Entner–Doudoroff pathway for sulfoquinovose degradation in *Pseudomonas putida* SQ1

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Sulfoquinovose (SQ; 6-deoxy-6-sulfoglucose) is the polar head group of the plant sulfolipid SQ-diacylglycerol, and SQ comprises a major proportion of the organosulfur in nature, where it is degraded by bacteria. A first degradation pathway for SQ has been demonstrated recently, a "sulfoglycolytic" pathway, in addition to the classical glycolytic (Embden–Meyerhof) pathway in *Escherichia coli* K-12; half of the carbon of SQ is abstracted as dihydroxyacetonephosphate (DHAP) and used for growth, whereas a C4-organosulfonate, 2,3-dihydroxypropane sulfonate (DHP), is excreted. The environmental isolate *Pseudomonas putida* SQ1 is also able to use SQ for growth, and excretes a different C4-organosulfonate, 3-sulfolactate (SL). In this study, we revealed the catabolic pathway for SQ in *P. putida* SQ1 through differential proteomics and transcriptional analyses, by in vitro reconstitution of the complete pathway by five heterologously produced enzymes, and by identification of all four organosulfonate intermediates. The pathway follows a reaction sequence analogous to the Entner–Doudoroff pathway for glucose-6-phosphate: it involves an NAD⁺-dependent SQ dehydrogenase, 6-deoxy-6-sulfoglucono-lactone (SGL) lactonase, 6-deoxy-6-sulfoglucolactone (SGL) dehydratase, and 2-keto-3,6-dideoxy-6-sulfoglucose (KDSG) aldolase. The aldolase reaction yields pyruvate, which supports growth of *P. putida*, and 3-sulfolactaldheyde (SLA), which is oxidized to SL by an NAD(P)⁺-dependent SLA dehydrogenase. All five enzymes are encoded in a single gene cluster that includes, for example, genes for transport and regulation. Homologous gene clusters were found in genomes of other *P. putida* strains, in other gamma-Proteobacteria, and in beta- and alpha-Proteobacteria, for example, in genomes of Enterobacteria, *Vibrio*, and *Halomonas* species, and in typical soil bacteria, such as *Burkholderia*, *Herbaspirillum*, and *Rhizobium*.

bacterial biodegradation | organosulfonate | sulfolipid | 6 deoxy 6 sulfoglucose | sulfur cycle

**Significance**

Phototrophic organisms worldwide produce estimated 10 gigatons of sulfoquinovose (SQ) per year; hence, complete degradation of SQ by bacteria is an important part of the biogeochemical sulfur cycle. Here, we show that *Pseudomonas putida* SQ1 catalyzes SQ to 3-sulfolactate (SL) in analogy to the Entner–Doudoroff pathway for glucose-6-phosphate, involving five newly discovered reactions, enzymes, and genes, and three newly discovered organosulfur intermediates. The SL can be mineralized by other bacteria, thus closing the sulfur cycle within a bacterial community. The genes for the SQ Entner–Doudoroff pathway can be found in genomes of a wide range of Proteobacteria, which shows that SQ utilization is a widespread and important, but still underrecognized, trait of bacteria in all environments where SQ is produced and degraded.

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an NAD\(^+\) dependent SQ dehydrogenase in cell free extracts of \emph{P. putida} SQ1 cells (12). Thus, we had experimental access to a second catabolic pathway for SQ, in addition to sulfoglycolysis in \emph{E. coli} K 12, apparently via an initial oxidation of SQ this time.

Most pseudomonads use glucose exclusively via the Entner Doudoroff pathway enzymes and do not encode fructose 6 phosphate kinase for glycolytic breakdown of glucose (e.g., the well studied isolate of \emph{P. putida}, strain KT2440) (16-20). Its major cytosolic pathway for glucose (Fig. 1 A) is relevant as an analogy to a possible SQ degradation pathway: Glucose is taken up into the cell and phosphorylated to GP, the analog of SQ (compare Fig. 1 A and B). Then, GP is oxidized by an NAD(P)\(^+\) dependent GP dehydrogenase to 6 phosphogluconolactone (PGL), and the PGL is hydrolyzed to 6 phosphogluconate (PG), the PG is dehydrated to 2 keto 3 deoxy 6 phosphogluconate (KDPG), and the KDPG is cleaved into pyruvate and GAP (Fig. 1 A). The five enzymes [i.e., glucose kinase (Glk), GP dehydrogenase (Zwf), PGL lactonase (Pgl), PG dehydratase (Edd), and KDPG aldolase (Eda)] are encoded in a single gene cluster (not shown; refer to ref. 20), which is highly conserved in \emph{P. putida} species, and also in \emph{P. putida} strain SQ1 (21). Even though it is conceivable that the classical Entner Doudoroff pathway enzymes for GP might also catalyze the analogous reactions for the substrate SQ (Fig. 1 B), the well studied \emph{P. putida} strains KT2440 and F1, for example, are unable to grow with SQ, in contrast to strain SQ1 (11).

For this study, we had SQ available as a substrate through chemical synthesis (11) and the analytical chemistry established for detection of SQ, its sulfosugar and C3 intermediates, and thus its enzyme activities (12), and we established a draft genome sequence of strain SQ1 for proteomics (21), which set the stage for an exploration of its SQ degradation pathway. Here, we demonstrate that \emph{P. putida} SQ1 uses SQ via what we term the “Sulfo Entner Doudoroff” pathway, in addition to the classical Entner Doudoroff pathway for glucose, via five newly discovered enzymes and genes, and via three newly identified organosulfur intermediates.

**Results**

Inducible NAD\(^+\)-Dependent SQ Dehydrogenase Activity and Conversion of SQ to SL in Cell-Free Extracts of SQ-Grown Cells. The NAD\(^+\) dependent SQ dehydrogenase activity was inducibly and highly produced during growth with SQ. The specific activity determined in cell free extracts (soluble protein fraction) of SQ grown cells (633 ± 18 mU/mg of protein) was more than 90 fold higher than the specific activity determined in extracts of glucose or succinate grown cells (each < 7 mU/mg of protein), as determined in a photometrical assay by formation of the coproduct NADH (recorded at 365 nm). For comparison, GP caused similar high NAD\(^+\) dependent dehydrogenase activity in extracts of glucose grown cells (576 ± 19 mU/mg of protein), and this activity was 12 fold decreased in extracts of SQ grown cells (45 ± 1 mU/mg of protein) and 25 fold decreased in succinate grown cells (24 ± 7 mU/mg of protein).
Identification of a Gene Cluster for SQ Degradation in *P. putida* SQ1. We compared the proteome of *P. putida* SQ1 during growth with SQ or glucose by 2D PAGE, and all prominent SQ specific protein spots were identified by peptide fingerprinting (PF) MS (Fig. 3A). In addition, non gel based, total proteome analyses of SQ and glucose grown cells were performed (Fig. 3B). As described in the following section, the proteomic data strongly suggested that one gene cluster (shown in Fig. 1C) is involved in SQ degradation in *P. putida* SQ1. Interestingly, such a gene cluster is not encoded in the genomes of *P. putida* strains KT2440, F1, and W619, which cannot grow with SQ (12, 21).

Four of the most prominent protein spots found exclusively on the 2D gels of SQ grown cells (Fig. 3A) identified four predicted genes in the same gene cluster (on the same contig) in the draft genome sequence of strain SQ1: [Integrated Microbial Genomes (IMG) locus tags] PpSQ1_00088, 00090, 00100, and 00094 (in the following sections, the IMG locus tag prefix PpSQ1_0 is omitted). The total proteome analysis confirmed and expanded on these results, in that two other loci in the gene cluster were also identified by proteins that also appeared to be highly abundant specifically in SQ grown cells. These additional loci were 0089 and 0091 (Fig. 3B). In contrast, strong expression of the well known enzyme homologs for the Entner Doudoroff pathway for glucose (well known in other *Pseudomonas* species) was detected for glucose grown cells, but not for SQ grown cells, of *P. putida* SQ1 (Fig. 3B).

The newly identified gene cluster (Fig. 1C) encodes five candidate enzymes for the proposed Entner Doudoroff pathway for SQ (Fig. 1B), and all five candidates were detected in the proteomic approach, specifically in SQ grown cells (Fig. 3A and B): two candidates for NAD(P)+ dependent SQ or SLA dehydrogenases, respectively; that is, 0090, a predicted short chain alcohol dehydrogenase, and 0088, a predicted succinate semialdehyde dehydrogenase. Further, one candidate each (Figs. 1C and 3A and B) for a lactonase (0091, predicted gluconolactonase), dehydratase (0089, predicted phosphogluconate dehydrogenase), and aldolase (0100, predicted 2,4 dihydroxyacet 2 ene 1,7 dioic acid aldolase) was identified. The other predicted genes in the cluster (Fig. 1C) might encode for transport (uptake of SQ and export of SL), regulation, and funneling of other SQ metabolites into the pathway (Discussion).

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**Fig. 2.** Complete disappearance of SQ in cell free extract of SQ grown *P. putida* SQ1 cells concomitant with a transient formation of metabolites SGL, SG, and KDSG, and formation of the end product SL. The reaction in soluble protein extract (soluble protein fraction) was started by addition of NAD+ in excess (Fig. 2). The chromatograms confirmed a complete disappearance of SQ during the reaction. In addition, formation of four sulfonated intermediates was detected, as indicated by four novel peaks with different retention times, molecular masses, and MS/MS fragmentation patterns, which, however, all exhibited fragment ions that are characteristic of organosulfonates (diagnostic ions from a loss of the sulfonate group, m/z = 81; Figs. S1 and S2).

One of the novel peaks represented SL, as identified by an identical retention time, molecular mass, and MS/MS fragmentation in comparison to authentic SL standard. The three other peaks exhibited molecular masses and MS/MS fragmentation patterns (Fig. S1) that corresponded to 6 deoxy 6 sulfogluconolactone (SGL), 6 deoxy 6 sulfoglucononate (SG), and 2 keto 3,6 dideoxy 6 sulfoglucuronic acid (KDSG), respectively, as transient intermediates of SQ degradation. The total ion chromatograms (TICs) recorded in the negative ion mode from the MS/MS fragmentation of the quasi molecular ions ([M H]+) of SQ, SGL, SG, and KDSG, as well as SL, are shown. Note that SGL and KDSG were each observed as [M H]+ ions of identical mass (m/z = 243) but that the compounds eluted at different HPLC retention times, as indicated for t = 5 min. Discussion of the MS/MS fragmentation of the metabolites SGL, SG, and KDSG, as well as SL, is provided in SI Materials and Methods.
Transcriptional analyses (RT PCR) (Fig. 3C) of the whole 13 gene cluster (Fig. 1C) confirmed that all of these genes were inducibly, and strongly, transcribed during growth with SQ, but not during growth with glucose. In addition, we constructed an insertion mutant via homologous recombination in gene 0090 (for SQ dehydrogenase, as discussed below) in *P. putida* SQ1, and the mutant strain did grow with glucose but had lost the ability to grow with SQ (Fig. S3).

**Recombinant Expression of the SQ and SLA Dehydrogenase Candidates and Activities of the Purified Enzymes.** The two identified dehydrogenase candidates of the SQ gene cluster, 0090 and 0088, were cloned and heterologously overexpressed in *E. coli*, and the proteins were purified (SI Materials and Methods and Fig. S4); for comparison, the GP dehydrogenase of strain SQ1 (3570, Zwf 1; Fig. 3B) was also produced recombinantly and purified (Fig. S4).

Only one dehydrogenase candidate, the predicted short chain alcohol dehydrogenase 0090, catalyzed an NAD<sup>+</sup> dependent reaction with SQ, and this reaction produced SGL from SQ (as discussed below). In the photometrical assay, recombinant SQ dehydrogenase 0090 exhibited a much higher catalytic efficiency (*kcat*/K<sub>m</sub>) with NAD<sup>+</sup> than with NADP<sup>+</sup> as an electron acceptor (Table 1). Further, SQ dehydrogenase 0090 exhibited no activity with GP as a substrate and with both cosubstrates tested, NAD<sup>+</sup> and NADP<sup>+</sup>, under the same assay conditions. For comparison, the recombinant GP dehydrogenase 3570 (Zwf 1) exhibited similar high catalytic efficiency with GP and NADP<sup>+</sup>, as well as NAD<sup>+</sup>, as a cosubstrate (Table 1), but no significant activity was detectable with SQ as a substrate and both cosubstrates tested; notably, the additional presence of SQ did not inhibit its activity with GP. The pH optimum for the SQ dehydrogenase reaction was between 8 and 9. Thus, we demonstrated that gene 0090 of the SQ gene cluster encodes for an NAD<sup>+</sup> dependent SQ dehydrogenase, which is poor at catalyzing a reaction with GP. In addition, we confirmed that NAD(P)<sup>+</sup> dependent GP dehydrogenase 3570 of the Entner-Doudoroff pathway is poor at catalyzing a reaction with SQ.

The second identified dehydrogenase of the SQ gene cluster, the annotated succinate semialdehyde dehydrogenase 0088 (Fig. 1C), turned out to catalyze the NAD(P)<sup>+</sup> dependent oxidation of SLA to SL, which was thus the last reaction of the proposed pathway (Fig. 1B): The enzyme exhibited high activity with SLA and both NAD<sup>+</sup> and NADP<sup>+</sup>, but no activity with SQ (or GP) in the photometrical assay, and the product of the SLA reaction was SL, as confirmed by HPLC MS (as discussed below). Notably, SLA as a substrate had to be generated enzymatically, either through a re action of recombinant SLA reductase (YihU) of *E. coli* K 12 in reverse with DHPS and NAD<sup>+</sup> (12) or directly from SQ by an in vitro reconstitution of the complete SQ pathway (as discussed below); therefore, we could not determine the kinetic parameters for the SLA dehydrogenase reaction. The enzyme did not catalyze a reverse reaction with SL and NADH when tested, which is a common observation for aldehyde dehydrogenases. Further, the enzyme exhibited high activity with succinate semialdehyde, with both NAD<sup>+</sup> and NADP<sup>+</sup> (Table 1).

**In Vitro Reconstitution of an Entner–Doudoroff Pathway for SQ.** The identified candidate lactonase (0091), dehydratase (0089), and al dolase (0100) genes for SQ degradation were also heterologously expressed in *E. coli*, and the proteins were purified (Fig. S4). The five proteins were added sequentially to a reaction mixture with SQ, and after each reaction step, samples were taken for HPLC MS analysis, as illustrated in Fig. 4.

The SQ dehydrogenase 0090 produced SGL from SQ (Fig. 4A and B), as indicated by the formation of a peak with a matching mass of the molecular ([M H<sup>+</sup>]<sup>+</sup>) ion and MS/MS fragmentation (Fig. S4A); the same peak was observed during the reactions with cell free extracts of SQ grown *P. putida* cells (Fig. 2). A second minor peak that also appeared represented SQ, as identified by a
matching mass of the \([\text{M H}^-]\) ion and MS/MS fragmentation (Fig. S1B); hence, the lactone hydrolyzed spontaneously to SG. After addition of the predicted SGL lactonase 0091, the peak for SGL had disappeared completely and the peak for SG had further increased (Fig. 4B and C). Thus, we confirmed that 0091 catalyzes a conversion of SGL to SG (Fig. 1C). Next, the predicted SG dehydratase 0089 was added, which resulted in an intermediate (Fig. 4C and D) that was identified as KDSG by a peak with a different retention time but identical molecular mass as SGL (compare Figs. 2 and 4), as well as matching MS/MS fragmentation that was different from the MS/MS fragmentation of SGL (compare Fig. S1A and C); the same peak was observed during the reactions with cell free extracts of SQ grown *P. putida* cells (Fig. 2). Correspondingly, the peak for SG had decreased (Fig. 4C and D). Thus, 0089 is a dehydratase that converts SG to KDSG (Fig. 1C). After addition of the predicted aldolase 0100, the KDSG peak had decreased and SLA had formed (Fig. 4D and E), as identified by comparison with SLA standard that had been

<table>
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<tr>
<th>Enzyme</th>
<th>Substrate</th>
<th>(K_m) mM</th>
<th>(V_{max}) (\mu\text{mol} \cdot \text{min}^{-1} \cdot \text{mg}^{-1})</th>
<th>(k_{cat}) s(^{-1})</th>
<th>(k_{cat}/K_m) (10^3) s(^{-1}) M(^{-1})</th>
</tr>
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<tr>
<td>SQ dehydrogenase (PpSQ1 00090)</td>
<td>SQ with NAD(^+)</td>
<td>0.5 ± 0.1</td>
<td>62.8 ± 2.0</td>
<td>33.8</td>
<td>67.6</td>
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<tr>
<td>GP dehydrogenase (Zwf 1) (PpSQ1 03570)</td>
<td>GP with NAD(^+)</td>
<td>2.4 ± 0.1</td>
<td>2.7 ± 0.1</td>
<td>1.4</td>
<td>0.6</td>
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<tr>
<td>SLA dehydrogenase (PpSQ1 00088)</td>
<td>SSA(^+) with NAD(^+)</td>
<td>0.14 ± 0.02</td>
<td>12.6 ± 0.4</td>
<td>11.8</td>
<td>84.2</td>
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*There was no SLA available as a substrate in the defined concentration (main text).

SSA, succinate semialdehyde.

Table 1. Kinetic parameters determined for recombinant dehydrogenases from *P. putida* SQ

![Fig. 4](https://example.com/fig4.png)  
**Fig. 4.** In vitro reconstitution of the Entner Doudoroff pathway for SQ. The transformation of SQ to SGL, SG, KDSG, and SLA, and of SLA to SL, by successive addition of recombinantly produced pathway enzymes was followed by HPLC MS. The initial substrate concentrations were 2 mM SQ and 3 mM NAD\(^+\), and 50 \(\mu\text{g} \cdot \text{mL}^{-1}\) of each enzyme was added. (A) Sample of SQ in reaction buffer \((t = 0 \text{ min})\). (B) Sample taken 45 min after addition of SQ dehydrogenase (gene PpSQ1 00090) \((t = 45 \text{ min})\). (C) Sample taken 45 min after addition of SGL lactonase (gene 0091) \((t = 90 \text{ min})\). (D) Sample taken 45 min after addition of SG dehydratase (gene 0089) \((t = 135 \text{ min})\). (E) Sample taken 45 min after addition of KDSG aldolase (gene 0100) \((t = 180 \text{ min})\). (F) Sample taken 45 min after addition of SLA dehydrogenase (gene 0088) and 2 mM NAD\(^+\) \((t = 225 \text{ min})\). The TICs recorded in the negative ion mode from the MS/MS fragmentation of the quasi molecular ions \([\text{M H}^-]\) of SQ, SGL, SG, KDSG, and SLA, as well as SLA and SL, are shown; note that SGL and KDSG were each observed as \([\text{M H}^-]\) ions of identical mass \((m/z = 241)\) but that the compounds eluted at different HPLC retention times, as indicated in the duplicated panels for TIC MS\(^3\) of \(m/z = 241\). Pyruvate, as the second product of the KDSG aldolase reaction (Fig. 1), could not be detected under the HPLC MS conditions we used but was confirmed by other analytical methods.

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generated enzymatically from DHPS (as discussed above). In addition, the existence of pyruvate after the aldolase reaction was confirmed through a positive lactate dehydrogenase reaction and by HPLC cochromatography with authentic pyruvate standard. Thus, we demonstrated that protein 0100 is an aldolase that cleaves KDSG to SLA and pyruvate (Fig. 1C). Finally, with the addition of the last enzyme of the SQ pathway, SLA dehydrogenase 0088, the SLA peak had disappeared completely and SL had formed (Fig. 4 E and F).

We also tested SG dehydratase 0089 and KDSG aldolase 0100 under the same reaction conditions for their potential activity with the analogous substrates of the classical Entner Doudoroff pathway, PG and KDGP (Fig. 1A), respectively, which are commercially available. No substrate turnover and product formation could be detected in the HPLC MS assay (not shown); hence, these enzymes of the SQ pathway in P. putida SQ1 also appeared to be highly specific for the sulfonated substrate, as is SG dehydratase.

Discussion

SQ is one of the most abundant organosulfur compounds in the biosphere, following glutathione, Cys, and Met, and the global production of SQ is estimated at 10 gigatons per year (2, 22). Although the biosynthesis of SQ and SQDG in plants, algae, cyanobacteria, and archaebacteria has been studied in considerable detail (e.g., 23, 24), much less is known about the degradation reactions and the recycling of the carbon and sulfur bound in SQ and SQDG. The lipid can easily be hydrolyzed by plant acyl hydrolases, which liberate SQ glycerol (1), and glucosidases can liberate SQ in the next step (25); however, it is still unclear whether higher plants are capable of splitting the carbon/sulfur bond in SQ at significant rates. Indeed, inorganic sulfate is the predominant source of sulfur for growth of plants and algae, for example, and plant growth can become sulfur/sulfate limited, for example, in soils that are sulfur deficient due to intensive agriculture and to the effective measures to reduce sulfur emissions to the atmosphere in recent years (26, 27); phytoplankton growth in freshwater environments can also become sulfate/sulfur limited (28). The recycling of the sulfur bound in SQ is catalyzed by heterotrophic bacteria, which can easily be enriched from soil (5, 7, 9), and which includes the degradation intermediates DHPS and SL, but no release of sulfate, if SQ utilizing bacteria are grown in pure culture (10-12). Later work demonstrated that SQ can be degraded completely by two member bacterial communities, that is, by a primary degrader with transient release of SL or DHPS and a secondary degrader with release of sulfate (11, 12). Pathways for the degradation of DHPS and SL, including desulfonation, have been described (13, 15, 29) where, briefly, DHPS is oxidized to SL and the SL is mineralized via one of three known pathways and desulfonative enzymes [i.e., SL sulfatase (SuyAB; EC 4.4.1.24), sulfatoacetaldehyde acetyltransferase (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25)]. However, details on the pathways, enzymes, and genes for the conversion of SQ to DHPS and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing. A first pathway, sulfoglycolysis leading to DHPS, was found in (Xsc; EC 2.3.3.15), cysteate sulfatase (CuyA; EC 4.4.1.25), sulfoacetaldehyde acetyltransferase (SuyAB; EC 4.4.1.24), sulfoglycolysis leading to DHPS, and SL were missing.
Interestingly, some of these strains are isolated gut symbionts (e.g., the Enterobacteriaceae strains *Hafnia alvei* ATCC51873, *Leminorella grimonii* DSM5078, *Serratia sp.* Ag2) and/or potential pathogens (e.g., *Vibrio* spp., *Halomonas* spp., *Salinarimonas*, *Microvirga* spp., *Plesiomonas* sp., *Halomonas* ATCC51873, *Hafnia alvei* ATCC51873, *Leminorella grimonii* DSM5078, *Edwardsiella tarda* 090813, *Acidocella* sp., *Halomonas* zhanjiangensis DSM21076, *Halomonas* sp. TD01, *Halomonas* sp. SMB101, *Microvirga* sp. 09A11 and *Leminorella*). Whether these isolated strains are indeed able to use SO for growth, and whether utilization of SO is indeed a relevant trait in the habitats from which these strains originated, needs to be addressed.

The use of either the glycolysis (Embden Meyerhof) or Entner Doudoroff pathway by microbes for the utilization of glucose as a growth substrate illustrates a direct connection between an organism’s environment and the thermodynamic and biochemical properties of the metabolic pathway it employs (32). We speculate that this same holds true for the newly discovered analogous pathways for SQ, i.e., for sulfoglycolysis in *E. coli* K12, which excretes SLA in its reduced form (as DHPS), and for the SQ Entner Doudoroff pathway in *P. putida* SQ1, which excretes SLA in its oxidized form (as SL). In glycolysis, glucose is phosphorylated twice and cleaved into two molecules of GAP, whereas in the Entner Doudoroff pathway, glucose is phosphorylated only once and oxidized to KDPG and the KDPG is cleaved to one pyruvate and one GAP. In the further reactions from GAP to pyruvate, two molecules of ATP per molecule of GAP can be conserved (as indicated in Fig. 1A), and, accordingly, microbes seem to prefer either the glycolysis (Embden Meyerhof) or Entner Doudoroff pathway for the utilization of glucose as a function of their energetic situation. Although energy deprived, fermentative anaerobes predominantly depend on the higher ATP yield of the glycolysis pathway, the Entner Doudoroff pathway is common among obligate aerobes and facultative anaerobes (18, 32). Furthermore, the fermentative organisms need to invest pyruvate carbon as an electron acceptor (e.g., for excreting lactate as a fermentation product), whereas in respiring organisms, the reducing equivalents (NADH) from GP oxidation in the Entner Doudoroff pathway and from dissimilation of pyruvate to CO2 can be preserved as (additional) ATP via proton motive force and ATPase. In contrast, life is acetic for microbes that use SO as a growth substrate via the SQ Entner Doudoroff pathway concomitant with the excretion of SL, compared with utilization of glucose by the classical Entner Doudoroff pathway. First, there is pyruvate and SLA produced from KDSG, not pyruvate and GAP as with KDPG; hence, no ATP can be produced by substrate level phosphorylation of GAP (Fig. 1A). Accordingly, the proteomic data for *P. putida* SQ1 suggested that GAP dehydrogenase was strongly downregulated in SQ grown cells but highly produced in glucose grown cells, whereas pyruvate dehydrogenase was highly produced for both (Fig. 3B). Second, there is only half of the carbon to re-appear from SQ, in form of one pyruvate. However, additional reducing equivalents (NADH) are gained from the last reaction of the SQ pathway in *P. putida* SQ1, from the oxidation of SLA to SQ as catalyzed by the SLA dehydrogenase (Fig. 1B). Hence, the SQ Entner Doudoroff pathway, inclusive of the SLA dehydrogenase reaction in *P. putida* SQ1, is represented by the equation

\[
SO + 2 NAD^+ \rightarrow pyruvate + SL + 2 NADH + 2 H^+.
\]

In the sulfoglycolytic pathway, there is DHAP and SLA produced from cleavage of SFP (12) rather than DHAP and GAP, as with fructose 1,6 bisphosphate in glycolysis, and the substrate level phosphorylation of the one DHAP (via GAP to pyruvate) allows for conservation of ATP. In addition, the reduction of SLA to DHPS, as catalyzed by the NADH dependent SLA reductase in *E. coli* K12, regenerates the electron acceptor NAD*+* that is needed for conversion of the DHAP via GAP to pyruvate (Fig. 1A), so that the overall equation of sulfoglycolysis inclusive of the SLA reductase reaction in *E. coli* K12 is

\[
SO + ADP + P_i \rightarrow pyruvate + DHPS + ATP.
\]

We therefore suspect that the SQ Entner Doudoroff pathway might be preferred among SQ utilizing microbes with respiratory energy metabolism, whereas SQ utilizing fermentative anaerobes might depend on the direct ATP yield of the sulfoglycolytic pathway and on the SLA reductase reaction as an additional electron accepting step that aids in the overall fermentation.

### Materials and Methods

A detailed version of the materials and methods used in this study can be found in [SI Materials and Methods](http://img.jgi.doe.gov); *P. putida* SQ1 (DSM 100120) (11) was cultivated in mineral salts medium at pH 7.2 (33) at 30 °C in the dark, with SO, glucose, or succinate as the sole carbon and energy source. SQ was cultivated in mineral salts medium at pH 7.2 (33) at 30 °C in the dark, with SO, glucose, or succinate as the sole carbon and energy source. The genome annotation was performed within the Joint Genome Institute’s IMG analysis system (34), and the annotation protocol used is described in the [SI Materials and Methods](http://img.jgi.doe.gov) for both (Fig. 3B).
IMG Project ID Gp0039102) was used to build a local Mascot database (35) for PS MS at the Proteomics Facility of the University of Konstanz. Two dimensional PAGE was performed using Bio Rad’s ReadyStrip immobilized pH gradient system (36) in RT PODS (primary sequences; Table S1), the E.Z.N.A Bacterial RNA preparation kit (Omega Bio Tek) was used; and for complementary DNA synthesis, the Maxima reverse transcriptase kit (Fermentas) was used for subsequent PCR assays (37). For insertional RNA preparation kit (Omega Bio Tek) was used and for complementary cDNA expression kit (Invitrogen); the proteins were purified using nickel nitriiilc acetic acid columns (12). The standard enzyme reaction mixture was 2 mM SQ in 50 mM Tris-HCl buffer (pH 7.5), plus 3 mM NAD(P)" and the corresponding enzymes (10 60 µg ml-1 each). SQ, SGL, KDSG, SLA, SL, GP, PGL, KDPG, and GAP were separated using hydrophilic interaction liquid chromatography and detected by electrospray ionization MS (12).

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