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Bacterial Lifestyle in a Deep-sea Hydrothermal Vent Chimney Revealed by the Genome Sequence of the Thermophilic Bacterium *Deferribacter desulfuricans* SSM1

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Abstract

The complete genome sequence of the thermophilic sulphur-reducing bacterium, *Deferribacter desulfuricans* SMM1, isolated from a hydrothermal vent chimney has been determined. The genome comprises a single circular chromosome of 2 234 389 bp and a megaplasmid of 308 544 bp. Many genes encoded in the genome are most similar to the genes of sulphur- or sulphate-reducing bacterial species within *Deltaproteobacteria*. The reconstructed central metabolisms showed a heterotrophic lifestyle primarily driven by C1 to C3 organics, e.g. formate, acetate, and pyruvate, and also suggested that the inability of autotrophy via a reductive tricarboxylic acid cycle may be due to the lack of ATP-dependent citrate lyase. In addition, the genome encodes numerous genes for chemoreceptors, chemotaxis-like systems, and signal transduction machineries. These signalling networks may be linked to this bacterium's versatile energy metabolisms and may provide ecophysiological advantages for *D. desulfuricans* SSM1 thriving in the physically and chemically fluctuating environments near hydrothermal vents. This is the first genome sequence from the phylum *Deferribacteres*.

Key words: *Deferribacter desulfuricans*; whole genome sequence; hydrothermal vent; chemolithotroph

1. Introduction

Generally, the greatest challenge to thermophilic microorganisms living on hydrothermal vents may be posed by the risk of being swept out of the range of the vent and thereby losing the temperature range and necessary chemical supplies. They solve this problem by clinging to rocks in communal mats or swimming with a whip-like flagellum as sensing temperature or chemical stimuli to guide their directional

movements.¹ *Deferribacter desulfuricans* SMM1^T (DSM 14783^T) has been isolated from a deep-sea hydrothermal vent chimney at the Suiyo Seamount in the Izu-Bonin Arc, Japan.² The strain SMM1 is thermophilic (optimal temperature, 60–65°C) and a strictly anaerobic heterotroph capable of using complex organic compounds such as yeast extract and tryptone, ethanol, and various organic acids as sources of energy and carbon. There are three other species in the genus *Deferribacter*—*D. abyssi* and *D. autotrophicus*, which

have been isolated from deep-sea hydrothermal vent environments, and *D. thermophilus*, which has been isolated from a seafloor petroleum reservoir.^{3–5} These bacteria are strictly anaerobic chemolithotrophs utilizing various organic compounds and H₂ as electron donors and nitrate, S⁰ (*D. desulfuricans*, *D. abyssi*, and *D. autotrophicus*), and Fe (III) and Mn (IV) (*D. thermophilus*, *D. abyssi*, and *D. autotrophicus*) as electron acceptors. Such versatility for energy generation may provide an ecological advantage for deep-sea vent-dominating chemolithotrophs as has been proposed for members of *Aquificales* and *Epsilonproteobacteria*.⁶ It has been shown, depending on the hydrothermal vent chimney environment, that *Deferribacter*-related species are the dominant species in these locations.^{7,8} Thus, it is intriguing to compare the genomes of *Deferribacter*-related species with other deep-sea vent chemolithotrophic species such as *Thiomicrospira crunogena*,⁹ *Nautilia profundicola*,¹⁰ *Sulfurovum* sp. NBC37-1,¹¹ *Nitratiruptor* sp. SB155-2,¹¹ and *Persephonella marina*¹² in order to highlight the genomic features that reflect their lifestyle in the environment of deep-sea hydrothermal vent chimneys. Here, we report the complete genome sequence of thermophilic *D. desulfuricans* SMM1 determined as the first published bacterial genome sequence from the phylum *Deferribacteres*. We provide a comparative analysis of the genome of *D. desulfuricans* SMM1 with those of five other chemolithotrophs isolated from deep-sea hydrothermal vent chimneys.

2. Materials and methods

2.1. Genome sequencing and assembly

Deferribacter desulfuricans SSM1 was grown heterotrophically as described previously,² and total DNA was isolated using proteinase K treatment followed by phenol extraction. The DNA was fragmented by HydroShear (Genomic Solutions), and three shotgun libraries were generated: small- and medium-insert (1.5 and 5 kb) plasmid libraries and a large-insert fosmid (35 kb) library as described previously.¹³ All three libraries provided 15 times coverage of the genome. Assemblies were accomplished using the PHRED/PHRAP/CONSED suite (<http://www.phrap.org>).¹⁴ Gaps between the assembled sequences were primarily closed by primer walking on gap-spanning library clones or with PCR products from genomic DNA. Quality assessment of the final assembly was performed as described previously.¹³

2.2. Gene identification and annotation

Putative non-translated genes were identified by using the Rfam¹⁵ and tRNAscan-SE¹⁶ programs, whereas rRNA genes were identified using the

BLASTN program.¹⁷ Protein-coding sequences (CDSs) were predicted using a combination of GLIMMER¹⁸ and GeneMarkS.¹⁹ The remaining parts of the genome were screened further to find missed CDSs by a BLASTX homology search against protein databases. The predicted CDSs were translated and submitted for BLAST analysis against the NCBI non-redundant (nr),²⁰ UniProt,²¹ and Kyoto Encyclopedia of Genes and Genomes (KEGG) GENES²² databases. The results were collated and presented via a home-made browser (GBROWN) for manual verification. The start sites were manually inspected and altered in an alignment comparison with the best match. The revised CDS set was searched against Pfam²³ in addition to the previously mentioned databases. Specific functional assignments suggested by matches with these databases were only accepted when they had a minimum 30% amino acid sequence identity over 70% of the gene length and were supported by Pfam domain assignments, or were consistent with gene context in the genome (e.g. membership in a potential operon with other genes with convincing matches to curated databases). The KEGG PATHWAY and MetaCyc²⁴ databases were used for pathway reconstruction. Signal peptides were predicted with SignalP,²⁵ whereas transmembrane helices were predicted with SOSUI.²⁶ Clusters of regularly interspaced repeats [clustered regularly interspaced short palindromic repeats (CRISPR)] were identified using the CRISPRFinder.²⁷

2.3. Comparative genomics analyses

Protein sequence data for bacterial genomes were obtained from the KEGG database.²² Pairwise ortholog families were identified with the InParanoid program.²⁸ In order to examine genome-wide relationships of *D. desulfuricans* in terms of gene repertoires, the ordination of bacterial genomes was generated using the non-metric multidimensional scaling (NMDS) method, which is a major branch of multivariate analysis. NMDS ordinations attempt to place all samples in an arbitrary two-dimensional space, in which the relative distances between the samples indicate the corresponding pairwise similarity. Hence, closely related organisms in the NMDS ordination would have similar gene repertoires. The gene context of each genome, based on clusters of orthologous groups (COGs),²⁹ was constructed with the following procedure. Each complete proteome was compared with the COG profile database (4450 families) using the RPSBLAST program.¹⁷ A significant match (*E*-value of 10⁻⁵) was determined for each COG, so that any outlier detected by the Smirnov–Grubbs test at the 0.01 significance level was excluded from the COG profile. Any proteome

was thus converted into a binary character matrix indicating the presence (1) or absence (0) of the COG families. The genome distance between species (A and B) was calculated by the formula: $D_{AB} = 1 - J_{AB}$, where J_{AB} is the Jaccard's coefficient, which reflects the similarity of gene content between A and B.³⁰ NMDS ordination was calculated using metaMDS in the vegan library running with the R programming language and environment (R package version 2.7.2: R Development Core Team, 2007, <http://www.R-project.org>).

2.4. Nucleotide sequence accession numbers

The sequences of the *D. desulfuricans* genome, consisting of the chromosome and plasmid sequences, are available at GenBank/EMBL/DDBJ under accession numbers AP011529 and AP011530, respectively.

3. Results and discussion

3.1. General genome features

The genome of *Deferribacter desulfuricans* SSM1 contains a single circular chromosome of 2 234 389 bp and a megaplasmid (pDF308) of 308 544 bp (Table 1). Their average G + C contents are 31.1% and 24.5%, respectively. The chromosome

displays two clear GC skew transitions that likely correspond to the DNA replication origin and terminus (Fig. 1). Annotation of the chromosomal sequence reveals 2117 CDSs, of which 1404 (66%) can be functionally assigned. The megaplasmid encodes 257 CDSs, whereas more than two-thirds are unique and exhibit no apparent similarity with any of the CDSs present in the database. Interestingly, 17 copies of gene cluster encoding two transposases belonging to the IS200 and IS605 family present in the megaplasmid but none were found in the chromosome. The chromosome contains two ribosomal RNA operons with a 16S–23S–5S rRNA gene alignment. In all, 43 tRNA genes were identified (Table 1). In addition to the regular tRNA genes, the *D. desulfuricans* genome also contains *selC* for the selenocysteine tRNA. The other components necessary for the selenocysteine system, e.g. selenocysteine synthetase (SelA), the specific elongation factor (SelB), selenophosphate synthetase (SelD), and seryl-tRNA synthetase (SerS), are also present in the genome. As for small RNA-encoding genes, potential genes for RNase P RNA (RnpB) and 6S RNA (SsrS) were assigned by using the Rfam database.

The *D. desulfuricans* chromosome contains three genomic islands, termed DDGI-1 (coordinates 278 054–313 125), DDGI-2 (coordinates 687 244–708 238), and DDGI-3 (coordinates 864 851–901 750), possibly acquired via horizontal gene transfer (Fig. 1 and Table 1). They have many specific features of genomic island, such as the tRNA gene locus at junctions and the presence of direct repeats and phage integrases (DEFDS_0277, DEFDS_0708, and DEFDS_0871), but no anomalous GC content.³¹ Most of the genes in the genomic islands encode hypothetical proteins, but some of those appeared to encode the functional proteins related to the adaptation mechanisms for the hydrothermal vent environments. For example, the DDGI-1 includes two heavy-metal transporting P-type ATPases (DEFDS_0300 and DEFDS_0301). The heavy-metal transporters could be responsible for heavy metal tolerance in the hydrothermal vent environment. The DDGI-2 has a toxin–antitoxin system (DEFDS_0716 and DEFDS_0717) involved in phage defence and the stress response.³²

Similar to most other thermophiles, *D. desulfuricans* has the CRISPR elements together with their associated genes (*cas*), which would serve as immunity against phages, possibly by an RNA-interference-like mechanism.³³ The CRISPR/Cas systems were identified in the chromosome (coordinates 77 878–86 387) and the plasmid (coordinates 267 868–276 377). Both systems have an identical repeat, and the *cas* genes also show a high relevance with each other. Regarding the repeat sequence and structure of the *cas* genes,

Table 1. Summary of genome features of *D. desulfuricans* SSM1

Characteristics	Chromosome	Plasmid
Size (bp)	2 234 389	308 544
G + C content (%)	31.1	24.5
No. of identified protein-coding genes		
Total	2117	257
Functionally assigned	1404	63
Conserved hypothetical	494	20
Hypothetical	219	174
Pseudogenes	17	9
Average gene length (bp)	976	993
Coding density (%)	93.7	88.2
No. of identified RNA genes		
rRNA operons	2	—
tRNA	43	—
Small RNA ^a	2	—
Size (bp) of genomic islands (% G + C content)		
DDGI-1	35 072 (31.4%)	—
DDGI-2	20 995 (28.2%)	—
DDGI-3	36 900 (31.0%)	—
CRISPR elements	2	2

^aIncludes genes for RNase P RNA and 6S RNA.

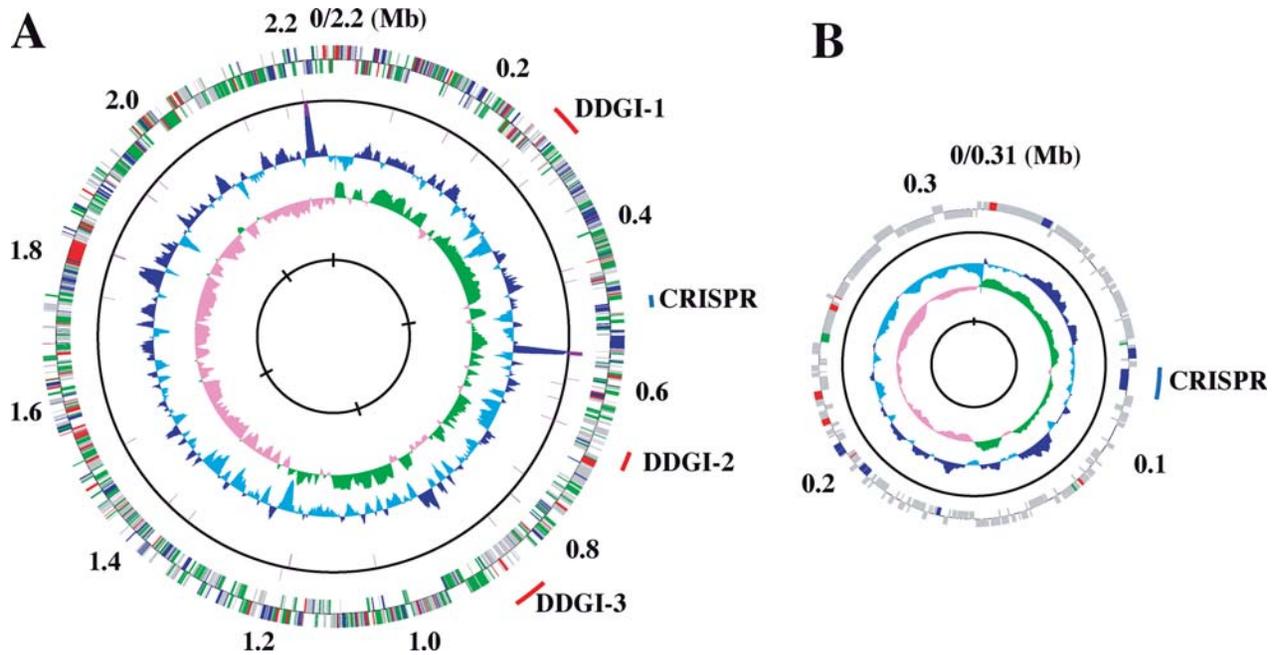


Figure 1. Circular representation of the *D. desulfuricans* SSM1 genome. (A) Chromosome. (B) Megaplasmid pDF308. From the inside, the first and second circles show the GC skew (values greater than or less than zero are indicated in green and pink, respectively) and the G + C percent content (values greater or smaller than the average percentage in the overall chromosome or plasmid are shown in blue and sky blue, respectively) in a 10-kb window with 100-bp step, respectively. The third and fourth circles show the presence of RNAs (rRNA, tRNA, and small RNA genes); CDSs aligned in the clockwise and counterclockwise directions are indicated in the upper and lower sides of the circle, respectively. Different colours indicate different functional categories: red for information storage and processing; green for metabolism; blue for cellular processes and signalling; grey for poorly characterized function; and purple for RNA genes. The outermost circle shows the location of genomic islands (red) and CRISPR/Cas systems (blue). The '0' marked on the outermost circles corresponds to the putative replication origin, and the putative replication termination site of the chromosome is at 1.23 Mb.

the systems of *D. desulfuricans* were closely related with those observed in other thermophiles, such as *Sulfurihydrogenibium azorensis*, *Thermoanaerobacter pseudethanolicus*, and the homo-acetogen *Clostridium thermocellum*. Therefore, the *D. desulfuricans* CRISPR/Cas systems may have been acquired horizontally via the megaplasmid.

3.2. Orthologous relationships among the bacterial species

Among the proteins identified in the *D. desulfuricans* genome, ~30% of them showed the highest similarity to those species from *Deltaproteobacteria*, especially *Geobacter*, *Pelobacter*, *Desulfovibrio*, and *Syntrophobacter* spp., and ~14% were found to be most similar to those from clostridial species. The remaining proteins showed the highest similarities to several species from *Aquificae* (5.3%), *Gammaproteobacteria* (4.8%), and *Epsilonproteobacteria* (3.7%). Approximately half of the proteins were shared between *D. desulfuricans* and *deltaproteobacterial* species, such as *Geobacter sulfurreducens* PCA (1106 orthologs), *Pelobacter carbinolicus* (1046 orthologs), *Syntrophobacter fumaroxidans* (985 orthologs), and *Desulfovibrio vulgaris* subsp. *vulgaris* Hildenborough (936 orthologs), although

D. desulfuricans is phylogenetically distant from *Deltaproteobacteria*.

For the next step of orthologous analysis, we performed multivariate analyses on the basis of the gene repertoires from 51 bacterial species in order to schematically express the orthologous relationships of *D. desulfuricans* among other bacterial species (Fig. 2A). As expected, the correlation map indicated that *D. desulfuricans* and the *deltaproteobacterial* species, which have strong orthologous relationships, gathered around the centre of map. The same analysis to focus on six species of the class *Deltaproteobacteria* with *D. desulfuricans* showed that *D. desulfuricans* is especially related to three species, *G. sulfurreducens* (gsu), *P. carbinolicus* (pca), and *D. vulgaris* (dvv), possessing sulphur- or sulphate-reducing properties (Fig. 2B). This result seems to attribute that these four species share many genes involved in physiological and metabolic properties such as anaerobiosis and assimilations system for small organic molecules (e.g. acetate, pyruvate, and lactate) as carbon and energy source.

3.3. Central metabolism

Deferribacter desulfuricans grows heterotrophically using a variety of organic acids (formate, acetate,

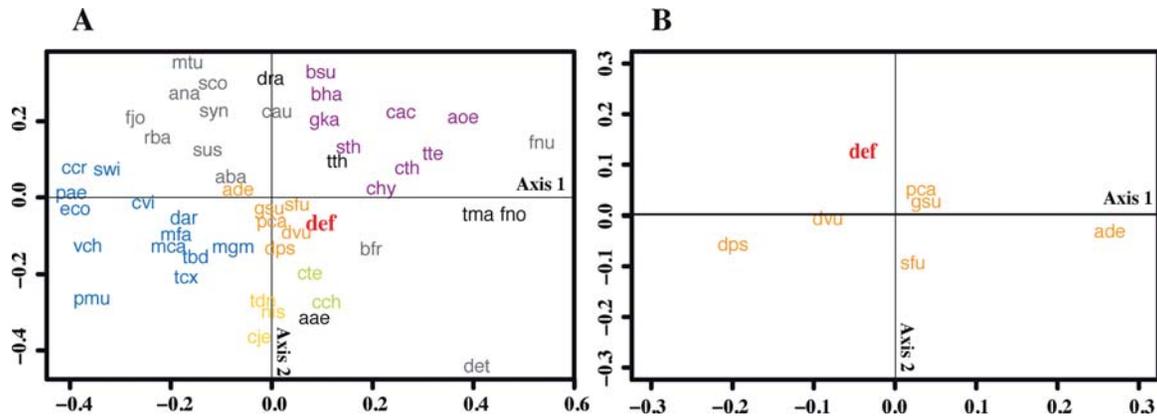


Figure 2. Ordination plot of bacterial genomes using NMDS. (A) Analysis with 50 species belonging to 12 phyla and 5 classes, and *D. desulfuricans* SSM1. (B) Analysis with six species within *Deltaproteobacteria* and *D. desulfuricans* SSM1. Distances were calculated from gene profiles based on COG families. The abbreviation corresponding to the KEGG organism code is used as the label for the species name (detailed explanations are described in Supplementary Table S1). The labels are colour-coded according to their taxonomic groups (phylum/class): red, *D. desulfuricans* SSM1 (def); orange, *Deltaproteobacteria*; yellow, *Epsilonproteobacteria*; blue, other *Proteobacteria*; purple, *Firmicutes*; green, *Chlorobi*; black, *Aquificae*, *Thermotogae*, and *Deinococcus-Thermus*; and grey, other bacteria.

propionate, pyruvate, and lactate) with nitrate or S^0 as a primary electron acceptor.² As shown in Fig. 3, the reconstructed central metabolic pathways from the *D. desulfuricans* genome certainly showed that these organic acids could be utilized as energy and carbon sources via the oxidative tricarboxylic acid (TCA) cycle and various anaerobic pathways. Acetate used as a *D. desulfuricans* SSM1 growth substrate can be activated to acetyl-CoA either via a single-step reaction by an acetyl-CoA synthetase (Acs: DEFDS_0854) or a two-step reaction by acetate kinase (AckA: DEFDS_1816) and phosphate acetyltransferase (Pta: DEFDS_1815). The AckA–Pta reaction can also operate in acetate production from acetyl-CoA in a fermentative metabolism of pyruvate, and the enzymatic action of AckA results in ATP production by substrate-level phosphorylation. Lactate may be oxidized to pyruvate by a malate dehydrogenase with a broad substrate specificity. In contrast to acetate and lactate, propionate is fed directly into the TCA cycle via succinyl-CoA. Propionyl-CoA, produced by the activation of propionate by acetyl-CoA synthetase, is converted to succinyl-CoA through a methylmalonyl pathway, including a propionyl-CoA carboxylase (DEFDS_1227–8), a methylmalonyl-CoA epimerase (DEFDS_1935), and a methylmalonyl-CoA mutase (MutA: DEFDS_2077 and MutB: DEFDS_1225). The catabolism of pyruvate reflects the anaerobic nature of *D. desulfuricans*. Conversion of pyruvate to acetyl-CoA is performed by either pyruvate ferredoxin oxidoreductase (POR: DEFDS_0568) or pyruvate-formate lyase (PFL: DEFDS_2103).

Deferribacter desulfuricans is capable of growing using formate as its sole source of carbon and energy. According to the reconstructed metabolic pathways from the *D. desulfuricans* genome, formate

is oxidized to CO_2 by membrane-bound formate dehydrogenase (Fdh: DEFDS_1329–31), which is energetically coupled with the respiratory nitrate or S^0 reduction. Methanogens and homo-acetogens are known to assimilate formate to acetyl-CoA via the Wood–Ljungdahl pathway (reductive acetyl-CoA pathway).^{3,4} Since the reductive acetyl-CoA pathway is absent in the *D. desulfuricans* genome, formate must be assimilated by another pathway. A potential reaction for formate assimilation is the direct or indirect conversion of formate and acetyl-CoA to pyruvate, the reverse reaction of pyruvate-formate lyase or the POR-catalysing carboxylation of CO_2 coupled with the formate oxidation by the Fdh protein. The pyruvate can then be converted to various biosynthetic intermediates by the TCA cycle and anaerobic pathways (Fig. 3).

The *D. desulfuricans* genome has a variety of anaerobic pathways, which include the three enzymes, malic enzyme (MaeB: DEFDS_1074), pyruvate carboxylase (Pyc: DEFDS_1275), and phosphoenolpyruvate carboxykinase (PckA: DEFDS_1461). These pathways replenish the intermediates of the TCA cycle for gluconeogenesis and amino acid biosynthesis, and their anaerobic CO_2 fixation may be an important function for *D. desulfuricans* living heterotrophically in a limited organic carbon such as hydrothermal vent environment. In the gluconeogenesis pathway, pyruvate may be dominantly produced by POR from acetyl-CoA and further converted to phosphoenolpyruvate by pyruvate phosphate dikinase (PpdK: DEFDS_0235).

The genome possesses genes for the Embden–Meyerhof–Parnas (EMP) pathway and the non-oxidative branch of the pentose phosphate pathway (Fig. 3). The EMP pathway includes fructose-1,6-

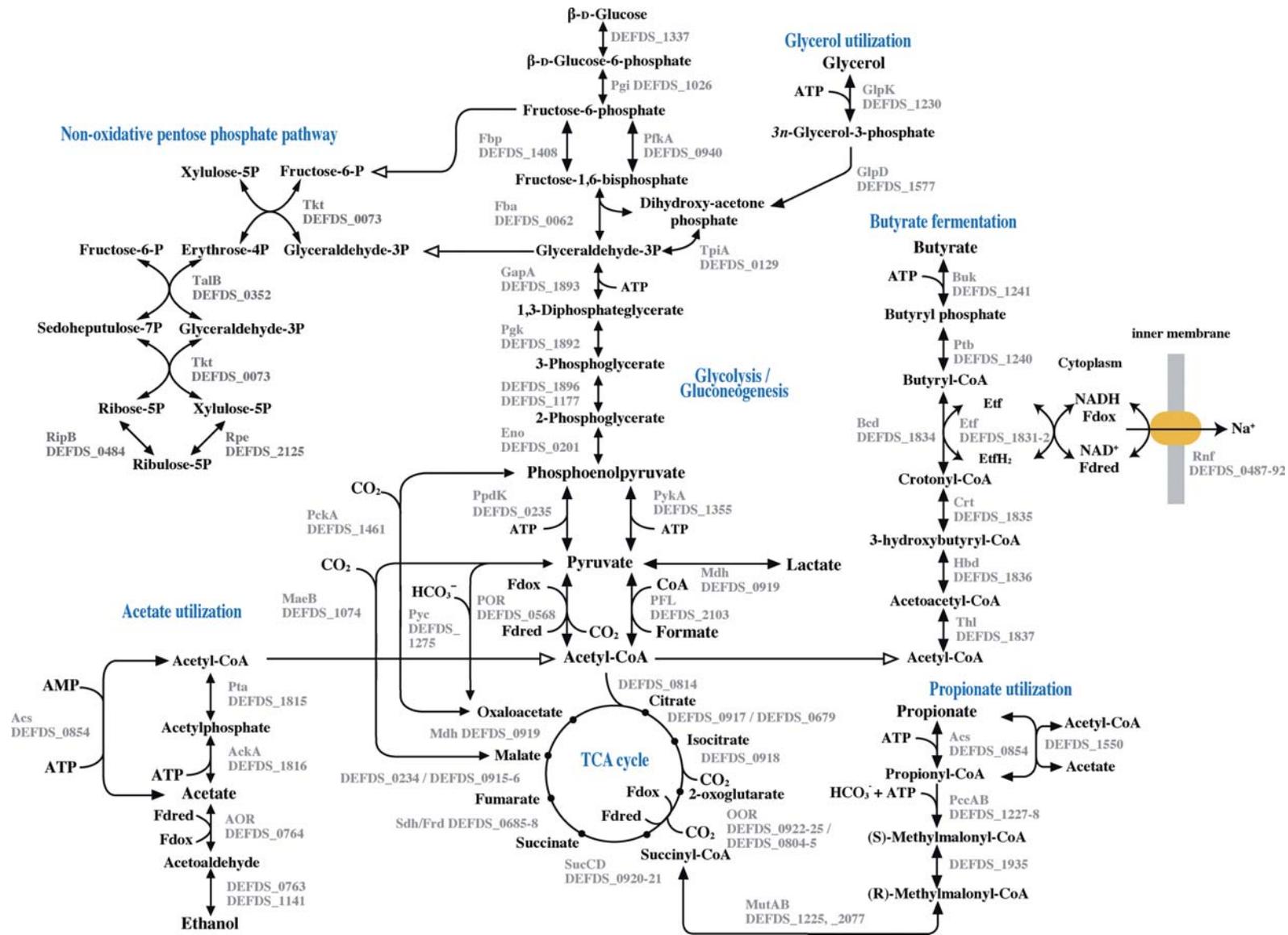


Figure 3. Central metabolism based on potential growth substrates and metabolic capacities reconstructed from the *D. desulfuricans* genome. This figure displays the flow of carbon in the metabolism of various organic acids (acetate, propionate, butyrate, lactate, and glycerol) predicted from the genome information of *D. desulfuricans* SSM1. The reversible and irreversible reactions catalysed by enzymes are indicated with both and single arrowhead, respectively. POR, pyruvate ferredoxin oxidoreductase; PFL, pyruvate formate-lyase; Pyc, pyruvate carboxylase; Pck, phosphoenolpyruvate carboxykinase; PykA, pyruvate kinase; Ppd, pyruvate phosphate dikinase; MaeB, malate dehydrogenase (oxaloacetate-decarboxylating); Mdh, malate dehydrogenase; SucCD, succinyl-CoA synthase; Sdh, succinate dehydrogenase; OOR, 2-oxoglutarate ferredoxin oxidoreductase; Fba, fructose-bisphosphatase; Pfk, 6-phosphofructokinase; Acs, acetyl-CoA synthetase; Ack, acetate kinase; Pta, phosphate acetyltransferase; AOR, aldehyde ferredoxin oxidoreductase; GlpK, glycerol kinase; GlpD, glycerol-3-phosphate dehydrogenase; Thl, acetoacetyl-CoA thiolase; Hbd, 3-hydroxybutyryl-CoA dehydrogenase; Crt, 3-hydroxybutyryl-CoA dehydratase (crotonase); Bcd, butyryl-CoA dehydrogenase; Ptb, phosphate butyryltransferase; Buk, butyrate kinase; Rnf, Rnf-type ion-translocating electron transport complex; Etf, electron transfer flavoprotein complex; PccAB, propionyl-CoA carboxylase; MutAB, methylmalonyl-CoA mutase; 2Pi, diphosphate; and Fdox/Fdred, ferredoxin, oxidized and reduced forms respectively.

bisphosphatase (DEFDS_1408), which is a key enzyme in gluconeogenesis. The TCA cycle of *D. desulfuricans* includes 2-oxoglutarate ferredoxin oxidoreductases (OOR: DEFDS_0922-25 and DEFDS_0804-5) instead of 2-oxoglutarate dehydrogenases that are typically found in aerobic bacteria. These enzymes catalyse the reversible oxidative decarboxylation of 2-oxoglutarate to form succinyl-CoA, while they are also key enzymes of the reductive TCA (rTCA) cycle. Therefore, the TCA cycle has the potential to proceed in the reverse direction. Although no ATP-dependent citrate lyase (AclAB) is present, the presence of other key enzymes of the rTCA cycle suggests that the rTCA cycle could be partially operative in *D. desulfuricans*. Actually, oxaloacetate is produced from pyruvate and phosphoenolpyruvate by the anaplerotic enzymes, Pyc and PckA, respectively, and then oxaloacetate is converted to 2-oxoglutarate by operating the TCA cycle in the reductive direction. Among the previously characterized members of the genus *Deferribacter*, *D. abyssi* and *D. autotrophicus* grow autotrophically.^{3,5} We have also isolated several strictly autotrophic strains of *D. desulfuricans* from different deep-sea hydrothermal environments (data not shown). Thus, the autotrophy may not be an unusual feature within the genus *Deferribacter*. The lack of an autotrophic phenotype in the strain SMM1 is presumably caused by the lack of the *aclAB* genes.

Genome analysis suggested the capability of butyrate-fermentation in *D. desulfuricans*, although it has not been confirmed experimentally. In this pathway, as shown in Fig. 3, butyryl-CoA is converted from acetyl-CoA by the four enzymes—acetoacetyl-CoA thiolase (Thl; DEFDS_1837), 3-hydroxybutyryl-CoA dehydrogenase (Hbd; DEFDS_1836), 3-hydroxybutyryl-CoA dehydratase (Crt; DEFDS_1835), and butyryl-CoA dehydrogenase (Bcd; DEFDS_1834)—and the electron transfer flavoprotein complex (Etf; DEFDS_1831-1832). The order of this gene cluster is conserved in the genomes of *Geobacter metallireducens*, *Geobacter uraniireducens*, and a butyrate-producing clostridial species, *Butyrivibrio fibrisolvens*.³⁵ Butyryl-CoA is converted to butyrate by phosphate butyryltransferase (DEFDS_1240) and butyrate kinase (DEFDS_1241) resulting in the generation of ATP by the substrate-level phosphorylation. This process can be reversible under a certain condition³⁶ and may thus serve for the butyrate utilization.

As shown in Fig. 3, the *D. desulfuricans* genome also contains a set of six genes (*rnfCDGAB*, DEFDS_0487-92) related to the potential membrane-bound electron transport complex (Rnf) recently found in various bacteria and archaea.³⁷⁻³⁹ In nitrogen-fixing bacteria, the Rnf complex transports electrons from NADH to ferredoxin, which donates electrons to

nitrogenase.⁴⁰ It is further proposed that the same enzyme apparently runs in the reverse direction: electron transfer from reduced ferredoxin to NAD⁺ driving the electrogenic pumping of Na⁺ out of the cell.³⁹ Regional synteny for the *rnf* genes in the *D. desulfuricans* genome was found in several clostridial genomes, such as *Clostridium tetani*, *Clostridium kluyveri*, and *Halothermothrix orenii*. It is supposed that the Rnf complex is involved in the regeneration of NADH for the fermentation of butyrate.⁴¹ Since the *D. desulfuricans* genome indicated the possible fermentation of butyrate and the requirement of reduced ferredoxin for the anabolic reactions, the Rnf complex may be operative in either the forward or reverse flow of electrons, or both. In addition, it is suggested that glycerol can be utilized by glycerol kinase (GlpK, DEFDS_1230), *sn*-glycerol-3-phosphate dehydrogenase (GlpD, DEFDS_1577), and triosephosphate isomerase (DEFDS_0129). However, no growth was observed when glycerol was used as the sole source of energy and carbon,² and this phenomenon is presumably explained by the lack of a glycerol-uptake-facilitator protein.

Supporting the heterotrophic ability of *D. desulfuricans*, a variety of transporters for mono-, di-, and tricarboxylates are encoded within the genome. Actually, the genes encoding two sodium:solute symporter (SSS) family proteins (DEFDS_1547 and DEFDS_1574) and a YaaH family protein, which are presumably involved in acetate uptake, were identified in the genome. In addition, the genes encoding five transporter systems of tripartite ATP-independent periplasmic (TRAP) family (DEFDS_0682-4, DEFDS_0770-2, DEFDS_1399-1400, DEFDS_1846-7, and DEFDS_2070-1) may be involved in uptake of various dicarboxylates such as fumarate, malate, and succinate. In terms of tricarboxylate transporters, the genes for two citrate transporters (DEFDS_1180 and DEFDS_2162) were identified in the genome. On the other hand, the genome encodes two phosphotransferase system sugar transporters for fructose and mannose, although *D. desulfuricans* could not grow by using sugar.

3.4. Respiration

Since *D. desulfuricans* SSM1 is capable of using molecular hydrogen (H₂) as an energy source,² a membrane-bound NiFe-hydrogenase (Hyd) (DEFDS_0075-77) would function as an H₂-uptake hydrogenase. As shown in Fig. 4, the oxidation of molecular hydrogen is coupled to the reduction of menaquinone. The genome has two distinctive nitrate-reducing enzymes for respiration, which are coupled to the electron transfer chains (Fig. 4). One is a membrane-bound (Nar: DEFDS_2086-89) and the other is a periplasmic

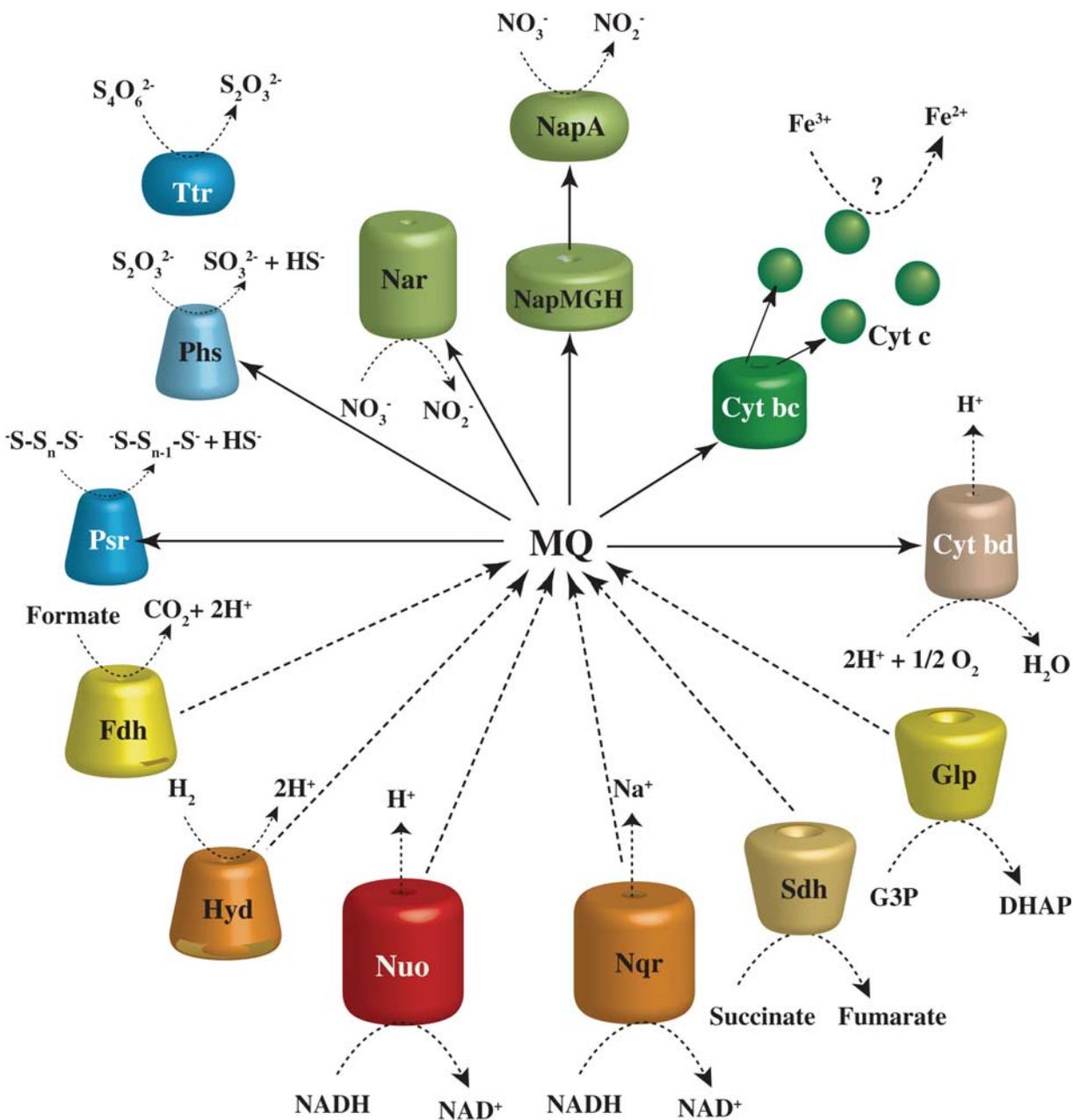


Figure 4. Genome-based models for the energy-conserving electron-transport pathways of *D. desulfuricans* SSM1. Reducing power acquired by catabolic metabolism (NADH, succinate, and *sn*-glycerol-3-phosphate) or by oxidation of hydrogen and/or formate is used to reduce sulphur compounds and nitrate, and potentially iron ions via the quinol pool for energy conservation or dissipation. Membrane-binding components are indicated with cylinders or cones, where the upper and the lower reactions are catalysed on the periplasmic side and the cytoplasmic side, respectively. Periplasmic components are indicated with ellipsoids or spheres. Hyd, membrane-binding NiFe-hydrogenase; Nar, respiratory membrane-bound nitrate reductase; Nap, periplasmic nitrate reductase; Psr, polysulphide reductase; Phs, thiosulphate reductase; Ttr, tetrathionate reductase; Fdh, formate dehydrogenase; Nuo, proton-pumping NADH dehydrogenase; Nqr, sodium-translocating NADH:quinone oxidoreductase; Sdh, succinate dehydrogenase; Cyt *bd*, cytochrome *bd* quinol oxidase; Cyt *bc*, cytochrome *bc* complex; Glp, *sn*-glycerol-3-phosphate dehydrogenase; G3P, *sn*-glycerol-3-phosphate; and DHAP, dihydroxyacetone phosphate.

(Nap: DEFDS_1819-23) nitrate reductase, which does not directly contribute to the generation of a proton motive force but contributes to redox balancing.⁴² It is generally known that bacteria have Nar-type nitrate reductases, but some bacterial species have a Nap-type or both types of nitrate reductase. Nap-type

nitrate reductase usually functions as a two-subunit enzyme comprising a catalytic subunit (NapA) that binds a bis-MGD cofactor and a [4Fe-4S] cluster, and an electron transfer subunit (NapB) that binds two *c*-type haems. However, since *D. desulfuricans* does not possess the *napB* gene, the nitrate reductase of *D.*

desulfuricans may be monomeric, which is differentiated from the heterodimeric NapAB structure typically found in bacteria. Actually, NapB-independent periplasmic nitrate reductases have been reported for some species in *Deltaproteobacteria* and *Clostridia*.⁴³ The organization of Nap genes in the *D. desulfuricans* genome is similar to that of *Desulfovibrio desulfuricans*. Although nitrate is sequentially reduced to N₂ (denitrification) or NH₄ (ammonification) in many cases, no enzyme for nitrite reduction was identified in the *D. desulfuricans* genome. This is consistent with experimental results, because the accumulation of nitrite is observed during culture of this organism.²

It has been reported that the reduction of energy-yielding sulphur compounds (sulphur-respiration) is catalysed by some key enzymes: a polysulphide reductase (Psr) in *Wolinella succinogenes* (*Epsilonproteobacteria*),⁴⁴ a thiosulphate reductase (Phs) in *Salmonella enterica* (*Gamma*proteobacteria),⁴⁵ and a hydrogenase-sulphur reductase multienzyme (Sre) in *Acidianus ambivalens* (*Crenarchaeota*) or *Aquifex aerolicus* (*Aquificae*).^{46,47} Psr and Phs reduce soluble polysulphide derived from S⁰ to sulphide, whereas Sre is considered to reduce S⁰ directly to sulphide. Genome analysis revealed that *D. desulfuricans* has three gene clusters encoding Psr/Phs enzymes, DEFDS_0670-72, DEFDS_1691-93, and DEFDS_1697-99. The genes in each cluster encode three subunits that construct the following membrane-bound complex enzyme: a catalytic subunit with molybdopterin (PsrA/PhsA), an electron transfer subunit with the [Fe-S] cluster (PsrB/PhsB), and a membrane anchor subunit (PsrC/PhsC). The amino acid sequences of the PsrA/PhsA subunits contain the motif necessary for translocation of the protein towards the periplasmic space via the twin arginine-translocation systems, suggesting that the polysulphide reduction should occur in the periplasmic space. Moreover, an alternative molybdopterin-containing enzyme, tetrathionate reductase (Ttr), is encoded by DEFDS_1446-47, but it is unclear whether this enzyme is involved in energy conservation because of the absence of a membrane anchor subunit. *Deferribacter desulfuricans* SSM1 presumably uses the polysulphides chemically formed from the reaction of S⁰ and sulphide, which readily occurs in hydrothermal vents,⁴⁸ and therefore it needs to transfer polysulphide to the periplasmic space across the outer membrane (Supplementary Fig. S1A). The periplasmic Sud protein in *W. succinogenes* has been proposed to serve as a polysulphide-binding protein and to transfer polysulphide-sulphur to the active site of polysulphide reductase.⁴⁹ A Psr/Phs gene cluster (DEFDS_0670-72) in the *D. desulfuricans* genome is associated with the genes coding an outer membrane porin and

lipoprotein (DEFDS_0667-68). The amino acid sequence of DEFDS_0667 represents the functional domain of porin_O_P (phosphate-selective porins O and P) that are conserved in anion-specific porins.⁵⁰ The lipoprotein DEFDS_0668 contains a rhodanese (thiosulphate sulphurtransferase) domain as well as the Sud protein, although there is no homology between the two proteins. Thus, these two proteins may facilitate sulphur respiration in *D. desulfuricans* as a polysulphide-specific porin in the outer membrane and a polysulphide-binding protein in the periplasmic space, respectively. This locus is adjacent to other genes related to respiration, two multihaem *c*-type cytochromes (DEFDS_0665-66) and a cytochrome *bc* complex (DEFDS_0674-77). Interestingly, a similar locus without the Psr/Phs genes was found in the genomes of the iron- and sulphur-reducing bacteria, *Geobacter* spp. and *Desulfuromonas acetoxidans* DSM 684 (Supplementary Fig. S1B).

The *D. desulfuricans* genome has a gene cluster (DEFDS_0741-60) that includes many genes encoding membrane-bound or periplasmic multihaem *c*-type cytochromes, which are potentially distributed in the inner or outer membranes or in the periplasmic space (Supplementary Fig. S2A). As demonstrated in *G. sulfurreducens* and *Shewanella oneidensis*, multihaem *c*-type cytochromes may be involved in the potential dissimilatory reduction of metal ions.⁵¹ Although *D. desulfuricans* SSM1 cannot grow by iron reduction, the capability of iron reduction is a symbolic physiological trait of the genus *Deferribacter*.³⁻⁵ On the basis of cultivation-dependent estimations, the members of the genus *Deferribacter* have been predicted to be the most numerically abundant iron-reducing prokaryotes in deep-sea vents.^{7,8,52} Therefore, the multihaem *c*-type cytochromes in *D. desulfuricans* may be a remnant of the metal reduction system.

As shown in Fig. 4, reductants produced from the oxidation of organic compounds would be oxidized by a proton-pumping NADH dehydrogenase (Nuo: DEFDS_1972-85) and succinate dehydrogenase (Sdh: DEFDS_0685-88) to provide reducing equivalents for the nitrate- and polysulphide reductions. The *D. desulfuricans* genome has an alternative complex for NADH oxidation, sodium-translocating NADH:quinone oxidoreductase (Nqr: DEFDS_1913-18). This complex possibly allows the generation of a sodium gradient, which could energize an Na⁺-dependent symporter of the organic substrates. This organism found to possess many sodium gradient-dependent symporters such as two solute:sodium symporters (SSS family), a nucleobase:cation symporter-2 (NCS2) family protein (DEFDS_1105), an alanine or glycine:cation symporter (AGCS) family protein (DEFDS_1601), and phosphate:sodium symporter (PNas) family protein (DEFDS_0081).

Table 2. Abundance of genetic components for signal transduction systems in the genomes of representative deep-sea vent chemolithotrophs

Signal transduction systems	Domains (Pfam)	<i>Deferribacter desulfuricans</i>	<i>Thiomicrospira crunogena</i>	<i>Nautilia profundicola</i>	<i>Nitratiruptor</i> sp. SB155-2	<i>Sulfurovum</i> sp. NBC37-1	<i>Persephonella marina</i>
Genome size (bp)		2 234 389	2 427 734	1 676 444	1 877 931	2 562 277	1 930 284
Two-component signal transduction systems							
Sensor histidine kinase	PF00512/ PF02518	23	13	11	15	20	8
Response regulator	PF00072	41	24	16	19	28	14
Hybrid		13	7	1	1	9	0
Total		77	44	28	35	57	22
Cyclic diGMP signalling systems							
GGDEF	PF00990	12	20	17	11	5	12
EAL	PF00563	1	5	3	2	1	4
HD-GYP	PF01966	3	3	2	0	0	2
GGDEF-EAL		3	16	11	19	12	12
Total		19	44	33	32	18	30
Chemotaxis							
Methyl-accepting chemotaxis proteins	PF00015	14	14	11	8	0	5
Chemotaxis proteins		32	13	3	13	0	6
Total		46	27	14	21	0	11

Signal transduction proteins were identified by querying the predicted gene products to the Pfam and COG databases. Genes with significant matches (E -value of less than $1E-5$) were assigned a product description and classified using a set of rules based on the domain architecture of the protein. The final results were manually verified.

3.5. Signal transduction, motility, and chemotaxis

Deferribacter desulfuricans SSM1 and its relatives inhabit the ever-changing steep physical and chemical gradients of hydrothermal vent chimney. The thermophilic microorganisms living on hydrothermal vents are generally sensing temperature or chemical stimuli to guide their directional movements by swimming with a whip-like flagellum. Thus, the *D. desulfuricans* genome should have the molecular machinery for sensing and responding to environmental changes. Indeed, *D. desulfuricans* has genes for various signalling systems, as other vent chemolithotrophs do^{9–11} (Table 2). More than 70 genes for two-component signal transduction (TCS) systems, including 23 histidine kinases, 41 response regulator genes, and 13 hybrid histidine kinases with regulator domains, were found in the *D. desulfuricans* genome. The frequency of TCS systems found in the *D. desulfuricans* genome is the highest (34 genes per megabase) among vent bacteria (ranging from 11 to 22 genes per megabase). Although most of them could not be functionally assigned due to very low homologies with well-defined systems, some functions were assumed to be phosphate regulation (PhoBR) and ammonium assimilation (NtrBC).

As an alternative signalling system, the *D. desulfuricans* genome has many genes relevant to a cyclic diguanylate (c-diGMP) signalling system,⁵³ although these were

less abundant than in other deep-sea vent bacteria (Table 2). This system is characterized by either diguanylate cyclase (GGDEF domain) or phosphodiesterase (EAL and HD-GYP domains) activity and is relevant to biofilm formation, motility, and virulence.⁵³ In addition, at least one PAS domain was found in seven histidine kinase proteins and two c-diGMP signalling proteins as additional input modules. PAS domains are known to sense changes in the redox conditions inside or outside cells.⁵⁴ It is worthy to note that the *D. desulfuricans* genome has a higher proportion of intracellular signalling systems than those of other deep-sea vent chemolithotrophs (Supplementary Fig. S3). These sensors may be essential for the versatile energy acquisition, carbon metabolisms, and the chemotaxis and redox taxis of *D. desulfuricans* SSM1 that are necessary under highly variable environmental conditions.

This genome encodes a large number of methyl-accepting chemotaxis proteins (14 MCPs) as observed in other deep-sea vent bacteria (5–14 MCPs), except for the immotile *Sulfurovum* sp. NBC37-1 (Table 2). These chemotaxis-specific receptors would, in part, contribute to the versatile sensing capabilities of *D. desulfuricans*. The MCP encoded by DEFDS_1855 possesses a Cache (Ca^{2+} channels and chemotaxis receptors) domain that is involved in the binding of amino acids and carbohydrates in the MCP of *Bacillus*

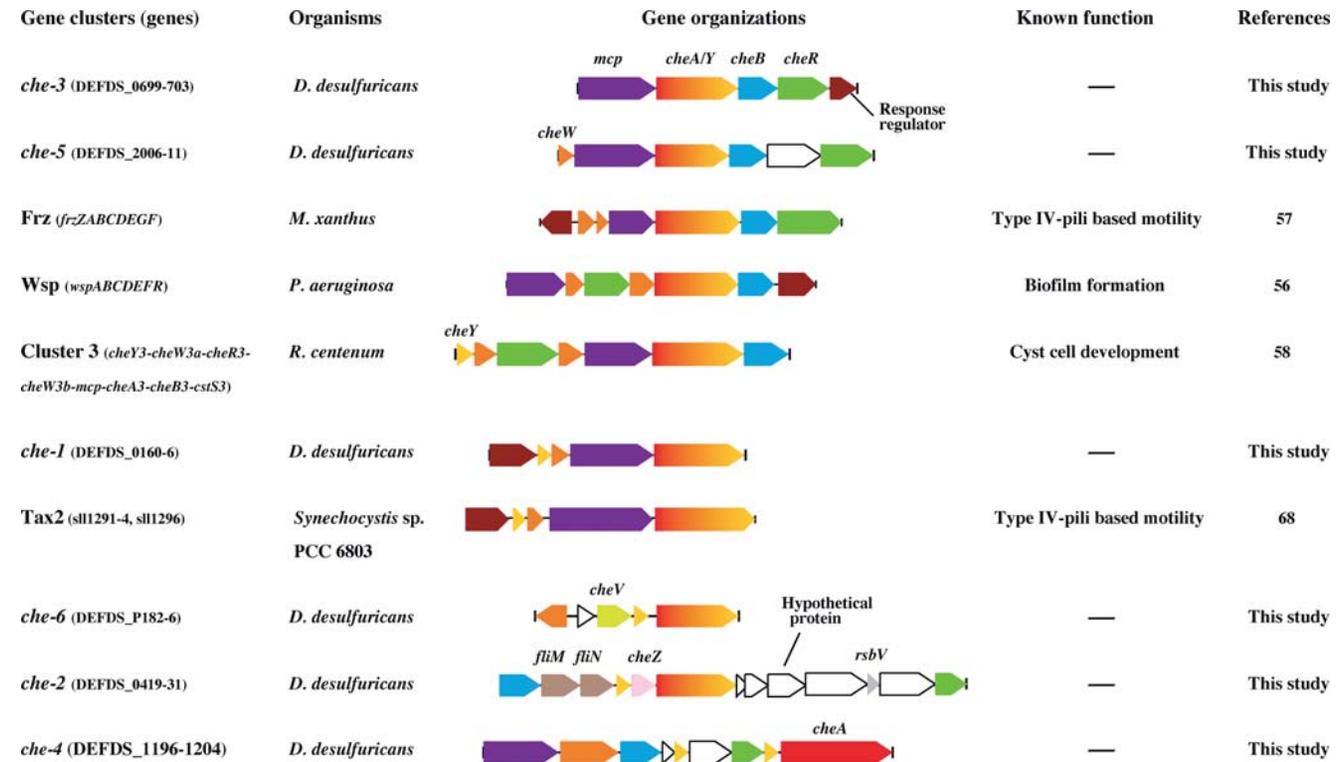


Figure 5. Gene arrangement of the representative chemotaxis-like gene clusters in the genomes of *D. desulfuricans* and related bacteria. Six chemotaxis-like gene clusters (*che-1* to *che-6*) identified in the *D. desulfuricans* genome are compared with those CheA/Y-containing clusters that have been experimentally verified: *M. xanthus* Frz,⁵⁷ *P. aeruginosa* Wsp,⁵⁶ *R. centenum* Cluster 3,⁵⁸ and *Synechocystis* sp. PCC 6803 Tax2.⁶⁸

subtilis.⁵⁵ It is also notable that multiple *che* clusters (six clusters of *che-1* to *che-6*) were identified in the genome of *D. desulfuricans*, whereas most deep-sea vent microorganisms usually have one or two *che* gene clusters (Table 2 and Fig. 5). The *che-2* cluster is associated with genes for flagellar biosynthesis, suggesting that flagellar formation and motility may be linked with the chemotaxis pathway. *Deferribacter desulfuricans* SSM1 has almost all of the genes necessary for the flagellar apparatus although motility has not yet been observed in this strain.² On the other hand, since motility has been confirmed in several strains of *D. desulfuricans* recently isolated by us, flagellar-based motility could be an intrinsic genetic potential in *D. desulfuricans*. Moreover, all *che* clusters, except for *che-4*, contain genes that encode a fusion protein (CheA/Y) consisting of histidine kinase (CheA) and response regulator (CheY) domains. In other bacteria, the gene clusters containing *cheA/Y* are involved in specific functions other than chemotaxis. For instances, the *Pseudomonas aeruginosa* Wsp cluster is involved in biofilm formation,⁵⁶ and the *Myxococcus xanthus* Frz cluster functionally controls type IV pili-based motility for cellular aggregation.⁵⁷ Also, the gene cluster 3 of *Rhodospirillum centenum* is involved in cyst cell development.⁵⁸ As shown in Fig. 5, the *che-3* and *che-5* gene clusters of *D. desulfuricans*, in particular, have a

similar gene organization to each other. There are significant homologies (more than 22% identity at the level of amino acid sequences) between CheA/Y proteins in *D. desulfuricans* and other organisms. Thus, various *D. desulfuricans* chemotaxis-like systems may be responsible not only for chemotaxis but also for other cellular functions involved in cell–cell interactions. In fact, this genome contains several gene clusters potentially involved in the formation of a type IV pilus that plays a role in the adhesion of bacteria to host cells and solid surfaces, and mediates bacterial twitching motility. Some genes encoding pilus-related proteins such as PilA of the major prepilin (DEFDS_1243), PilB of the assembly ATPase (DEFDS_1109 and DEFDS_1256), PilQ of secretin (DEFDS_1255), and PilD of prepilin peptidase (DEFDS_0112) were detected. Considering the presence of these genes, it is possible to propose a lifestyle of clinging to the chimney surface for survival under a constantly variable environment.⁵⁹

3.6. Adaptation to thermal environment

As in other thermophilic microbes, the proteome of *D. desulfuricans*, which can grow up to 70°C should be stable at least at the maximum growth temperature. Generally, it is known that a protein's amino acid

composition has a great influence on its thermostability, and the proteins of thermophiles show a tendency to possess fewer non-charged amino acids and more charged amino acids than those of mesophiles.⁶⁰ Actually, all of the proteins encoded in the *D. desulfuricans* genome were found to have fewer histidine, glutamine, and threonine residues, but more glutamic acid and lysine residues than mesophiles (Supplementary Fig. S4). Both charged amino acids presumably contribute to increase the thermostability of the protein by enhancing the occurrence of salt bridges and ion pairs.⁶¹

Also, the stabilization of DNA and RNA at a high temperature is indispensable for survival in the hydrothermal environment. It has been suggested that polyamines, RNA methyltransferases, and protamine P1 could contribute to the thermoadaptation of *Geobacillus kaustophilus*, which has a similar maximum temperature for growth (74°C) as *D. desulfuricans*.⁶² In *Thermus thermophilus*, which can grow up to 85°C, the inactivation of genes for polyamine biosynthesis or tRNA (adenine-N1)-methyltransferase (TrmI) results in a thermolabile phenotype.⁶³ The *D. desulfuricans* genome encodes genes necessary for putrescine and spermidine synthesis, *speA* (DEFDS_1288) and *speBDE* (DEFDS_0967-9). In addition, we identified two genes for norspermidine synthesis—carboxynorspermidine dehydrogenase (DEFDS_1287) and carboxynorspermidine decarboxylase (DEFDS_1286). Norspermidine and norspermine are commonly found in hyperthermophilic bacteria.⁶⁴ These polyamines stabilize DNA by binding to nucleic acids and can induce aggregation or conformational changes of DNA.⁶⁵ On the other hand, a homolog (DEFDS_0605) of TrmI found in *T. thermophilus*, and four tRNA and three tRNA/rRNA methyltransferase genes in total were identified in *D. desulfuricans*. The genes described above appear to contribute to the thermoadaptation of *D. desulfuricans* as well as other thermophilic bacteria.

Deferribacter desulfuricans possesses many molecular chaperons used for protein folding and unfolding such as DnaJ-DnaK-GrpE (DEFDS_2113-4) and the HrcA repressor (DEFDS_2113-6), GroEL-GroES (DEFDS_0240-39), and small heat shock proteins categorized into Hsp20 family (DEFDS_1576 and DEFDS_1707). This organism also possesses ATP-dependent heat shock-responsive proteases, which is thought to be concerned in providing thermotolerance to cell on exposure to heat stress, such as HslVU (DEFDS_2155-6), ClpPX (DEFDS_0193-4), and Lon (DEFDS_0195 and DEFDS_1706).

3.7. Antioxidant system

Deferribacter desulfuricans SSM1 is a strict anaerobe: its genome possesses many genes potentially associated

with resistance to oxidative stress. DEFDS_1019 and DEFDS_0573 encode a superoxide reductase (SOR) and a rubredoxin (Rd), respectively. The SOR–Rd proteins can catalyse the reduction of superoxide to hydrogen peroxide. Putative rubrerythrins (Rbr) encoded by DEFDS_0019, DEFDS_1568, and DEFDS_1971 further reduce hydrogen peroxide to water.⁶⁶ DEFDS_1568 is located adjacent to the gene encoding the peroxide repressor (*perR*) (DEFDS_1567). A series of these genes presumably construct the antioxidant system of *D. desulfuricans* SSM1 inhabiting the oxic–anoxic transition zone in the deep-sea hydrothermal environment. Additionally, genes for peroxiredoxins (DEFDS_0018 and DEFDS_1350), thioredoxin (DEFDS_1167), and thioredoxin reductase (DEFDS_0503) may be involved in the antioxidant system.

On the other hand, *D. desulfuricans* possesses genes encoding two potential dioxygen scavenging systems. The first one is a cytochrome *bd* quinol oxidase (DEFDS_1619-1620), which is a respiratory terminal oxidase, and the second one is a rubredoxin-oxygen oxidoreductase (Roo), whose gene is located next to the rubredoxin gene (DEFDS_0573). In the sulfate-reducing *Desulfovibrio*-related species, the latter enzyme is proposed to be the cytoplasmic terminal oxidase for the non-energy-conserving respiratory reduction of O₂ or nitric oxide.⁶⁷ Thus, the *bd*-type oxidase and Roo of *D. desulfuricans* may also serve to relieve the environmental and intracellular oxidative stresses.

3.8. Conclusions

Genome analysis of *D. desulfuricans* SSM1 revealed its versatile energy and carbon metabolisms and its machineries for sensing and responding to the environmental changes in hydrothermal vent habitats. We showed that the molecular systems such as the multiheme *c*-type cytochrome clusters, two-component signal transducers, and abundant chemotaxis components could be tightly linked to the adaptation mechanisms required to adapt in physically and chemically variable environments. The multiple signal transduction systems for sensing dynamic changes in carbon source and temperature, and the type IV pili, which are likely to be useful for clinging to the chimney, allow *D. desulfuricans* to survive in such a harsh environment. The genome sequence of *D. desulfuricans* SSM1 should provide many clues for the better understanding of bacterial life in environments around hydrothermal vents from the ecological and evolutionary points of view. The sequences, as well as the gene information shown in this paper, are available in the web databases, ExtremoBase (<http://www.jamstec.go.jp/gbrowser/cgi-bin/top.cgi>) and DOGAN (<http://www.bio.nite.g.o.jp/dogan/Top>).

Supplementary data: Supplementary data are available at www.dnaresearch.oxfordjournals.org.

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