

1 Identification of a parasitic symbiosis between respiratory metabolisms in  
2 the biogeochemical chlorine cycle

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7 Running title: Parasitic symbiotic perchlorate respiration

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## 15 Abstract

16 A key step in the chlorine cycle is the reduction of perchlorate ( $\text{ClO}_4^-$ ) and chlorate ( $\text{ClO}_3^-$ ) to  
17 chloride by microbial respiratory pathways. Perchlorate-reducing bacteria and chlorate-reducing  
18 bacteria differ in that the latter cannot use perchlorate, the most oxidized chlorine compound.  
19 However, a recent study identified a bacterium with the chlorate reduction pathway dominating a  
20 community provided only perchlorate. Here we confirm a metabolic interaction between  
21 perchlorate- and chlorate-reducing bacteria and define its mechanism. Perchlorate-reducing  
22 bacteria supported the growth of chlorate-reducing bacteria to up to 90% of total cells in  
23 communities and co-cultures. Chlorate-reducing bacteria required the gene for chlorate reductase  
24 to grow in co-culture with perchlorate-reducing bacteria, demonstrating that chlorate is  
25 responsible for the interaction, not the subsequent intermediates chlorite and oxygen. Modeling of  
26 the interaction suggested that cells specialized for chlorate reduction have a competitive  
27 advantage for consuming chlorate produced from perchlorate, especially at high concentrations of  
28 perchlorate, because perchlorate and chlorate compete for a single enzyme in perchlorate-  
29 reducing cells. We conclude that perchlorate-reducing bacteria inadvertently support large  
30 populations of chlorate-reducing bacteria in a parasitic relationship through the release of the  
31 intermediate chlorate. An implication of these findings is that undetected chlorate-reducing  
32 bacteria have likely negatively impacted efforts to bioremediate perchlorate pollution for decades.

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## 40 Introduction

41 The chlorine cycle consists of the biological, geological, and chemical processes that interconvert  
42 organic and inorganic chlorine compounds (Atashgahi et al 2018). Chlorine oxyanions are a  
43 group of inorganic chlorine compounds of particular interest in biology due to their high  
44 reduction potentials ( $E^{0'} > 0.7 \text{ V}$ ) (Liebensteiner et al 2016, McCullough and Hazen 2003,  
45 Winterbourn 2008, Youngblut et al 2016b). Hypochlorite ( $\text{ClO}^-$ ) and chlorite ( $\text{ClO}_2^-$ ) are highly  
46 reactive compounds that damage cells through oxidative chemistry (Gray et al 2013, Hofbauer et  
47 al 2016, Melnyk et al 2015), while chlorate ( $\text{ClO}_3^-$ ) and perchlorate ( $\text{ClO}_4^-$ ) are used as electron  
48 acceptors in respiration by some bacteria and archaea (Youngblut et al 2016b). Uniquely among  
49 chlorine oxyanions, perchlorate is chemically stable in solution, and a necessary step in the  
50 chlorine cycle is the reduction of perchlorate to chloride by microbial respiration (Coates and  
51 Achenbach 2004, Youngblut et al 2016b). Where this microbial activity is absent, geochemical  
52 reactions in the atmosphere lead to the accumulation of perchlorate and, to a lesser degree,  
53 chlorate (Kounaves et al 2010, Melnyk and Coates 2015, Youngblut et al 2016b). Both  
54 atmospheric deposition of chlorine oxyanions and microorganisms respiring chlorine oxyanions  
55 appear to be widespread (Coates et al 1999, Rajagopalan et al 2009), yet the biogeochemistry of  
56 this key part of the chlorine cycle is not well understood (Youngblut et al 2016b).

57 An important unresolved question is whether the microbial respiration of chlorine oxyanions in  
58 the environment is performed by individual cells or by groups of cells with different parts of the  
59 biochemical pathway (Barnum et al 2018, Clark et al 2016). Many redox metabolisms from other  
60 elemental cycles have been found to occur through pathways that are divided between different  
61 cells, including nitrate reduction (Van de Pas-Schoonen et al 2005); ammonia oxidation (Daims et  
62 al 2016, Winogradsky 1892); sulfur oxidation and reduction (Anantharaman et al 2018, Kelly et  
63 al 1997); and organic chlorine reduction (Groster and Edwards 2006). Complete pathways might

64 even be rare in environmental systems: a recent description of metagenome-assembled genomes  
65 from aquifer sediment found that only a minority of organisms with genes for nitrate reduction or  
66 sulfur oxidation had the complete pathway (Anantharaman et al 2016). In many cases, respiratory  
67 metabolisms have been observed to involve both cells with complete pathways and cells with  
68 partial pathways, a form of symbiosis that can range from mutualistic to antagonistic (Costa et al  
69 2006, Dolinšek et al 2016, Hallin et al 2018, Lilja and Johnson 2016).

70

71 Chlorate reduction could be considered a partial pathway of perchlorate reduction, as the two  
72 pathways share substantial similarities (Youngblut et al 2016b). The key difference is whether or  
73 not the initial step of the pathway is catalyzed by a perchlorate reductase (Pcr), which reduces  
74 both perchlorate and chlorate, or by a chlorate reductase (Clr), which can only reduce chlorate  
75 (Figure 1A) (Wolterink et al 2003). Both metabolisms occur in the bacterial periplasm, where  
76 perchlorate and/or chlorate are reduced to chlorite, chlorite is converted to chloride and oxygen  
77 by a chlorite dismutase (Cld) (Bender et al 2002, Coates et al 1999, Hofbauer et al 2014, Van  
78 Ginkel et al 1996), and oxygen is reduced to water by one or more terminal oxidases (Clark et al  
79 2014, Clark et al 2016, Sun 2008). Energy is conserved by the reduction of perchlorate, chlorate,  
80 and oxygen but not in the conversion of chlorite to oxygen and chloride (Figure 1A) (Rikken et al  
81 1996). Genes for these enzymes are found together within horizontally transferred genomic DNA  
82 or plasmid DNA, typically with accessory genes for signaling and regulation, reactive chlorine  
83 stress response, protein and cofactor assembly, and genetic mobility (Clark et al 2013, Melnyk et  
84 al 2011, Melnyk and Coates 2015). Some bacteria and archaea have been experimentally  
85 observed or engineered to reduce perchlorate or chlorate to chlorite, relying on a second organism  
86 or chemical reactions to remove chlorite (Clark et al 2016, Liebensteiner et al 2013, Liebensteiner  
87 et al 2015, Martínez-Espinosa et al 2015). However, selection for perchlorate- or chlorate-  
88 reducing microorganisms from the environment has only yielded bacteria with the canonical  
89 pathways described above (Barnum et al 2018, Youngblut et al 2016b).

90

91     Though the pathways for chlorine oxyanion respiration have been studied in parallel for decades  
92     (Malmqvist et al 1994, Rikken et al 1996), research on interactions between them is sparse. One  
93     set of studies explored how unusually high accumulation of chlorate by the perchlorate-reducing  
94     bacterium *Dechlorosoma sp.* HCAP-C (PCC) could support chlorate-reducing bacteria (Dudley  
95     and Nerenberg 2007, Dudley et al 2008, Salamone and Nerenberg 2006). Addition of a chlorate-  
96     reducing bacterium in co-culture with strain HCAP-C decreased the concentration of chlorate,  
97     and while models of the system suggested growth of the chlorate-reducing bacterium, the  
98     community structure *in situ* was not determined (Dudley and Nerenberg 2007, Salamone and  
99     Nerenberg 2006). Accumulation of chlorate by strain HCAP-C was proposed to occur because a  
100     single enzyme (Pcr) catalyzes two sequential reactions in the pathway (reduction of perchlorate to  
101     chlorate, and chlorate to chlorite) (Dudley et al 2008, Nerenberg et al 2006). As that trait is shared  
102     by all known perchlorate-reducing bacteria, and several perchlorate-reducing bacteria have been  
103     reported to accumulate chlorate, albeit at much lower concentrations (Cameron Thrash et al 2010,  
104     Thrash et al 2010b, Youngblut et al 2016a), it was speculated that chlorate-reducing bacteria may  
105     be a common feature of natural perchlorate-reducing communities (Nerenberg et al 2006,  
106     Salamone and Nerenberg 2006).

107

108     No subsequent research examined the possibility of interaction between chlorine oxyanion  
109     reduction pathways in communities until recently, when we observed a genome with chlorate  
110     reduction genes in a perchlorate-enriched community (Barnum et al 2018). Surprisingly, the  
111     putative chlorate-reducing population was 10-fold more abundant than the perchlorate-reducing  
112     population. Because no chlorate had been added to the cultures, the chlorate-reducing population  
113     either had unknown perchlorate reduction genes or was metabolizing intermediates of the  
114     perchlorate reduction pathway (Barnum et al 2018).

115

116 In the present study, we investigate the interaction between perchlorate-reducing bacteria and  
117 chlorate-reducing bacteria. After sequencing the genomes of perchlorate-reducing cultures  
118 obtained from estuary sediment enrichments (Carlström et al 2016), we detected contaminating  
119 bacteria that had not been completely removed during isolation. We discovered that several  
120 cultures were not predominantly perchlorate-reducing bacteria, as expected, but dominated by  
121 chlorate-reducing bacteria. We therefore used a combination of co-cultures, genetics, and  
122 modeling to confirm the interaction, define its mechanism, and explain how such a community  
123 structure could be produced. We conclude that the environmental chlorine cycle involves the  
124 interaction of a complete pathway and a partial pathway in the reduction of perchlorate to  
125 chloride.

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## 129 Materials and Methods

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### 131 *Genome sequencing, assembly, binning, and annotation*

132 Genomic DNA was extracted using a MoBio PowerSoil DNA Extraction Kit with a cell lysis  
133 protocol consisting of vortexing and heating at 70 °C for 5 min, repeated twice (MoBio  
134 Laboratories, Inc., Carlsbad, CA). DNA library preparation and DNA sequencing were performed  
135 by the Adam Arkin Laboratory or the Vincent J. Coates Genomics Sequencing Laboratory at the  
136 California Institute of Quantitative Biosciences (QB3, Berkeley, CA) using an Illumina MiSeq  
137 V2 (150PE or 250PE) and Illumina HiSeq4000 (100PE), respectively. Paired-end reads from  
138 each sample were trimmed using Sickle v. 1.33 with default parameters (Joshi and Fass 2011),  
139 error-corrected using SGA v. 0.10.15 (Simpson and Durbin 2012), and assembled using  
140 MEGAHIT v. 1.1.2 with the parameters --no-mercy and --min-count 3 (Li et al 2015). After  
141 assembly, reads were mapped back to each assembly using the Burrows-Wheeler Alignment Tool  
142 v. 0.7.10 (BWA) BWA-MEM algorithm (Li 2013). All manipulation of reads was performed on  
143 high-performance computing clusters administered by the Computational Genomics Resource  
144 Laboratory (CGRL).

145

146 Genome assemblies were screened for contamination using Anvi'o v. 3.1 (Eren et al 2015).  
147 Briefly, contigs >2,000 bp were manually binned into genomes using the hierarchical clustering  
148 generated from sequence characteristics and read coverage. When multiple genomes were present  
149 in a single assembly, contigs were binned into metagenome-assembled genomes (MAGs).  
150 Because perchlorate and chlorate respiration involve horizontally transferred genes that are  
151 subject to poor assembly, the BLAST feature in Bandage v. 0.8.0 (Wick et al 2015) was used to  
152 identify key genes and confirm their presence and absence in genomes as previously described  
153 (Barnum et al 2018). The completeness and contamination of each genome and metagenome-

154 assembled genome was measured using CheckM (Parks et al 2015), which measures the single  
155 copy genes expected within a lineage and defines contamination as redundant genes with less  
156 than 90% amino acid identity. Structural annotation of genomes was performed using Prokka v.  
157 1.11 (Seemann 2014), and key genes were identified using custom profile Hidden Markov models  
158 (HMMs) trained on previously confirmed proteins using HMMER v. 3.1b2 (Finn et al 2015). All  
159 reads and genome sequences are available through the NCBI Bioproject accession PRJNA387015  
160 (Barnum et al 2018).

161

#### 162 *Strains, media, and culture conditions*

163 A complete set of strains and cultivation conditions are included in Supplementary Table 1.  
164 Growth medium for perchlorate-reducing cultures consisted of either a freshwater defined  
165 medium (Coates et al 1999) or a marine defined medium (Coates et al 1995) at pH 7.2 with,  
166 unless noted otherwise, 10 mM acetate as the electron donor and carbon source and 10 mM  
167 perchlorate as the electron acceptor. All media and stocks were made anaerobic by sparging with  
168 N<sub>2</sub>. Growth experiments were performed at 30 C in crimp-sealed tubes with an N<sub>2</sub> atmosphere.  
169 Concentrations of perchlorate, chlorate, and acetate were measured using ion chromatography.  
170 Cells were quantified by optical density at 600 nm (OD600). Isolation of chlorate-reducing strains  
171 was performed by streaking twice onto aerobic solid media and confirmed by Sanger sequencing  
172 of individual colonies' 16S rRNA genes.

173

#### 174 *Quantification of perchlorate- and chlorate-reducing microorganisms*

175 Primers to measure the model perchlorate-reducing bacterium *Azospira suillum* PS and model  
176 chlorate-reducing bacterium *Pseudomonas stutzeri* PDA were designed to bind variable regions  
177 of their respective small ribosomal subunit gene (16S rRNA) sequence and amplify ~150 bp  
178 sequence. Primers to measure all chlorate-reducing bacteria were designed to bind the chlorate  
179 reductase gene (*clrA*). The *clrA* gene consists of two phylogenetic groups (here termed groups 1



180 and 2) with highest similarity to the alpha subunits of selenate reductase or dimethylsulfide  
181 dehydrogenase, respectively (Clark et al 2013). Specific primer selection involved identifying  
182 highly conserved sequence positions within each *ctrA* group but not across closely related genes.  
183 Related genes were identified by searching the NCBI NR database with BLASTP (Camacho et al  
184 2009). Primer-BLAST used Primer Pair Specificity to check against select genomes in the NCBI  
185 non-redundant database (Supplementary Table 2). Template DNA was quantified using qPCR  
186 with three technical replicates; a standard curve of known concentration; and SYBR qPCR  
187 Master Mix (Thermo Fisher Scientific) on a StepOnePlus qPCR machine (Applied Biosciences).  
188 Measurements were performed on four biological replicates sampled at the time of inoculation  
189 and at the last timepoint preceding stationary phase. Quantification of total extracted DNA used  
190 the Quant-iT dsDNA Assay Kit (Thermo Fisher Scientific).

191

192 The relative abundance of isolated chlorate-reducing strains in the enriched communities was  
193 determined from previous 16S rRNA gene amplicon data under Sequence Reads Archive  
194 accession SRP049563 (Carlström et al 2016). We obtained amplicon sequence variants (ASVs) to  
195 differentiate between closely related taxa by using DADA2 v.1.10 with default settings and  
196 without pooling (Callahan et al 2016, Callahan et al 2017). 16S rRNA gene sequences from  
197 representative DPRM and DCRM were compared to ASVs using BLASTN (Camacho et al  
198 2009). Each ASV was assigned the taxonomy of the sequence with the highest percent identity  
199 above a threshold of 95% (approximately genus-level similarity). Relative abundance was  
200 calculated from the number of reads composing each ASV and the total reads per sample.

201

## 202 *Genetics*

203 Genetic deletions and insertions in *Pseudomonas stutzeri* PDA were performed using protocols,  
204 strains, and plasmids from previous work (Clark et al 2016). All primers, plasmids, and strains  
205 are included in Supplementary Tables 1 and 3. Vectors were introduced into *Pseudomonas*

206 *stutzeri* PDA via conjugation with *Escherichia coli* WM3064. These vectors had regions of  
207 homology allowing allelic exchange for a clean deletion, which were obtained by selection on  
208 kanamycin and counter-selection on sucrose.

209

## 210 *Modeling*

211 Modeling of perchlorate and chlorate reduction used the Equilibrium Chemistry Approximation  
212 (Tang and Riley 2013), a modification of Michaelis-Menton kinetics that can account for  
213 competition between organisms for substrates and competition between substrates for an  
214 enzyme's active site. The reaction rate for perchlorate reduction to chlorate by perchlorate-  
215 reducing bacteria is provided by Equation 1:

216

217

$$V_{PRB}^{ClO_4} = V_{max}^{ClO_4} \cdot [B_{PRB}] \cdot \frac{[ClO_4]}{K_M^{ClO_4} \cdot \left( 1 + \frac{[ClO_4]}{K_{PRB,O}^{ClO_4}} + \frac{[ClO_3]}{K_{PRB,M}^{ClO_3}} + \frac{[B_{PRB}]}{K_{PRB,M}^{ClO_4}} \right)} \cdot \frac{[DOC]}{K_{PRB,M}^{DOC} \cdot \left( 1 + \frac{[DOC]}{K_{PRB,M}^{DOC}} + \frac{[B_{PRB}]}{K_{PRB,M}^{DOC}} + \frac{[B_{CRB}]}{K_{CRB,M}^{DOC}} \right)} \quad (1)$$

218

219 Where V (concentration time<sup>-1</sup>) is reaction rate and V<sub>max</sub> (time<sup>-1</sup>) is the maximum growth rate; B,  
220 [ClO<sub>4</sub>], [ClO<sub>3</sub>], and [DOC] (concentration) are, respectively, the density of cells and the  
221 concentration of perchlorate, chlorate, and dissolved organic carbon (acetate). K<sub>m</sub> (concentration)  
222 is the half-saturation concentration for each substrate. Together, these terms define how  
223 maximum reaction rate is limited by the concentration of perchlorate and acetate, as well as the  
224 competition of Pcr for chlorate and perchlorate.

225

226 The reaction rate for chlorate reduction was described similarly for perchlorate-reducing bacteria  
227 (Equation 2) and chlorate-reducing bacteria (Equation 3). To simplify modeling, we present  
228 chlorate reduction as one step instead of three steps (involving the intermediates chlorite and

229 oxygen). We included the assumption that chlorate-reducing bacteria are unaffected by  
 230 perchlorate.

231

232

$$V_{PRB}^{ClO_3} = V_{PRB,max}^{ClO_3} \cdot [B_{PRB}] \cdot \frac{[ClO_3]}{K_{PRB,M}^{ClO_3} \cdot \left( 1 + \frac{[ClO_4]}{K_{PRB,M}^{ClO_4}} + \frac{[ClO_3]}{K_{PRB,M}^{ClO_3}} + \frac{[B_{PRB}]}{K_{PRB,M}^{ClO_3}} + \frac{[B_{CRB}]}{K_{CRB,M}^{ClO_3}} \right)} \cdot \frac{[DOC]}{K_{PRB,M}^{DOC} \cdot \left( 1 + \frac{[DOC]}{K_{PRB,M}^{DOC}} + \frac{[B_{PRB}]}{K_{PRB,M}^{DOC}} + \frac{[B_{CRB}]}{K_{CRB,M}^{DOC}} \right)} \quad (2)$$

233

$$V_{CRB}^{ClO_3} = V_{CRB,max}^{ClO_3} \cdot [B_{CRB}] \cdot \frac{[ClO_3]}{K_{CRB,M}^{ClO_3} \cdot \left( 1 + \frac{[ClO_3]}{K_{CRB,M}^{ClO_3}} + \frac{[B_{PRB}]}{K_{PRB,M}^{ClO_3}} + \frac{[B_{CRB}]}{K_{CRB,M}^{ClO_3}} \right)} \cdot \frac{[DOC]}{K_{CRB,M}^{DOC} \cdot \left( 1 + \frac{[DOC]}{K_{CRB,M}^{DOC}} + \frac{[B_{PRB}]}{K_{PRB,M}^{DOC}} + \frac{[B_{CRB}]}{K_{CRB,M}^{DOC}} \right)} \quad (3)$$

234

235 The biomass yield and stoichiometry were calculated using the framework provided by Rittmann  
 236 and McCarty (Rittmann and McCarty 2001). Calculations required redox potentials and balanced  
 237 half-reactions for the reduction of perchlorate to chlorate, the reduction of chlorate to chloride  
 238 (via an oxygen intermediate), and the oxidation of acetate to carbon dioxide. Detailed methods  
 239 and Python code are available at [https://github.com/tylerbarnum/perchlorate-and-chlorate-](https://github.com/tylerbarnum/perchlorate-and-chlorate-reduction-2019)  
 240 [reduction-2019](https://github.com/tylerbarnum/perchlorate-and-chlorate-reduction-2019). Unless otherwise noted, simulations of the model involved a theoretical case with  
 241 all values equal for perchlorate-reducing bacteria and chlorate-reducing bacteria except for the  
 242 ability to use perchlorate as a substrate (Table 1).

243

244

## 245 Results

246

### 247 *Infiltration of perchlorate-reducing cultures by chlorate-reducing bacteria*

248 Genomic sequencing of perchlorate-reducing cultures revealed large populations of chlorate-  
249 reducing bacteria, hinting to a metabolic interaction between perchlorate and chlorate reduction.  
250 The cultures had been obtained previously by selecting colonies from perchlorate-reducing  
251 enrichments and confirming their isolation with Sanger sequencing of the 16S ribosomal RNA  
252 gene (Carlström et al 2016). Despite appearing axenic, the nine cultures produced a total of 16  
253 genomes after assembly and binning: four draft genomes from axenic cultures, and 11 high-  
254 quality draft metagenome-assembled genomes (MAGs) and one medium-quality draft MAG from  
255 mixed cultures (Figure 1B) (Supplementary Table 4). Every less-abundant MAG was either at  
256 low relative abundance (0.9-9.5%) or in the same taxonomic family as the most-abundant MAG,  
257 which likely caused the failure to detect contaminating strains through 16S rRNA gene  
258 sequencing. Annotation of MAGs and assembly graphs identified genes for perchlorate reduction  
259 (*pcr*, *cld*, and a terminal oxidase) in only nine genomes. Unexpectedly, while perchlorate and  
260 acetate, a non-fermentable carbon source, were the only energy substrates available in the growth  
261 medium, MAGs lacking *pcr* were the most abundant organisms in several cultures (Figure 1B).  
262 Instead, these three MAGs contained a complete chlorate reduction pathway (*clr*, *cld*, and a  
263 terminal oxidase) (Supplemental Figure 1).

264

265 The putative chlorate-reducing bacteria accounted for 69-90% of cells in the perchlorate-reducing  
266 cultures (Figure 1B), which is similar to what we previously observed in a perchlorate-enriched  
267 community (Barnum et al 2018). The dominance of putative chlorate-reducing bacteria could be  
268 visually confirmed by comparing the number of colonies that develop on anaerobic tubes  
269 containing chlorate or perchlorate as the sole terminal electron acceptor (Figure 1C). Subsequent  
270 isolation and characterization of *Marinobacter vinifirmus* UCB, *Azoarcus marinus* PHD, and

271 *Pseudomonas stutzeri* CAL confirmed the strains to be strictly chlorate-respiring microorganisms,  
272 as no perchlorate was consumed after two weeks of incubation (data not shown) or co-  
273 metabolized during dissimilatory chlorate reduction by any strain (Figure 1D). Because these  
274 strains cannot consume perchlorate themselves, the most parsimonious explanation of the  
275 observed community structure is that a perchlorate-reducing population supported a larger  
276 chlorate-reducing population.

277

278 *Perchlorate reduction supports chlorate-reducing bacteria in simple and complex communities*

279 The interaction between perchlorate- and chlorate-reducing bacteria was validated using defined  
280 co-cultures. Perchlorate- and chlorate-reducing strains were inoculated at equal cell densities  
281 (OD600) into anaerobic media with perchlorate as the sole electron acceptor, and the relative  
282 number of chlorate-reducing cells between inoculation and the start of stationary phase was  
283 measured using the copy number of chlorate reductase alpha subunit (*clrA*) determined by qPCR.  
284 Chlorate-reducing strains grew in every co-culture with perchlorate-reducing bacteria (Figure  
285 2A). No growth was observed in control media that lacked an electron acceptor (Supplementary  
286 Figure 2). The fitness of the chlorate-reducing bacteria was dependent on the partner perchlorate-  
287 reducing bacterium, with *Denitromonas halophilus* SFB-1 supporting the most growth of  
288 chlorate-reducing bacteria and *Dechloromonas agitata* CKB supporting the least growth (Figure  
289 2A). Thus, all tested perchlorate-reducing strains supported some growth of chlorate-reducing  
290 bacteria.

291

292 To determine if this interaction occurs in more complex communities, we quantified the  
293 abundance of isolated strains in the original perchlorate-reducing enrichments using previously  
294 published 16S rRNA gene amplicon data (Carlström et al 2016). Indeed, amplicon sequence  
295 variants (ASVs) corresponding to isolated chlorate-reducing strains in the genera *Azoarcus* and  
296 *Pseudomonas*, which are not known to contain perchlorate-reducing species, were highly

297 abundant (>20%) in six of ten communities at low salinity (Figure 2B). In those communities, the  
298 ASVs affiliated with chlorate reduction accounted for 23-46% of total bacteria and archaea in the  
299 community and 40-84% of putative chlorate- and perchlorate-reducing taxa. Chlorate-reducing  
300 bacteria and perchlorate-reducing bacteria were found in various combinations in communities.  
301 That many different perchlorate-reducing bacteria can support the growth of chlorate-reducing  
302 bacteria, in both co-cultures and communities, demonstrated the interaction is based not on strain-  
303 specific traits but on conserved features of the metabolic pathways involved.

304

305 *Chlorate-reducing bacteria require the perchlorate reduction intermediate chlorate*

306 Chlorate-reducing bacteria are able to use all components of the perchlorate reduction pathway  
307 except perchlorate (Figure 1A), so we sought to determine which intermediates were responsible  
308 for the metabolic interaction. We deleted different steps of the chlorate reduction pathway in the  
309 model chlorate-reducing bacterium *Pseudomonas stutzeri* PDA (PDA). Measuring the fitness of  
310 each of these mutants in co-culture with the model perchlorate-reducing bacterium *Azospira*  
311 *suillum* PS (PS) would demonstrate which steps of the chlorate reduction pathway were essential  
312 for growth from perchlorate reduction intermediates. Genes encoding enzymes for reactions  
313 upstream of an exchanged intermediate are non-essential for growth, whereas genes encoding  
314 enzymes for reactions downstream of the exchanged intermediate are essential. For example, if  
315 chlorite were the exchanged intermediate, PS growing by perchlorate reduction would support  
316 growth of PDA strains lacking *clrA* but not PDA strains lacking *clt* (Figure 3A).

317

318 In the co-cultures inoculated with equal cell densities of PS and PDA, growth of wild type PDA  
319 was characterized by a final relative abundance of 27% (final ratio PDA/PS = 0.37) (Figure 3B).  
320 In contrast, deletion of any steps of the chlorate reduction pathway prevented growth of PDA: the  
321 final abundance of PDA deletion strains (PDA<sub>del</sub>/PS < 0.048) was equivalent to that expected with  
322 no growth of PDA (PDA/PS < 0.060) (Figure 3A). While all chlorate reduction genes were

323 necessary, the particular necessity of chlorate reductase (*clrA*) demonstrated that chlorate is the  
324 only intermediate exchanged in enough quantity to support measurable growth. That is, chlorite  
325 dismutase and terminal oxidases are present in the PDA *clrA* deletion strain, yet any release of  
326 chlorite or oxygen by PS during perchlorate reduction was not sufficient to support growth of  
327 PDA. Thus, the basis of the metabolic interaction is the transfer of chlorate from perchlorate-  
328 reducing cells to chlorate-reducing cells.

329

330 Other observations supported chlorate as the exchanged intermediate. Perchlorate-reducing  
331 bacteria accumulated chlorate at concentrations between 1% and 22% mol/mol of initial  
332 perchlorate (~10 mM) (Figure 3C), as reported previously (Thrash et al 2010a, Thrash et al  
333 2010b). Additionally, chlorate accumulated in pure cultures of PS (<0.3 mM) but was consumed  
334 in co-cultures of PS and wild type PDA (Figure 3D). However, there was no clear relationship  
335 between the maximum concentration of chlorate that accumulated in pure cultures of perchlorate-  
336 reducing bacteria (Figure 3C) and the fitness of chlorate-reducing bacteria in co-culture (Figure  
337 2A). Notably, kinetics differed between PS cultures with and without wild type PDA (Figure 3D,  
338 Supplemental Figure 3). When PDA was present, the maximum growth rate and maximum  
339 perchlorate reduction rate by PS decreased and the onset of growth and perchlorate reduction was  
340 earlier when compared to the pure PS culture (Figure 3D). Similar changes in growth kinetics  
341 were observed in other co-cultures (Supplemental Figure 2). The kinetics of chlorate production  
342 and consumption thus seemed to be an important factor in the interaction.

343

344 *Specificity for chlorate enables chlorate-reducing cells to exploit perchlorate-reducing cells*

345 An understanding of the kinetics of the interaction was necessary to understand how chlorate  
346 release could produce the observed community structure. For example, how can accumulation of  
347 chlorate to only 3% of initial perchlorate concentration support chlorate-reducing bacteria at 27%  
348 of the community (Figure 3)? More generally, how can a population with the partial pathway

349 outcompete a population with the complete pathway up to a factor of nearly ten (Figures 1-2)? To  
350 answer these questions, we used simulations of an Equilibrium Chemistry Approximation kinetics  
351 model, which included the effects of substrate competition within and between cells. We focused  
352 on the theoretical case where (1) the kinetics of chlorite and oxygen are ignored and (2) chlorate-  
353 and perchlorate-reducing populations were identical (maximum growth rate, yield, etc.) except  
354 for substrate utilization (Table 1, Equations 1-3): populations could use both perchlorate and  
355 chlorate or only chlorate. Therefore, the model's salient features were the yields and rates from  
356 the production and consumption of chlorate, as well as the competition of perchlorate and  
357 chlorate for Pcr. In simulations with the perchlorate-reducing population alone, these parameters  
358 led to the accumulation of chlorate during perchlorate reduction (Figure 4A). Importantly, growth  
359 rate was lower while the  $\text{ClO}_3^-:\text{ClO}_4^-$  ratio was low (Figure 4B). Chlorate influenced growth rate  
360 so strongly because chlorate reduction to chloride provided more energy (622.9 kJ/mol chlorate)  
361 than perchlorate reduction to chlorate (211.7 kJ/mol perchlorate). At low  $\text{ClO}_3^-:\text{ClO}_4^-$  ratios, the  
362 perchlorate-reducing population was less likely to reduce chlorate and more likely to reduce  
363 perchlorate (Figure 4C).

364

365 Accordingly, we hypothesized that a population that could only reduce chlorate would have a  
366 higher growth rate at low  $\text{ClO}_3^-:\text{ClO}_4^-$  ratios than the perchlorate-reducing population. We tested  
367 this by adding the chlorate-reducing population to the simulation at equal initial concentration.  
368 The chlorate-reducing population outcompeted the perchlorate-reducing population and decreased  
369 the concentration of chlorate (Figure 4D), consistent with experimental observations. In support  
370 of our hypothesis, at low  $\text{ClO}_3^-:\text{ClO}_4^-$  ratios the chlorate-reducing population consumed almost all  
371 of the chlorate and had a higher growth rate (about 2-fold) than the perchlorate-reducing  
372 population (Figure 4E). With chlorate-reducing cells present, the consumption of chlorate delayed  
373 the increase of the  $\text{ClO}_3^-:\text{ClO}_4^-$  ratio (Figures 4B and 4E). Thus, in this simple theoretical case,  
374 chlorate-reducing cells had a growth advantage because they, unlike perchlorate-reducing cells,



375 could consume chlorate at high perchlorate concentrations (Figure 4F). Additionally, the  
376 consumption of chlorate by chlorate-reducing bacteria created a positive feedback by maintaining  
377 a low  $\text{ClO}_3^-:\text{ClO}_4^-$  ratio (Figures 4C and 4F).

378

379 We used additional simulations to observe how initial conditions affect the interaction. Varying  
380 the initial ratio of chlorate-reducing cells to perchlorate-reducing cells did not alter the ecological  
381 success or the fraction of chlorate acquired by the chlorate-reducing population (Supplemental  
382 Figure 4A-B); Chlorate-reducing cells ultimately dominated by acquiring a large percent of  
383 chlorate unless initially outnumbered 100-fold (Supplemental Figure 4C). Varying perchlorate  
384 concentration, however, did alter the success of chlorate-reducing cells (Supplemental Figure 4D-  
385 F). Even when chlorate-reducing cells outnumbered perchlorate-reducing cells, the perchlorate-  
386 reducers consumed nearly all available chlorate except at perchlorate concentrations above  $\sim 1$   
387 mM (Supplemental Figure 4E). Also, varying the affinity of different populations for perchlorate  
388 or chlorate altered the ecological success of chlorate-reducing cells (Supplemental Figure 5).  
389 While not necessarily predictive of behavior in the environment or over different temporal and  
390 spatial scales, these simulations provide an intuitive description of the interaction: chlorate-  
391 reducing cells exploit a niche made available by differences in enzyme kinetics and substrates.

392

## 393 Discussion

394 This study confirms and further interrogates the interaction between perchlorate reduction and  
395 chlorate reduction. Here we clearly demonstrate that bacteria with the perchlorate reduction  
396 pathway supported – and could be outcompeted by – bacteria with the chlorate reduction  
397 pathway. The interaction between perchlorate and chlorate reduction occurred in both controlled  
398 (i.e. co-cultures) and uncontrolled systems (i.e. enrichment and isolation) and in both freshwater  
399 and marine conditions. The basis of the interaction was the exchange of chlorate from

400 perchlorate-reducing cells to chlorate-reducing cells. Chlorate was available for consumption  
401 likely due to competition of perchlorate and chlorate for a single enzyme in the periplasm of  
402 perchlorate-reducing cells (Dudley et al 2008). Simulations showed that the chlorate-reducing  
403 cells are successful because chlorate can be reduced even at a low  $\text{ClO}_3^-:\text{ClO}_4^-$  ratio, a state that  
404 chlorate consumption perpetuates. In summary, chlorate-reducing bacteria were a common  
405 feature of perchlorate reduction and had a large effect on the structure and function of  
406 perchlorate-reducing communities.

407

408 The basis of the interaction alters our understanding of the chlorine cycle. Perchlorate reduction  
409 involves the combined activity of perchlorate-reducing microorganisms, chlorate-reducing  
410 microorganisms, and any chemical reduction of their intermediates (Figure 5). A role for chlorite-  
411 consuming or oxygen-consuming partial pathways in perchlorate reduction was not observed here  
412 (Figure 3), and an interaction based on the exchange of chlorite has been engineered (Clark et al  
413 2016) but not yet observed in nature. This is likely due to the high activity ( $k_{\text{cat}}/K_M$ ) of chlorite  
414 dismutase ( $10^6\text{-}10^8 \text{ M}^{-1} \text{ s}^{-1}$ ) relative to perchlorate reductase ( $\sim 10^5 \text{ M}^{-1} \text{ s}^{-1}$ ) (Dubois 2014,  
415 Youngblut et al 2016a). Because chlorate is less reactive than chlorite, cells that inadvertently  
416 reduce chlorate to chlorite would experience greater reactive chlorine stress; chlorite dismutase  
417 (Cld) can detoxify chlorite produced in this manner (Celis et al 2015). Additionally, the exchange  
418 of chlorate is less constrained by the reducing state of the environment than the exchange of  
419 chlorite. But chlorate does react with common environmental reductants such as reduced iron  
420 minerals (Brundrett et al 2019, Engelbrekton et al 2014), and the reactivity of chlorate with iron  
421 increases with salinity (Brundrett et al 2019), which may contribute to the lower frequency of  
422 chlorate-reducing bacteria in higher-salinity perchlorate-reducing enrichments (Figure 2B). The  
423 concentrations of reductants, chlorate, and perchlorate may all influence the relative contribution  
424 of perchlorate-reducing microorganisms and chlorate-reducing microorganisms to chlorine  
425 oxyanion respiration.

426

427 Interactions like that described here, where low accumulation of an intermediate supports large  
428 populations with a partial respiratory pathway, may be common across elemental cycles. Some  
429 evidence exists for the importance of these interactions in denitrification, for example.  
430 *Pseudomonas* strain G9, which contains a complete denitrification pathway producing inhibitory  
431 concentrations of nitrite, could grow only in co-culture with *Alcaligenes faecalis* strain TUD,  
432 which only reduces nitrite to dinitrogen, and the two strains were found at steady state at  
433 approximately equal cell densities (Van de Pas-Schoonen et al 2005). Nitrite accumulation caused  
434 by inter-enzyme competition in *Pseudomonas stutzeri* strain A1501 was decreased by dividing  
435 nitrite production and consumption between different strains (Lilja and Johnson 2016). In  
436 denitrifying communities, then, it may be beneficial for some organisms to *lack* steps in the  
437 denitrification pathway. This was the case for a pooled transposon mutant library of *Azospira*  
438 *suillum* PS, where mutants with insertions in nitrite reductase, which is deleterious in pure  
439 culture, outcompeted cells with intact denitrification pathways (Melnyk et al 2015). Much  
440 remains to be learned about community structure impacts resulting from pathway distribution  
441 across different populations.

442

443 The importance of studying metabolic interactions in biogeochemical transformations is to learn  
444 how such interactions influence concentrations and rates. Previous studies that added chlorate-  
445 reducing bacteria to cultures of the perchlorate-reducing bacterium HCAP-C, which accumulates  
446 far more chlorate than the typically observed (Cameron Thrash et al 2010, Thrash et al 2010b,  
447 Youngblut et al 2016a), had conflicting results where chlorate-reducing bacteria either slightly  
448 accelerated (Salamone and Nerenberg 2006) or substantially decelerated the rate of perchlorate  
449 reduction (Dudley and Nerenberg 2007). We observed that adding chlorate-reducing bacteria to  
450 cultures of the model perchlorate-reducing bacterium *Azospira suillum* PS decreased the  
451 concentration of chlorate, maximum growth rate, and maximum perchlorate reduction rate

452 (Figure 3D). Similar effects on growth rate were observed with perchlorate-reducing bacteria that  
453 accumulated varying concentrations of chlorate (Supplemental Figure 2, Figure 3C), and we  
454 directly demonstrated success of chlorate-reducing populations at the expense of perchlorate-  
455 reducing populations (Figure 2). Because chlorate reduction appears to substantially influence  
456 concentrations and rates during perchlorate reduction, chlorate-reducing bacteria could affect  
457 efforts to bioremediate perchlorate. For example, a description of perchlorate-reducing  
458 bioreactors with gene-centric metagenomics identified *Azoarcus* and *Pseudomonas* as among the  
459 most abundant genera, yet the *Azoarcus* isolate did not reduce perchlorate (Stepanov et al 2014).  
460 Our results predict that those organisms are chlorate-reducing bacteria that persisted in the  
461 bioreactors for over 10 years (Stepanov et al 2014). Understanding how this metabolic interaction  
462 affects perchlorate reduction kinetics in different systems, and how it could be controlled, may be  
463 a promising line of future research.

464

465 A close interaction between metabolisms also has evolutionary implications, as co-occurrence can  
466 influence gene evolution and exchange. For example, in nitrifying microorganisms, niche  
467 differentiation led to high affinity and low affinity ammonia-oxidizing enzymes that function best  
468 at different pH (Martens-Habbena et al 2009) and to the exchange of ammonia monooxygenase to  
469 nitrite-oxidizing bacteria (Daims et al 2015). Not enough chlorate reductases and perchlorate  
470 reductases have been evaluated to draw general conclusions from their substrate affinities and  
471 catalytic rates. However, several chlorate-reducing bacteria contain genes or gene fragments of  
472 perchlorate reductase components (*napC* and *pcrD*) adjacent to the chlorite dismutase (*clt*), and  
473 these genes were most likely acquired from perchlorate-reducing bacteria (Clark et al 2013).  
474 Because environmental reduction of perchlorate or chlorate will likely involve both perchlorate-  
475 reducing microorganisms and chlorate-reducing microorganisms, a history of gene exchange  
476 between the two metabolisms is unsurprising.

477

## 478 Conclusions

479 Perchlorate reduction supports chlorate reduction through the release of the intermediate chlorate.  
480 The fundamental cause of the interaction is that the perchlorate reductase enzyme catalyzes both  
481 perchlorate reduction to chlorate and chlorate reduction to chlorite – therefore chlorate competes  
482 with perchlorate for perchlorate reductase, limiting subsequent steps of the perchlorate reduction  
483 pathway. Chlorate reduction, despite being a partial pathway, is ecologically successful because it  
484 can consume chlorate unabated and, in doing so, exacerbates the imbalance between perchlorate  
485 and chlorate. As for several other respiratory metabolisms, the respiration of chlorine oxyanions  
486 in the environment should be expected to involve cells performing complete and partial  
487 respiratory pathways. These findings have clear implications for understanding the evolution and  
488 the kinetics of chlorine oxyanion reduction.

489

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495

## 496 Contributions

497 JDC guided the research. LNL and TPB isolated strains. LNL extracted DNA for sequencing.  
498 TPB assembled and analyzed genomes, designed primers, and performed amplicon sequence  
499 variant analysis. TPB and KAH performed all experiments and measurements. YC developed the  
500 model. YC and TPB performed and interpreted modeling simulations. TPB wrote the manuscript  
501 and created the figures with guidance from JDC. All authors contributed to data analysis,  
502 reviewed the manuscript, and approved of its publication.

503

504 Conflict of interest statement

505 The authors declare no conflict of interest.

506

507

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## 757 Table and Figure Legends

758 **Table 1.** Parameters for growth kinetics model. Populations were identical except for enzyme  
759 affinity for perchlorate, which for population 2 was set to be negligible (\*).

760

761 **Figure 1.** Isolation of chlorate-reducing bacteria from perchlorate-reducing cultures. (A)  
762 Pathways for the respiration of perchlorate (red) and chlorate (orange) involve the enzymes  
763 perchlorate reductase (Pcr) or chlorate reductase (Clr), chlorite dismutase (Cld), and a terminal  
764 oxidase reducing oxygen to water (TO). (B) Binning and key genes of genomes from perchlorate-  
765 reducing cultures. A previously sequenced perchlorate-reducing enrichment is included for  
766 comparison (“1% NaCl Enrichment”). Filled squares indicate gene presence. Relative abundance  
767 (%) was calculated as normalized coverage divided by total coverage for all genomes. Compl.  
768 (%) refers to percent completeness (single copy genes); dashed lines indicate medium quality (M)  
769 and high quality (H) completeness. All genomes had negligible contamination (<3%). (C)  
770 Magnified image of colonies that developed in agar media supplied perchlorate or chlorate from a  
771 co-culture of *Denitromonas halophilus* SFB-1 and *Pseudomonas stutzeri* CAL. The inoculum for  
772 perchlorate agar media was 10-times more concentrated. (D) Dissimilatory reduction of chlorate  
773 and not perchlorate by isolated chlorate-reducing bacteria.

774

775 **Figure 2.** Co-cultivation of perchlorate-reducing bacteria (red, PRB) and chlorate-reducing  
776 bacteria (orange, CRB) in defined and undefined communities (A) Fold change of *clrA* in defined  
777 co-cultures between lag phase and late exponential phase batch growth. For the co-culture  
778 consisting of *P. stutzeri* PDA and *A. suillum* PS, primers for 16S rRNA genes was used. Arrows  
779 indicate the upper and lower bounds of fold change estimated from the initial and final OD600 of  
780 the co-culture. Boxplots indicate quartiles in the sample. (B) Relative abundance of 16S rRNA  
781 gene amplicon sequence variants grouped by similarity to the 16S rRNA genes of perchlorate-

782 and chlorate-reducing taxa. \*, strains most closely related to perchlorate-reducing MAGs for  
783 which 16S rRNA genes were not available.

784

785 **Figure 3.** Determination of the perchlorate reduction intermediate that supports growth chlorate-  
786 reducing bacteria in defined co-cultures. (A) Genotype and phenotype (in pure culture) of  
787 chlorate reduction pathway mutants constructed in *Pseudomonas stutzeri* PDA (PDA). A chlorate  
788 reduction mutant would be unable to grow unless it can use the intermediate produced by  
789 perchlorate-reducing bacteria as a respiratory electron acceptor. (B) Fitness of chlorate reduction  
790 mutants in co-culture with *Azospira suillum* PS (PS) provided 10 mM perchlorate and 40 mM  
791 lactate, which PDA does not ferment. Relative abundance was calculated from qPCR  
792 measurements of both the PS and PDA 16S rRNA genes. \*, significance of  $p < 0.05$  (two-sided  
793 T-test); n.s.,  $p > 0.05$ . Boxplots indicate quartiles in the sample with outliers as circles. (C)  
794 Maximum concentration of chlorate during dissimilatory perchlorate reduction by different  
795 strains of perchlorate-reducing bacteria (PRB) supplied 10 mM perchlorate. (D) Concentrations  
796 of perchlorate and chlorate during dissimilatory perchlorate reduction by PS or PS and PDA.  
797 Errors bars represent standard deviation of at least three replicates.

798

799 **Figure 4.** Modeling of perchlorate reduction and chlorate reduction. Simulated growth curves for  
800 perchlorate-reducing bacteria (A-C) alone and (D-F) with chlorate-reducing bacteria.  $[\text{ClO}_3^-] /$   
801  $[\text{ClO}_4^-]$ , the ratio between chlorate concentration and perchlorate concentration; fraction  $\text{ClO}_3^-$  to  
802 CRB indicates the relative amount of chlorate consumed by the chlorate-reducing population at  
803 each time step; growth rate, the change in cell concentration between each time step.

804

805 **Figure 5.** Model for the production and degradation of chlorine oxyanions. The perchlorate  
806 reduction pathway (red) accumulates chlorate, which can react with reductants and generate  
807 reactive chlorine species (gray) or be consumed by the chlorate reduction pathway (orange). We

808 did not find evidence for the release of chlorite and oxygen by the perchlorate and chlorate  
809 reduction pathways, though both chemicals can react with any reductants in the periplasm.  
810 Perchlorate and chlorate reduction remove the products of atmospheric oxidation of chlorine  
811 (dashed yellow). Co-metabolic or inadvertent enzyme activities are not shown.

812  
813 **Supplemental Figure 1.** Visualization of assemblies and binning using Bandage to verify  
814 binning of key genes. Only mixed cultures with perchlorate-reducing bacteria and chlorate-  
815 reducing bacteria are shown: cultures (A) “UCB,” (B) “CAL,” and (C) “PHD.” The de Bruijn  
816 graph assembly is visualized by displaying contigs (lines), and connections between contigs that  
817 could not be resolved during assembly. Thickness of lines indicates sequencing depth. In each  
818 assembly, contigs with the same color were found in the same bin. Bins containing contigs with  
819 chlorate reduction genes (*clr*, *cld*) are colored orange, bins containing contigs with perchlorate  
820 reduction genes (*pcr*, *pcd*) are colored red, and bins without either set of genes are other colors.  
821 Arrows indicate the contig(s) with key genes. Mean sequencing depth for those contigs and each  
822 genome bin are indicated in parentheses.

823  
824 **Supplementary Figure 2.** Growth phenotypes of the different combinations of perchlorate- and  
825 chlorate-reducing bacteria. Individual replicates are shown due to interesting variation. Blue, co-  
826 cultures with 10 mM perchlorate; red, perchlorate-reducing bacteria with 10 mM perchlorate;  
827 solid orange, chlorate-reducing bacteria with 10 mM chlorate; and dashed orange, chlorate-  
828 reducing bacteria with no electron acceptor.

829  
830 **Supplemental Figure 3.** Growth curves of chlorate reduction pathway mutants in *Pseudomonas*  
831 *stutzeri* PDA (PDA) in co-culture with *Azospira suillum* PS (PS). Errors bars represent standard  
832 deviation of four replicates.

833

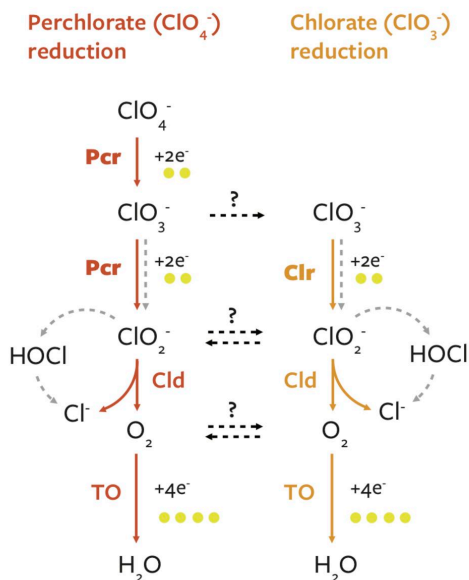
834 **Supplementary Figure 4.** Simulations of the kinetics-based model that varied the initial  
835 concentrations of perchlorate-reducing bacteria and chlorate-reducing bacteria (A, B, C) or  
836 perchlorate-reducing bacteria and perchlorate (D, E, F). For each simulation, the final ratio of the  
837 populations (A, C) and the total percent of chlorate consumed by the chlorate-reducing population  
838 (B, E) were determined after 1000 hours with 1-hour time steps. (C, F) depict the relationship  
839 between the two measurements. The default conditions used in the main text are highlighted in  
840 white:  $10^{-5}$  M ( $\sim 0.001$  g/L) cells and 10 mM perchlorate.

841

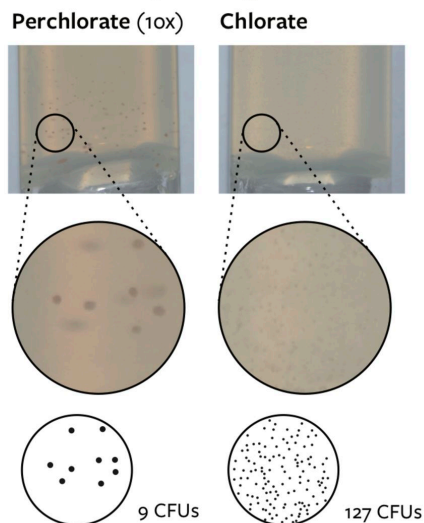
842 **Supplementary Figure 5.** Simulations of the kinetics-based model that measured the final ratio  
843 of chlorate-reducing bacteria to perchlorate-reducing bacteria after varying (A) the affinity of  
844 perchlorate-reducing bacteria for chlorate and perchlorate and (B) the affinity of chlorate-  
845 reducing bacteria and perchlorate-reducing bacteria for chlorate. The default conditions used in  
846 the main text are highlighted in white:  $6 \mu\text{M Km}$  for chlorate (for both populations) and  $6 \mu\text{M Km}$   
847 for perchlorate (for perchlorate-reducing bacteria only).



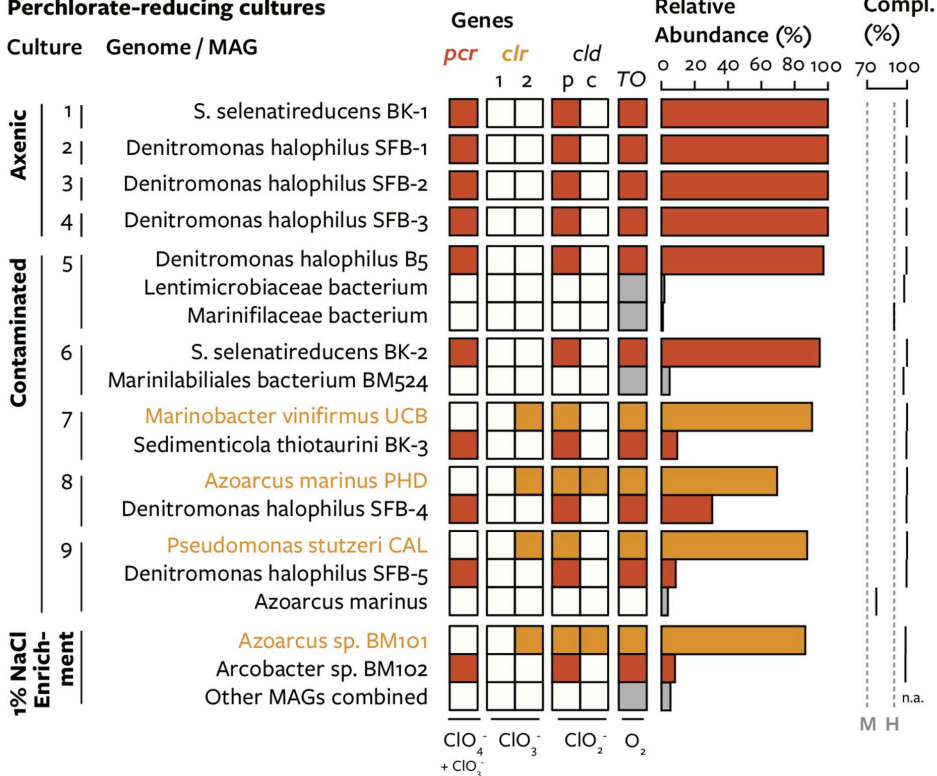
### A. $\text{ClO}_x^-$ reduction pathways



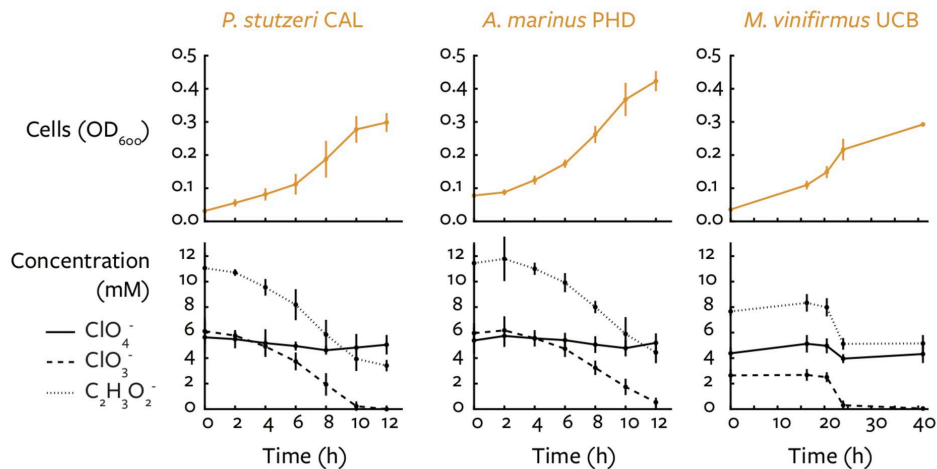
### C. Hidden colony-forming units



### B. Perchlorate-reducing cultures

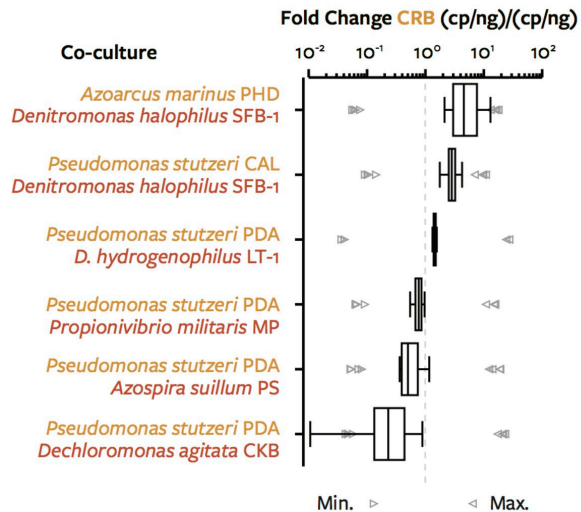


### D. Chlorate-reducing isolates

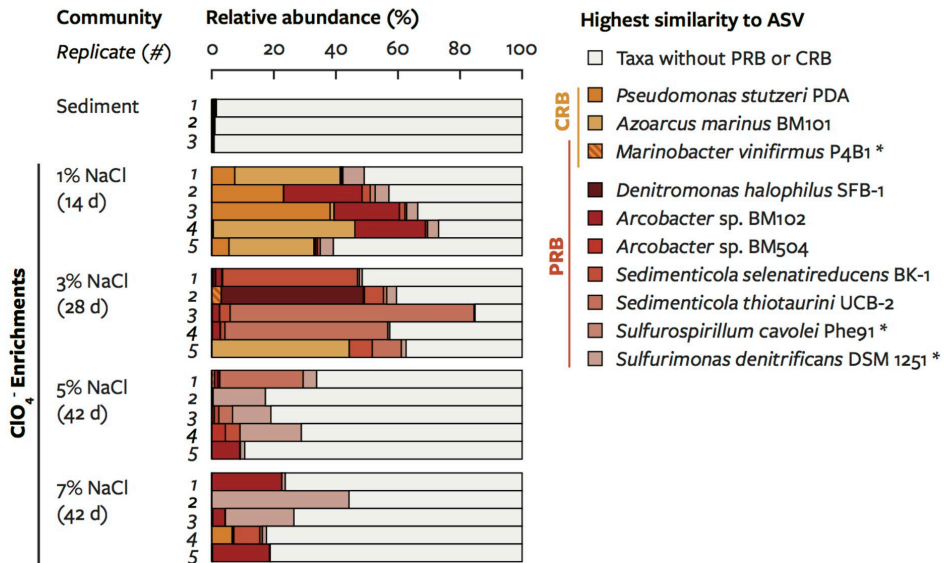




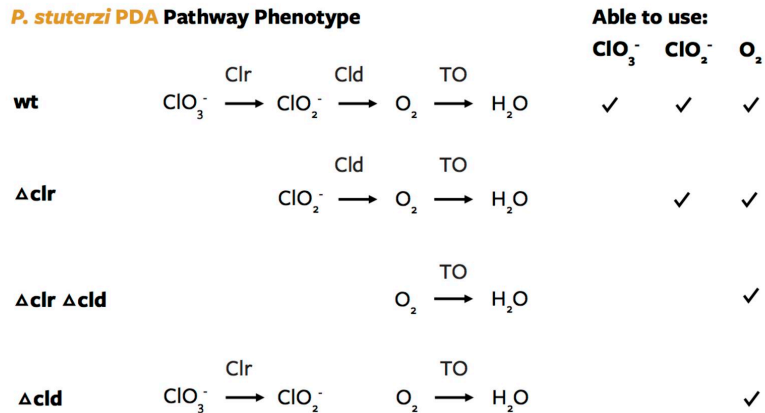
## A. Defined co-cultures



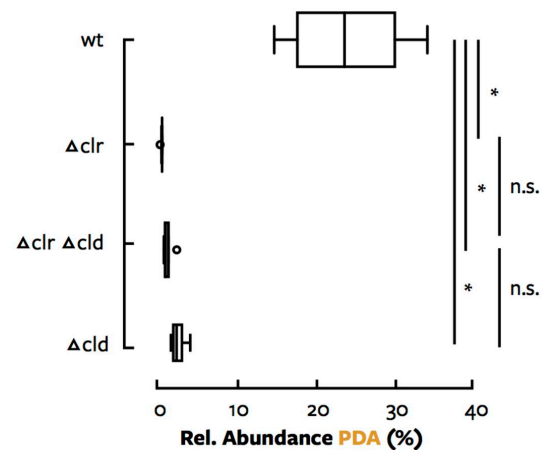
## B. Communities



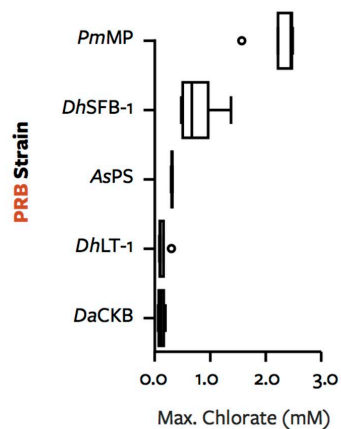
### A. *P. stutzeri* PDA Pathway Phenotype



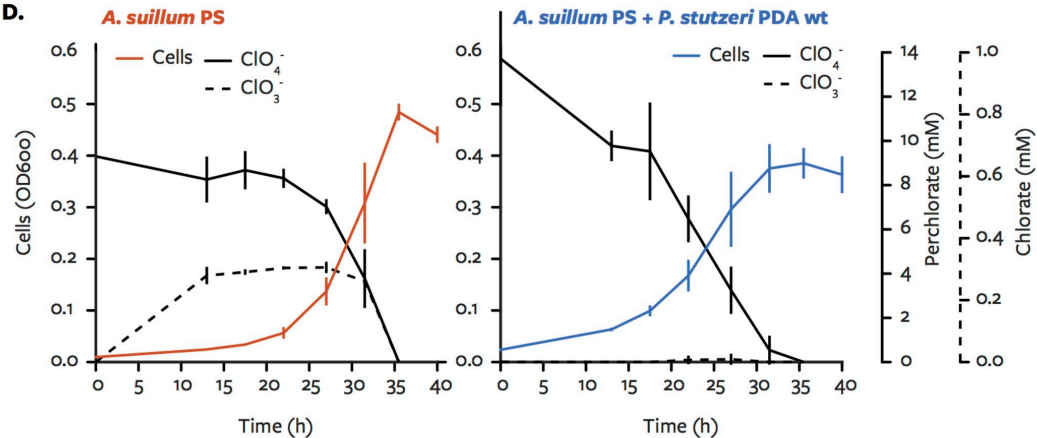
### B. Fitness in Co-culture with *A. suillum* PS

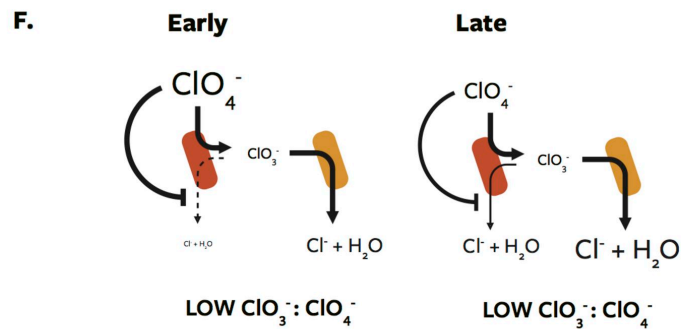
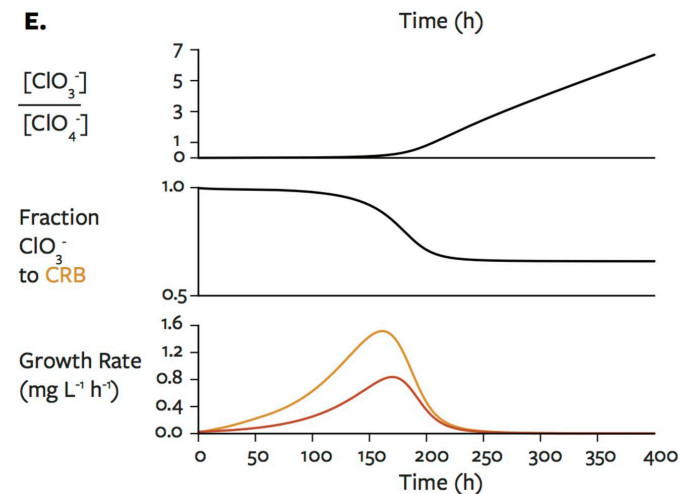
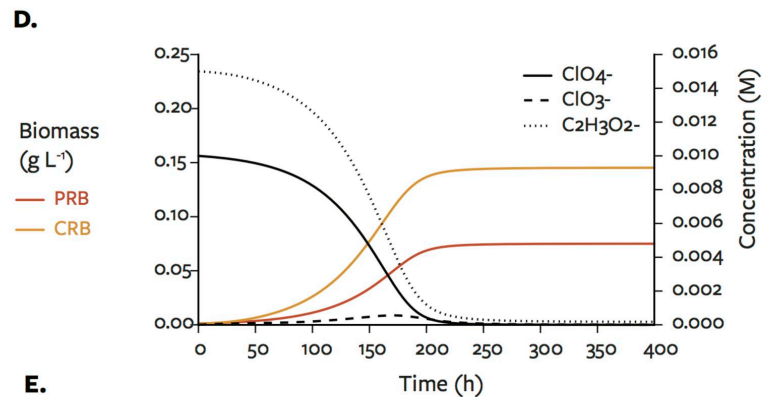
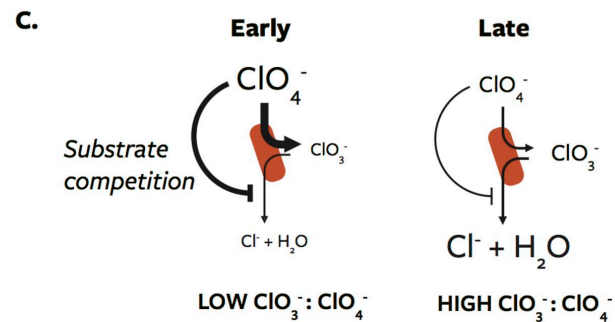
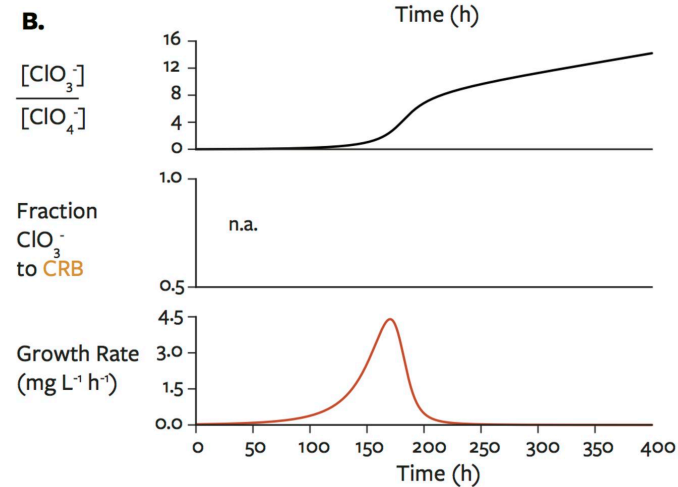
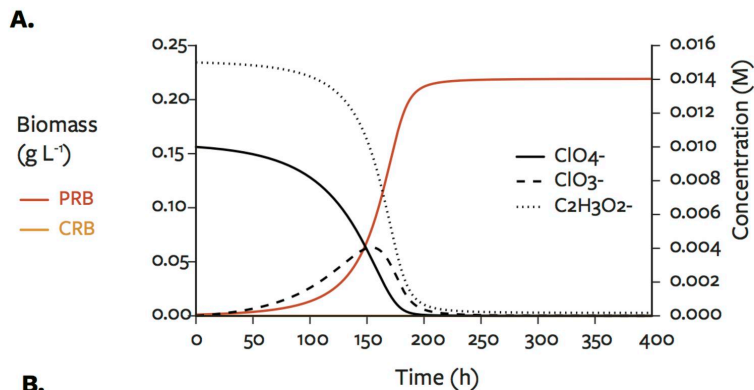


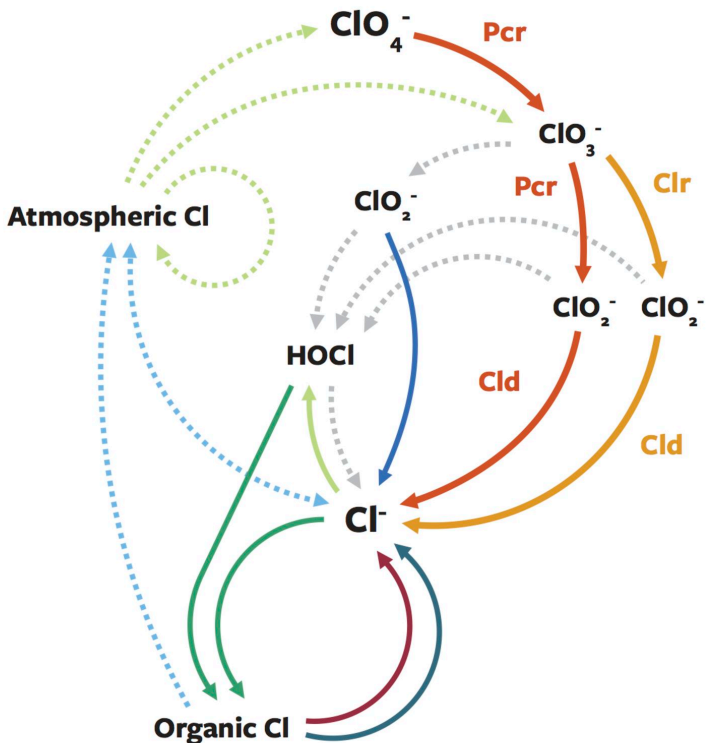
### C.



### D.







### ClO<sub>x</sub><sup>-</sup> degradation

- Perchlorate reduction
- Chlorate reduction
- Chlorite detoxification
- ... Abiotic reduction

### ClO<sub>x</sub><sup>-</sup> production

- ... Volatilization and deposition
- ... Atmospheric oxidation
- Enzymatic oxidation

### Organic Cl cycling

- Halogenation
- Organohalide respiration
- Dehalogenation

<b>Parameter</b>	<b>Population 1</b>	<b>Population 2</b>
Km ClO <sub>4</sub> <sup>-</sup> (mM)	0.006	10000 *
Km ClO <sub>3</sub> <sup>-</sup> (mM)	0.007	0.007
Km C <sub>2</sub> H <sub>3</sub> O <sub>2</sub> <sup>-</sup> (mM)	1	1
Max. growth rate (h <sup>-1</sup> )	0.5	0.5
Death rate (h <sup>-1</sup> )	0	0
Type	Perchlorate reducer	Chlorate reducer
* <i>Set to be negligible</i>		