Supporting Information

For

Diverse Dechlorinators and Dechlorination Genes Enriched through Amendment of Chlorinated Natural Organic Matter Fractions

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Additional Information on Experimental Methods

Preparation of Cl-NOM

Organic rich sediment was collected from Pelican Lake, MN (46° 36' 42.7566''N, 94° 9' 26.4024''W) and dried at 105ºC for 4 hrs. The organic matter was extracted sequentially from the sediment (100 g total) with an accelerated solvent extractor (ASE) (Thermo Scientific) using first water, then methanol, and finally hexane:acetone (50:50). Each extract (water, methanol, or hexane:acetone) was collected in separate bottles. The ASE method for each solvent had an oven temperature of 100ºC. The 50 ml ASE vials were filled with the dried sediment and then had a static time of 10 min. Half of the solvent was then replaced in 2 subsequent extraction steps as is typical of ASE extractions. All of the extracts were rotovapped and blown down to dryness with nitrogen, after which they were resuspended in a phosphate buffer (100 mL, 0.1 M, pH 4). The extract obtained with each solvent was then split evenly between two flasks, one which was chlorinated with hypochlorous acid (to generate the "Cl-NOM"), while the other was simply retained ("NOM"). For the chlorination step, hypochlorous acid was added to a final concentration of 1 µM every 20 minutes for a total of 10 additions. All three fractions of both the Cl-NOM and the NOM were cleaned via solid phase extraction with C18 columns. Methanol, acetone, and hexane/acetone (1:1) were used to extract the Cl-NOM or NOM off of the columns. The extracts were blown down to dryness and resuspended in 5 ml of methanol.

Enrichment of Soil with Different Hydrophobicities of NOM and Cl-NOM

Soil contaminated with PCBs was collected from upstate New York by a consulting firm and was stored in an anaerobic chamber (Coy) after arrival until its use. The soil contained approximately 40 mg/kg of total PCBs. As stated, enrichment cultures (140-ml) were set up in the anaerobic chamber and contained 5 g of soil, 100 ml of low chloride reduced anaerobic mineral medium (RAMM) [1], and 25 µl of different fractions of concentrated NOM or Cl-NOM. The headspace of the serum bottles contained 5% hydrogen and 95% nitrogen. Sterile negative controls were autoclaved three times for 40 minutes before the addition of a mixture of the three different fractions of the Cl-NOM. Enrichment cultures were sampled using sterile pipettes, removing 1 ml and 5 ml of well-mixed slurry for DNA analysis and chloride analysis, respectively. The low chloride RAMM contained 0.27 g KH_2PO_4, 0.35 g K_2HPO_4, 0.97 g NH_4Br, 51 mg $CaBr_2$, 90.5 mg MgBr, 36.3 mg $FeBr_3$, and 10 ml of the reduced chloride mineral solution mixed into 1 L of ultrapure water (MilliQ, Millipore). Resazurin was added as an indicator. If needed, the media was then pH adjusted to approximately 7.0. The mineral solution contained 72.4 mg $MnBr_2$*4 $H_2$0, 5 mg H_3BO_3, 3.2 mg CuBr, 1 mg $NaMoO_4$*2H_2O, 80 mg $CoBr_2$*H_2O, 4.5 mg $NiBr_2$, and 5 mg Na_2SeO_3 in 1 L of ultrapure water (MilliQ, Millipore). The chloride concentration of the prepared microcosms was approximately 1.5 mg/L.

Enrichment with Contaminants

As stated, after enrichment with the different NOM or Cl-NOM fractions for 115 days, the triplicate serum bottles for each treatment were mixed together, then subdivided into 6 new serum bottles containing 45 ml of the mixed enrichment in each. The total volume of half of the new serum bottles (3 for each treatment) was brought up to 70 ml with the reduced chloride RAMM and the total volume of the other half of the new serum bottles (again, 3 bottles for each treatment) was brought up to 100 ml with the reduced chloride RAMM. This differential volume was used because TCE was measured via headspace analysis while TeCB was measured by liquid-liquid extraction.

Analytical Methods

For TeCB and 1,2,3-TCB analysis, 2 ml of the culture was measured into a glass vial with a Teflon lined top. One ml of hexane was added to the sample and shaken for 2 min. The hexane layer was removed. This was repeated and the two hexane layers were combined and dried with sodium sulfate. The hexane extract was analyzed using a gas chromatograph (HP

5890) coupled to an electron capture detector (GC-ECD). A sample of the hexane extract (5 µl) was injected onto an Agilent HP-5 column via autosampler (HP 7673). The initial oven temperature was maintained at 110ºC for 1 min, then increased 10ºC/min until 200ºC where it was held for an additional 5 min. Multiple possible degradation products of TeCB were analyzed (1,2,3-TCB, 1,3,5-TCB, 1,3-dichlorobenzene (1,3-DCB), and 1,2-DCB), but only 1,2,3-TCB was ever detected.

TCE was measured via headspace injection (10 µl) onto an Agilent HP-5 column on a GC-ECD. Standards were prepared in the same way as the cultures, with different known quantities of TCE added to 70 ml pure water (milli-Q, Millipore) in sealed 140-ml serum bottles. The GC method consisted of a constant oven temperature at 35ºC. All possible isomers of DCE were also measured by this method (1,1-DCE, *trans*-DCE, and *cis*-DCE) but only *cis*-DCE was ever detected. The method detection limits of the DCE congeners and TCE were 1 µM and less than 100 nM, respectively.

Quantitative PCR

The qPCR primers used for the reductive dehalogenase and dehalogenase gene detection were developed in previous research[2] from DNA sequences of dehalogenase genes identified in metagenomics analysis of the same soil used in the study presented here. Putative reductive dehalogenase, haloalkane dehalogenase, and 2-haloacid dehalogenase genes were targeted in Temme et al. (2018). The qPCR primers developed from this metagenome specific to the reductive and hydrolytic dehalogenase genes are shown in Table SI 1.

Total 16S rRNA gene quantity was determined using a general primer set that targets the V3 region[4]. The qPCR mixture for all of the primer sets contained 1X SYBR green MasterMix (Bio-Rad Laboratories), 100 nM of each primer, 1 mg/L of BSA, and 1 µl of undiluted template. The general qPCR cycle was an initial 95ºC denaturation for 2 minutes followed by 40 cycles of 95ºC denaturation for 15 s and 30 s anneal/extension at the specific annealing temperature for each primer set (Table S1). A melting curve analysis was completed at the end of each run for quality control/assurance. The number of gene copies in each sample was determined with a standard curve of standard dilutions ranging from 10^8 to 10^0. These standards were purchased as gblocks from IDT. Standards for total 16S rRNA gene analysis were prepared as described in Temme et al. (2018). The standard with the lowest concentration that was still linear was determined to be the limit of quantification. The limit of quantification for the generic primer set targeting the V3 region was 1000 gene copies/µl and the limits of quantification for the functional genes were 10 copies/µl.

Table S1. Primer sequences.

PCBRDaseF	CCTGAACAGCTATGGGAATAC	129	56.0	Putative reductive dehalogenase gene
PCBRDaseR	CAGCCGGTAATCAATACTCC			
PCBHaDhg1F	CCATCAAATCGGGAGCTAAA	129	59.0	Putative haloalkane dehalogenase gene
PCBHaDhg1R	CGTATGTGGATACAGGAAAGG			
PCBHaDhg2F	GGAACGCTTGATCTTGGAA	110	55.0	Putative haloalkane dehalogenase gene
PCBHaDhg2R	CAAGGTAAGGGCGATGATATG			
PCB 2-haloacidDhgF	GTTTCGCATCCGGGTAAA	104	58.0	Putative 2-haloacid dehalogenase gene
PCB 2-haloacidDhg	GCTGACTTTCACGCTCAA			

Community Analysis

As stated in the manuscript, Illumina paired end sequencing (2x300) was completed on the V4-V6 region of the 16S rRNA gene and used for bacterial community analysis. Amplification and sequencing were completed at the University of Minnesota Genomics Center (UMGC). The V4-V6 region was amplified with primers 515F-GTGCCAGCMGCCGCGGTAA and 806R-GGACTACHVGGGTWTCTAAT. These were selected from those available at UMGC because they captured the highest percentage of the *Chloroflexi* bacteria in the Ribosomal

Database Project database, which were anticipated to be important in Cl-NOM cycling[5]. The data was analyzed via the Minnesota Supercomputing Institute (MSI). Quality filtering was performed with a pipeline available on MSI that uses Trimmommatic and FastQC. The number of reads in each sample were rarified to the least number of reads in one of the samples. The processed reads were then analyzed using QIIME using the denovo clustering pipeline. The reads were also analyzed using a pipeline with the MOTHUR clustering algorithms, but this did not significantly change the results (data not shown). Once the relative fraction of a given population was calculated, this was converted to a numerical value (number of 16S rRNA genes) based on the total number of 16S rRNA genes present in the sample as obtained via qPCR. This conversion from relative abundance to quantities has been verified in the literature as a way to account for changes in biomass [6–9].

Statistical analysis

To determine whether particular bacterial populations may have benefitted from the amendment of Cl-NOM, Spearman's rank correlation was used. The analysis was performed separately at each phylogenetic class, though family and genus levels were focused on. First, any family or genera in less than 5 of the samples (triplicate samples of the 5 time points of the 6 treatments) and with fewer than 1000 16S rRNA gene copies/ml in at least one sample were filtered out of the dataset. Using QIIME, the Spearmen's rank correlation was then performed for each of the filtered genera and families to determine which populations increased over time in the treatments amended with Cl-NOM. The calculated *P*-values were corrected for multiple comparisons using the false discovery rate (FDR) method. The families or genera with negative Spearman's rho and *P*-values greater than 0.05 were removed. Further filtering was conducted by determine which of the remaining genera or families increased more in treatments amended with fractions of Cl-NOM when compared to the treatments amended with the same fraction of NOM, based on the *P*-values from the Dunn's Multiple Comparison Test. Spearman's rank coefficient was also used to determine which of the filtered genera significantly grew with the production of *cis*-DCE and the dechlorination of TCE for each treatment. Families or genera with negative Spearman's rho and corrected *P*-values greater than 0.05 were removed. Instead of correlating with time as was done with the Cl-NOM/NOM experiments, the test was used to determine which bacteria correlated with dechlorination of TCE or the production of *cis*-DCE because these dechlorination results were more variable between the triplicates. The results obtained for the correlation with TCE degradation and *cis*-DCE production were similar and only the *cis*-DCE results are included. The TeCB enrichments were analyzed differently because only two time points (Day 0 and Day 50) were taken. Instead, the Kruskal Wallis test in QIIME was used to determine whether the two time points were different followed by FDR corrected *P*-values to determine which genera grew significantly more in the samples with 1,2,3-TCB formation. Samples with *P*-values less than 0.05 are included.

Contaminant Dechlorination Results

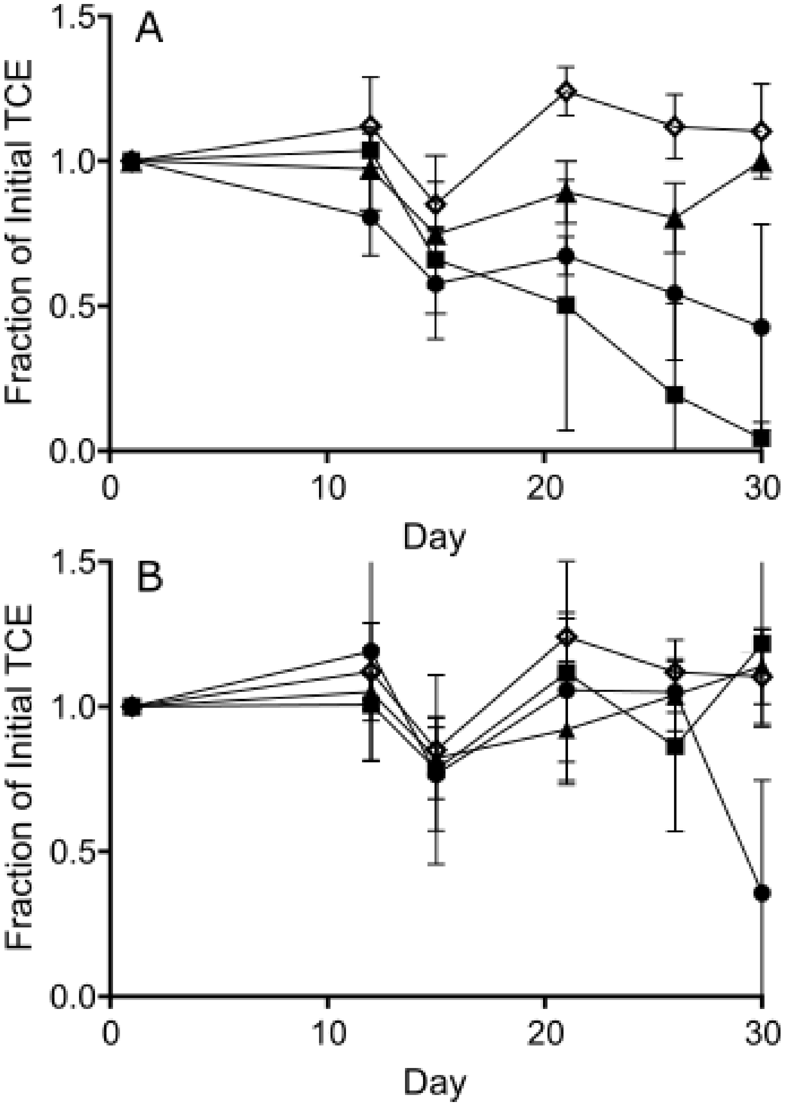

Figure S1. Fraction of initial TCE remaining over time in the treatments previously enriched on (A) Cl-NOM fractions and (B) NOM fractions; 100 µM TCE was added to each treatment. Symbols are: sterile negative control (◇), least hydrophobic fraction (●), moderate hydrophobic fraction (■), and most hydrophobic fraction (▲). Error bars represent standard deviations of triplicate experiments.

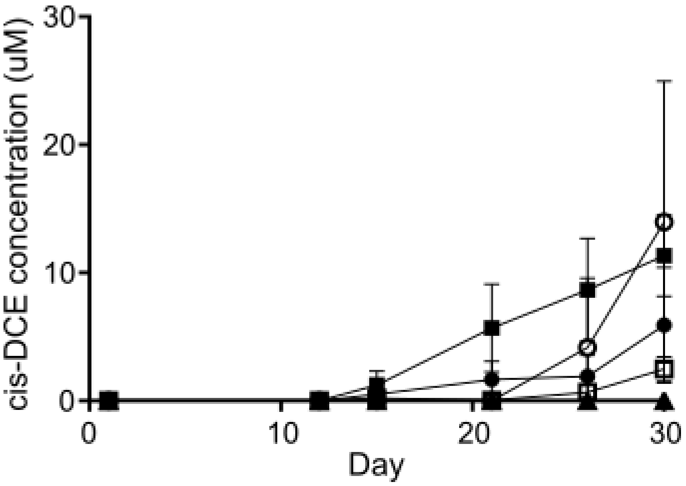

Figure S2. *Cis*-DCE formation over time in the treatments previously enriched on Cl-NOM fractions (closed symbols) and NOM enrichments (open symbols). Symbols are: least hydrophobic fraction (●), moderate hydrophobic fraction (■). No *cis*-DCE was detected in the most hydrophobic fraction or sterile negative control. Error bars represent standard deviations of triplicate experiments.

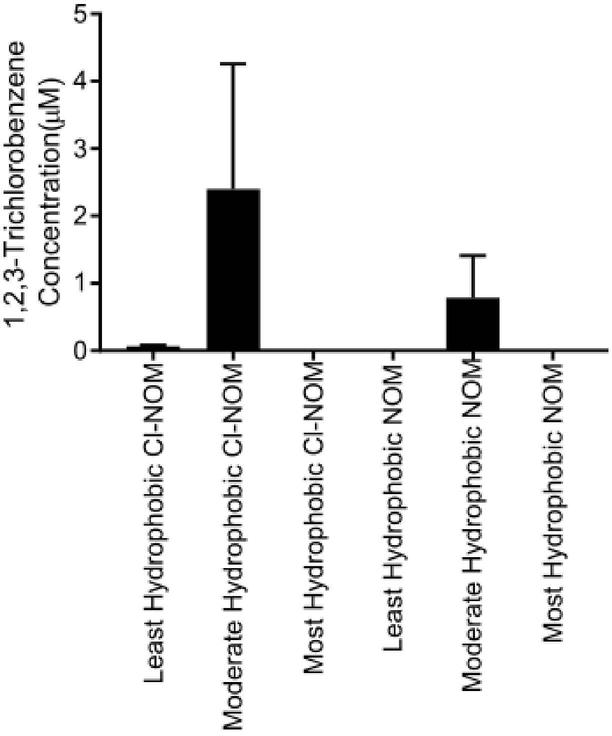

Figure S3. The concentration of 1,2,3-trichlorobenzene after 80 days of incubation with tetrachlorobenzene. Error bars represent standard deviations of triplicate experiments.

Tables with Spearman’s and concentrations

Genera with Significant Growth in Cl-NOM Enrichments

Table S2. Genera that grew significantly more in at least one of the treatments amended with the least hydrophobic Cl-NOM fraction compared to the treatments amended with the least hydrophobic NOM fraction, based on the Spearman’s ρ. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the five days sampled (Days 1, 17, 50, 83, and 113).

	ρ	*P*-value	1	17	50	83	113	ρ	*P*-value	1	17	50	83	113
Euryarchaeota														
Methanobacteria; Methanobacteriales; Methanobacteriaceae	0.62	0.05	0.00	0.00	0.89	3.14	3.22	0.00	0.00	0.00	0.62	0.00	1.39	1.43
Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina	0.70	0.02	1.43	0.00	2.78	2.58	3.63	0.00	0.00	1.29	0.70	0.00	1.77	1.53
Acidobacteria														
Solibacteres; Solibacterales; AKIW659	0.86	< 0.01	1.10	0.00	3.77	5.04	5.17	0.60	0.08	2.38	0.86	4.04	4.65	3.92
Solibacteres; Solibacterales; Solibacteraceae; Solibacter	0.82	< 0.01	1.95	0.00	2.90	3.94	4.59	0.85	< 0.01	0.00	0.82	3.02	3.96	4.02
Actinobacteria														
OPB41	0.58	0.08	0.68	0.00	0.91	1.44	3.78	0.00	0.00	0.00	0.58	1.60	1.68	1.14
Bacteroidetes														
Bacteroidia; Bacteroidales; Porphyromonadaceae	0.41	0.29	0.00	1.15	0.44	0.67	2.23	0.00	0.00	0.81	0.41	1.42	1.68	0.74
Chloroflexi														
Anaerolineae; Anaerolineales; Anaerolinaceae; WCHB1-05	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.83	1.22	0.00
Cyanobacteria														
Oscillatoriophycideae	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes														

Bacilli; Lactobacillales; Carnobacteriaceae	0.00	0.00	0.00	0.63	0.00	1.68	0.00	0.30	0.53	0.64	0.00	0.00	1.06	1.59
Bacilli; Lactobacillales; Enterococcaceae; Vagococcus	0.00	0.00	0.00	0.56	0.44	0.00	1.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clostridia; Clostridiales	0.84	< 0.01	1.66	2.24	5.15	6.05	6.16	0.79	< 0.01	2.82	0.84	4.70	5.47	4.94
Clostridia; Clostridiales; Mogibacteriaceae; Anaerovorax	0.86	< 0.01	0.00	0.00	3.87	4.57	4.65	0.87	< 0.01	0.64	0.86	3.41	5.05	4.77
Clostridia; Clostridiales; Tissierellaceae; Sedimentibacter	0.82	< 0.01	2.60	4.91	5.70	6.28	6.29	0.64	0.04	2.80	0.82	4.62	5.18	4.61
Clostridia; Clostridiales; Christensenellaceae	0.84	< 0.01	2.97	0.89	4.73	5.91	6.11	0.77	< 0.01	3.10	0.84	4.64	5.63	5.11
Clostridia; Clostridiales; Clostridiaceae	0.69	0.02	1.07	1.42	5.00	4.89	4.75	0.54	0.15	0.64	0.69	2.67	3.16	2.97
Clostridia; Clostridiales; Eubacteriaceae	0.00	0.00	0.00	0.59	0.00	1.11	0.00	0.00	0.00	0.00	0.00	0.00	1.06	0.00
Clostridia; Clostridiales; Eubacteriaceae; Acetobacterium	0.61	0.06	2.72	2.37	2.17	3.47	3.66	0.00	0.00	2.51	0.61	2.31	2.12	2.72
Clostridia; Clostridiales; Eubacteriaceae	0.00	0.00	0.00	0.00	0.00	1.01	0.00	0.00	0.00	0.81	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Gracilibacteraceae; Gracilibacter	0.91	< 0.01	2.34	3.62	4.64	5.50	5.75	0.77	< 0.01	2.57	0.91	4.49	5.29	4.90
Clostridia; Clostridiales; Gracilibacteraceae	0.90	< 0.01	0.00	2.41	3.16	3.93	4.15	0.79	< 0.01	0.00	0.90	2.51	3.66	3.28
Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes	0.79	< 0.01	0.00	0.00	1.65	2.82	3.88	0.00	0.00	0.00	0.79	0.00	0.00	0.00
Clostridia; Clostridiales; Lachnospiraceae; Blautia	0.62	0.05	0.00	0.00	1.01	2.58	2.71	0.00	0.00	0.91	0.62	0.00	0.00	0.00
Clostridia; Clostridiales; Lachnospiraceae	0.92	< 0.01	0.00	0.00	2.90	4.34	4.73	-0.29	0.55	1.53	0.92	2.27	1.06	0.75
Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus	0.79	< 0.01	4.02	5.15	5.51	6.31	6.35	0.85	< 0.01	3.19	0.79	5.69	6.18	5.88
Clostridia; Clostridiales; Peptococcaceae; WCHB1-84	0.81	< 0.01	0.77	4.10	4.53	5.60	5.63	0.64	0.04	1.55	0.81	4.91	5.44	4.63
Clostridia; Clostridiales; Peptococcaceae	0.71	0.01	1.76	2.88	3.25	4.11	4.27	0.73	0.01	0.64	0.71	3.76	4.23	3.77
Clostridia; Clostridiales; Ruminococcaceae	0.82	< 0.01	2.52	2.04	4.51	5.59	5.69	0.84	< 0.01	2.26	0.82	4.10	4.95	4.48
Clostridia; Clostridiales; Ruminococcaceae; Oscillospira	0.81	< 0.01	0.68	0.00	1.13	4.50	4.85	0.00	0.00	0.65	0.81	0.73	0.96	0.70
Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus	0.00	0.00	0.68	0.00	0.00	1.43	2.86	0.00	0.00	0.65	0.00	0.00	0.00	0.00

Clostridia; Clostridiales; Veillonellaceae; BSV43	0.79	< 0.01	1.86	2.28	4.82	5.54	5.49	0.69	0.03	1.90	0.79	2.91	3.97	4.60
Clostridia; Clostridiales; Veillonellaceae; Sporomusa	0.76	< 0.01	2.90	2.82	5.37	6.38	6.40	0.68	0.03	2.81	0.76	4.38	4.95	4.74
Clostridia; Clostridiales; Veillonellaceae	0.67	0.03	0.00	1.84	2.41	2.18	3.39	0.73	0.01	0.00	0.67	0.59	0.82	2.63
Proteobacteria														
Deltaproteobacteria; Desulfuromonadales; Geobacteraceae	0.50	0.17	0.00	0.00	1.70	2.75	1.06	0.00	0.00	0.00	0.50	0.69	0.88	0.00
Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter	0.80	< 0.01	2.30	2.94	4.67	4.93	4.66	-0.46	0.24	2.99	0.80	2.27	2.32	1.54
Deltaproteobacteria; Desulfuromonadales; Geobacteraceae	0.00	0.00	0.00	0.00	2.35	0.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria; Deltaproteobacteria; Myxococcales; Myxococcaceae; Anaeromyxobacter	0.87	< 0.01	2.20	4.28	5.40	5.85	5.86	0.00	0.00	1.29	0.87	2.21	2.04	1.44
WS2														
Kazan-3B-09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.84	0.00	0.00	1.06	0.00

Table S3. Genera that grew significantly more in at least one of the treatments amended with the moderately hydrophobic Cl-NOM fraction compared to the treatments amended with the moderately hydrophobic NOM fraction, based on the Spearman's ρ. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the five days sampled (Days 1, 17, 50, 83, and 113).

	ρ	***P*-value**	**1**	**17**	**50**	**83**	**113**	**ρ**	***P*-value**	**1**	**17**	**50**	**83**	**113**
Euryarchaeota														
Methanobacteria; Methanobacteriales; Methanobacteriaceae	0.60	0.06	1.17	0.00	3.39	5.15	3.44	0.00	0.00	0.00	0.00	1.23	1.54	2.61
Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina	0.44	0.21	0.00	0.70	0.00	4.20	1.18	0.74	0.01	0.00	0.00	0.69	3.26	3.79
Acidobacteria														
Solibacteres; Solibacterales; AKIW659	0.70	0.02	1.20	0.70	1.97	4.19	3.87	0.81	0.00	0.56	1.83	4.13	4.91	4.80
Solibacteres; Solibacterales; Solibacteraceae; Solibacter	-0.04	0.92	3.63	1.17	0.73	3.38	2.28	0.77	0.01	1.03	0.93	1.92	4.13	4.67
Actinobacteria														
OPB41	0.00	0.00	0.00	0.00	1.25	1.62	0.00	0.00	0.00	0.00	0.00	1.13	0.00	0.00
Bacteroidetes														
Bacteroidia; Bacteroidales; Porphyromonadaceae	0.60	0.06	0.00	3.28	4.40	5.78	3.69	0.00	0.00	0.00	0.00	1.13	0.00	0.54
Chloroflexi														
Anaerolineae; Anaerolineales; Anaerolinaceae; WCHB1-05	0.72	0.02	0.00	0.00	3.04	5.07	3.37	0.00	0.00	0.00	0.57	0.00	0.00	0.68
Cyanobacteria														
Oscillatoriophycideae	0.71	0.02	0.00	1.43	0.00	2.41	4.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes														
Bacilli; Lactobacillales; Carnobacteriaceae	0.65	0.05	0.00	3.82	4.02	4.63	4.22	0.00	0.00	0.73	0.00	0.40	0.00	0.00
Bacilli; Lactobacillales; Enterococcaceae; Vagococcus	0.56	0.09	0.00	2.98	3.00	3.85	2.40	0.00	0.00	0.00	0.00	0.00	0.00	0.78
Clostridia; Clostridiales	0.75	0.01	2.19	3.70	4.57	5.93	5.13	0.84	< 0.01	0.83	2.97	4.72	5.37	4.97

Clostridia; Clostridiales; Mogibacteriaceae; Anaerovorax	0.66	0.04	0.72	2.72	3.77	5.03	3.21	0.78	< 0.01	0.00	1.68	3.60	4.31	4.49
Clostridia; Clostridiales; Tissierellaceae; Sedimentibacter	0.61	0.06	3.56	5.00	5.03	5.97	5.20	0.62	0.06	0.86	3.75	4.72	5.27	4.75
Clostridia; Clostridiales; Christensenellaceae	0.71	0.02	3.92	2.60	4.23	5.69	5.29	0.84	< 0.01	1.34	1.98	4.53	5.66	5.53
Clostridia; Clostridiales; Clostridiaceae	0.38	0.29	2.71	2.27	3.28	4.00	3.71	0.51	0.20	1.57	1.85	2.85	3.85	3.30
Clostridia; Clostridiales; Eubacteriaceae	0.88	0.00	0.00	0.00	3.43	5.39	4.52	0.00	0.00	0.00	0.00	0.00	0.00	0.68
Clostridia; Clostridiales; Eubacteriaceae; Acetobacterium	0.71	0.02	3.40	2.27	5.79	6.74	5.90	0.00	0.00	1.06	2.23	1.41	3.55	0.68
Clostridia; Clostridiales; Eubacteriaceae	0.71	0.02	0.00	0.66	3.61	4.77	3.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Gracilibacteraceae; Gracilibacter	0.86	< 0.01	0.72	3.80	4.17	5.77	5.43	0.80	< 0.01	1.68	2.90	4.32	5.52	5.21
Clostridia; Clostridiales; Gracilibacteraceae	0.63	0.06	0.00	2.20	2.46	3.98	2.46	0.74	0.01	0.00	1.23	2.89	3.55	3.20
Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Lachnospiraceae; Blautia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Lachnospiraceae	0.00	0.00	1.27	0.00	0.37	0.00	1.07	0.00	0.00	0.29	1.84	1.69	2.25	0.00
Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus	0.47	0.18	4.60	5.09	4.53	5.80	5.33	0.77	< 0.01	1.56	4.85	5.57	6.24	5.90
Clostridia; Clostridiales; Peptococcaceae; WCHB1-84	0.61	0.06	0.00	1.52	3.71	4.98	2.99	0.59	0.09	0.73	3.69	4.39	4.55	4.06
Clostridia; Clostridiales; Peptococcaceae	0.58	0.08	0.82	0.90	2.01	3.52	2.47	0.67	0.04	0.00	2.81	3.62	4.16	3.72
Clostridia; Clostridiales; Ruminococcaceae	0.79	< 0.01	3.49	2.22	3.71	5.00	4.88	0.85	< 0.01	1.30	2.10	2.90	4.71	5.16
Clostridia; Clostridiales; Ruminococcaceae; Oscillospira	0.37	0.31	0.72	0.00	0.37	1.47	2.08	0.00	0.00	-0.44	0.49	0.00	0.00	0.68
Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus	0.00	0.00	1.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Veillonellaceae; BSV43	0.17	0.67	3.51	2.19	2.61	5.09	2.63	0.62	0.06	1.39	2.37	2.68	4.39	4.11
Clostridia; Clostridiales; Veillonellaceae; Sporomusa	0.47	0.18	3.97	2.63	2.96	4.32	5.12	0.55	0.14	1.55	2.73	3.28	4.06	3.48
Clostridia; Clostridiales; Veillonellaceae	0.45	0.20	0.00	0.80	0.79	0.79	2.02	0.41	0.35	0.00	0.59	1.73	1.19	1.83
Proteobacteria														

Deltaproteobacteria; Desulfuromonadales; Geobacteraceae	0.55	0.10	0.00	3.18	2.79	3.82	2.58	0.00	0.00	0.00	0.00	1.29	1.29	0.68
Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter	0.56	0.09	2.37	6.12	5.77	6.65	5.75	0.48	0.23	0.66	3.94	3.84	4.82	4.33
Deltaproteobacteria; Desulfuromonadales; Geobacteraceae	0.62	0.06	0.00	3.19	3.02	4.15	2.64	0.00	0.00	0.00	0.78	0.00	2.25	0.00
Proteobacteria; Deltaproteobacteria; Myxococcales; Myxococcaceae; Anaeromyxobacter	0.40	0.27	0.00	1.27	2.36	3.14	0.91	0.74	0.01	0.00	2.08	2.02	3.68	3.29
WS2														
Kazan-3B-09	0.74	0.01	0.00	0.00	1.38	0.95	3.37	0.00	0.00	0.00	1.37	0.00	0.00	0.88

Table S4. Genera that grew significantly more in at least one of the treatments amended with the most hydrophobic Cl-NOM fraction compared to the treatments amended with the most hydrophobic NOM fraction, based on the Spearman's ρ. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the five days sampled (Days 1, 17, 50, 83, and 113).

	ρ	***P*-value**	**1**	**17**	**50**	**83**	**113**	**ρ**	***P*-value**	**1**	**17**	**50**	**83**	**113**
Euryarchaeota														
Methanobacteria; Methanobacteriales; Methanobacteriaceae	0.89	< 0.01	0.00	0.00	1.71	3.62	3.99	0.00	0.00	0.00	0.00	0.00	1.39	1.43
Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina	0.93	< 0.01	0.00	0.89	3.56	4.23	4.42	0.00	0.00	1.29	0.00	0.00	1.77	1.53
Acidobacteria														
Solibacteres; Solibacterales; AKIW659	0.83	< 0.01	0.00	0.61	3.89	3.47	4.09	0.60	0.08	2.38	2.72	4.04	4.65	3.92
Solibacteres; Solibacterales; Solibacteraceae; Solibacter	0.86	< 0.01	2.76	1.17	3.65	4.74	4.98	0.85	0.00	0.00	0.00	3.02	3.96	4.02
Actinobacteria														
OPB41	0.00	0.00	0.00	0.00	1.77	0.68	0.00	0.00	0.00	0.00	0.00	1.60	1.68	1.14
Bacteroidetes														
Bacteroidia; Bacteroidales; Porphyromonadaceae	0.20	0.56	1.99	0.61	0.71	1.21	2.21	0.00	0.00	0.81	0.58	1.42	1.68	0.74
Chloroflexi														
Anaerolineae; Anaerolineales; Anaerolinaceae; WCHB1-05	0.00	0.00	0.60	0.61	0.00	0.69	0.76	0.00	0.00	0.00	0.58	0.83	1.22	0.00
Cyanobacteria														
Oscillatoriophycideae	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Firmicutes														
Bacilli; Lactobacillales; Carnobacteriaceae	0.00	0.00	0.00	0.61	0.87	0.00	1.44	0.30	0.53	0.64	0.58	0.00	1.06	1.59
Bacilli; Lactobacillales; Enterococcaceae; Vagococcus	0.00	0.00	0.00	1.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Clostridia; Clostridiales	0.87	< 0.01	1.53	2.44	4.79	4.82	5.22	0.79	< 0.01	2.82	3.91	4.70	5.47	4.94
Clostridia; Clostridiales; Mogibacteriaceae; Anaerovorax	0.91	< 0.01	1.35	1.73	3.77	4.05	4.40	0.87	< 0.01	0.64	1.16	3.41	5.05	4.77
Clostridia; Clostridiales; Tissierellaceae; Sedimentibacter	0.37	0.24	2.52	5.83	5.80	5.58	5.69	0.64	0.04	2.80	3.38	4.62	5.18	4.61
Clostridia; Clostridiales; Christensenellaceae	0.92	< 0.01	2.60	2.77	4.56	4.99	5.56	0.77	< 0.01	3.10	2.55	4.64	5.63	5.11
Clostridia; Clostridiales; Clostridiaceae	0.64	0.02	0.00	0.00	4.68	3.38	3.64	0.54	0.15	0.64	2.87	2.67	3.16	2.97
Clostridia; Clostridiales; Eubacteriaceae	0.00	0.00	0.00	0.00	0.53	1.21	1.03	0.00	0.00	0.00	0.00	0.00	1.06	0.00
Clostridia; Clostridiales; Eubacteriaceae; Acetobacterium	0.00	0.00	2.35	2.57	2.75	1.48	2.50	0.00	0.00	2.51	2.60	2.31	2.12	2.72
Clostridia; Clostridiales; Eubacteriaceae	0.00	0.00	0.00	0.00	0.53	0.00	0.00	0.00	0.00	0.81	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Gracilibacteraceae; Gracilibacter	0.95	< 0.01	1.35	4.30	4.57	5.07	5.52	0.77	< 0.01	2.57	2.83	4.49	5.29	4.90
Clostridia; Clostridiales; Gracilibacteraceae	0.85	< 0.01	0.00	2.74	3.49	3.57	3.76	0.79	< 0.01	0.00	0.93	2.51	3.66	3.28
Clostridia; Clostridiales; Lachnospiraceae; Anaerostipes	0.00	0.00	0.60	0.00	0.78	1.53	0.00	0.00	0.00	0.00	0.58	0.00	0.00	0.00
Clostridia; Clostridiales; Lachnospiraceae; Blautia	0.00	0.00	0.00	0.00	0.53	0.00	0.00	0.00	0.00	0.91	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Lachnospiraceae	0.72	< 0.01	0.00	0.00	0.63	0.69	2.21	-0.29	0.55	1.53	2.28	2.27	1.06	0.75
Clostridia; Clostridiales; Peptococcaceae; Desulfosporosinus	0.88	< 0.01	4.54	5.34	5.24	6.30	6.50	0.85	< 0.01	3.19	5.12	5.69	6.18	5.88
Clostridia; Clostridiales; Peptococcaceae; WCHB1-84	0.61	0.03	0.00	4.06	4.00	4.21	4.65	0.64	0.04	1.55	4.13	4.91	5.44	4.63
Clostridia; Clostridiales; Peptococcaceae	0.87	< 0.01	1.59	3.10	3.47	4.11	4.09	0.73	0.01	0.64	2.74	3.76	4.23	3.77
Clostridia; Clostridiales; Ruminococcaceae	0.99	< 0.01	0.00	2.70	4.83	5.13	5.53	0.84	< 0.01	2.26	2.54	4.10	4.95	4.48
Clostridia; Clostridiales; Ruminococcaceae; Oscillospira	0.78	< 0.01	0.00	0.00	0.87	1.67	3.15	0.00	0.00	0.65	0.58	0.73	0.96	0.70
Clostridia; Clostridiales; Ruminococcaceae; Ruminococcus	0.60	0.03	0.60	0.00	0.53	1.05	4.06	0.00	0.00	0.65	0.00	0.00	0.00	0.00
Clostridia; Clostridiales; Veillonellaceae; BSV43	0.64	0.02	2.45	2.67	4.14	4.78	4.82	0.69	0.03	1.90	2.54	2.91	3.97	4.60

Clostridia; Clostridiales; Veillonellaceae; Sporomusa	0.88	< 0.01	2.69	2.95	3.52	3.55	5.20	0.68	0.03	2.81	3.24	4.38	4.95	4.74
Clostridia; Clostridiales; Veillonellaceae	0.00	0.00	0.00	3.16	2.85	1.72	2.31	0.73	0.01	0.00	0.00	0.59	0.82	2.63
Proteobacteria														
Deltaproteobacteria; Desulfuromonadales; Geobacteraceae	0.18	0.59	0.00	0.00	2.30	1.28	0.00	0.00	0.00	0.00	0.58	0.69	0.88	0.00
Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter	0.66	0.02	0.75	2.90	4.46	4.09	3.60	-0.46	0.24	2.99	2.47	2.27	2.32	1.54
Deltaproteobacteria; Desulfuromonadales; Geobacteraceae	0.26	0.44	0.00	0.89	1.39	1.48	0.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria; Deltaproteobacteria; Myxococcales; Myxococcaceae; Anaeromyxobacter	0.60	0.03	0.70	3.52	5.25	4.63	4.56	0.00	0.00	1.29	1.76	2.21	2.04	1.44
WS2														
Kazan-3B-09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.84	0.00	0.00	1.06	0.00

Genera with Significant Growth in Trichloroethene Enrichment

Table S5. Genera in which growth was significantly correlated to *cis*-DCE formation, in treatments initially enriched on the least hydrophobic fraction of Cl-NOM or NOM, based on the Spearman's ρ and *P*-value. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the three days sampled (Days 1, 20, and 49).

	ρ	*P*-value	1	20	49	ρ	*P*-value	1	20	49
Euryarchaeota										
Methanomicrobia	0.00	0.00	0.00	1.22	0.00	0.00	0.00	0.00	2.45	0.00
Armatimonadetes										
SHA-37	0.81	0.02	0.95	4.49	5.43	0.00	0.00	0.00	0.00	0.00
SJA-176; RB046	0.00	0.00	0.00	0.00	1.31	0.00	0.00	0.00	0.00	0.00
Bacteroidetes										
Bacteroidia; Bacteroidales	0.79	0.03	3.43	6.20	6.34	-0.16	0.98	5.98	6.85	6.17
Bacteroidia; Bacteroidales; Porphyromonadaceae; Paludibacter	0.91	0.01	0.00	5.98	6.51	-0.02	0.98	2.73	5.55	5.03
Bacteroidia; Bacteroidales; SB-1	0.67	0.09	0.82	4.49	5.18	-0.17	0.98	5.07	5.58	5.33
Chloroflexi										
Anaerolineae; Anaerolineales; Anaerolinaceae; Anaerolinea	0.68	0.09	2.09	2.97	5.58	0.00	0.00	0.00	0.00	0.00
Anaerolineae; WCHB1-50	0.00	0.00	0.98	0.00	0.00	0.14	0.98	4.26	5.24	5.00
Firmicutes										
Bacilli; Bacillales; Planococcaceae; Rummeliibacillus	0.77	0.03	0.00	3.14	5.45	0.00	0.00	0.00	0.00	0.00
Bacilli; Lactobacillales; Carnobacteriaceae	0.63	0.13	0.82	5.43	6.07	-0.23	0.98	5.25	5.75	5.26
Bacilli; Lactobacillales; Carnobacteriaceae; Trichococcus	0.63	0.13	1.19	6.38	7.00	-0.16	0.98	6.16	6.62	6.18
Clostridia; Clostridiales; Eubacteriaceae	0.85	0.01	0.00	4.46	5.52	-0.05	0.98	5.44	6.24	5.97
Clostridia; Clostridiales; Peptococcaceae; Dehalobacter	0.94	0.00	4.10	5.97	6.83	-0.06	0.98	4.70	5.06	3.41
Clostridia; Clostridiales; Peptococcaceae; WCHB1-84	0.78	0.03	5.25	5.85	6.23	0.77	0.36	0.81	2.85	4.58
Clostridia; Clostridiales; Veillonellaceae; Pelosinus	0.78	0.03	4.71	5.32	5.73	0.63	0.91	3.37	2.90	4.61
Clostridia; SHA-98; D2; unknown	0.00	0.00	0.00	2.49	2.98	0.00	0.00	0.00	0.00	1.49

Proteobacteria										
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae	0.74	0.05	1.15	6.77	7.15	0.29	0.98	5.16	6.18	6.26
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae	0.78	0.03	0.00	4.21	4.75	0.00	0.00	0.81	2.45	1.18
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas	0.81	0.02	4.62	5.54	5.76	-0.08	0.98	2.79	5.14	4.73
Betaproteobacteria; Burkholderiales	0.37	0.46	3.02	4.29	4.29	-0.60	0.91	3.61	3.13	1.18
Deltaproteobacteria; Myxococcales	0.00	0.00	0.00	1.22	1.31	0.00	0.00	0.00	0.00	0.00
Tenericutes										
Mollicutes; RF39	0.81	0.02	0.00	4.96	5.48	0.00	0.00	0.00	0.00	0.00
Verrucomicrobia										
Pedosphaerae; Pedosphaerales	0.00	0.00	0.87	1.49	0.00	0.00	0.00	0.00	0.00	1.18

Table S6. Genera in which growth was significantly correlated to *cis*-DCE formation, in treatments initially enriched on the moderately hydrophobic fraction of Cl-NOM or NOM, based on the Spearman's ρ and *P*-value. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the three days sampled (Days 1, 20, and 49).

	ρ	*P*-value	1	20	49	ρ	*P*-value	1	20	49
Euryarchaeota										
Methanomicrobia	0.76	0.04	1.85	1.28	4.04	0.00	0.00	0.65	0.00	0.00
Armatimonadetes										
SHA-37	0.00	0.00	0.00	0.00	1.35	0.00	0.00	0.00	0.00	0.00
SJA-176; RB046	0.84	0.01	0.00	4.72	5.03	0.00	0.00	0.88	0.00	0.00
Bacteroidetes										
Bacteroidia; Bacteroidales	0.58	0.17	2.71	7.23	6.87	0.38	0.62	1.84	6.83	6.27
Bacteroidia; Bacteroidales; Porphyromonadaceae; Paludibacter	0.00	0.00	0.00	2.66	1.29	0.75	0.21	0.65	6.63	6.70
Bacteroidia; Bacteroidales; SB-1; unknown	0.90	0.00	0.90	6.55	6.99	0.88	0.05	0.00	3.53	5.44
Chloroflexi										
Anaerolineae; Anaerolineales; Anaerolinaceae; Anaerolinea	0.95	0.00	0.00	4.40	5.15	-0.67	0.38	2.91	4.71	0.00
Anaerolineae; WCHB1-50	0.94	0.00	0.00	3.05	4.90	0.00	0.00	0.00	0.00	0.00
Firmicutes										
Bacilli; Bacillales; Planococcaceae; Rummeliibacillus	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacilli; Lactobacillales; Carnobacteriaceae	0.78	0.04	0.86	3.49	4.82	0.19	0.80	0.75	5.15	3.36
Bacilli; Lactobacillales; Carnobacteriaceae; Trichococcus	0.87	0.01	0.74	5.22	5.61	0.37	0.63	0.00	6.23	5.54
Clostridia; Clostridiales; Eubacteriaceae	0.97	0.00	1.02	4.15	4.44	0.15	0.82	3.09	5.82	5.38
Clostridia; Clostridiales; Peptococcaceae; Dehalobacter	0.97	0.00	3.79	4.71	6.94	0.79	0.15	3.47	6.65	7.12
Clostridia; Clostridiales; Peptococcaceae; WCHB1-84	0.14	0.78	4.82	4.86	4.84	0.28	0.74	3.30	0.00	2.66
Clostridia; Clostridiales; Veillonellaceae; Pelosinus	0.86	0.01	4.79	5.52	5.82	0.49	0.61	4.02	3.38	4.77
Clostridia; SHA-98; D2; unknown	0.97	0.00	1.93	4.55	5.55	0.62	0.46	2.27	4.71	5.12
Proteobacteria										

Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae	0.61	0.14	4.54	5.60	5.54	0.24	0.76	4.13	5.82	5.63
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae	0.00	0.00	1.70	0.00	0.00	0.00	0.00	1.59	1.39	0.00
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas	0.16	0.76	3.01	3.07	3.28	0.24	0.76	4.02	3.14	3.12
Betaproteobacteria; Burkholderiales	0.90	0.00	2.92	4.03	4.28	0.80	0.15	3.31	2.81	4.56
Deltaproteobacteria; Myxococcales	0.94	0.00	0.96	4.17	4.56	0.20	0.78	0.00	4.22	3.76
Tenericutes										
Mollicutes; RF39	0.71	0.06	1.09	5.45	5.44	0.00	0.00	1.97	0.00	0.00
Verrucomicrobia										
Pedosphaerae; Pedosphaerales	0.89	0.00	1.60	2.90	5.03	0.79	0.15	3.56	4.97	5.32

Table S7. Genera that grew significantly more in TCE-amended treatments initially enriched on the most hydrophobic fraction of Cl-NOM and NOM, based on the Spearman's ρ. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the three days sampled (Days 1, 20, and 49). Statistical correlations to *cis*-DCE formation could not be calculated because no cis-DCE was detected in these enrichments.

	1	20	49	1	20	49
Euryarchaeota						
Methanomicrobia	0.00	0.00	0.00	0.00	0.00	0.00
Armatimonadetes						
SHA-37	0.00	1.54	1.42	2.78	3.18	3.00
SJA-176; RB046	0.00	0.00	0.00	0.00	1.68	1.56
Bacteroidetes						
Bacteroidia; Bacteroidales	2.67	4.91	4.49	4.20	5.48	4.86
Bacteroidia; Bacteroidales; Porphyromonadaceae; Paludibacter	0.00	2.10	5.64	0.86	1.40	1.56
Bacteroidia; Bacteroidales; SB-1	0.00	1.18	0.00	0.00	1.45	0.00
Chloroflexi						
Anaerolineae; Anaerolineales; Anaerolinaceae; Anaerolinea	1.80	1.63	1.45	0.00	2.93	3.15
Anaerolineae; WCHB1-50	0.00	1.40	0.00	0.00	0.00	0.00
Firmicutes						
Bacilli; Bacillales; Planococcaceae; Rummeliibacillus	0.00	0.00	0.00	0.00	0.00	0.00
Bacilli; Lactobacillales; Carnobacteriaceae	1.16	0.00	0.00	1.33	2.65	1.36
Bacilli; Lactobacillales; Carnobacteriaceae; Trichococcus	1.94	0.00	1.61	0.00	2.75	0.00
Clostridia; Clostridiales; Eubacteriaceae	0.00	0.00	2.68	1.22	1.43	2.97
Clostridia; Clostridiales; Peptococcaceae; Dehalobacter	4.42	5.63	5.78	5.22	5.49	5.82
Clostridia; Clostridiales; Peptococcaceae; WCHB1-84	4.19	4.95	4.58	5.40	5.50	4.49
Clostridia; Clostridiales; Veillonellaceae; Pelosinus	3.93	4.47	2.95	4.28	1.60	4.08
Clostridia; SHA-98; D2	1.77	0.00	3.67	1.61	0.00	0.00

Proteobacteria						
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae	3.76	5.84	5.73	4.66	5.55	5.75
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae	0.84	2.77	2.42	0.76	1.44	2.71
Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingomonas	3.99	4.91	4.63	4.69	4.72	3.06
Betaproteobacteria; Burkholderiales	3.31	4.20	4.22	4.05	3.16	4.03
Deltaproteobacteria; Myxococcales	0.00	1.34	1.16	0.00	1.17	1.36
Tenericutes						
Mollicutes; RF39	0.00	1.60	3.11	0.00	0.00	1.36
Verrucomicrobia						
Pedosphaerae; Pedosphaerales	0.68	1.24	2.26	0.00	0.00	1.25

Genera with Significant Growth in Tetra-chlorobenzene Enrichments

Table S8. Genera in which growth was significantly correlated to 1,2,3-TCB formation across all of the treatments based on the FDR corrected *P*-value. The log concentrations of the 16S rRNA genes (log [copies/ml]) are listed for the two days sampled (Days 1 and 50) for each of the treatments.

[redacted]													
	P-value	1	50	1	50	1	50	1	50	1	50	1	50
						Acidobacteria							
Acidobacteriia; Acidobacteriales; Koribacteraceae; Koribacter	0.0044	2.2	3.0	1.2	6.2	4.1	1.2	5.1	1.7	1.6	6.9	3.8	3.1
						Bacteroidetes							
Bacteroidia; Bacteroidales	0.0005	3.4	5.4	6.0	6.7	2.7	4.0	1.8	5.9	2.7	6.0	4.2	5.0
Bacteroidia; Bacteroidales; SB-1	0.0061	0.8	5.0	5.1	5.6	0.9	1.4	0.0	5.3	0.0	5.5	0.0	2.7
						Firmicutes							
Clostridiales; Gracilibacteraceae; Gracilibacter	0.0044	5.3	6.6	6.2	7.0	5.5	6.5	6.0	7.1	5.1	7.2	6.1	6.6
Clostridiales; Gracilibacteraceae	0.0012	3.4	4.6	3.6	4.9	3.5	4.4	3.9	4.9	3.1	5.1	4.0	4.6
Clostridiales; Ruminococcaceae	0.0006	5.3	6.5	6.1	7.0	5.9	6.2	5.9	7.0	5.0	7.1	5.9	6.7
Clostridia; Clostridiales; Syntrophomonadaceae; Syntrophomonas	0.0002	2.4	4.9	5.2	6.3	5.8	2.7	4.9	5.3	4.0	6.3	4.4	3.5
Clostridia; SHA-98; D2	0.0002	0.0	0.0	0.0	5.2	1.9	0.0	2.3	0.0	1.8	5.5	1.6	0.0
						Planctomycetes							
Phycisphaerae; Pla1		0.0	0.0	0.0	4.8	0.0	1.3	1.9	1.7	0.8	5.1	1.1	0.0
Planctomycetia; Pirellulales; Pirellulaceae	0.0406	1.7	1.2	2.7	4.2	2.8	0.0	3.3	3.5	0.0	4.4	3.8	1.4
						Proteobacteria							
Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Sulfurospirillum	0.0303	0.0	1.2	4.4	5.9	5.2	5.5	5.0	5.0	4.1	6.1	2.7	5.4
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas	0.0059	4.0	5.2	7.0	6.8	5.4	5.0	5.0	7.5	4.3	6.2	4.6	5.2
Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae	0.0147	0.9	1.2	5.4	5.2	3.9	4.1	4.0	6.0	1.7	4.9	3.7	3.0

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