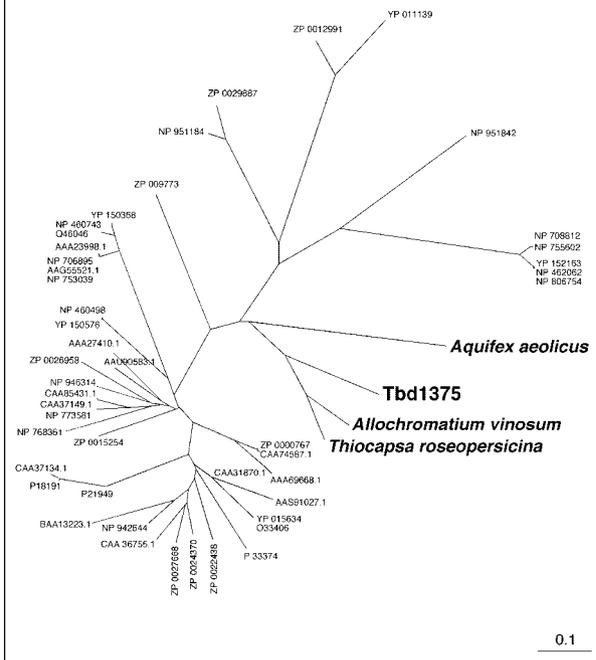
### B. Isp1



### C. Isp2



### D. HynL



likely to play a role in sulfur-compound oxidation, including sulfide:quinone oxidoreductase (Tbd1407, Tbd2225) and rhodanese (thiosulfate-sulfurtransferase; Tbd1650, Tbd2399, Tbd2489). Genes for dimethyl sulfoxide (DMSO) reductase (Tbd0570–Tbd0572) and tetrathionate reductase (Tbd1739–Tbd1741) are also present in the *T. denitrificans* genome, but these may have a role as anaerobic electron acceptors rather than in sulfur-compound oxidation. No genes for the  $\alpha$ - and  $\beta$ -subunits of DMSO dehydrogenase were detected. The type strain of *T. denitrificans* (NCIMB 9548) and some strains of *T. thioparus* can oxidize and grow on thiocyanate as a sole electron donor (47), and three genes of *T. thioparus* encode the thiocyanate hydrolase enzyme that initiates thiocyanate degradation (GenBank AB007989; *scnBAC*). In contrast, *T. denitrificans* strain ATCC 25259 does not oxidize thiocyanate, and its genome lacks the genes encoding thiocyanate hydrolase.

**Hydrogen metabolism.** Analysis of the genome of *T. denitrificans* ATCC 25259 has revealed the presence of genes encoding two [NiFe]hydrogenases. Hydrogenases are metalloenzymes that catalyze the reversible oxidation of  $H_2$  to protons and are vital components of the energy metabolism of many microbes. Notably, hydrogenases have not previously been reported in *T. denitrificans*, and the sequenced strain does not appear to be able to grow on hydrogen as a sole electron donor under denitrifying conditions (H. Beller, unpublished data); however, hydrogen oxidation appears to be required for nitrate-dependent U(IV) oxidation by *T. denitrificans* (5).

One of the hydrogenases encoded in the *T. denitrificans* genome is putatively a cytoplasmic, heterotetrameric, group 3b [NiFe]hydrogenase (following the classification system described by Vignais et al. [87]). The four-gene cluster (Tbd1260–Tbd1263) does not appear to be near any accessory or maturation genes encoding proteins necessary for assembly of the functional holoenzyme. Although group 3b hydrogenases have primarily been found in hyperthermophilic archaea (87), BLASTP analysis revealed that a group of similar predicted proteins (43 to 53% identity for the four subunits) occur in *Azotobacter vinelandii*, a mesophilic,  $\delta$ -proteobacterium; gene organization in *T. denitrificans* and *A. vinelandii* was also similar. Group 3b hydrogenases in the hyperthermophile *Pyrococcus furiosus* are among the better characterized and are thought to play a role in disposing of excess reductant generated during fermentation (whereby NADPH can serve as the physiological electron donor for  $H_2$  evolution) (87). The role of a group 3b hydrogenase in *T. denitrificans*, if indeed this hydrogenase is expressed in functional form, is not currently known.

The other hydrogenase encoded in the *T. denitrificans* genome is putatively a periplasmic, group 1 [NiFe]hydrogenase (following the classification system described by Vignais et al.

[87]). Although the sequences of the small (HynS) and large (HynL) subunits of this hydrogenase are similar to those in many bacteria and archaea, they occur in an unusual gene cluster (*hynS-isp1-isp2-hynL*; Tbd1378–Tbd1375) that has only been observed in four other microbes to date (none of which is a mesophilic, chemolithoautotrophic bacterium like *T. denitrificans*): the phototrophic sulfur bacteria *Thiocapsa roseopersicina* (66) and *A. vinosum* (16), the hyperthermophilic bacterium *Aquifex aeolicus* (GenBank NP 213658.1–213655.1), and the archaeon *Acidianus ambivalens* (53). Typically, *hynS* and *hynL* are adjacent to one another, but they are separated by two intervening genes in these species. Not only is the organization of the *hynS-isp1-isp2-hynL* gene cluster in *T. denitrificans* identical to that of the other four species, the sequence similarity of the four predicted proteins is also relatively high among these species (Fig. 4). The degree of sequence identity for HynS, Isp1, Isp2, and HynL in *T. denitrificans* compared to *T. roseopersicina*, *A. aeolicus*, and *A. vinosum* ranges from 26 to 68%. A phylogenetic tree of Isp1 in *T. denitrificans* ATCC 25259 and the small complement of related proteins from the GenBank nr database (BLASTP E values  $< 10^{-5}$ ) reveals similarity not only to Isp1 copies of other species but also to NarI (the  $\gamma$  subunit of cytoplasmic nitrate reductase) and Hmc5 (part of the high-molecular-weight, transmembrane, electron transport protein complex found in *Desulfovibrio vulgaris*) (Fig. 4B). Alignment of the predicted amino acid sequence of Isp1 from *T. denitrificans* with other sequences represented in Fig. 4B shows that four histidine residues (located in two of the five predicted transmembrane helices in Isp1, NarI, and Hmc5) are highly conserved. Similar observations have been made for other Isp1 sequences (16, 53, 66), and Berks et al. (8) elucidated how the conserved histidines (and the two *b*-hemes that they putatively bind, one in each half of the membrane bilayer) play a role in mediating transport of electrons across the cytoplasmic membrane as part of an electron-carrying arm of a redox loop in the integral membrane proteins NarI and HyaC (a *b*-type cytochrome associated with periplasmic [NiFe]hydrogenases). On the basis of these and other observations, it is likely that Isp1 serves two functions: (i) to anchor HynSL on the periplasmic side of the cytoplasmic membrane, where  $H_2$  can be converted to  $2H^+$  and  $2e^-$  by HynSL, and (ii) to mediate transmembrane electron transfer from HynSL to the quinone pool of electron transport chains and thereby participate in a chemiosmotic mechanism of energy conservation. Notably, in serving these functions, Isp1 may be substituting for the *b*-type cytochrome HupC/HoxZ/HupZ/HyaC that is typically found in group 1 [NiFe]hydrogenases but which is apparently absent in the *T. denitrificans* genome. A phylogenetic tree of Isp2 in *T. denitrificans* (Fig. 4C) reveals a similarity not only to Isp2 sequences of other

FIG. 4. Phylogenetic relationships among predicted amino acid sequences for HynS (A), Isp1 (B), Isp2 (C), and HynL (D) in *T. denitrificans* and the best BLASTP matches from the GenBank nr database. For limbs that show species names rather than GenBank accession numbers, the corresponding accession numbers are as follows: (HynS) *A. vinosum* (AAU93828.1), *T. roseopersicina* (AAC38281.1), *A. aeolicus* (NP 213658.1); (Isp1) *A. vinosum* (AAU93829.2), *T. roseopersicina* (AAC38283.1), *A. aeolicus* (NP 213657.1), *D. vulgaris* Hmc5 (YP 009755), *A. ambivalens* (CAC86885.1), *D. desulfuricans* NarI (ZP 00128546.1); (Isp2) *A. vinosum* (AAY89333.1), *T. roseopersicina* (AAC38284.1), *A. aeolicus* (NP 213656.1), *A. ambivalens* (CAC86886.1), *Polaromonas* sp. (ZP 00503323.1), *C. aurantiacus* (ZP 00356812), *A. vinosum* DsrK (AAC35401.2), *C. tepidum* DsrK (NP 663117.1), *D. vulgaris* Hmc6 (YP 009754.1); (HynL) *A. vinosum* (AAY89334.1), *T. roseopersicina* (AAC38282.1), *A. aeolicus* (NP 213655.1).

species but also to sequences of various iron-sulfur-containing proteins such as heterodisulfide reductases, DsrK (from other sulfur-compound oxidizers *A. vinosum* and *C. tepidum*), and Hmc6 from *D. vulgaris*; such similarities have been noted previously for other *Isp2* copies (16, 66).

The two adjacent gene clusters (Tbd1380–Tbd1374 and Tbd1381–Tbd1386 [on opposite DNA strands]) that code for the group 1 [NiFe]hydrogenase of *T. denitrificans* include a number of genes putatively involved in biosynthesis and maturation of the hydrogenase. This clustering of maturation genes along with the *hynS-isp1-isp2-hynL* cluster in *T. denitrificans* distinguishes its gene organization from that of *T. roseopersicina* and *A. aeolicus*, which do not have accessory genes in the immediate vicinity of the *hynS-isp1-isp2-hynL* cluster. In the Tbd1380–Tbd1374 gene cluster, Tbd1374 codes for a homolog of *UreJ* and is probably involved in Ni transport; *hynD* (Tbd1380) codes for a putative maturation protease. Most or all of the genes in the *hypCABDFE* gene cluster (Tbd1381–Tbd1386) encode proteins that are putatively involved with insertion of Ni, Fe, CO, and CN in the active site of the hydrogenase (87).

**Aerobic respiration.** The genome of *T. denitrificans*, a facultative anaerobe, encodes all the necessary machinery for aerobic respiration, including NADH:ubiquinone oxidoreductase (complex I; Tbd1142–Tbd1155), succinate dehydrogenase (complex II; Tbd1182–Tbd1185), and cytochrome *bc*<sub>1</sub>-type ubiquinol oxidoreductase (complex III; Tbd1831–Tbd1833) (9). These components can provide the reducing equivalents needed for terminal respiration with nitrate or oxygen, the latter in conjunction with one of three terminal cytochrome *c* oxidases encoded by two gene clusters on the *T. denitrificans* genome. The first cluster encodes a cytochrome *aa*<sub>3</sub>-type cytochrome *c* oxidase (Tbd0325, Tbd0326, Tbd0328, Tbd0330) and a *cbb*<sub>3</sub>-type cytochrome *c* oxidase (Tbd0338–Tbd0341), whereas the second cluster (Tbd0640–Tbd0643) encodes a second *cbb*<sub>3</sub>-type cytochrome *c* oxidase. The presence of both *aa*<sub>3</sub>- and *cbb*<sub>3</sub>-type oxidases, in addition to the denitrification machinery, allows *T. denitrificans* to survive under a wide range of redox conditions; presumably, the *aa*<sub>3</sub> oxidase operates under high oxygen tension, *cbb*<sub>3</sub> oxidases operate under microaerophilic conditions, and the denitrification complex operates under anaerobic conditions (58, 61).

**Denitrification.** *T. denitrificans* has all necessary genes encoding the four essential enzymes that catalyze denitrification (reduction of nitrate to nitrogen gas): nitrate reductase, nitrite reductase, nitric oxide reductase, and nitrous oxide reductase (60, 94). The membrane-bound, dissimilatory nitrate reductase is encoded in a *narKK<sub>2</sub>GHJI* cluster (Tbd1401–Tbd1406), whereas the NarXL two-component regulatory system is encoded on the reverse DNA strand (Tbd1400–Tbd1399). This gene organization is similar to that described for *Pseudomonas aeruginosa* PAO1 and *P. fluorescens* C7R12 (60). A *nir* operon including the CDS for cytochrome *cd*<sub>1</sub>-nitrite reductase (*nirS*; Tbd0077) is present in *T. denitrificans*, and this protein was in fact purified from a different strain of *T. denitrificans* (strain DSM 807) (36). *T. denitrificans* ATCC 25259 contains two *norCB* gene clusters that include the *norCB* structural genes encoding nitric oxide reductase, a membrane-anchored protein complex. RT-qPCR analyses carried out with thiosulfate-oxidizing, denitrifying cells (Table 3) indicated that the *norCB* genes Tbd0562–Tbd0561 had >50-fold-higher expression levels than

*norCB* genes Tbd0822–Tbd0823, strongly indicating that the former genes are of greater functional importance. The predicted NorC amino acid sequence for the less-expressed copy (Tbd0822) contains >120 more residues at the C terminus than the highly expressed copy (Tbd0562) or a similar copy in *Azoarcus* sp. strain EbN1 (GenBank YP 157125); these additional amino acid residues for Tbd0822 include a second CXXCH heme-binding motif. The enzyme catalyzing the final step of denitrification, nitrous oxide reductase, is associated with the structural gene *nosZ* (Tbd1389) and, like NirS, was purified from *T. denitrificans* strain DSM 807 (36). Organization of *nos* genes in *T. denitrificans* is similar, but not identical, to that described for *Ralstonia metallidurans* CH34 (60). As has been observed for some other  $\beta$ -proteobacteria (60), *nosR* (Tbd1390) is located downstream from *nosZ* in *T. denitrificans*.

***c*-type cytochromes.** *T. denitrificans* strain ATCC 25259 has a higher number of *c*-type cytochromes than most bacteria with finished genomes, as suggested by analysis of the characteristic CXXCH heme-binding motif throughout the genome. Fifty-six genes, or approximately 2% of the total CDS, contained at least one CXXCH motif (some encoded proteins, such as DnaJ and ribosomal protein L31, are not truly *c*-type cytochromes; Table 4). In the context of bacteria reported to have relatively high numbers of *c*-type cytochromes, the number in *T. denitrificans* is less than that cited for *Geobacter sulfurreducens* (111, or 3.2% of the total CDS) (54) but more than for *Shewanella oneidensis* (39, or 0.8% of the total CDS) (34) and *Pseudomonas aeruginosa* (35, or 0.6% of the total CDS) (77). Overall, *c*-type cytochromes in *T. denitrificans* range in predicted molecular mass from 9.5 to 138 kDa and in number of heme groups from one to three (with only one triheme *c*-type cytochrome and the vast majority as monoheme proteins) (Table 4). Although the functions of some *c*-type cytochromes in *T. denitrificans* can be confidently predicted, such as NirS and NorC, some are of less certain or unknown function (Table 4). The ability of *T. denitrificans* to catalyze anaerobic, nitrate-dependent oxidation of metals with high reduction potentials, such as Fe(II) or U(IV) (5, 78), may be mediated by *c*-type cytochromes, as few other electron carriers in a bacterial cell would have sufficiently high reduction potentials to accept electrons from compounds such as uraninite, or UO<sub>2</sub> (the UO<sub>2</sub><sup>2+</sup>/UO<sub>2</sub> couple has an E<sub>0</sub>' value of +0.26V) (5).

**Autotrophy.** The genome of this obligate chemolithoautotroph encodes both form I and form II ribulose 1,5-bisphosphate carboxylase/oxygenase (RubisCO) enzymes for CO<sub>2</sub> fixation (21, 35). The form I genes (*cbbl* and *cbbs*) occur in an operon with *cbbQ* and *cbbo* genes (*cbblSQO*; Tbd2624–Tbd2621). The form II gene, *cbbm*, is in a separate operon that also includes *cbbQ* and *cbbo* genes; the operon has the form *cbbmQO* (Tbd2638–Tbd2636). Both operons are preceded by divergently transcribed *cbbr* genes encoding LysR-type transcriptional regulators (Tbd2625 and Tbd2639). The *cbbQ* and *cbbo* genes encode proteins involved in the posttranslational activation of RubisCO (33). The two copies of each gene are quite distinct: the two CbbQ proteins have 71% identical residues, whereas the two CbbO proteins only share 34% identity. The two RubisCO operons, although separate, fall within a 33-kb region that also includes an operon of 10 genes (Tbd2641–Tbd2650) encoding the carboxysome shell proteins (14). The carboxysome operon does not begin with *cbblS*,

TABLE 4. CDS potentially encoding *c*-type cytochromes in the *T. denitrificans* genome<sup>a</sup>

CDS	Annotation <sup>b</sup>	Molecular mass (Da) <sup>c</sup>	No. of hemes
Tbd0055	Cytochrome <i>c</i> family protein	20,116	1
Tbd0064	Cytochrome <i>c</i> -553	23,727	2
Tbd0070	Probable <i>nirN</i>	63,589	1
Tbd0076	Probable <i>nirC</i>	10,547	1
Tbd0077	<i>nirS</i> (cytochrome <i>cd</i> <sub>1</sub> )	62,992	1
Tbd0094	Hypothetical protein	17,109	1
Tbd0128	Cytochrome <i>c</i>	38,000	2
Tbd0129	Cytochrome <i>c</i>	21,784	2
Tbd0137	Diheme cytochrome <i>c</i>	19,427	2
Tbd0138	Cytochrome <i>c</i> -type protein	14,395	1
Tbd0146	Probable cytochrome <i>c</i> <sub>5</sub>	26,734	2
Tbd0187	Cytochrome <i>c</i>	21,387	2
Tbd0219	Flavin adenine dinucleotide–flavin mononucleotide-containing dehydrogenase	138,251	1
Tbd0325	<i>aa</i> <sub>3</sub> -type cytochrome <i>c</i> oxidase, subunit II	41,279	1
Tbd0339	<i>cbb</i> <sub>3</sub> -type cytochrome <i>c</i> oxidase, subunit II	28,037	1
Tbd0341	<i>cbb</i> <sub>3</sub> -type cytochrome <i>c</i> oxidase, subunit III	33,124	2
Tbd0436	Excinuclease ATPase subunit	103,145	1
Tbd0562	<i>norC</i>	15,845	1
Tbd0564	<i>soxA</i>	30,960	1
Tbd0567	<i>soxX</i>	12,712	1
Tbd0571	DMSO reductase chain B	25,909	1
Tbd0640	<i>cbb</i> <sub>3</sub> -type cytochrome <i>c</i> oxidase, subunit III	33,873	2
Tbd0642	<i>cbb</i> <sub>3</sub> -type cytochrome <i>c</i> oxidase, subunit II	22,314	1
Tbd0723	Possible high-affinity Fe <sup>2+</sup> /Pb <sup>2+</sup> permease	69,511	1
Tbd0752	Mannose-sensitive hemagglutinin pilin biogenesis ATPase protein MshE	62,481	1
Tbd0820	Cytochrome <i>c</i> (in or near nonfunctional <i>nor</i> cluster)	57,261	2
Tbd0822	<i>norC</i> -related (potentially not functional)	30,200	2
Tbd0840	Probable cytochrome <i>c</i> <sub>5</sub>	16,718	1
Tbd0917	<i>soxX</i>	13,246	1
Tbd0918	<i>soxA</i>	30,875	1
Tbd1169	Ferredoxin, 2Fe-2S	12,259	1
Tbd1357	Unknown	16,635	1
Tbd1398	Putative cytochrome <i>c</i> -type protein	15,842	1
Tbd1404	<i>narH</i>	59,191	1
Tbd1484	Cytochrome <i>c</i>	9,544	1
Tbd1520	Putative Fe-S protein	48,430	1
Tbd1542	ATPase involved in DNA replication	61,297	1
Tbd1564	Probable ribonuclease E	95,354	1
Tbd1585	Putative pyruvate formate-lyase-activating enzyme	40,800	1
Tbd1831	Putative cytochrome <i>c</i> <sub>1</sub>	27,211	1
Tbd1840	Unknown	11,061	1
Tbd2026	Possible cytochrome <i>c</i> <sub>4</sub> or <i>c</i> -553	11,253	1
Tbd2027	Cytochrome <i>c</i> , class IC	11,521	1
Tbd2034	Possible cytochrome subunit of sulfide dehydrogenase	10,395	1
Tbd2060	Possible alpha-mannosidase	64,835	1
Tbd2157	Cytochrome <i>c</i>	18,742	1
Tbd2170	Activase of anaerobic class III ribonucleotide reductase	24,585	1
Tbd2181	Unknown	20,904	1
Tbd2476	<i>dsrJ</i>	17,948	3
Tbd2477	<i>dsrL</i>	71,328	1
Tbd2545	Diheme cytochrome <i>c</i>	37,973	2
Tbd2726	Cytochrome <i>c</i>	11,096	1
Tbd2727	Conserved protein of unknown function	74,616	1
Tbd2738	Zinc-dependent hydrolase	26,287	1

<sup>a</sup> As defined by the presence of at least one CXXCH heme-binding motif. Tbd0039 (which encodes ribosomal protein L31) and Tbd1539 (which encodes DnaJ) include the CXXCH motif but were excluded from this table.

<sup>b</sup> Best attempt at annotation based on examination of best BLASTP hits, top 10 PSI-BLAST hits, and genomic context.

<sup>c</sup> Molecular mass predicted for the unprocessed gene product without cofactors.

unlike other known examples (14). These three operons, all located on the reverse strand, are oriented to be transcribed in the same direction. The carboxysome operon includes the gene (Tbd2649) for carbonic anhydrase (CA) epsilon (74). The carboxysome operon is also preceded by a divergently transcribed *cbbR* gene (Tbd2651) encoding a LysR-type transcriptional

regulator. In addition to the epsilon-type CA, a eukaryotic-type CA (Tbd2167) is encoded elsewhere in the genome. Since there is no evidence that the carboxysome operon is functional (14, 72), this alternative CA may be the primary source of this activity.

Inasmuch as *T. denitrificans* can grow under both aerobic

and denitrifying conditions, and form I and form II RubisCO in this species were shown to have markedly different abilities to discriminate between CO<sub>2</sub> and O<sub>2</sub> (35), it is possible that form I and II RubisCO are differentially expressed in *T. denitrificans* as a function of O<sub>2</sub> concentration. Molecular oxygen competes with CO<sub>2</sub> for the active site of RubisCO and thereby decreases its efficiency for carbon fixation. Hence, form I, which has a higher CO<sub>2</sub>/O<sub>2</sub> specificity, should be more highly expressed under aerobic conditions, whereas form II should be more highly expressed under anaerobic conditions.

Genes for all enzymes to complete the Calvin-Benson-Bassham cycle are present. Transketolase, NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12), phosphoglycerate kinase, pyruvate kinase, and fructose 1,6-bisphosphate aldolase (Tbd0159–Tbd0163) are encoded by an operon, whereas fructose 1,6-/sedoheptulose-1,7-bisphosphatase (Tbd2577), ribose 5-phosphate isomerase (Tbd2364), and phosphoribulokinase (Tbd2447) are encoded by isolated genes. Genes encoding ribulose 5-phosphate 3-epimerase and phosphoglycolate phosphatase (Tbd2230–Tbd2229) are adjacent but may not be cotranscribed.

**Central intermediary metabolism.** Organic storage materials in *T. denitrificans* have not been reported, but the presence of genes encoding glycogen synthase (Tbd2057), maltooligosyl trehalose synthase (Tbd1174), and various glucan branching enzymes (e.g., an  $\alpha$ -1,4-D-glucan branching enzyme; Tbd1173, Tbd2058) and glucano- and glycosyl-transferases suggests that the bacterium synthesizes a polyglucose storage product (cf. *Halothiobacillus neapolitanus* [10]). The gene for the key enzyme of the Embden-Meyerhof-Parnas (EMP) pathway necessary for it to effect gluconeogenesis (fructose 1,6-bisphosphatase) is present in the genome (Tbd2577). The synthesis of such a storage product would provide a rationale for the presence of genes for glucokinase (Tbd2062, Tbd2216), which could thus assist in the endogenous catabolism of stored polyglucose. Several genes encoding enzymes for polysaccharide hydrolysis also appear to be present:  $\beta$ -galactosidase (Tbd2429), several glycosidases (Tbd0727, Tbd0923, Tbd1172) and glycosyl transferases (e.g., Tbd0289, Tbd0293, Tbd0294, Tbd0301, Tbd2139), an  $\alpha$ -mannosidase (Tbd2060), and an  $\alpha$ -arabinofuranosidase (Tbd1789).

Genes encoding all the enzymes of the EMP pathway necessary for it to function in the forward direction for the conversion of glucose to pyruvate are present in the genome, including the gene for phosphofructokinase (Tbd1502), which is unique to the degradative EMP pathway. Genes for all the enzymes of the oxidative pentose phosphate pathway for the oxidation of glucose to carbon dioxide are also present in the genome. Some of the enzymes of the EMP and oxidative pentose phosphate pathways are also common to the Calvin-Benson-Bassham reductive pentose phosphate cycle for carbon dioxide fixation, and ribose 5-phosphate for nucleic acid synthesis can be produced from glucose 6-phosphate by glucose 6-phosphate dehydrogenase, phosphogluconolactonase, and 6-phosphogluconate dehydrogenase (encoded by Tbd2121–Tbd2123). In addition, genes encoding alcohol dehydrogenase (EC 1.1.1.1; Tbd1767) and other short-chain alcohol dehydrogenases (Tbd0924, Tbd1469, Tbd1549, Tbd1699, Tbd1886, Tbd2701, Tbd2756), lactate dehydrogenase (Tbd1998), and phosphoketolase (EC 4.1.2.9) (Tbd0049, Tbd0831) suggest

that *T. denitrificans* might be able to produce ethanol and lactate (by homo- or hetero-fermentative metabolism) from endogenous glucose under anoxic conditions. This would parallel the heterolactic fermentation of stored polyglucose carried out anaerobically by *Halothiobacillus neapolitanus* (11). Glucose 6-phosphatase and glycerol phosphatase are absent from the *T. denitrificans* genome, reflecting the lack of need to produce free glucose or glycerol.

Genes for some enzymes of the Entner-Doudoroff pathway are present, but the gene encoding 2-keto-3-deoxy-6-phosphogluconate (KDPG) aldolase is notably absent, meaning that *T. denitrificans* cannot express a functional Entner-Doudoroff pathway. We failed to detect KDPG aldolase in the genome in BLAST searches conducted using database polypeptide sequences from *Escherichia coli* and *Zymomonas*, *Gluconobacter*, and *Neisseria* spp. The gene putatively encoding 6-phosphogluconate (6-PG) dehydratase (Tbd2730), whose product is KDPG, may be a false identification, as a TBLASTN search of the *T. denitrificans* genome with the 6-PG dehydratase protein sequence of *Xanthomonas axonopodis* (GenBank NP\_642389) failed to detect any matching sequences, although direct BLAST2(P) comparison of the polypeptide encoded by Tbd2730 did show low (27 to 29%) identity to the 6-PG dehydratases of *Xanthomonas* sp. and *Helicobacter pylori* (GenBank NP\_223740). The highest identities of Tbd2730 indicated by BLAST analyses were to dihydroxyacid dehydratases, and comparisons by BLASTP of the polypeptide sequences of the dihydroxyacid dehydratase of *Sinorhizobium meliloti* (GenBank AL591792) with the 6-PG dehydratase of *Xanthomonas* sp. also showed 29% identity. Assigning putative function must thus be done with caution.

Genes for all the enzymes of the Krebs tricarboxylic acid cycle were identified in the genome. The E1 and E2 subunits of 2-oxoglutarate dehydrogenase are encoded by Tbd1188 and Tbd1189, whereas the E3 subunit (common also to pyruvate dehydrogenase) is encoded by Tbd0652. The genes encoding the E1, E2, and E3 subunits of pyruvate dehydrogenase are Tbd0652, Tbd0654, and Tbd0655, whereas Tbd1847 putatively encodes all three subunits, with highest identity to the *pdhA*, *pdhB*, and *pdhL* genes of *Ralstonia eutropha*. It was surprising to find genes for the E1 and E2 subunits of 2-oxoglutarate dehydrogenase, as *T. denitrificans* strains (including ATCC 25259) do not express an active 2-oxoglutarate dehydrogenase enzyme when growing autotrophically (57, 83). This inability is shared with other obligate chemolithotrophs and methanotrophs, including *Nitrosomonas europaea* and *Methylococcus capsulatus*, and has been proposed as a contributory factor in the obligate growth modes of these bacteria (15, 41, 48, 73, 89, 90, 92). The E3 component of the pyruvate and 2-oxoglutarate dehydrogenases is also known to be controlled by multiple regulatory mechanisms (93), so it may be that failure of obligate chemolithotrophs to express active 2-oxoglutarate dehydrogenase results from regulation at the E3 gene expression level.

While identifying genes encoding some Krebs cycle enzymes, it was found that a gene (Tbd2119) showed significant identity to both fumarase (fumarate hydratase; EC 4.2.1.2) and aspartate ammonia-lyase (EC 4.3.1.1). BLASTP analysis showed the translated sequence of Tbd2119 to share 55% sequence identity with the aspartate ammonia-lyase of *Geobacter sulfurreducens* (GenBank NP\_951538.1), 55%

identity with the fumarase sequence of *Pelobacter propionicus* (GenBank ZP\_00677090.1), and 41% with the fumarase C of *E. coli*. We suggest that the role of the Tbd2119 gene product is as a fumarase in the Krebs cycle. This similarity of genes for fumarase and aspartate ammonia-lyase is common across the database sequences for numerous organisms, possibly indicating multifunctional roles for the genes or their encoded proteins.

Genes encoding isocitrate lyase and malate synthase have not been detected using BLASTP searches with the translated polypeptide sequences of the genes from *E. coli*, meaning that the glyoxylate cycle cannot be present and hence exogenous acetate could not be metabolized as a sole source of carbon by that route.

**Transport systems for organic nutrients.** Permease systems for inorganic ions and numerous ABC transporter components are encoded within the genome, but relatively few specific systems have been detected for the uptake of sugars or organic acids. Those detected include various components constituting a tripartite ATP-independent periplasmic (TRAP)-type C<sub>4</sub>-dicarboxylate transporter system (Tbd0466, Tbd0467, Tbd0468, Tbd2151, Tbd2164) and phosphotransferase system components including enzyme I (Tbd2414), HPr (Tbd2413), two enzyme IIA subunits specific for mannose/fructose (Tbd2412, Tbd0531), and Hpr(ser) kinase/phosphorylase (Tbd0530). The absence from the *T. denitrificans* genome of a gene encoding enzyme IIC (the sugar permease component) suggests that the role of this PTS system may be regulatory rather than for sugar transport (30). The genome of *T. denitrificans* also encodes two sodium:solute symporter family proteins that may be involved in acetate uptake (Tbd0088, Tbd0212). A sodium:solute symporter protein, ActP, has been shown to be involved in acetate uptake in *E. coli* (GenBank P32705). A functional transport system for acetate in *T. denitrificans* was indicated by the uptake of <sup>14</sup>C-labeled acetate into bacteria growing chemolithotrophically (acetate provided 6 to 11% of the cell carbon of strain ATCC 25259) (84). As well as being used for lipid biosynthesis, [<sup>14</sup>C]acetate was incorporated only into the protein-amino acids glutamate, proline, and arginine, as reported for other obligate chemolithotrophs and methanotrophs that lack 2-oxoglutarate dehydrogenase (19, 41, 73, 92). Incorporation of acetate-carbon into glutamate by *T. denitrificans* was unaffected by exogenous glutamic acid, which was presumably not taken up significantly by the bacteria. The possibility remains to be tested that chemolitho-organotrophic growth by *T. denitrificans* might be possible if the organism were presented with compounds such as acetate, or a suitable C<sub>4</sub>-dicarboxylic acid, in the presence of thiosulfate and nitrate as the energy source. This would be akin to the chemolithoorganotrophic growth of *Nitrosomonas europaea* on fructose or pyruvate and ammonia (15, 37).

**Inorganic ion transport and heavy metal resistance.** A number of genes were identified in *T. denitrificans* that putatively encode transporters that can mediate either the uptake or efflux of a range of inorganic ions. In all, at least 18 complete ABC (ATP Binding Cassette) transporters predominantly for inorganic molecules are present in the genome, allowing for the uptake of Fe<sup>3+</sup>, thiosulfate, nitrate, nitrite, and many other ions (18). Numerous non-ABC-type transporters allowing for uptake of other ions, such as various sulfur-containing com-

TABLE 5. Comparison of encoded efflux-mediated heavy metal resistance systems among the genomes of *T. denitrificans* and other selected bacteria

Bacterial species	Genome size (Mbp)	No. of HME RNDs	No. of CDF	No. of CPx-type ATPases
<i>Thiobacillus denitrificans</i> <sup>a</sup>	2.9	5	3	3
<i>Geobacter sulfurreducens</i> PCA <sup>a</sup>	3.8	3	2	2
<i>Ralstonia metallidurans</i> <sup>b</sup>	6.9	12	3	5
<i>Pseudomonas aeruginosa</i> <sup>b</sup>	6.3	1	3	4
<i>Escherichia coli</i> <sup>b</sup>	4.6	1	2	2

<sup>a</sup> Putative heavy metal-exporting protein families for *T. denitrificans* and *G. sulfurreducens* PCA (GenBank AE01780) were identified as described by Nies (55). Confirmatory data on metal transport in *G. sulfurreducens* was obtained from an unpublished source (H. A. Vronis and D. R. Lovley, 105<sup>th</sup> Gen. Meet. Am. Soc. Microbiol., poster I-054, 2005).

<sup>b</sup> From Nies (55).

pounds and bicarbonate, are also present. The genome of *T. denitrificans* also contains a surprisingly large number of metal resistance systems, particularly considering its relatively small genome size (Table 5). In total, the *T. denitrificans* genome encodes as many as 17 possible metal resistance systems (described by Nies [55]), including five heavy metal efflux (HME) systems from the resistance-nodulation-cell division (RND) family of transporters; three cation diffusion facilitators (CDF); three CPx-type ATPases (heavy metal-specific P-type ATPases); and five additional gene clusters encoding possible resistance systems specific for metals such as Ni<sup>2+</sup> (*nreB*), Pb<sup>2+</sup> (*pbrT*), Hg<sup>2+</sup> (3), chromium (as chromate; *chrA*), and Cu<sup>2+</sup>/Ag<sup>2+</sup> (26, 32). Although the *T. denitrificans* genome has fewer systems than the model metal-resistant bacterium *Ralstonia metallidurans* (55), it has more than most other bacteria characterized to date (Table 5). Notably, *T. denitrificans* (or species with >98% 16S rRNA gene sequence similarity) was found to be prevalent in an inactive uranium mine with relatively high concentrations of uranium, nickel, cobalt, and zinc (80).

Several of the efflux-mediated heavy metal resistance systems, along with various systems involved in metal uptake and storage, are found in large gene clusters on the *T. denitrificans* genome (Fig. 1). The largest of these metal transport clusters, Tbd0704–Tbd0726, encodes proteins allowing for high-affinity Fe<sup>3+</sup> acquisition, Fe<sup>3+</sup> storage, Pb<sup>2+</sup> resistance, and heavy metal resistance. Genes involved in high-affinity Fe<sup>3+</sup> acquisition include homologs of a portion of the *Vibrio parahaemolyticus* polyhydroxycarboxylate-type siderophore biosynthesis, secretion, and uptake gene cluster *pvuApvsABCDE psuA* (Tbd0722–Tbd0717, Tbd0715) (81) and *tonBexbBD* (Tbd0713–Tbd0711), which allows for active transport across the outer membrane of Fe<sup>3+</sup>-bound siderophore. Also found are genes encoding the Fe<sup>3+</sup> storage proteins bacterioferritin and bacterioferritin-associated ferredoxin (Tbd0704–Tbd0705), Pb<sup>2+</sup> resistance (Tbd0723), and CDF family heavy metal resistance (Tbd0726). A second large gene cluster (encompassing genes on both the forward and reverse strands) encodes proteins primarily associated with metal resistance (Tbd1324–Tbd1341). This cluster includes a multi-copper oxidase (Tbd1324) (32), a periplasmic Cu<sup>2+</sup>-binding protein (Tbd1326) (26), two HME-RND systems (Tbd1327–Tbd1329, Tbd1333–Tbd1335), and a Hg<sup>2+</sup> resistance system, *merRTPA* (Tbd1338–Tbd1341) (3).

**Future prospects.** The availability of the *T. denitrificans* genome has fostered new insights into this bacterium and will effectively focus further investigations into its biochemistry and physiology. Among the new insights reported here are the following genomic characteristics: an unusually large number of genes encoding c-type cytochromes, a relatively large complement of genes associated with inorganic ion transport and heavy metal resistance, and the presence of genes encoding two [NiFe]hydrogenases, which is particularly significant because no physiological, biochemical, or genetic information on hydrogenases has previously been reported for this species. The genome also provides much more information on the genetic basis of sulfur-compound oxidation in chemolithotrophic  $\beta$ -proteobacteria (particularly with respect to *sox* and *dsr* genes). Much more work will be required to understand the genetic and biochemical basis of unusual and enigmatic metabolic capabilities of this bacterium, including the coupling of denitrification with sulfur-compound oxidation, the use of mineral electron donors, and the anaerobic, nitrate-dependent oxidation of metals. Whole-genome transcriptional studies with cDNA microarrays are currently under way to address such questions.

#### ACKNOWLEDGMENTS

We thank A. Lapidus and C. Detter (Department of Energy Joint Genome Institute), M. Land (Oak Ridge National Laboratory), and M. Shin, T. Legler, F. Bourguet, W. Marrs, and A. Krefft (Lawrence Livermore National Laboratory) for their valuable contributions.

This work was performed under the auspices of the U.S. Department of Energy by the University of California, Lawrence Livermore National Laboratory, under contract W-7405-Eng-48.

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