Guided cobalamin biosynthesis supports Dehalococcoides mccartyi reductive dechlorination activity

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Dehalococcoides mccartyi strains are corrinoid-auxotrophic Bacteria and axenic cultures that require vitamin B12 (CN-Cbl) to conserve energy via organohalide respiration. Cultures of D. mccartyi strains BAV1, GT and FL2 grown with limiting amounts of 1 \( \mu \text{g} \text{L}^{-1} \) CN-Cbl quickly depleted CN-Cbl, and reductive dechlorination of polychlorinated ethenes was incomplete leading to vinyl chloride (VC) accumulation. In contrast, the same cultures amended with 25 \( \mu \text{g} \text{L}^{-1} \) CN-Cbl exhibited up to 2.3-fold higher dechlorination rates, 2.8–9.1-fold increased growth yields, and completely consumed growth-supporting chlorinated ethenes. To explore whether known cobamide-producing microbes supply Dehalococcoides with the required corrinoid cofactor, co-culture experiments were performed with the methanogen Methanosarcina barkeri strain Fusaro and two acetogens, Sporomusa ovata and Sporomusa sp. strain KB-1, as Dehalococcoides partner populations. During growth with H\(_2\)/CO\(_2\), M. barkeri axenic cultures produced 4.2 \( \pm \) 0.1 \( \mu \text{g} \text{L}^{-1} \) extracellular cobamide (factor III), whereas the Sporomusa cultures produced phenolyl- and \( p-\text{cresolyl-} \)cobamides. Neither factor III nor the phenolic cobamides supported Dehalococcoides reductive dechlorination activity suggesting that M. barkeri and the Sporomusa sp. cannot fulfil Dehalococcoides’ nutritional requirements. Dehalococcoides dechlorination activity and growth occurred in M. barkeri and Sporomusa sp. co-cultures amended with 10 \( \mu \text{M} \) \( S,\text{S}^-\text{-dimethylbenzimidazole (DMB)} \), indicating that a cobalamin is a preferred corrinoid cofactor of strains BAV1, GT and FL2 when grown with chlorinated ethenes as electron acceptors. Even though the methanogen and acetogen populations tested did not produce cobalamin, the addition of DMB enabled guided biosynthesis and generated a cobalamin that supported Dehalococcoides’ activity and growth. Guided cobalamin biosynthesis may offer opportunities to sustain and enhance Dehalococcoides activity in contaminated subsurface environments.

1. Introduction

Chlorinated compounds, including tetrachloroethene (PCE) and trichloroethene (TCE), are widespread and toxic environmental pollutants [1,2]. Strains of the organohalide-respiring species Dehalococcoides mccartyi couple growth to the reductive dechlorination of a variety of chlorinated priority pollutants including polychlorinated biphenyls (PCBs), chlorobenzenes and chlorinated solvents. Some D. mccartyi strains dechlorinate PCE, TCE, dichloroethenes (DCEs) and vinyl chloride (VC) to non-toxic ethene, and thus are of great interest to restore aquifers contaminated with chlorinated ethenes [2–4].

Dehalococcoides mccartyi strains grow in completely synthetic, defined media, but cannot de novo synthesize the corrin ring and require exogenous vitamin B\(_{12}\) (cyanocobalamin, CN-Cbl) [2]. Corrinoids, such as CN-Cbl, contain a heterocyclic tetrapyrole ring with a central cobalt atom [5]. Some Archaea and Bacteria synthesize corrinoids with an upper \( \beta \)-ligand moiety and a lower \( \alpha \)-ligand moiety, so-called cobamides, which participate in important biological processes such as methanogenesis, acetogenesis and organohalide
respiration [5–7]. Cobamides with 5',6'-dimethylbenzimidazole (DMB) as the lower α-ligand are cobalamins such as adenosylcobalamin, hydroxocobalamin and cyanocobalamin (CN-Cbl). A cobalamin or a cobamide serve as cofactors for the PCE and TCE reductive dehalogenases (RDases) of several organohalide-respiring genera such as Dehalobacter, Desulfotobacterium and Sulfurospirillum, and exemplify the crucial roles these corrinoids play in the energy metabolism of organohalide-respiring Bacteria [7–10].

Genome sequence analysis demonstrated that D. mccartyi strains are corrinoid auxotrophs and lack the ability for de novo corrinoid synthesis [11,12]. A previous survey demonstrated that only about half (209 out of 410) CN-Cbl-requiring Bacteria possessed genes encoding corrinoid biosynthesis pathways [11]. Genes encoding the BtuBFCD type CN-Cbl/cobamide transport system were found in most (more than 90%) of the corrinoid-auxotrophic Bacteria [11], indicating external CN-Cbl/cobamide uptake rather than de novo biosynthesis is a common strategy of microorganisms to acquire this essential cofactor. Thus, it is not surprising that Dehalococcoides also possess BtuBFCD gene homologues as well as cobinamide (i.e. a cobamide lacking the lower α-ligand) salvage genes (cobU and cbiZ) to save the energy cost associated with adenosylcobalamin (Ado-Cbl) de novo biosynthesis [11].

Enhanced Dehalococcoides growth and faster dechlorination rates were observed in co- or tri-cultures of D. mccartyi strain 195 and corrinoid-producers such as Acetobacterium woodii, Desulfovibrio desulfuricans and Desulfovibrio vulgaris Hildenborough, suggesting that strain 195 benefited from the corrinoids produced in the co-cultures [13,14]. Recently, interspecies cobalamin transfer from Geobacter loeleyi to D. mccartyi strains BAV1 and FL2 was demonstrated in CN-Cbl-free co-cultures [15]. Geobacter sulfurreducens did not support Dehalococcoides activity unless DMB was supplied to the growth medium suggesting that only the cobamides with specific types of lower ligands, such as DMB, meet Dehalococcoides’ nutritional requirements.

In anoxic subsurface environments, Dehalococcoides are members of diverse microbial communities, and some populations synthesize cobamides with different lower α-ligands [16,17]. Cobalamin and the naturally occurring cobamides tested in this study are shown in figure 1. For example, 5'-hydroxybenzimidazolyl-cobamide (factor III) or adenyl-cobamide (pseudo vitamin B12) are typically produced by methanogenic Archaea as the cofactors for methyltransferases involved in methane formation [18]. Acetogenic Bacteria synthesize benzimidazolyl- or phenolyl-type cobamides required for specific enzymes of the Wood-Ljungdahl pathway [18]. Cobalamin (5',6'-dimethylbenzimidazolyl-cobamide) was identified as the corrinoid produced by A. woodii, phenolyl- and p-cresolyl-cobamide were purified from S. ovata, and 5'-methylbenzimidazolyl-cobamide was isolated from sulfate-reducers, such as Desulfobacterium autotrophicum and Desulfobulbus propionicus [19,20].

In this study, we investigated Dehalococcoides reductive dechlorination activity and growth during the co-cultivation with corrinoid-producing methanogenic Archaea and acetogenic Bacteria. Co-cultures established in CN-Cbl-free medium demonstrated interspecies cobamide transfer and identified the specific type(s) of corrinoid that Dehalococcoides can use. Knowledge of how Dehalococcoides’ nutritional requirements are met in natural communities will reveal the ecophysiology of strictly organohalide-respiring, corrinoid-auxotrophic Chloroflexi. Understanding the bottlenecks (i.e.

**Figure 1.** Structures of cobalamin and the lower α-ligands of several characterized cobamides. In vitamin B12 (cyanocobalamin, CN-Cbl), a cyano group is the upper β-ligand and DMB is the lower α-ligand (circled). The structures were redrawn from [16,17]. DMB, 5',6'-dimethylbenzimidazole; 5'-OH-BEN, 5'-hydroxybenzimidazole.
controls) limiting the activity of organohalide-respiring Chlorella may lead to innovative engineering approaches that enhance reductive dechlorination rates and extents and enable more efficient bioremediation applications.

2. Methods

(a) Pure cultures and growth conditions

*Dehalococcoides mccartyi* strain BAV1 (ATCC BAA-2100), strain GT (ATCC BAA-2099) and strain FL2 (ATCC BAA-2098) were grown in 160 ml serum bottles containing 100 ml reduced, bicarbonate-buﬀered, deﬁned mineral salts medium amended with acetate (5 mM) and a N₂–CO₂ (80/20, v/v) headspace [21–23]. Following autoclaving, the bottles were amended with 10 ml hydrogen and 25 μg l⁻¹ CN-Cbl as described [15]. Neat TCE (5 μl, 99%, Fisher, Pittsburgh, PA, USA) and cis-DCE (5 μl, 99.5%, Sigma-Aldrich-Fluka, St Louis, MO, USA) were added with a microlitre syringe (Hamilton, Reno, NV, USA). Following equilibration, the bottles received 3 per cent (v/v) inocula from dechlorinating cultures maintained under the same conditions. In addition, culture bottles amended with 1 μg l⁻¹ CN-Cbl were maintained to evaluate the effects of low CN-Cbl concentrations on *Dehalococcoides* growth yields and dechlorination activities. Pure cultures of *M. barkeri* strain Fusaro (DSM 804), *S. ovata* (DSM 2662) and *Sporomusa* sp. strain KB-1 (16S rRNA gene GenBank accession no. AY780559.1) were maintained in the same deﬁned medium prior to inoculation. The positive control inocula were transferred to sterile 50 ml plastic tubes and incubated for 20 min in a boiling water bath. Following centrifugation at 15 000g for 15 min, the supernatants were collected and the pellets were extracted a second time. The combined supernatants were mixed with 0.01 volumes of a 3 per cent acetic acid solution prior to loading onto a Sep-Pak C18 cartridge (Waters Corp, Milford, MA, USA), which had been equilibrated with 2 ml 100 per cent methanol and 40 ml deionized water. Following sample loading, the cartridge was washed with 10 ml deionized water (20 interstitial volumes) and 7.5 ml 10 per cent methanol (15 interstitial volumes) prior to the final elution step with 10 ml 50 per cent methanol (20 interstitial volumes). The slightly pink-coloured solution obtained from the final elution step was vacuum dried and the residues were suspended in 0.5 ml sterile, deionized water.

(b) Co-cultures

Triplicate co-cultures containing one of the three *D. mccartyi* strains and either *M. barkeri* or one of the *Sporomusa* sp. were established in 160 ml vessels inside an anaerobic chamber as described [15]. The vessels were amended with 5 mM acetate and contained a H₂–CO₂ (80/20, v/v) headspace. To avoid CN-Cbl carry-over, cells for inoculation were collected by centrifugation at 14 000g for 10 min at room temperature, and suspended in CN-Cbl-free medium prior to inoculation. The positive control inocula were prepared in the same way and inoculated into culture vessels amended with 25 μg l⁻¹ CN-Cbl. *Dehalococcoides mccartyi* pure cultures without CN-Cbl served as negative controls. Additional co-culture replicates received 10 mM acetate and either KCN (100 mM stock solution) was added to reach a final concentration of 10 mM. The suspensions were vigorously shaken, each transferred to sterile 50 ml plastic tubes and incubated for 20 min in a boiling water bath. Following centrifugation at 15 000g for 15 min, the supernatants were collected and the pellets were extracted a second time. The combined supernatants were mixed with 0.01 volumes of a 3 per cent acetic acid solution prior to loading onto a Sep-Pak C18 cartridge (Waters Corp, Milford, MA, USA), which had been equilibrated with 2 ml 100 per cent methanol and 40 ml deionized water. Following sample loading, the cartridge was washed with 10 ml deionized water (20 interstitial volumes) and 7.5 ml 10 per cent methanol (15 interstitial volumes) prior to the final elution step with 10 ml 50 per cent methanol (20 interstitial volumes). The slightly pink-coloured solution obtained from the final elution step was vacuum dried and the residues were suspended in 0.5 ml sterile, deionized water.

(c) DNA extraction and 16S rRNA gene quantification

Cells from *Dehalococcoides* pure cultures and co-cultures were harvested from 1 ml culture suspension as described [15,24]. Briefly, total genomic DNA was extracted using the MO BIO Soil DNA isolation kit (MO BIO, Carlsbad, CA, USA), and a high eﬃciency bead rupor homogenizer (Omini International, Kennesaw, GA, USA) following the manufacturer’s protocols. Samples were processed with the bead rupor homogenizer at a speed 3.25 m s⁻¹ for 5 min. Quantitative real-time PCR (qPCR) to enumerate *Dehalococcoides* 16S rRNA gene copies followed established protocols using primer set Dhc1200F/Dhc1271R and probe FAM-BHQ1 Dhc1240 [24].

(d) Corrinoid measurements

(i) Microbiological B₁₂ assay

Quantification of extracellular cobamides in pure and co-cultures was performed using a microbiological assay with *Lactobacillus delbrueckii* subsp. lactis (ATCC 7830) as the cobamide-auxotroph test organism following described procedures [15]. To detect intracellular cobamides, whole cells from 1.5 ml *S. ovata* or *Sporomusa* sp. strain KB-1 cultures were collected by centrifugation at 14 000g for 2 min, suspended in sterile water, and broken either by heating at 95°C for 15 min or by sonicating with a Branson 250 Sonifier Analog Cell Disruptor (Branson Ultrasonics Corp., Danbury, CT, USA) for 15 min at 50 per cent duty cycle at an output of 60 W.

(ii) Total cobamide extraction and puriﬁcation

Total intracellular cobamides were extracted and puriﬁed using an established protocol with the following modifications [25]. *Sporomusa ovata* or *Sporomusa* sp. strain KB-1 cultures (1 litre each) grown with H₂/CO₂ were centrifuged at 15 000g for 15 min at 4°C. Following removal of the supernatants, each cell pellet was suspended in 5 ml deionized water, the pH was adjusted to 5–6 with 3 per cent (v/v) glacial acetic acid, and KCN (100 mM stock solution) was added to reach a final concentration of 10 mM. The suspensions were vigorously shaken, each transferred to sterile 50 ml plastic tubes and incubated for 20 min in a boiling water bath. Following centrifugation at 15 000g for 15 min, the supernatants were collected and the pellets were extracted a second time. The combined supernatants were mixed with 0.01 volumes of a 3 per cent acetic acid solution prior to loading onto a Sep-Pak C18 cartridge (Waters Corp, Milford, MA, USA), which had been equilibrated with 2 ml 100 per cent methanol and 40 ml deionized water. Following sample loading, the cartridge was washed with 10 ml deionized water (20 interstitial volumes) and 7.5 ml 10 per cent methanol (15 interstitial volumes) prior to the final elution step with 10 ml 50 per cent methanol (20 interstitial volumes). The slightly pink-coloured solution obtained from the final elution step was vacuum dried and the residues were suspended in 0.5 ml sterile, deionized water.

(iii) HPLC analysis of cyanocobamides

Cyanocobamides were analysed using an Agilent 1200 series HPLC system equipped with an Eclipse XDB-C18 column (5 μm, 4.6 × 150 mm) and a diode array detector at a detection wavelength of 361 nm. Samples (20 μl each) were injected and separated at 30°C at a flow rate of 1.0 ml min⁻¹ using 0.1 per cent acetic acid in water (eluent A) and 0.1 per cent acetic acid in methanol (eluent B) as mobile phases. The initial ratio of 90 per cent A/10 per cent B was linearly decreased to 35 per cent A/65 per cent B over a 12 min time window followed by a 4 min hold, before equilibration with 90 per cent A. CN-Cbl was identiﬁed by comparing retention times and absorption spectra with authentic CN-Cbl standards (more than 98% purity, Fisher Scientiﬁc, Pittsburgh, PA, USA) dissolved in deionized water.

(e) Other analytical methods

Methane, ethene and chlorinated ethenes were quantiﬁed using an Agilent 7890 gas chromatograph equipped with a ﬂame ionization detector and a DB-624 capillary column (60 m × 0.32 mm × 1.8 μm) as described [22]. Acetate was analysed using an Agilent 1200 series HPLC system equipped with an Aminex HPX-87H column (Bio-Rad, Hercules, CA, USA). Samples were acidiﬁed with 1 M H₂SO₄ in a ratio of 19:1 (v/v) and separated with 4 ml aqueous H₂SO₄ as the mobile phase at a ﬂow rate of 0.6 ml min⁻¹ and quantiﬁed using a UV detector set to 210 nm.

3. Results

(a) CN-Cbl-dependent reductive dechlorination and growth of *D. mccartyi* strains

In deﬁned medium amended with 25 μg l⁻¹ CN-Cbl, strain BAV1 and strain GT cultures produced stoichiometric
amounts of ethene from 50.3 ± 0.4 μmoles of cis-DCE (figure 2a) and 36.5 ± 0.9 μmoles of TCE (figure 2c) provided as electron acceptor, respectively. Strain FL2 cultures produced a mixture of VC and ethene (23.9 ± 1.7 and 10.3 ± 0.9 μmoles, respectively) during a 3-week incubation period (figure 2e). Cultures that received 1 μg l⁻¹ CN-Cbl exhibited lower dechlorination rates and incomplete dechlorination. Strain BAV1 cultures dechlorinated cis-DCE (50.3 ± 0.4 μmoles) to VC (42.0 ± 3.1 μmoles) and small amounts of ethene (4.3 ± 0.4 μmoles) by day 17. VC remained the major dechlorination product (90.8 ± 0.1%) after 27 days and ethene accounted for 9.2 ± 0.1% (figure 2f). In strain GT cultures, more than one third of the initial TCE amount (36.5 ± 0.9 μmoles) remained after 27 days of incubation, and cis-DCE (4.3 ± 0.2 μmoles), VC (7.7 ± 0.7 μmoles) and ethene (4.7 ± 1.1 μmoles) were detected (figure 2d). TCE was dechlorinated at a rate of 9.0 ± 1.1 μmoles 1⁻¹ d⁻¹ or about 2.2-fold slower compared with the TCE dechlorination rates (19.6 ± 0.2 μmoles 1⁻¹ d⁻¹) observed in strain GT cultures that received 25 μg l⁻¹ CN-Cbl (figures 2c,d). Similarly, strain FL2 cultures dechlorinated TCE at lower rates (i.e. 9.8 ± 2.3 versus 22.2 ± 0.8 μmoles 1⁻¹ d⁻¹ in medium amended with 25 μg l⁻¹ CN-Cbl), and after a 4-week incubation period, 40.3 ± 6.8% of the initial TCE was still present with cis-DCE (7.9 ± 0.4 μmoles) and VC (6.8 ± 2.1 μmoles) as the dechlorination products but no ethene was formed (figure 2f).

CN-Cbl concentrations in the medium decreased concomitantly with reductive dechlorination and Dehalococcoides growth, and the initial CN-Cbl concentration of 1 μg l⁻¹ declined to below 20 ng l⁻¹ during the 18-day incubation period (figure 2b,d,f). By day 27, reductive dechlorination of the remaining chlorinated ethenes ceased, and the CN-Cbl concentrations in strain GT, strain FL2 and strain BAV1 cultures were 7.7 ± 2.0 ng l⁻¹, below 5 ng l⁻¹ (i.e. below the quantification limit of the microbiological B12 assay), and below 2 ng l⁻¹ (i.e. below the detection limit), respectively. CN-Cbl was depleted at higher rates in the 25 μg l⁻¹ CN-Cbl-amended Dehalococcoides cultures. At day 17, when BAV1 cultures had completely dechlorinated cis-DCE to ethene, CN-Cbl concentrations dropped to 0.7 ± 0.1 μg l⁻¹, averaging an uptake rate of 1500 ng l⁻¹ d⁻¹ versus 63 ng l⁻¹ d⁻¹ in the BAV1 cultures amended with 1 μg l⁻¹ CN-Cbl (figure 2a,b). Strain GT and strain FL2 cultures depleted CN-Cbl from an initial amount of 26.5 ± 1.0 μg l⁻¹ to 0.03 ± 0.03 and 1.0 ± 0.7 μg l⁻¹, respectively, at 25- and 24-fold higher rates compared with those rates observed in the corresponding cultures amended with 1 μg l⁻¹ CN-Cbl (figure 2c–f).

qPCR analysis demonstrated that limiting amounts of 1 μg l⁻¹ CN-Cbl affected Dehalococcoides growth yields, which were calculated as described [22]. For example, 1.4 ± 0.8 × 10⁷ BAV1 cells per μmole of Cl⁻ released were obtained in cultures amended with 1 μg l⁻¹ CN-Cbl, whereas 1.3 ± 0.1 × 10⁸ BAV1 cells per μmole of Cl⁻ released (a 9.1-fold increase) were measured in cultures amended with 25 μg l⁻¹ CN-Cbl (table 1). Similar results were observed in strain GT cultures with an average 2.8-fold higher growth yield in medium amended with 25 μg l⁻¹ CN-Cbl (table 1).

(b) Cobamide production in methanogenic and acetogenic cultures

During a 43-day incubation period, extracellular cobamide concentrations gradually increased to 4.2 ± 0.1 μg l⁻¹ in M. barkeri strain Fusaro cultures concomitantly with methane formation (figure 3b). No extracellular cobamides were detected in the acetate-producing S. ovata (figure 3b) and Sporomusa sp. strain KB-1 cultures, which was unexpected because Sporomusa spp. are known cobamide producers.
Table 1. Comparison of Dehalococcoides mccartyi growth yields in axenic and in co-cultures amended with DMB.

<table>
<thead>
<tr>
<th>culture</th>
<th>CN-Chl (µg l(^{-1}))</th>
<th>DMB(^a)</th>
<th>D. mccartyi 16S rRNA gene copies per ml</th>
<th>growth yield (cells per µmole Cl(^{-}) released)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>inoculum</td>
<td>final</td>
<td>fold increase(^e)</td>
</tr>
<tr>
<td>axenic cultures</td>
<td></td>
<td>6.3 ± 2.0 × 10(^6)</td>
<td>1.3 ± 0.4 × 10(^8)</td>
<td>2.1</td>
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<tr>
<td>BAV1</td>
<td>1</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>GT</td>
<td>1</td>
<td>—</td>
<td>4.0 ± 0.5 × 10(^6)</td>
<td>2.1 ± 0.3 × 10(^8)</td>
</tr>
<tr>
<td>FL2</td>
<td>1</td>
<td>—</td>
<td>2.4 ± 0.3 × 10(^6)</td>
<td>2.3 ± 0.7 × 10(^6)</td>
</tr>
<tr>
<td>co-cultures</td>
<td></td>
<td>2.4 ± 0.3 × 10(^6)</td>
<td>3.7 ± 1.1 × 10(^6)</td>
<td>15.3</td>
</tr>
<tr>
<td>BAV1/KB-1</td>
<td>+</td>
<td>6.3 ± 2.0 × 10(^6)</td>
<td>1.9 ± 0.1 × 10(^9)</td>
<td>29.8</td>
</tr>
<tr>
<td>BAV1/Fusaro</td>
<td>—</td>
<td>+</td>
<td>6.3 ± 2.0 × 10(^6)</td>
<td>2.0 ± 0.1 × 10(^9)</td>
</tr>
<tr>
<td>GT/KB-1</td>
<td>+</td>
<td>—</td>
<td>4.0 ± 0.5 × 10(^6)</td>
<td>2.1 ± 0.3 × 10(^8)</td>
</tr>
<tr>
<td>GT/Fusaro</td>
<td>—</td>
<td>+</td>
<td>4.0 ± 0.5 × 10(^6)</td>
<td>1.6 ± 0.0 × 10(^8)</td>
</tr>
<tr>
<td>FL2/KB-1</td>
<td>—</td>
<td>+</td>
<td>2.4 ± 0.3 × 10(^6)</td>
<td>9.5 ± 1.6 × 10(^9)</td>
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<tr>
<td>FL2/Fusaro</td>
<td>+</td>
<td>—</td>
<td>2.4 ± 0.3 × 10(^6)</td>
<td>9.0 ± 2.7 × 10(^8)</td>
</tr>
</tbody>
</table>

\(\text{DMB}^a\) supplied at 10 µM.

\(\text{Biomass collected at day 27.}\)

\(\text{Data averaged from triplicates.}\)

\(\text{No growth occurred.}\)

when grown via H\(_2\)/CO\(_2\) reductive acetogenesis. Cobamides were also not detected in Sporomusa cell lysates suggesting that Sporomusa produced cobamide(s), to which the indicator organism L. delbrueckii subsp. lactis did not respond (i.e. the cobamide cannot be detected and quantified with the microbiological B\(_2\) assay).

(c) Reductive dechlorination in co-cultures

In D. mccartyi strain BAV1 and M. barkeri strain Fusaro co-cultures amended with 25 µg l\(^{-1}\) CN-Chl, reductive dechlorination and methane formation occurred concomitantly. Strain BAV1 dechlorinated 53.1 ± 0.6 moles of cis-DCE to stoichiometric amounts of ethene with concomitant methane formation (86.9 ± 15.9 moles) by strain Fusaro within 25 days (figure 4c). In BAV1/Fusaro co-cultures not amended with CN-Chl, methane was formed (225.2 ± 26.2 moles per bottle) and maximum amounts of 3.7 ± 0.2 µg l\(^{-1}\) cobamide were measured as CN-Chl equivalents using the microbiological B\(_2\) assay in the culture suspensions after 30 days (figure 4b). Only negligible reductive dechlorination activity occurred in these co-cultures, and less than 12 per cent of the initial amount of cis-DCE was dechlorinated to VC (6.1 ± 0.1 moles). Negative controls (i.e. strain BAV1 cultures without CN-Chl) produced 9.8 ± 0.9 moles of VC (figure 4c).

Dehalococcoides/S. ovata co-cultures amended with 25 µg l\(^{-1}\) CN-Chl exhibited acetate formation concomitantly with complete reductive dechlorination of 65.9 ± 1.7 moles of cis-DCE to ethene (figure 4d), indicating growth of both populations. Both S. ovata and Sporomusa sp. strain KB-1 grew in co-cultures lacking CN-Chl but extracellular cobamides were not detected using the microbiological B\(_2\) assay, and only 10.6 ± 3.6 and 10.4 ± 0.5 moles of VC were produced in BAV1/S. ovata and BAV1/Sporomusa sp. strain KB-1 co-cultures, respectively (figure 4c,f). These findings demonstrate that Sporomusa sp. were unable to support BAV1 reductive dechlorination activity. Activities of D. mccartyi strains GT and FL2 were also tested in the co-cultures with M. barkeri strain Fusaro, S. ovata and Sporomusa sp. strain KB-1. Only insignificant dechlorination of TCE to cis-DCE (less than 0.5% of the initial amount of TCE) occurred in these co-cultures (data not shown).

(d) Guided biosynthesis of cobalamin in Sporomusa

The CN-Chl standard (5 mg l\(^{-1}\)) eluted at a retention time of 6.94 min (figure 5a). HPLC separation of cyanocobamides extracted from Sporomusa sp. strain KB-1 (figure 5b) and S. ovata (data not shown) cells collected from cultures not amended with DMB yielded two major peaks with retention times of 9.80 and 11.25 min, matching previous reports that two types of cobamides, phenolyl-cobamide and p-cresolyl-cobamide, were synthesized by S. ovata [26]. The addition of 10 µM DMB to the culture medium did not affect growth, and Sporomusa sp. strain KB-1 cultures reached similar OD 600 nm values of 0.040–0.041 (data not shown). Distinct cyanocobamide patterns were observed in Sporomusa sp. strain KB-1 cultures amended with DMB. The peak areas corresponding to phenolyl-cobamide and p-cresolyl-cobamide both decreased by about 80 per cent, and a major peak with a retention time of 6.94 min, identical to that of
information occurred and extracellular cobamide concentrations in cultures. Filled circle, methane; open circle, acetate, cross symbol, cobamide(s) reported as CN-Cbl equivalents. Error bars represent the standard deviations of triplicate samples and are not shown if they are smaller than the symbols.

authentic CN-Cbl, emerged (figure 5c). These findings provide evidence for guided biosynthesis [27], and cyanocobalamin was the major cobamide when 10 μM DMB was added to the growth medium.

(e) Recovery of Dehalococcoides dechlorination activity in DMB-amended co-cultures

The addition of 10 μM DMB to non-dechlorinating Dehalococcoides/Sporomusa sp. strain KB-1 co-cultures stimulated reductive dechlorination activity. DMB-amended BA1/KB-1 and GT/KB-1 co-cultures completely dechlorinated cis-DCE (52.1 ± 0.5 μmoles) and TCE (34.4 ± 0.7 μmoles) to ethene, respectively (figure 6a,b). FL2/KB-1 co-cultures reduced the initial TCE amount to VC (8.5 ± 1.2 μmoles) and ethene (28.5 ± 2.0 μmoles) (figure 6c). Concomitant with cis-DCE or TCE dechlorination, extracellular cobamides measured using the microbiological B₁₂ assay after 17 days of incubation gradually increased from below the detection limit (i.e. less than 2 ng l⁻¹) to 2.5 ± 0.4, 0.9 ± 0.4 and 1.0 ± 0.3 μg l⁻¹ in strain BA1/strain KB-1, strain GT/strain KB-1 and strain FL2/strain KB-1 co-cultures, respectively (figure 6d–c).

Guided cobalamin biosynthesis through lower ligand exchange with DMB was also observed in Dehalococcoides/M. barkeri strain Fusaro co-cultures (figure 6d–f). Methane formation occurred and extracellular cobamide concentrations increased to 1.4–19 μg l⁻¹. In addition, cis-DCE and TCE were completely dechlorinated to ethene in the strain BA1 and strain GT co-cultures, respectively, and strain FL2 co-cultures dechlorinated the initial TCE amount (34.4 ± 0.7 μmoles) of VC (16.0 ± 4.1 μmoles) and ethene (18.8 ± 5.3 μmoles).

Negligible Dehalococcoides growth was observed in the co-cultures without DMB. In contrast, Dehalococcoides cell densities increased 29.8- to 51.5-fold in the DMB-amended co-cultures with Sporomusa sp. strain KB-1. Strain BA1 cells increased from 6.3 ± 2.0 × 10⁶ cells ml⁻¹ (cells introduced with the inoculum) to 1.9 ± 0.1 × 10⁸ cells ml⁻¹, strain GT cells increased from 4.0 ± 0.5 × 10⁶ to 2.1 ± 0.3 × 10⁹ cells ml⁻¹, and strain FL2 cells increased from 2.4 ± 0.3 × 10⁶ to 9.5 ± 1.6 × 10⁷ cells ml⁻¹. In the DMB-amended M. barkeri strain Fusaro co-cultures, D. mccartyi strain BA1, strain GT and FL2 cell densities increased 31- to 41-fold and 37-fold to reach 2.0 ± 0.1 × 10⁸, 1.6 ± 0.0 × 10⁸ and 9.0 ± 2.7 × 10⁷ cells ml⁻¹, respectively (table 1).

4. Discussion

CN-Cbl is a required cofactor for the characterized D. mccartyi strains grown in axenic culture [2]. The responses of D. mccartyi strain 195 to different CN-Cbl concentrations in the medium revealed that maximum TCE dechlorination rates and growth yields required CN-Cbl of 25 μg l⁻¹ or higher concentrations [13]. In cultures of D. mccartyi strains BA1, GT and FL2 amended with 1 μg l⁻¹ CN-Cbl, CN-Cbl was quickly depleted to below 10 ng l⁻¹, and TCE and cis-DCE dechlorination was incomplete. Ethene formation, about 2-fold higher dechlorination rates, and 2.8–9.1-fold increases in Dehalococcoides growth yields were observed in cultures that received 25 μg l⁻¹ CN-Cbl. These findings demonstrate that Dehalococcoides' requirement for this essential cofactor must be understood to achieve and sustain desirable reductive dechlorination rates and endpoints at sites impacted with chloroorganic contaminants. Reductive dechlorination and growth of D. mccartyi strain BA1 and strain FL2 were sustained in co-cultures with the PCE-to-cis-DCE dechlorinating species G. lovleyi strain SZ, which possesses the complete cobamide biosynthesis pathway [15]. The cobamide concentrations in these dechlorinating co-cultures ranged from 10 to 30 ng l⁻¹, suggesting that the cobamide flux may be the relevant factor to sustain Dehalococcoides' dechlorination activity in microbial communities. Genes encoding the prokaryotic BtuBFCD corrinoid uptake system, which belongs to the ABC-type (ATP-binding cassette) transporter family, were identified in all sequenced Dehalococcoides genomes [11]. In vitro experiments demonstrated that the outer membrane corrinoid receptor BtuB of Escherichia coli had a high affinity for CN-Cbl with a half-saturation concentration of 0.5 nM (0.68 μg l⁻¹) [28]. Dehalococcoides reductive dechlorination activity was sustained in D. mccartyi/G. lovleyi co-cultures with cobamide concentrations of 10–30 ng l⁻¹, suggesting that D. mccartyi strains also possess high affinity cobamide uptake systems.

A crucial question is the source of the corrinoid cofactor to sustain Dehalococcoides reductive dechlorination activity in the environment, particularly in chlorinated solvent-contaminated aquifers. The Dehalococcoides-containing consortium KB-1 used for bioaugmentation contains methanogens and
Figure 4. Dechlorination and extracellular cobamide production in Dehalococcoides mccartyi strain BA1/Methanosarcina barkeri strain Fusaro and strain BA1/Sporomusa ovata co-cultures. (a) Strain BA1/M. barkeri strain Fusaro co-culture amended with 25 μg l⁻¹ CN-Cbl (positive control); (b) strain BA1/strain Fusaro co-culture without CN-Cbl addition; (c) strain BA1 culture without CN-Cbl (negative control); (d) Strain BA1/S. ovata co-culture amended with 25 μg l⁻¹ CN-Cbl (positive control); (e) strain BA1/S. ovata co-culture without CN-Cbl addition; (f) strain BA1/S. ovata sp. strain KB-1 co-culture without CN-Cbl addition. Filled triangle, cis-DCE; open inverted triangle, vinyl chloride; filled square, ethene; open circle, acetate; cross symbol, cobamide(s) reported as CN-Cbl equivalents. Error bars represent the standard deviations of triplicate samples and are not shown if they are smaller than the symbols.

Figure 5. Demonstration of guided cobalamin biosynthesis. HPLC chromatograms of (a) authentic CN-Cbl standard (5 mg l⁻¹ dissolved in water); (b) cyano-phenolyl and cyano-p-cresolyl cobamides extracted from 1 l of S. ovata sp. strain KB-1 culture grown autotrophically with H₂/CO₂; and (c) cyanocobalamin extracted from 1 litre of S. ovata sp. KB-1 culture grown autotrophically with H₂/CO₂ and the addition of 10 μM DMB, mAU = milliabsorbance units. (Online version in colour.)

CO₂-reducing acetogens [29]. Both methanogenic Archaea and acetogenic Bacteria are known to synthesize cobamides with different lower ligands (figure 1). 5'-Hydroxybenzimidazolyl-cobamide (factor III) and adenyl-cobamide (pseudo vitamin B₁₂) are the predominant cobamides isolated from methanogenic Archaea [30], and factor III was identified in M. barkeri cultures [31]. In Dehalococcoides co-cultures with M. barkeri strain Fusaro, more than 4 μg l⁻¹ CN-Cbl equivalents, presumably factor III, were quantified in culture suspensions; however, only negligible reductive dechlorination activity, similar to negative control cultures, was observed, indicating that factor III cannot fulfil Dehalococcoides’ corrinoid requirement. These findings are supported by a previous study that reported that D. mccartyi strain 195 reductive dechlorination activity was not enhanced in co-cultures with Methanobacterium congolense [14]. Pure culture studies with D. mccartyi strain 195 corroborated that purified factor III and phenolic cobamides did not support reductive dechlorination, and growth only occurred when cobamides containing benzimidazolyl types of lower ligands were available [32]. Although the specific cobamides produced by Methanobacterium congolense and many other methanogens have not been thoroughly explored, the data reported here confirm that at least the 5'-hydroxybenzimidazolyl-cobamide produced by some methanogens cannot fulfil the D. mccartyi corrinoid cofactor requirement.

Cobamides containing a phenolic-type lower ligand, i.e. phenolyl- and p-cresolyl-cobamide, were first purified from S. ovata, and were found in other Bacteria capable of H₂/CO₂ reductive acetogenesis [26]. Sporomusa sp. strain KB-1 was isolated from the dechlorinating KB-1 consortium and shares 98.5 per cent sequence identity with the 16S rRNA gene of S. ovata
(AJ279800.1). Both Sporomusa isolates produced phenolyl- and p-cresolyl-cobamide, suggesting that they represent the characteristic cobamides of the genus Sporomusa.

The test organism for the microbiological B_{12} assay, L. delbrueckii, did not respond to S. ovata or Sporomusa sp. strain KB-1 culture suspensions or cell lysates, indicating that the cobamides with phenolic lower ligands cannot fulfil the corrinoid cofactor requirement of L. delbrueckii. Many prokaryotes, including D. mccartyi strains and L. delbrueckii, use adenosyl-cobalamin-dependent class II ribonucleotide reductases (RNRs), which catalyse the conversion of ribonucleotides to deoxyribonucleotides [11]. Since D. mccartyi genomes harbour multiple copies of class II RNR genes, it is possible that the lack of dechlorination activity and Dehalococcoides growth in the Sporomusa co-cultures was not only caused by non-functional RDases but also because of non-functional RNRs.

Interestingly, Dehalococcoides dechlorination activity and growth occurred in the DMB-amended co-cultures. In the presence of 10 \( \mu \)M DMB, CN-Cbl was the predominant corrinoid synthesized by Dehalococcoides sp. strain KB-1 cultures, indicating that guided biosynthesis allows Sporomusa sp. to generate a corrinoid cofactor that fulfils Dehalococcoides’ nutritional requirements. Similar observations were made in D. mccartyi/G. sulfurreducens co-cultures that were amended with DMB [15], suggesting that guided biosynthesis may be a relevant process for supplying D. mccartyi strains with the required cobalamin cofactor.

In DMB-amended Sporomusa sp. strain KB-1 co-cultures with each of the D. mccartyi strains BAV1, GT and FL2, the dechlorinators attained population sizes of 2.1 ± 0.2 \times 10^8, 2.1 ± 0.3 \times 10^8 and 9.0 ± 1.4 \times 10^7 cells per \mu\text{mole} of chloride released, respectively. These cell numbers were 1.7-, 1.4- and 2.2-fold higher compared with axenic cultures that received 25 \( \mu \)g l^{-1} CN-Cbl. Dehalococcoides mccartyi strains are known to grow better in mixed cultures, presumably because community members supply Dehalococcoides with unknown growth factors. Hence, it is possible that M. barkeri strain Fusaro and the Sporomusa isolates provided the D. mccartyi strains with not yet identified compounds that enhance growth yields. Another possible explanation for the lower growth yields observed with CN-Cbl is the cell’s energetic burden associated with the replacement of the upper cyanide ligand [33].

The microbial synthesis of non-native cobamides in the presence of excess non-native lower ligand is known as guided biosynthesis [17,27,34]. Guided biosynthesis has been demonstrated with model organisms such as Propionibacterium shermanii, E. coli and Streptomyces griseus to obtain desired cobamides [17]. Factor III synthesized by Methanobacterium thermoautotrophicum was replaced by a cobalamin in medium amended with DMB without affecting methane formation and growth [35]. Synthesis of a cobalamin in the presence of DMB has also been demonstrated in M. barkeri cultures [36]. The co-culture experiments with D. mccartyi strains demonstrated that the addition of DMB to the medium enabled guided biosynthesis and the formation of a cobalamin by M. barkeri strain Fusaro and Sporomusa sp. strain KB-1. Sporomusa sp. strain KB-1 replaced the phenolic cobamides with a cobalamin without apparent effects on its own growth suggesting that cobalamin can replace the phenolyl- and p-cresolyl-cobamides during growth with H_{2}/CO_{2}.

Survival of corrinoid auxotrophs such as Dehalococcoides relies on cobamides and corrinoid precursors (e.g. cobamides) produced and released by corrinoid-synthesizing Archaea and Bacteria. It is currently unclear to what extent and under what conditions microorganisms capable of de novo corrinoid synthesis produce and release cobamides and/or corrin ring precursors to the surrounding medium. While methanogens and acetogens readily release cobamides...
into the medium, at least under laboratory cultivation conditions, the formation of cobalamin requires DMB. Key questions are the origin of DMB in anoxic environments (i.e. who is synthesizing DMB?), and whether the availability of DMB limits cobalamin biosynthesis and *Dehalococcoides* activity. The biosynthesis pathway(s) of DMB under anoxic conditions has remained elusive, and the flux of DMB in subsurface environments has not been evaluated. While our experiments have demonstrated cobalamin production through guided biosynthesis, the relevance of this process in natural microbial communities has yet to be demonstrated. All *D. mccartyi* strains harbour *cobT*, *cobC* and *cobS* genes implicated in the cobalamin assembly from DMB and cobinamide [37], suggesting *Dehalococcoides* has the ability to assemble cobalamin if the precursors are available. Independently of whether *Dehalococcoides* or other microbes perform the final cobalamin assembly, the sources and fluxes of its precursors, in particular DMB, need to be understood in natural and disturbed microbial communities to identify *Dehalococcoides*’ nutritional limitations and potentially predict and manipulate reductive dechlorination activity. Limited dechlorination activity of *Dehalococcoides* and related corrinoid-auxotroph, organohalide-respiring Chloroflexi (e.g. *Dehalogenimonas* [38,39], *Dehalo bacterium* [40]) is regarded as a major constraint to achieve detoxification at sites contaminated with chlorinated contaminants. Hence, elucidating the nutritional requirements and ecophysiology of organohalide-respiring Chloroflexi in natural and contaminated environments will help develop predictive understanding and new strategies for stimulating in situ reductive dechlorination activity.

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