Characterizing the metabolism of Dehalococcoides with a constraint-based model

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Characterizing the Metabolism of *Dehalococcoides* with a Constraint-Based Model

M. Ahsanul Islam, Elizabeth A. Edwards, Radhakrishnan Mahadevan*

Department of Chemical Engineering and Applied Chemistry, University of Toronto, Toronto, Ontario, Canada

**Abstract**

*Dehalococcoides* strains respire a wide variety of chloro-organic compounds and are important for the bioremediation of toxic, persistent, carcinogenic, and ubiquitous ground water pollutants. In order to better understand metabolism and optimize their application, we have developed a pan-genome-scale metabolic network and constraint-based metabolic model of *Dehalococcoides*. The pan-genome was constructed from publicly available complete genome sequences of *Dehalococcoides* sp. strain CBDB1, strain 195, strain BAV1, and strain VS. We found that *Dehalococcoides* pan-genome consisted of 1118 core genes (shared by all), 457 dispensable genes (shared by some), and 486 unique genes (found in only one genome). The model included 549 metabolic genes that encoded 356 proteins catalyzing 497 gene-associated model reactions. Of these 497 reactions, 477 were associated with core metabolic genes, 18 with dispensable genes, and 2 with unique genes. This study, in addition to analyzing the metabolism of an environmentally important phylogenetic group on a pan-genome scale, provides valuable insights into *Dehalococcoides* metabolic limitations, low growth yields, and energy conservation. The model also provides a framework to anchor and compare disparate experimental data, as well as to give insights on the physiological impact of "incomplete" pathways, such as the TCA-cycle, CO₂ fixation, and cobalamin biosynthesis pathways. The model, referred to as iAI549, highlights the specialized and highly conserved nature of *Dehalococcoides* metabolism, and suggests that evolution of *Dehalococcoides* species is driven by the electron acceptor availability.

**Introduction**

Genome sequencing has enabled the characterization of biological systems in a more comprehensive manner. Recent research in bioinformatics and systems biology has resulted in the development of numerous systematic approaches for the analysis of cellular physiology that have been reviewed elsewhere [1–4]. However, constraint-based reconstruction and analysis (COBRA), a mathematical framework for integrating sequence data with a plethora of experimental ‘omics’ data has been shown to be successful in the genome-wide analysis of cellular physiology [5–7]. In addition, this approach has also been utilized to explore the metabolic potential, as well as the gene essentiality analysis of *Dehalococcoides* [8–13]; however, the COBRA approach has not yet been implemented for *Dehalococcoides*, or any other known dechlorinating bacterium.

Using acetate as a carbon source and hydrogen as an electron donor, small, disc-shaped anaerobic bacteria *Dehalococcoides* are capable of dehalogenating a variety of halogenated organic compounds as electron acceptors, of which many are problematic ground water pollutants [14–17]. *Dehalococcoides* ethenogen strain 195 (strain 195) is the first member of this phylogenetic branch that was grown as an isolate [18]. Subsequently, a number of *Dehalococcoides* strains were isolated: strain CBDB1 [19], strain BAV1 [20], strain FL2 [21,22], strain GT [23], and strain VS [24]. The strains respire through a membrane-bound electron transport chain (ETC) [25–27], which is incompletely defined. Reductive dehalogenases (RDases), encoded by reductive dehalogenase homologous (rdh) genes, are pivotal membrane-associated enzymes of the ETC [26,27]. Genome sequencing has revealed the presence of multiple non-identical putative rdh genes in each strain [28–31]. Since these microbes respire chlorinated pollutants by RDase-catalyzed reductive dechlorination reaction, rdh genes determine a significant part of *Dehalococcoides* phenotypes. Functional characterization of only 5 of the over 190 rdh genes reveals that cobalamin — a corrinoid compound — is an essential cofactor for the corresponding RDases [32–36]. Hydrogenase (H₂ase) is another key enzyme of *Dehalococcoides* ETC [26,27,29,30]. Interestingly, the genomes of *Dehalococcoides* strains encode 5 different types of H₂ases: membrane-bound *hup, ehh, hyc*, and cytoplasmic *hva* [29,30,37,38]. The presence of multiple types of H₂ases clearly emphasizes the importance of H₂ in their energy metabolism [18–21]. This multiplicity of H₂ases and RDases further highlights redundancy in the organisms’ energy...
conservation process that may ensure a rapid and efficient response of their energy metabolism towards changing growth conditions [39,40].

In addition to RDase and H2ase, the ETC likely requires an in vivo electron carrier to mediate electron transport between these enzymes. Previous studies have shown that the reductive dechlorination reaction requires an in vivo electron donor of redox potential ($E_0$) $\leq -360$ mV [25,27], similar to other dechlorinating bacteria [17,41,42]. The cob(II)alamin of corrinoid cofactor in the RDase enzyme is reduced to cob(I)alamin during the reductive dechlorination reaction; hence, necessitating a low-potential donor because the redox potential ($E_0$) of Co(II)/Co(I) couple is between $-500$ and $-600$ mV [17,41,43]. While quinones, such as menaquinone or ubiquinone could act as electron carriers in anaerobes [44–46], experimental evidence suggests this is not the case in Dehalococcoides [27,47]. Moreover, the redox potentials for quinones (Menaquinone ox/red $E_0 = -70$ mV, Ubiquinone ox/red $E_0 = +113$ mV; [48]) are not compatible with the RDases’ requirement of a low-potential donor. Furthermore, cytochrome b — a typical donor for the quinones to participate in the redox reactions of anaerobic ETCs [49,50] — appears to be absent in the genomes of Dehalococcoides [29,30]. However, the genomes have ferredoxin, an iron-sulphur protein, which can act as the low-potential donor for RDases because ferredoxin is the most electronegative electron carrier yet found in the bacterial ETCs [42,48,51–55].

Although, Dehalococcoides are capable of harnessing free energy from the RDase catalyzed exergonic reductive dechlorination reactions by coupling to ATP generation for growth [14,17], their pure culture growth is much less robust than their growth in mixed cultures [24,56,57]; even in mixed cultures, their growth yield is not as high as that predicted from the free energy of reductive dechlorination [26,58]. Thus, in order to better understand dechlorination-metabolism, and given that to-date sequenced

Figure 1. Composition of the Dehalococcoides pan-genome. Core, dispensable, and unique genomes are represented by blue, green, and orange, respectively. Genes in these genomes are also categorized as metabolic (spotted pattern), non-metabolic (plain), and hypothetical (grid pattern) on the basis of various bioinformatic analyses (see text for details).

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Dehalococcoides genomes are more than 85% identical at the amino acid level [38,59], we developed a pan-genome-scale constraint-based in silico metabolic model of Dehalococcoides. The model was constructed from the complete genome sequences of 4 geographically distinct strains: strain CBDB1 from the Saale river near Jena, Germany [60,61], strain BAV1 from Oscoda, Michigan, USA [62,63], strain 195 from a wastewater treatment plant in Ithaca, New York, USA [18,64,65], and strain VS from Victoria, Texas, USA [24,66]. Although the model comprises multiple genomes, it analyzed the outcome of metabolic genes only. Also, it did not include information about cellular regulation due to the lack of adequate knowledge about Dehalococcoides regulatory networks. Nonetheless, the model was primarily used to investigate the intrinsic metabolic limitations, in addition to addressing open questions regarding Dehalococcoides physiology, such as the incomplete nature of various metabolic pathways, and attendant implications on metabolism and growth. We also identified the environmental conditions from the model simulations that resulted in faster in silico growth of Dehalococcoides. Furthermore, the constraint-based model, along with the comparative analysis of 4 genomes, clarifies both similarities and differences among the strains in terms of their core metabolism and other biosynthetic processes leading to an improved understanding of metabolism and evolution in Dehalococcoides.

Results/Discussion

Dehalococcoides Metabolic Network

Pan-metabolic-genes of Dehalococcoides. The concept of a pan-genome was first investigated by Tettelin and colleagues for the 8 isolates of common human pathogen *Streptococcus agalactiae* [67]. While pan-genome analyses for other organisms have been

![Figure 2. Distribution of dispensable and unique metabolic genes in different Dehalococcoides strains.](image-url)
reported [68], no such analysis has been performed to-date for any dechlorinating bacterium, or any other microbe of bioremediation importance. In addition, most of the reported pan-genome analyses were conducted on pathogenic isolates for designing vaccines by assessing their virulence evolution and diversity. Here, we developed the \textit{Dehalococcoides} pan-genome from the complete sequenced genomes of four \textit{Dehalococcoides} strains. Method details are provided in the Materials and Methods and in Figures 1–4 in Text S2. The pan-genome comprises 2061 genes (Figure 1). Of these 2061 genes, 1118 genes are in the core, 457 are dispensable, and 486 are unique (Figure 1). The genes are further classified as metabolic, non-metabolic, and hypothetical based on information obtained from the literature and various biochemical databases, such as SWISSPROT [69], UniProt [70], IMG [71], and PDB [72]. We defined metabolic genes as those that are exclusively related to metabolic processes such as carbon and energy metabolism of \textit{Dehalococcoides}. Genes that are involved in DNA repair and metabolism, as well as encoding putative transposable elements and insertion elements [29,30] are classified as non-metabolic. Putative genes with a non-specific metabolic function or genes without any function or annotation are categorized as hypothetical (Figure 1).

Most of the metabolic genes (413 out of 549) were found in the core genome while only a small number of those were identified in the dispensable (75) and unique (61) genomes. This abundance of core metabolic genes in the pan-genome indicate that the central metabolism of \textit{Dehalococcoides} is very well conserved across strains since core genes are shared by all [2,67,73–75]. We further categorized the metabolic genes in the dispensable and unique genomes based on both function and strain (Figure 2). Clearly, the majority of differences among the strains (45 out of the 75 dispensable genes and 47 out of the 61 unique genes) are due to the \textit{rdh} genes (Figure 2). In addition, only strain195 has nitrogen fixing genes and associated transporters related to the nitrogen fixation process. As a result of these genes, together with unique \textit{rdh}s, strain 195 has the most unique genes of the 4 genomes compared. Due to the presence of a suite of multiple non-identical \textit{rdh} genes, each strain metabolizes a unique set of specific chlorinated substrates [38,76,77]. Hence, the differences in \textit{rdh} genes largely define the strain specific phenotypes of \textit{Dehalococcoides}.

Though there were differences in \textit{rdh} genes, most of these were found in the dispensable genome (Figure 2 and Table 14 in Text S1) while only 9 \textit{rdh}A (5 \textit{rdh}A and 4 \textit{rdh}B genes with >35% amino acid sequence identity) were shared by all strains and found in the core genome (Table 13 in Text S1). The presence of majority of \textit{rdh} genes in the dispensable genome further supports the hypothesis that they were acquired through lateral gene transfer events [29,59,78].

**Features of the reconstructed metabolic network of *Dehalococcoides*.** The reconstructed metabolic network of \textit{Dehalococcoides}, denoted as iAI549 according to the established naming convention [79], accounted for 549 open reading frames (ORF) or protein coding genes (27% of the total 2061 genes). Metabolic genes were identified from the genome annotations which were verified with various bioinformatic analyses (see Materials and Methods). In addition, we annotated or revised the annotation for 70 ORFs based on information obtained from different biochemical databases (Table 2 in Text S1 provides a full list of reannotated genes). General features of \textit{Dehalococcoides} metabolic network (iAI549) are provided in Table 1.

iAI549 includes 518 model reactions and 549 metabolites where 497 reactions are gene associated and 21 (4%) are non-gene associated (Table 1). The non-gene associated reactions (Table 1 in Text S1) were added in order to fill gaps in the reconstructed network based on simulations. Although no gene associations were identified for these reactions, we provided a list of core hypothetical genes (Table 16 in Text S1) which potentially could contain genes associated with these reactions and are prime candidates for further biochemical testing. The network also comprises 36 exchange reactions, including one demand reaction called the biomass synthesis reaction (\textit{BIO\_DHC\_DM\_61}), to facilitate the transport of various metabolites into and out of the cell. The composition of the \textit{in silico} minimal medium is shown in Table 2, while detailed composition of \textit{BIO\_DHC\_DM\_61} is available in Text S2. We further categorized the genes and

<table>
<thead>
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<th>Genes</th>
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<th>Number of included genes</th>
<th>Number of excluded genes</th>
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<td>Number of intracellular biomass metabolites</td>
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doi:10.1371/journal.pcbi.1000887.t001

doi:10.1371/journal.pcbi.1000887.t002

**Table 1. General features of *Dehalococcoides* metabolic network (iAI549).**

<table>
<thead>
<tr>
<th>Abbreviation</th>
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<th>Equation</th>
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<tr>
<td>Acetate exchange</td>
<td>\text{EX_ac(e)}</td>
<td>\text{ac} \leftrightarrow</td>
</tr>
<tr>
<td>Vitamin B12 or cobalamin exchange</td>
<td>\text{EX_cb1(e)}</td>
<td>\text{cb1} \leftrightarrow</td>
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<tr>
<td>Chloride exchange</td>
<td>\text{EX_cl(e)}</td>
<td>\text{cl} \leftrightarrow</td>
</tr>
<tr>
<td>Carbon dioxide exchange</td>
<td>\text{EX_co2(e)}</td>
<td>\text{co2} \leftrightarrow</td>
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<td>Proton exchange</td>
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<td>\text{EX_h2o(e)}</td>
<td>\text{h2o} \leftrightarrow</td>
</tr>
<tr>
<td>Dichlorobenzene exchange</td>
<td>\text{EX_dcb(e)}</td>
<td>\text{dcb} \leftrightarrow</td>
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<td>Ethene exchange</td>
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<td>\text{hcb} \leftrightarrow</td>
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<td>Ammonium exchange</td>
<td>\text{EX_nh4(e)}</td>
<td>\text{nh4} \leftrightarrow</td>
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<tr>
<td>Inorganic phosphate exchange</td>
<td>\text{EX_pi(e)}</td>
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<td>\text{EX_so4(e)}</td>
<td>\text{so4} \leftrightarrow</td>
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doi:10.1371/journal.pcbi.1000887.t003

**Table 2. Composition of the *in silico* minimal medium of *Dehalococcoides*.**
reactions of iAI549 into 7 different functional categories or subsystems based on the associated metabolic pathways (Figures 7 and 8 in Text S2). The differences among the strains are mainly observed in the energy metabolism category, which includes 51 dispensable and 34 unique metabolic genes, and most of these are rbsd (Figure 7 in Text S2). However, almost all the reactions of iAI549 (96% of the total 518) are core, which again indicates that the basic central metabolism of Dehalococcoides is strictly conserved (Figure 8 in Text S2). Although a number of dispensable metabolic genes are found in different subsystems, most of these genes are actually paralogs of the core metabolic genes. This relationship explains why, for example, there are 13 dispensable genes in the transport subsystem, 3 genes each in the lipid and nucleotide metabolism, but no corresponding dispensable reactions (Figure 8 in Text S2). Since rbsd were found in core, unique and dispensable genomes, we assigned the reductive dechlorination reaction as a core reaction. Therefore, the truly unique metabolic reactions of iAI549 are the nitrogen fixing reaction (EC-1.18.6.1) and the molybdate (required for synthesizing rdh) transport reaction (TC-3.A.1.8) belonging to strain 195 only.

Furthermore, we compared iAI549 to a number of in silico genome-scale models of other Bacteria and Archaea (Table 3): iAF1260 for Escherichia coli [90], YO844 for Bacillus subtilis [81], RM588 for Geobacter sulfurreducens [82], and iAF692 for Methanosarcina barkeri [83]. We found that iAI549 had the lowest number of total reactions because of the limited scope of Dehalococcoides metabolism. In addition, these numbers also suggest that facultative anaerobes (E. coli and B. subtilis) are more versatile in their lifestyle and metabolism compared to obligate anaerobes (Dehalococcoides, Geobacter and Methanosarcina). These differences are further supported by the presence of a high number of transporters in iAF1260 and YO844 compared to the presence of only 32 transporters in iAI549 (Table 3). A large number of reactions of iAI549 are found to be involved in the amino acid metabolism since the genes for de novo synthesis of all the amino acids except methionine are identified to be present in the genomes [29,30]. Also, iAI549 comprises only 41 reactions for the central carbon metabolism — glycolysis, gluconeogenesis, TCA-cycle, pentose phosphate pathway, carbohydrate metabolism — compared to 262 reactions in iAF1260; an incomplete TCA-cycle and an inactive glycolysis pathway explain this low number for iAI549. Since Dehalococcoides lacks a typical bacterial cell wall [18–20], iAI549 has only 81 reactions for the lipid metabolism category. Furthermore, the cofactor and prosthetic group biosynthesis comprises 101 reactions of iAI549 compared to 162 reactions of iAF1260 because the pathways for synthesizing vitamin B₁₂ and quinones are predicted to be incomplete in Dehalococcoides [29,30].

Model-Based Simulations of Dehalococcoides Physiology

Exploring the central metabolism of Dehalococcoides. The reconstructed network for glycolysis, gluconeogenesis, the TCA-cycle and the pentose phosphate pathway of iAI549 highlighted some of the key limitations of Dehalococcoides central metabolism. Although putative genes for glycolysis and gluconeogenesis were identified, no gene for a glucose or fumarate transporter was found in any of the genomes, explaining the inability of Dehalococcoides to use glucose or fumarate as a carbon source. The TCA-cycle of Dehalococcoides (Figure 3A) is incomplete, as previously reported [29,30]. We could identify putative genes for 2-oxoglutarate synthase and succinyl Co-A synthetase (with 26% amino acid sequence identity to the Methanococcus jannaschii gene), and fumarate reductase/succinate dehydrogenase (with 31–33% amino acid sequence identity to the E. coli gene) (Table 3 in Text S1), but we could not find a gene encoding the citrate synthase (CS) in Dehalococcoides. In a scenario without CS, carbon assimilation could occur using a reductive TCA-cycle. However, the biosynthetic formation of citrate by Dehalococcoides etenogenes strain 195 was recently demonstrated using 13C-labeled isotopomer experiments, although the gene encoding the putative Re-type CS enzyme was not identified [84]. The two Dehalococcoides genes that are most similar to the only biochemically characterized Re-type CS gene from Clostridium kluyveri DSM555 [85] are annotated as isopropyl malate and homocitrate synthase; however, these genes share only 27% amino acid sequence identity with CS gene from C. kluyveri. Hence, further experiments are required to establish the role of these genes, as well as the aforementioned putative TCA-cycle genes in Dehalococcoides. Nonetheless, these isolate labeling studies suggest the formation of 2-oxoglutarate from citrate through the oxidative branch of the TCA-cycle.

In order to analyze the effect of the presence of the CS reaction on Dehalococcoides growth, we conducted growth simulations with and without this reaction in iAI549. Only a subtle difference in the growth rate (0.0137 h⁻¹ vs. 0.014 h⁻¹) and yield (0.72 gDCW/eq vs. 0.71 gDCW/eq) was observed (Figures 4A, 4B and Table S2 in Text S2). Hence, regardless of whether the TCA-cycle is oxidative (Figure 4B) or reductive (4A), the fact that it is incomplete explains why Dehalococcoides are unable to use acetate as their energy source. Interestingly, iAI549 has one anaplerotic
Figure 3. The reconstructed TCA-cycle and CO2 fixation pathway of Dehalococcoides. The arrows show the directionality of the reactions. (A) Grey: citrate synthase gene currently not identified in iAI549, but the pathway is suggested to be present by Tang et al. [84]; Orange: pathways for which homologous putative genes (≥30% amino acid sequence identity) were tentatively identified in Dehalococcoides, but are suggested to be absent by Tang et al. [84]; Red: pathways for which putative genes are confirmed to be present by both iAI549 and Tang et al. [84]. In all cases, the TCA-cycle of Dehalococcoides is not closed which explains their inability to use acetate as an energy source. (B) Dehalococcoides' requirement of CO2 in addition to acetate for their in silico growth. The numbers are flux values in mmol.gDCW \(^{-1}\).h\(^{-1}\). During pyruvate synthesis, Dehalococcoides require 67% carbon (molar basis) from acetate and 33% (molar basis) from CO2. Thus, Dehalococcoides fix carbon via the pyruvate-ferredoxin oxidoreductase or pyruvate synthase (POR) pathway.

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reaction — pyruvate carboxylase (PC) — which produces oxaloacetate from pyruvate (Figures 3A, 4A, and 4B). Generally, anaerobic reactions generate intermediates of a TCA-cycle, but in the absence of a CS reaction, PC is essentially the sole pathway for producing oxaloacetate in the TCA-cycle of iAI549.

**CO₂ fixation by Dehalococcoides.** Analysis of iAI549 also revealed the presence of a carbon fixation step via pyruvate-ferredoxin oxidoreductase or pyruvate synthase (POR) enzyme encoded by 4 putative *Dehalococcoides* genes (gene number 181, 182, 183, 184; Table 3 in Text S1). Anaerobes such as *Geobacter sulfurreducens* and *Methanococci barkeri* are also reported to utilize this step in their central metabolism [82,86]. POR is essential for the *in silico* growth of *Dehalococcoides* using iAI549 since it is the only pathway for producing pyruvate from acetate (Figures 3A, 4A, and 4B). Growth simulations of iAI549 further predict that 33% of the total moles of carbon fixed into the biomass is from extracellular CO₂ via POR, and the balance (67%) is from extracellular acetate through acetyl-CoA synthetase (Figure 3B); thus, clearly highlighting the important requirement for extracellular CO₂ in addition to acetate as a carbon source for *Dehalococcoides*.

Moreover, the presence of both POR and carbon-monoxyde dehydrogenase enzymes (CODHR) encoded by 4 putative genes of iAI549 (gene number 170, 171, 172, 174; Table 3 in Text S1) initially suggested that the Wood-Ljungdahl pathway [87] of CO₂ fixation might be active in *Dehalococcoides*. However, the absence of several key enzyme encoding genes, such as the menyltetrahydrofylate reductase and a methyltransferase in the folate-dependent branch of the Wood-Ljungdahl pathway [88-90] indicated that the pathway was incomplete in *Dehalococcoides* (Figure 5 in Text S2). All of these observations are consistent with the carbon labeling studies by Tang et al. [84].

**Implications of the incomplete cobalamin synthesis pathway in Dehalococcoides.** Cobalamin or vitamin B₁₂ is essential for RDase activity; however, the pathway for producing cobalamin is incomplete in *Dehalococcoides* [29,30,91] (Figure 5). The complete *de novo* biosynthesis (aerobic or anaerobic) of vitamin B₁₂ requires around 30 genes [92], of which only 18 genes (Tables 3–7 in Text S1) are identified in *Dehalococcoides*. Seven (7) of these genes belong to the “anaerobic” pathway while 2 are found to be involved in the “aerobic” pathway of cobalamin biosynthesis. Several key enzyme encoding genes required for the precorrin ring formation, cobalt insertion, and methylation were not found in *Dehalococcoides* genomes (Figure 5). However, 7 genes of iAI549 (3 core, 1 dispensable, and 3 unique genes: 161, 162, 163, 433, 524, 525, 526; Tables 3, 5, and 7 in Text S1) that encode a putative cobalamin transporter were identified; thus, indicating that *Dehalococcoides* could uptake vitamin B₁₂ from the medium in the form of either cobinamide or cobalamin [93]. In fact, vitamin B₁₂ has been shown to be required for the growth of pure cultures, and its addition to the medium has been reported to enhance the growth rate of *Dehalococcoides* [91].

Therefore, in order to examine the influence of cobalamin on the growth of *Dehalococcoides*, we conducted growth simulations for two scenarios using iAI549: 1) *Dehalococcoides* growth rate as a function of weight fraction of cobalamin in the biomass and cobalamin salvage rate from the medium (Figure 6A), and 2) *Dehalococcoides* growth yield assuming it could synthesize its own cobalamin (i.e., adding all the reactions to iAI549 required for *de novo* cobalamin synthesis) compared to the yield when B₁₂ is salvaged from the medium (Figure 6B). Predictably, the growth rate decreases to zero at low cobalamin salvage rates (Figure 6A). Also, the cobalamin salvage rate at which metabolism becomes limited by B₁₂ is a strong function of the cobalamin fraction in the biomass, which has never been experimentally measured for *Dehalococcoides* (Figure 6A). From the second simulation, it is clear that the energetic cost for synthesizing cobalamin *de novo* is not very significant since the predicted yield with and without a cobalamin synthesis pathway is almost identical (Figure 6B). Only if one assumes a biomass cobalamin fraction 10 times higher than the maximum reported, a small (4%) reduction in the growth yield (from 0.72 gDCW/eq to 0.69 gDCW/eq) is predicted as a penalty for synthesizing cobalamin *de novo* (Figure 6B and Table 3 in Text S2). This low synthesis cost, along with the fact that cobalamin is essential, yet its synthesis pathway is incomplete in *Dehalococcoides* suggests perhaps that *Dehalococcoides* might have evolved syntrophically with cobalamin secreters and never faced significant evolutionary pressure to acquire a complete cobalamin synthesis pathway in their genomes.

**Does carbon or energy limit the *in silico* growth of Dehalococcoides?** Growth of *Dehalococcoides* is more rapid in mixed microbial communities than in pure cultures [24,57,60,94] although the reasons for this discrepancy are not entirely clear. The difference in reported growth yields between pure and mixed cultures is more significant (p = 0.0005 at 95% confidence level) than the difference in reported growth rates (p = 0.05 at 95% confidence level) (Tables 25, 26 in Text S2). Thus, in order to examine the growth-limiting conditions, we simulated *Dehalococcoides* growth yields under two different conditions: 1) allowing unlimited flux of amino acids in the medium at a hydrogen flux of 10 mmol.gDCW⁻¹.h⁻¹ (equivalent to the dechlorination rate obtained from average pure-culture growth yields and rates; Tables 24, 25 in Text S2), and 2) doubling the hydrogen flux (20 mmol. gDCW⁻¹.h⁻¹) without allowing any amino acid flux in the medium. The first condition mimics a carbon-rich environment while the second one represents an energy-rich situation. The model predicts that adding unlimited amount of any or all of the amino acids in the growth medium (obviating the need for the cell to synthesize these amino acids) increased the growth yield by a maximum of 55% (1.13 gDCW/eeq) compared to the case with no amino acids in the medium (0.72 gDCW/eeq) (Figure 7A). However, doubling only the hydrogen flux enhanced the growth yield by 65% (from 0.72 gDCW/eeq to 1.19 gDCW/eeq) (Figure 7A).

To further analyze this aspect of energy limitation, we simulated *in silico* growth yields of *Dehalococcoides* as a function of both acetate flux (carbon availability) and energy flux, represented by the energy transfer efficiency. This analysis (Figure 7B) shows that the growth of *Dehalococcoides* is energy-limited but not carbon-limited since growth yield increases proportionally to increase in energy transfer efficiency regardless of acetate flux. Moreover, simulations also reveal that growth yield of *Dehalococcoides* in a pure culture is only 30% efficient (corresponding to the green arrow) compared to 65% efficient (corresponding to the red arrow) in a mixed culture (Figure 7B). These simulations point towards electron flux from...
Figure 5. Reconstructed cobalamin biosynthesis pathway of Dehalococcoides. Dashed orange lines indicate cell membrane, grey lines indicate missing pathways, and red lines indicate existing pathways, putative genes of which are identified in Dehalococcoides during the reconstruction of iAI549. The arrows are denoting the directionality of the reactions. Since the genomes encode a putative cobalamin transporter, Dehalococcoides may salvage vitamin B₁₂ either in the form of cobinamide or cobalamin from the environment as indicated by ‘cobinamide transport’ and ‘cobalamin transport’ reactions in the figure. The adenosylcobalamin, which is the end product of the entire pathway, is a biomass constituent and is assumed to take part in Dehalococcoides cell formation.

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hydrogen to the RDase as the rate-limiting step, which is somehow more efficient in mixed cultures. It is possible that interspecies hydrogen transfer, such as in a mixed culture is more direct than hydrogen provided in the medium (as for pure cultures). Electrons supplied from an electrode that was polarized to a very low potential were shown to stimulate Dehalococcoides metabolism [95], possibly illustrating such an effect; if true, these results suggest a mechanism for the enhanced growth of Dehalococcoides and to a faster dechlorination of pollutants.

As described earlier, experimental studies clearly illustrate the favorable growth of Dehalococcoides in syntrophic microbial consortia compared to their isolated pure cultures. This obviously points towards the existence of some undefined beneficial metabolic interactions among the consortia members. Although iAI549 simulations suggested more efficient electron transfer and energy utilization in a mixed culture, this result requires further experimental validation. Because these microbes harness energy for their growth from reductive dechlorination reactions, their increased growth will certainly accelerate the bioremediation process. Hence, the current challenge is to understand the reason behind their favorable growth in a mixed microbial community prevailing in their natural habitat. Therefore, a genome-scale metabolic model of a syntrophic community of dechlorinating bacteria, where Dehalococcoides are the dominant members, can be useful to understand the factors influencing their growth. This information may also help to develop a defined bacterial community with enhanced bioremediation capability, in addition to developing effective strategies for exploiting these microbes for effective bioremediation of contaminated sites around the world.

Conclusions

Although genome-scale constraint-based models are available for several microbes from all three forms of life, iAI549 is the first such endeavor for dechlorinating bacteria. This constraint-based flux balance model is consistent with the specialized nature of Dehalococcoides metabolism. The model supports the idea that evolution of the chlorinated compound specific rdx genes conferred the strain-specific metabolic phenotype to Dehalococcoides. In addition to cataloguing significant metabolic similarities among Dehalococcoides strains, the model also provides valuable insights regarding physiological and metabolic bottlenecks of these microbes. Reconstructed central metabolic pathways, for example, identified underlying reasons for Dehalococcoides’ requirement of a separate energy source in addition to a carbon source for growth, as well as a carbon fixation step. Also, growth simulations revealed the energy-limited rather than carbon or cobalamin-limited growth of these organisms. In the process of developing the model, detailed tables of metabolic gene correspondences among 4 genomes, reannotations based on pathway analysis, and intrinsic kinetic and stoichiometric parameters were developed for the user community. We also created lists of core hypothetical genes and non-gene associated model reactions; these lists will be useful for designing enzyme assays for functional annotation of the hypothetical genes. Finally and most importantly, this pan-genome-scale metabolic model now provides a common and scalable framework as well as a knowledgebase, which can be used for visualization and interpretation of various omics-scale data from transcriptomics, proteomics and metabolomics for any Dehalococcoides strain; such analysis will further our understanding of these environmentally important organisms so that the outcome of bioremediation can be improved.

Materials and Methods

Dehalococcoides Pan-Genome

In order to develop the pan-genome of Dehalococcoides, we obtained strain CBDB1 genome sequence from JCVI [http://cmr.jcvi.org/tigr-scripts/CMR/CmrHomePage.cgi] while strain 195 and strain BAV1 genome sequences were downloaded from the IMG database [http://img.jgi.doe.gov/cgi-bin/pub/main.cgi]. Strain VS genome sequence was obtained from Alfried Spormann at Stanford University, CA. The genome sequences were compared using OrthoMCL [96], a widely accepted method for finding orthologs across different genomes [97]. OrthoMCL is based on reciprocal best BLAST hit (RBH), but recognizes co-ortholog groups using a Markov graph clustering (MCL) algorithm [98]. The Dehalococcoides pan-genome was developed following a previously described approach [67,68] outlined in Figures 1–4 in Text S2 and in the following section.

First, we identified putative orthologs between a reference genome and a subject genome which were selected arbitrarily from the 4 genomes compared. The analysis was conducted by OrthoMCL keeping the parameters of the algorithm in default settings. Subsequently, those genes that were present only in subject genome 1 were identified and combined with the reference genome to create the augmented genome 1 (Figure 1 in Text S2). Then, the augmented genome 1 was compared and analyzed with subject genome 2 as described above to construct the augmented genome 2. The pan-genome was obtained by comparing the augmented genome 2 and subject genome 3. The number of genes in a pan-genome was reported to depend on both the order of genomes analyzed and the reference genome [67]; hence, we constructed 6 pan-genomes for 6 different genome-order combinations. Of these 6 pan-genomes, we selected the one with the highest number of genes (2061) as Dehalococcoides pan-genome in order to capture the entire gene repertoire of Dehalococcoides species [74]. We also identified the core, dispensable and unique genomes for Dehalococcoides pan-genome using methods described previously [2,67], (Figures 2–4 in Text S2).

Reconstructing the Metabolic Network of Dehalococcoides

The pan-genome was used to reconstruct the pan-genome-scale metabolic network, and the constraint-based model of Dehalococcoides metabolism was developed from this reconstruction. Since the strains of Dehalococcoides share a high degree of sequence identity, we arbitrarily chose strain CBDB1 genome as a reference and constructed the metabolic network from its annotated genome sequence [29], publications regarding its physiology, and various genomic and biochemical databases [7]. Then, we included other metabolic genes from the pan-genome into the reconstructed network that were missing from strain CBDB1 genome. Five gene
correspondence tables for the four genomes were prepared (Tables 3–7 in Text S1) for facilitating gene identification and cross-reference regardless of the genome of interest. We developed and manually curated the reconstructed network using the procedures described previously [3,7,99,100] with the SimPheny platform (Genomatica Inc., San Diego, CA). Since genome annotations are error prone [101], annotated genes of strain CBDB1, as well as the pan-genome genes with defined metabolic functions were verified by identifying their homologs in other well characterized organisms, including Escherichia coli, Bacillus subtilis, Geobacter sulfurreducens and Saccharomyces cerevisiae with BLAST [102]. Subsequently, confidence levels were assigned based on the degree of sequence identities or reciprocal best BLAST hits. Dehalococcoides genes, for instance, having >40% amino acid sequence identity with homologs in the protein databases (SWISSPROT [103], IMG [71], PDB [72], GO [104]) were given a confidence level of 3, and genes with >50% and <30% identity were assigned a confidence level of 2 and 1, respectively. In addition, these genes were also evaluated on the basis of both gene order or conserved synteny [105], along with phylogenetic analysis with the updated versions of biological databases, such as UniProt [70], IMG [71], GO [104], and PDB [72]. Afterwards, both elementally and charge balanced biochemical reactions were assigned to the genes to create the gene-protein-reaction (GPR) associations [3]. These reactions were further verified by biochemical literature as well as enzyme databases, such as KEGG [106], BRENDA [107], MetaCyc [108], and ENZYME [109]. In some instances, genes required for some biosynthetic reactions essential for producing all the precursor metabolites for cell biomass were not identified. Such reactions (21 in number detailed in Table 1 in Text S1) were added to the reconstructed network as non-gene associated reactions.

Estimation of Biomass Composition and Maintenance Energy Requirements

The biomass composition (dry basis) of 1 gram of Dehalococcoides cells was calculated from various published and experimental data, and expressed in mmol (millimoles)/g DCW (dry cell weight) (Tables 19–24 in Text S2). Due to the lack of detailed experimental data on the cellular composition of Dehalococcoides, the weight fractions of protein, lipid, carbohydrate, soluble pools and ions of the cell were estimated from the published genome-scale model of Methanosarcina barkeri [83]. We choose to use data from M. barkeri model — an archaean — because Dehalococcoides cells are enclosed by the archaeal S-layer like protein instead of a typical bacterial cell wall [18–20]. The weight percent of DNA was estimated from the cell morphology, length of the genome sequence [110] and molar mass of the DNA, and the weight percent of RNA was calculated from the experimental data on a Dehalococcoides containing mixed microbial culture (see Text S2 for details). In addition, the detailed composition of each macromolecule as well as the composition of cofactors, and other soluble pools and ions are presented in Tables 19–24 in Text S2. The distribution of amino acids, nucleotides and cofactors in the biomass was calculated from the data reported previously [111,112] while the weight fractions of different fatty acids were estimated from White et al. [113]. These compositions were then integrated into the model as a biomass synthesis reaction, BIO_DHC_DM_61 (see Text S2 for additional details).

Maintenance energy accounts for the ATP requirements of cellular processes, such as turnover of the amino acid pools, polymerization of cellular macromolecules, and ion transport, which are not included in the biomass synthesis reaction [114–116]. These ATP requirements can be either growth associated (GAM), i.e., related to assembly and polymerization of macromolecules (eg. proteins, DNA, etc.), or non-growth associated (NGAM) that corresponds to maintaining membrane potential for keeping cellular integrity [114,115,117]. Due to the lack of experimental chemostat data required for calculating both maintenance parameters [118], the NGAM for a Dehalococcoides cell (1.8 mmol ATP/g DCW h⁻¹) was calculated from the experimental decay rate (0.09 day⁻¹) [24] and the average of pure-culture experimental growth yields (0.69 g DCW/eeq; Table 25 in Text S2) following the procedures described previously [114,116]. The GAM was estimated by regression, using an initial estimate of 26 mmol ATP/g DCW for a typical bacterial cell (Table 28 in Text S2) [111]. The initial estimate of GAM and the calculated NGAM were then used to simulate (using flux balance analysis, described below) the average of reported pure-culture experimental growth rates (0.014 h⁻¹; Table 26 in Text S2). A GAM of 61 mmol ATP/g DCW gave the best prediction of the experimental growth rate.

In Silico Analysis of Dehalococcoides Metabolism

Flux Balance Analysis (FBA) relies on the imposition of a series of constraints including stoichiometric mass balance constraints derived from the metabolic network, thermodynamic reversibility constraints and any available enzyme capacity constraints [3,119,120]. The imposition of these constraints leads to a linear optimization (Linear Programming, LP) problem formulated to maximize a cellular objective function such as the growth rate. Hence, the biomass synthesis reaction is assumed to be the objective function to be maximized to solve the LP problem in SimPheny. In addition, a number of reversible reactions were added in the network for exchanging external metabolites, such as acetate (ac), chloride (Cl⁻), carbon dioxide (CO₂), sulphate (SO₄²⁻) etc., to represent the in silico minimal medium (Table 2) for Dehalococcoides. As discussed earlier, cobalamin is essential for Dehalococcoides growth, but they are unable to synthesize it de novo; hence, they salvage cobalamin from the medium. In order to analyze whether cobalamin flux can limit Dehalococcoides growth, we performed a robustness analysis on the cobalamin exchange reaction for different weight fractions of cobalamin in the biomass. We also simulated growth rates by incorporating all the pathways required for de novo cobalamin synthesis in iAB49 for analyzing cobalamin synthesis cost, and its effect on Dehalococcoides growth. Finally, to identify whether the growth of Dehalococcoides was carbon or energy limited, the growth simulations were conducted by varying acetate fluxes and energy transfer efficiencies since acetate and H₂ are the carbon and energy sources of these
A

Growth yield (gDCW/eq)

0.0
0.2
0.4
0.6
0.8
1.0
1.2

MM
Tyr
Glu
Gln
Gly
Ala
Thr
Asp
All AA
2X H₂ flux

B

Growth yield (gDCW/eq)

0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0

Acetate flux (mmol gDCW⁻¹ h⁻¹)
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0

Energy transfer efficiency
Effect of carbon and energy sources on the growth yield of Dehalococcoides. (A) The experimental growth yield of Dehalococcoides in the minimal medium (0.69 gDCW/eeq) is compared with increased growth yields achieved by allowing unlimited fluxes of all amino acids at a H2 flux of 10 mmol.gDCW⁻¹.h⁻¹ (corresponding to the experimental dechlorination rate), as well as doubling the H2 flux (20 mmol.gDCW⁻¹.h⁻¹). It shows that unlimited flux of amino acids (carbon source) increased the in silico growth yield of Dehalococcoides by 55%, whereas doubling the H2 flux (electron donor or energy source) alone enhanced the yield by 65%. (B) Analysis of the energy limited growth of Dehalococcoides. Since the growth yield of Dehalococcoides varies linearly with the energy transfer efficiency, their yield can be improved by increasing the flux of their energy source or electron donor to generate more ATP per electron. However, the variation in acetate fluxes has no effect on growth yields. Red and green arrows show growth yields and corresponding efficiencies for Dehalococcoides growth in mixed and pure cultures, respectively. 'MM' = minimal medium; 'Tyr' = tyrosine; 'Glu' = glutamate; 'Gln' = glutamine; 'Gly' = glycine; 'Ala' = alanine; 'Thr' = threonine; 'Asp' = aspartate; 'AA' = all amino acids; '2x H2 flux' = 20 mmol.gDCW⁻¹.h⁻¹.

supporting information

Data S1 SBML File for Dehalococcoides Metabolic Model, iA549.

Found at: doi:10.1371/journal.pcbi.1000887.s003 (0.3 MB PDF)

Text S2 This file contains the tables of detailed macromolecular composition of a gram of Dehalococcoides cell, experimental values of various pan-model parameters and the detailed procedure to calculate those parameters, as well as supplemental text regarding energy conservation process of Dehalococcoides. In addition, all the supplemental figures are included at the end of this document.

Found at: doi:10.1371/journal.pcbi.1000887.s002 (5.41 MB PDF)

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Author Contributions

Conceived and designed the experiments: EAE RM. Performed the experiments: MAI. Analyzed the data: MAI. Wrote the paper: MAI.

References


Constraint-Based Modeling of *Dehalococcoides*