

Reductive dechlorination of 1,2-dichloroethane in the presence of chloroethenes and 1,2-dichloropropane as co-contaminants

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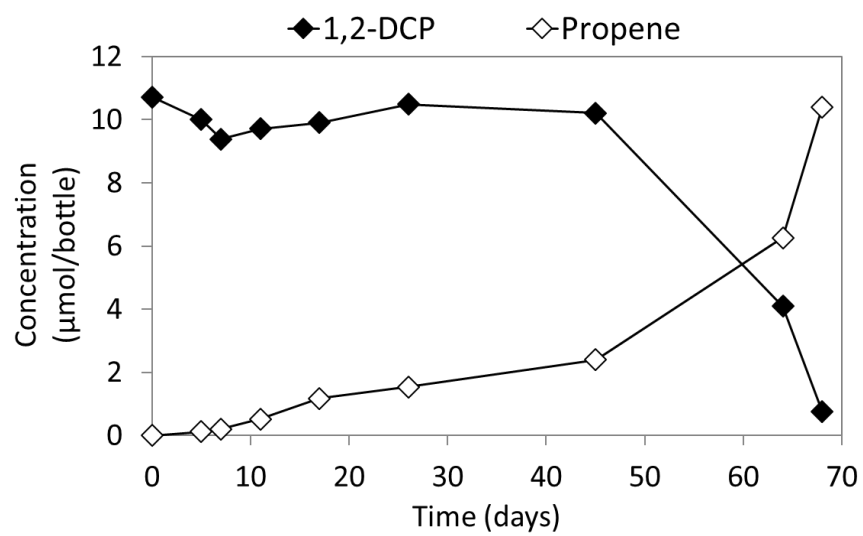


Fig. S1: Reductive dechlorination of 1,2-DCP in EA transfer culture.

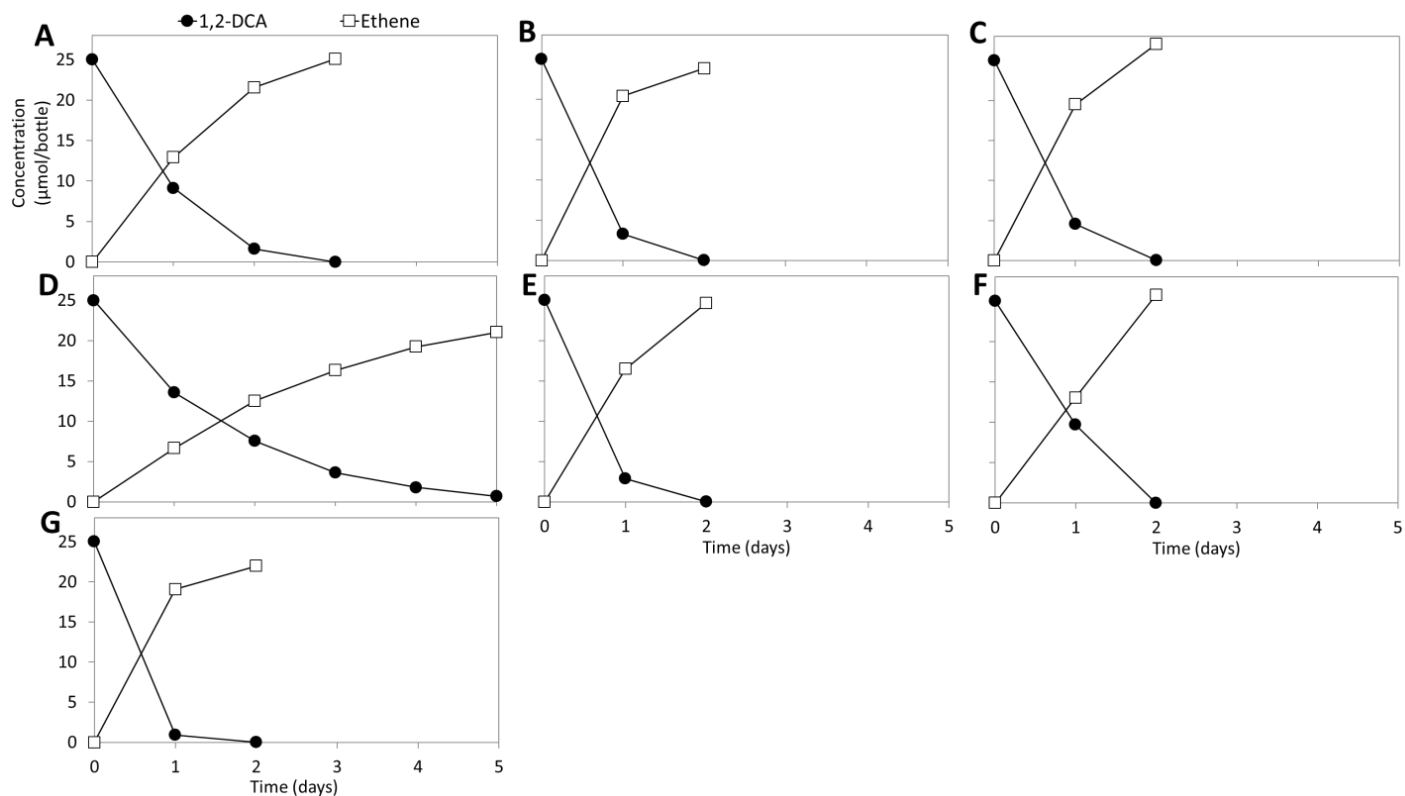


Fig. S2: Reductive dechlorination of 1,2-DCA alone in EA and EB transfer cultures previously amended with 1,2-DCA plus PCE (cultures EA-T2 and EB-T2) (A and D); 1,2-DCA plus cDCE (cultures EA-T3 and EB-T3) (B and E); 1,2-DCA plus VC (cultures EA-T4 and EB-T4) (C and F); 1,2-DCA plus 1,2-DCP (culture EA-T9) (G). Each concentration value represents the average measurement of duplicate cultures.

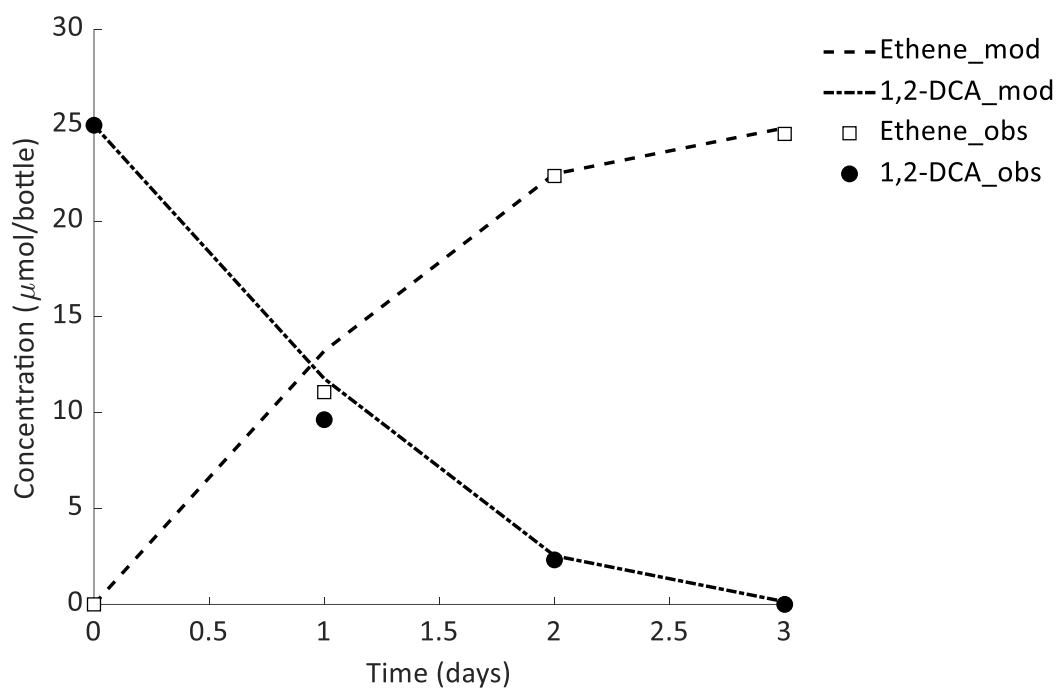


Fig. S3: Modeled (mod) and observed (obs) concentrations in culture EA-T1_A.

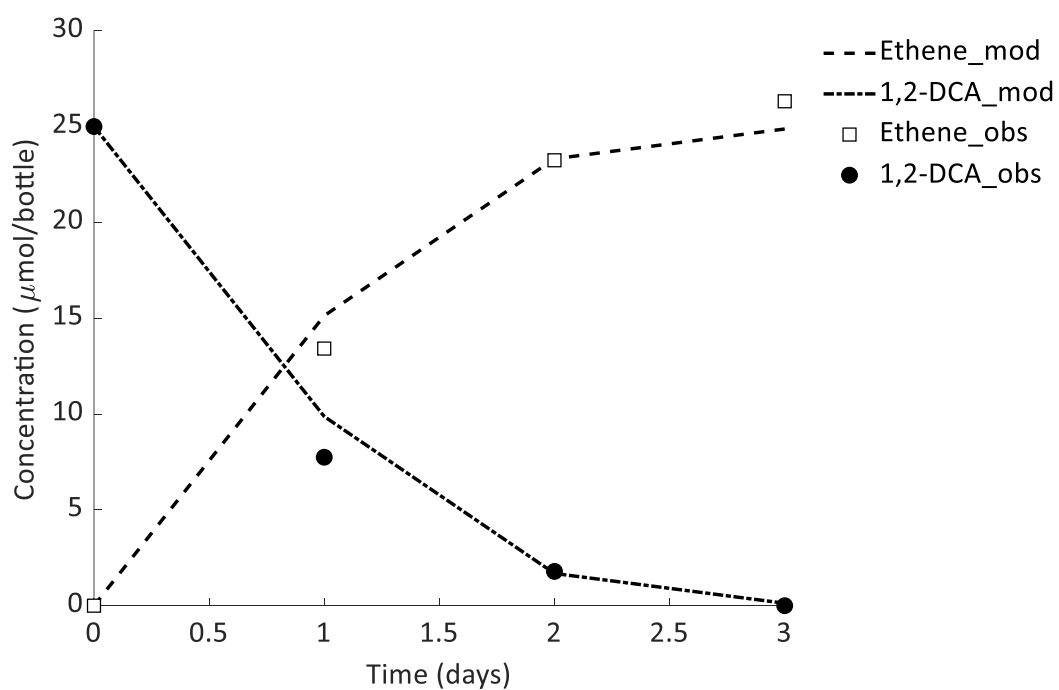


Fig. S4: Modeled (mod) and observed (obs) concentrations in culture EA-T1_B.

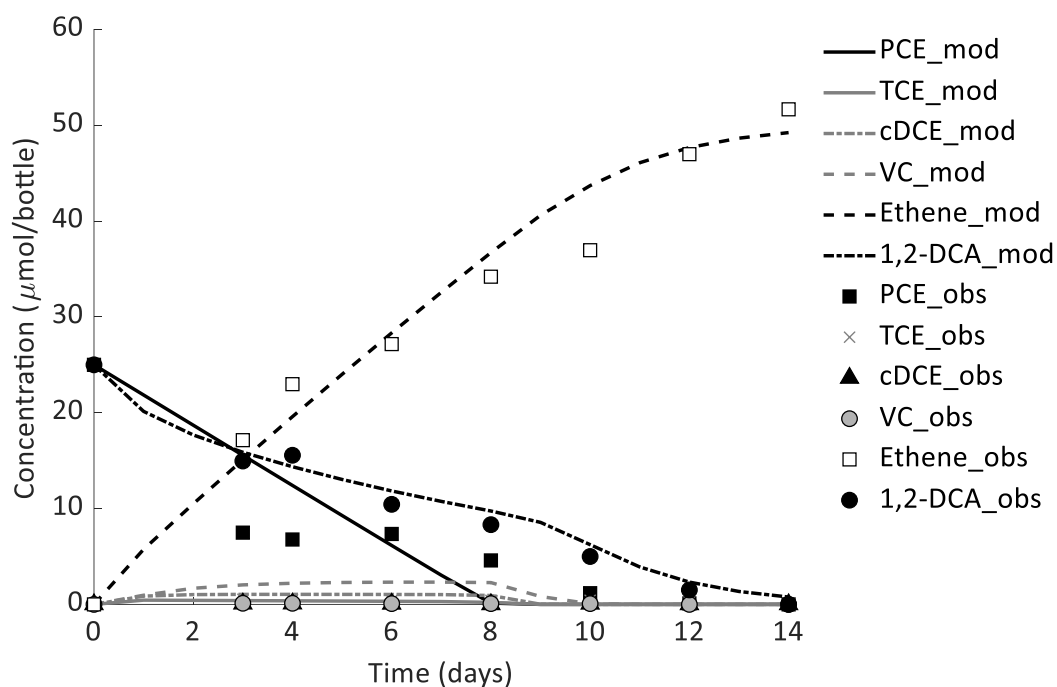


Fig. S5: Modeled (mod) and observed (obs) concentrations in culture EA-T2_A.

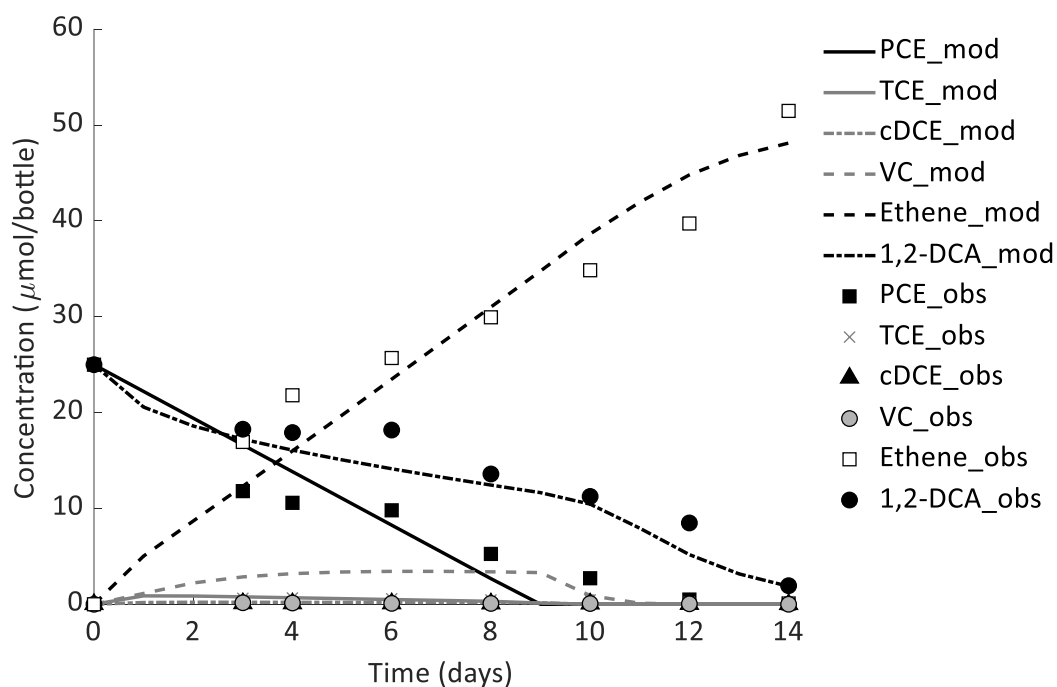


Fig. S6: Modeled (mod) and observed (obs) concentrations in culture EA-T2_B.

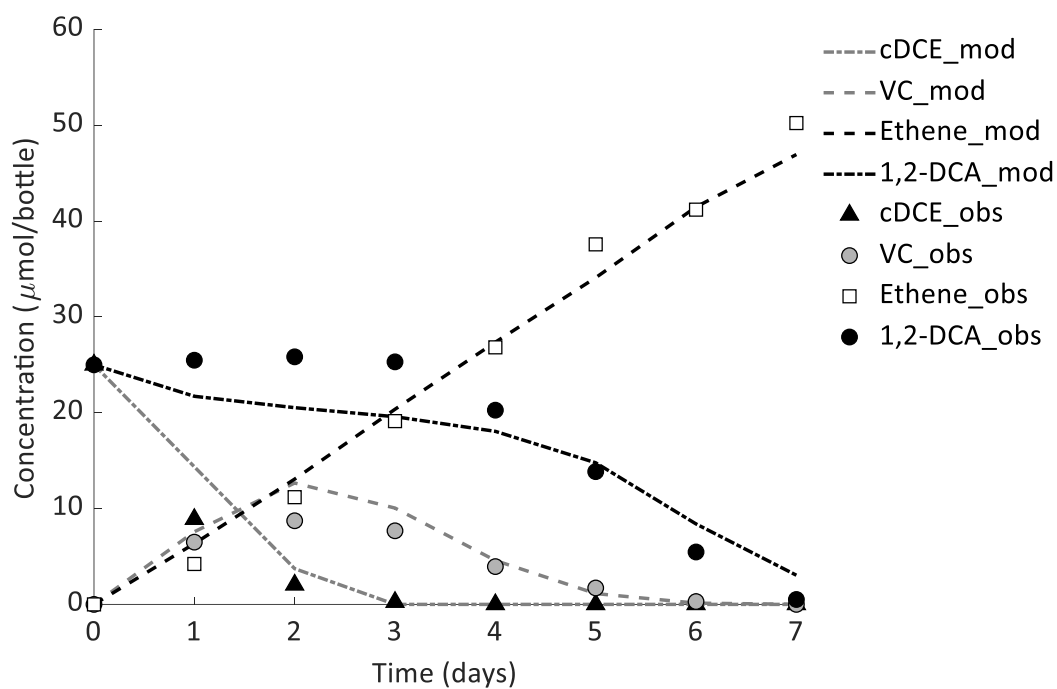


Fig. S7: Modeled (mod) and observed (obs) concentrations in culture EA-T3_A.

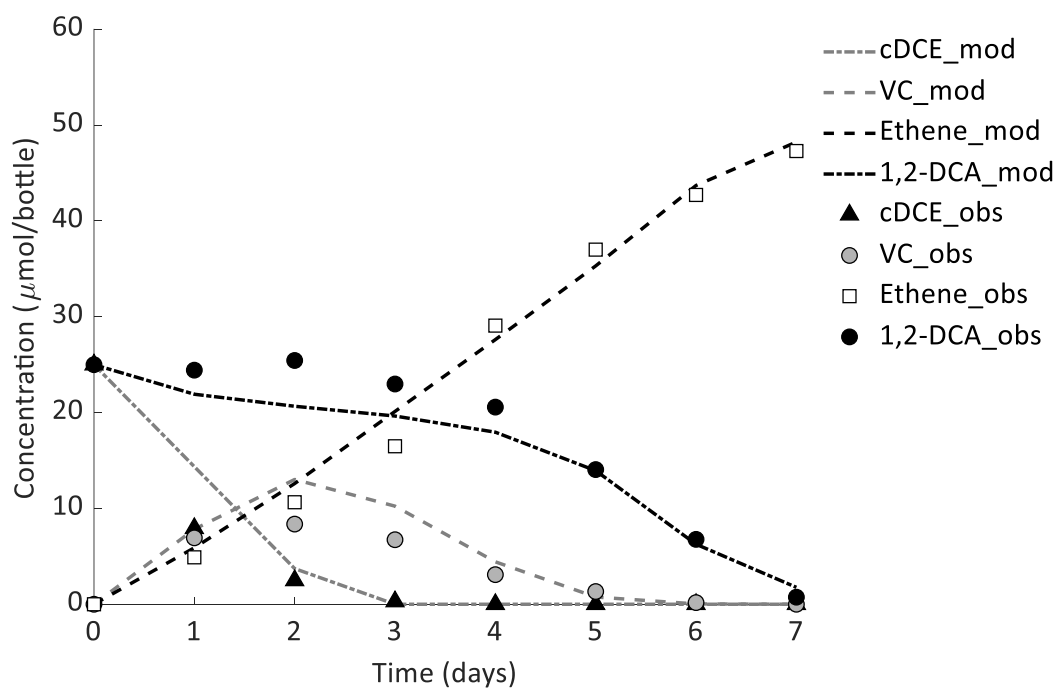


Fig. S8: Modeled (mod) and observed (obs) concentrations in culture EA-T3_B.

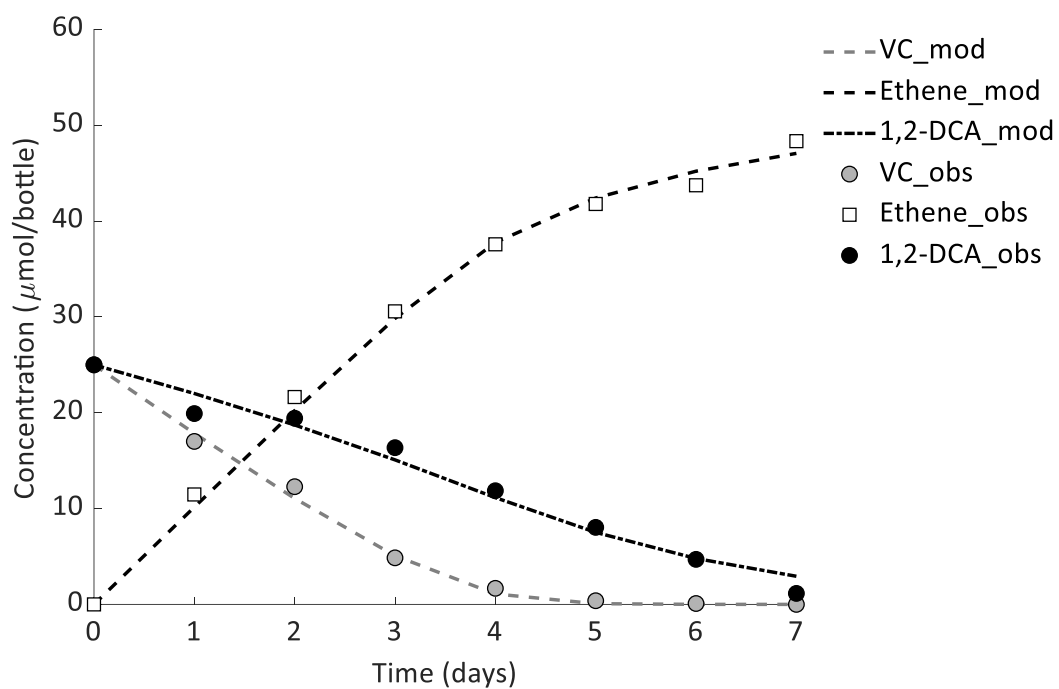


Fig. S9: Modeled (mod) and observed (obs) concentrations in culture EA-T4_A.

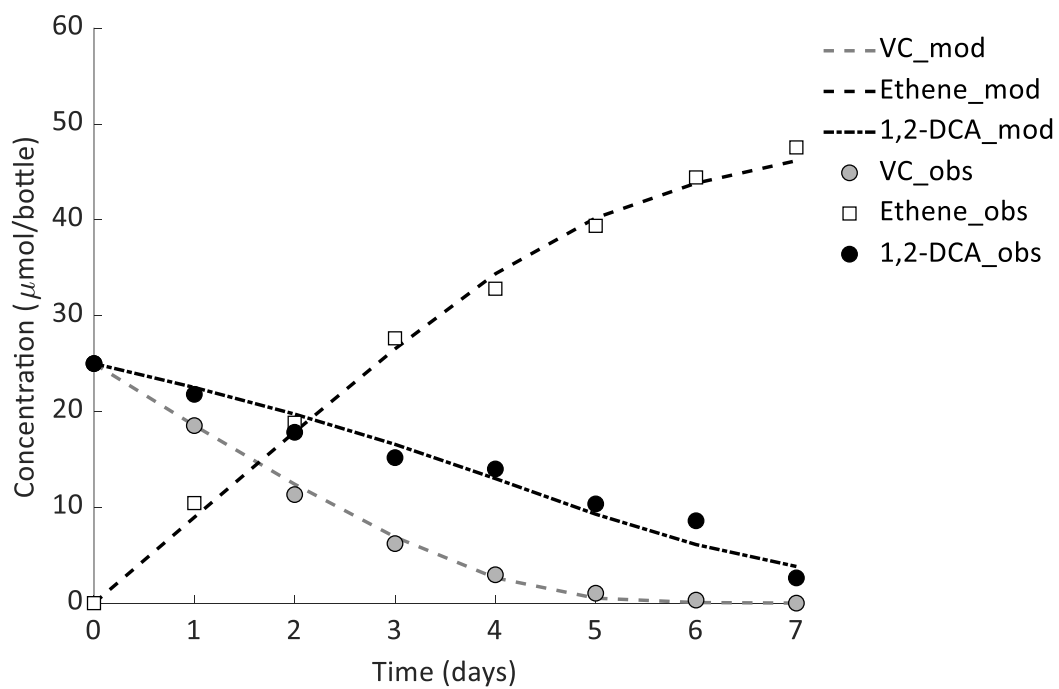


Fig. S10: Modeled (mod) and observed (obs) concentrations in culture EA-T4_B.

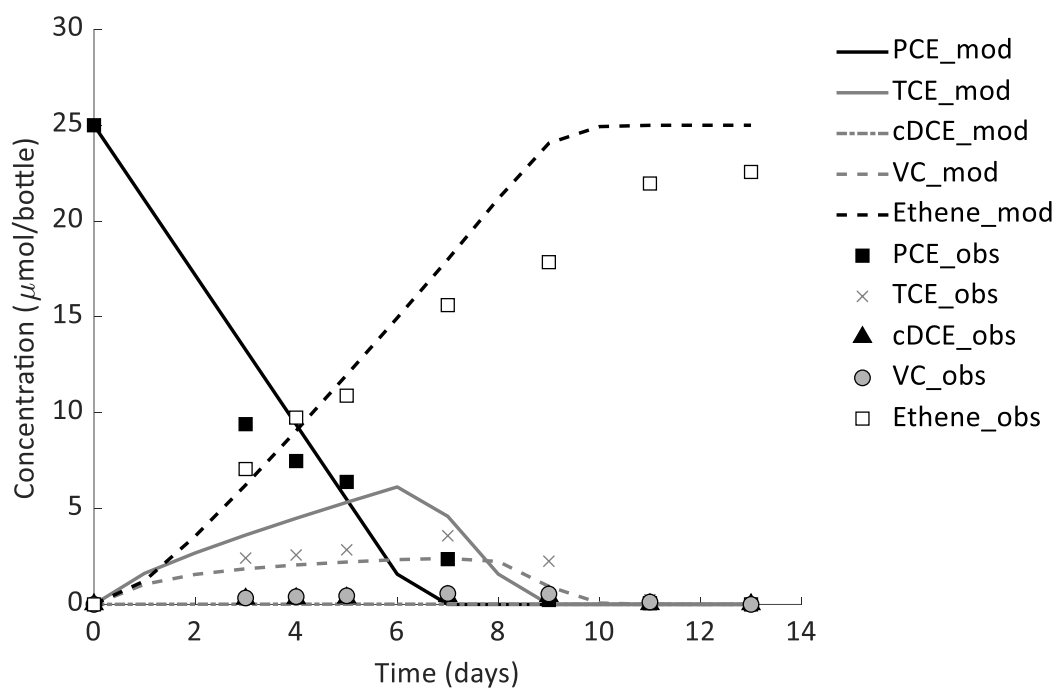


Fig. S11: Modeled (mod) and observed (obs) concentrations in culture EAT5_A.

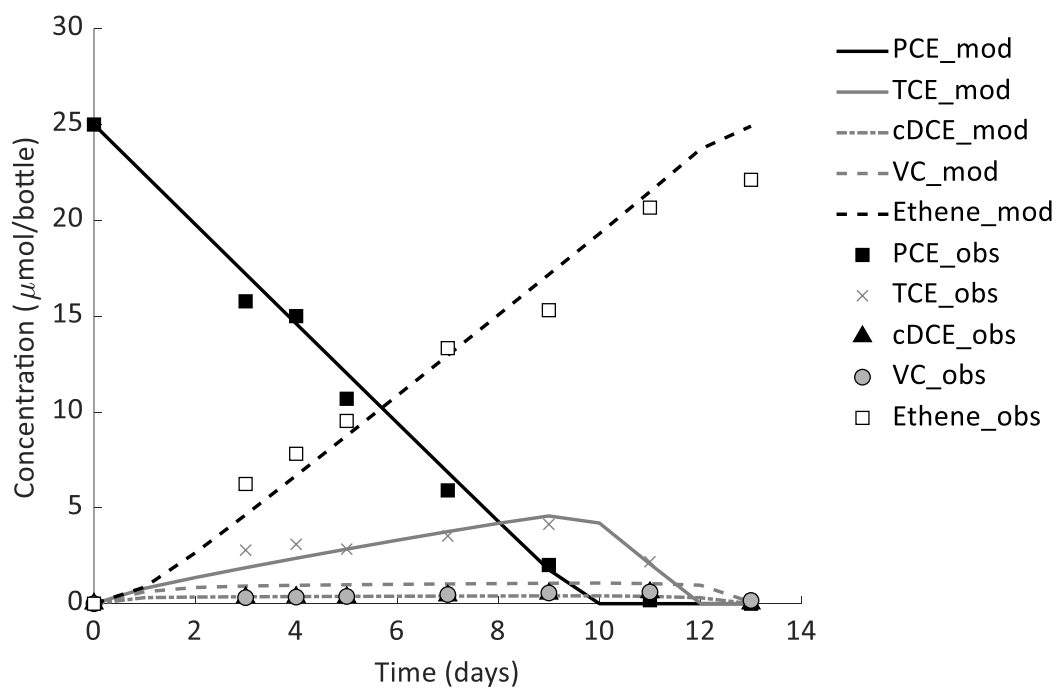


Fig. S12: Modeled (mod) and observed (obs) concentrations in culture EAT5_B.

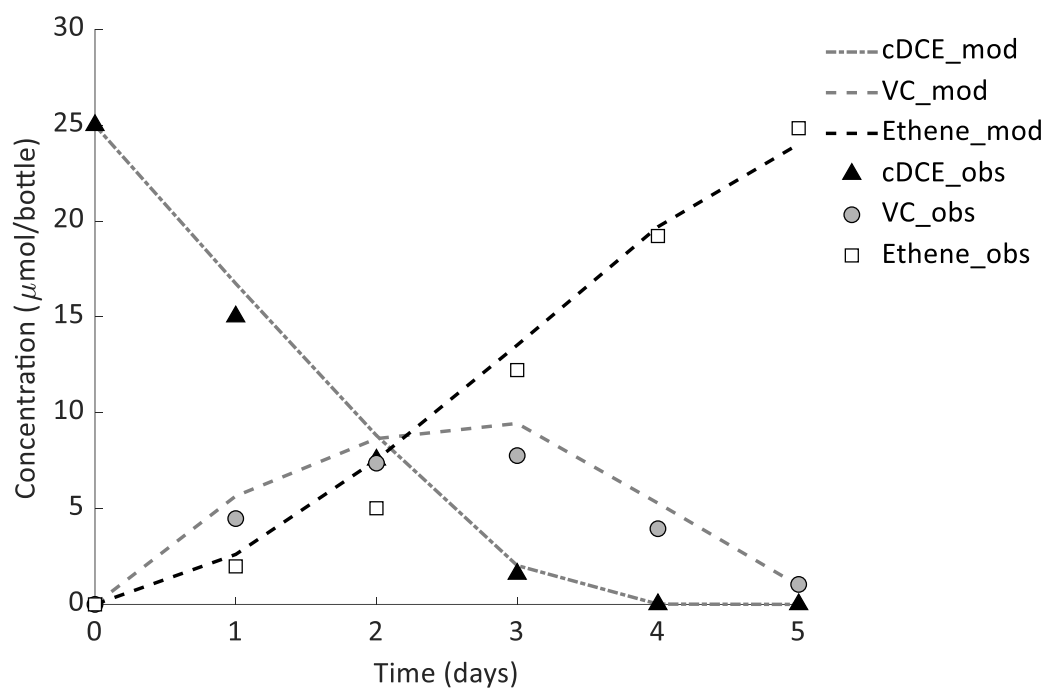


Fig. S13 Modeled (mod) and observed (obs) concentrations in culture EA-T6_A.

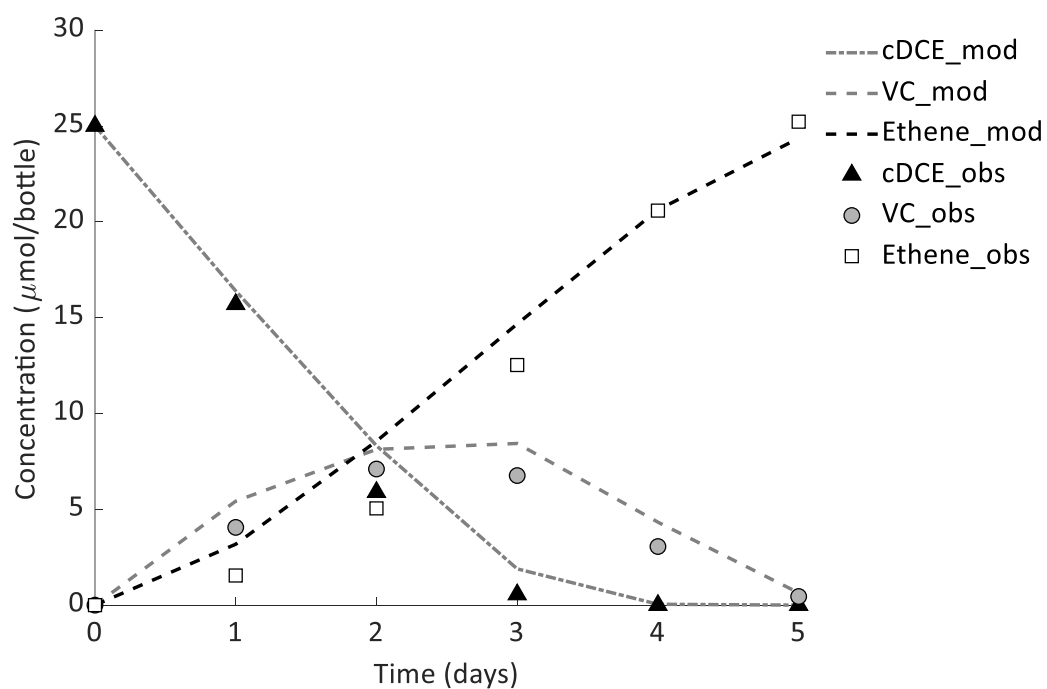


Fig. S14: Modeled (mod) and observed (obs) concentrations in culture EA-T6_B.

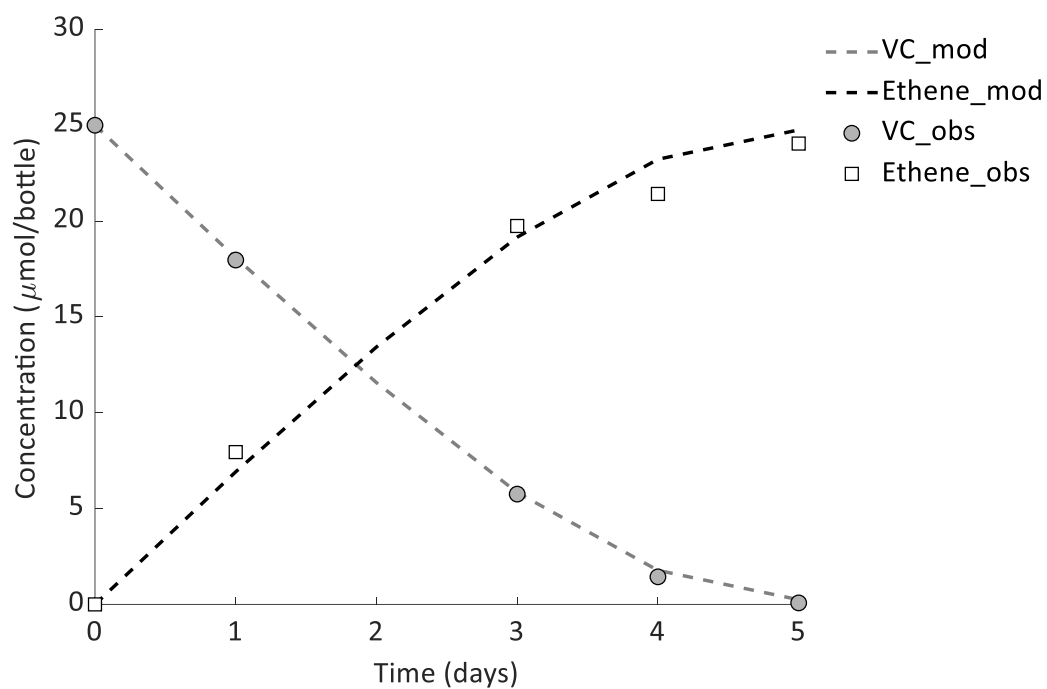


Fig. S15: Modeled (mod) and observed (obs) concentrations in culture EA-T7_A.

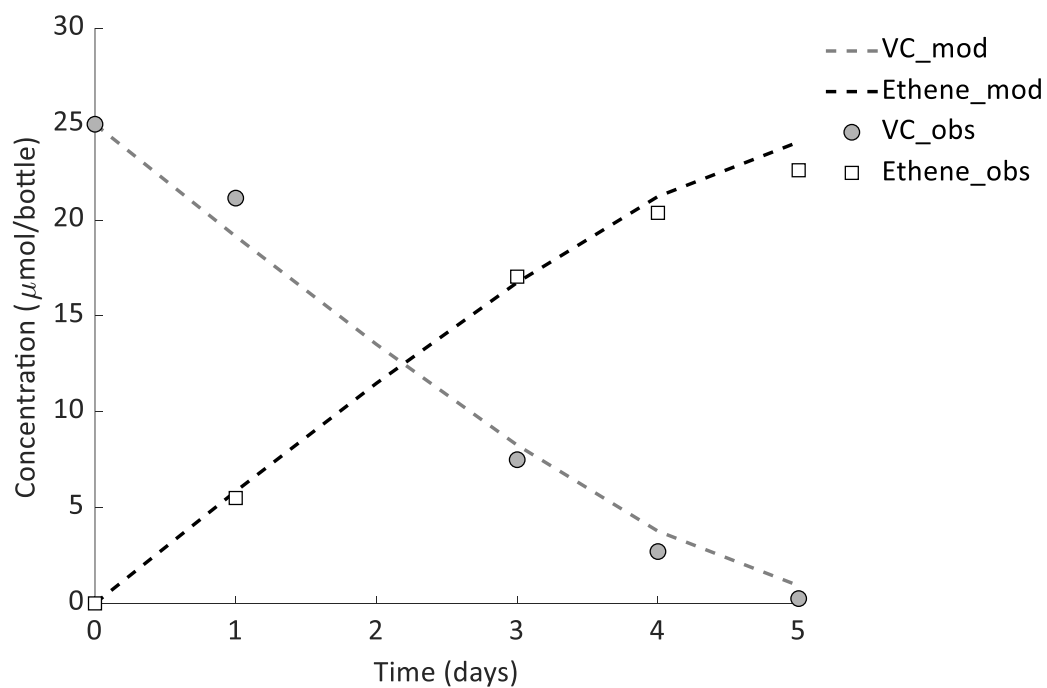


Fig. S16: Modeled (mod) and observed (obs) concentrations in culture EA-T7_B.

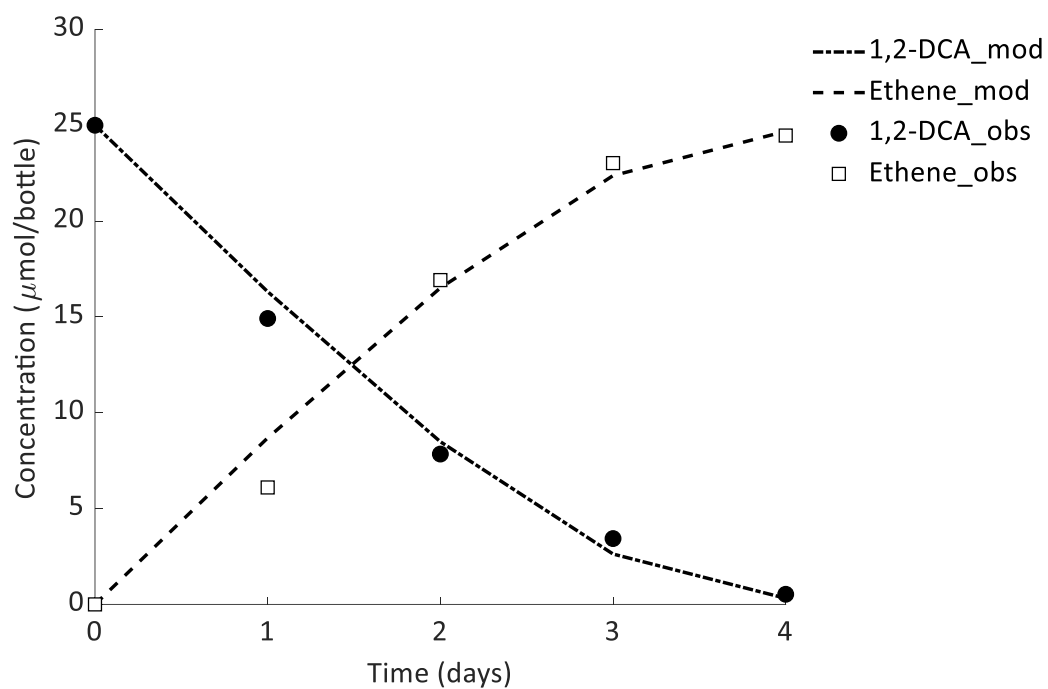


Fig. S17: Modeled (mod) and observed (obs) concentrations in culture EA-T8_A.

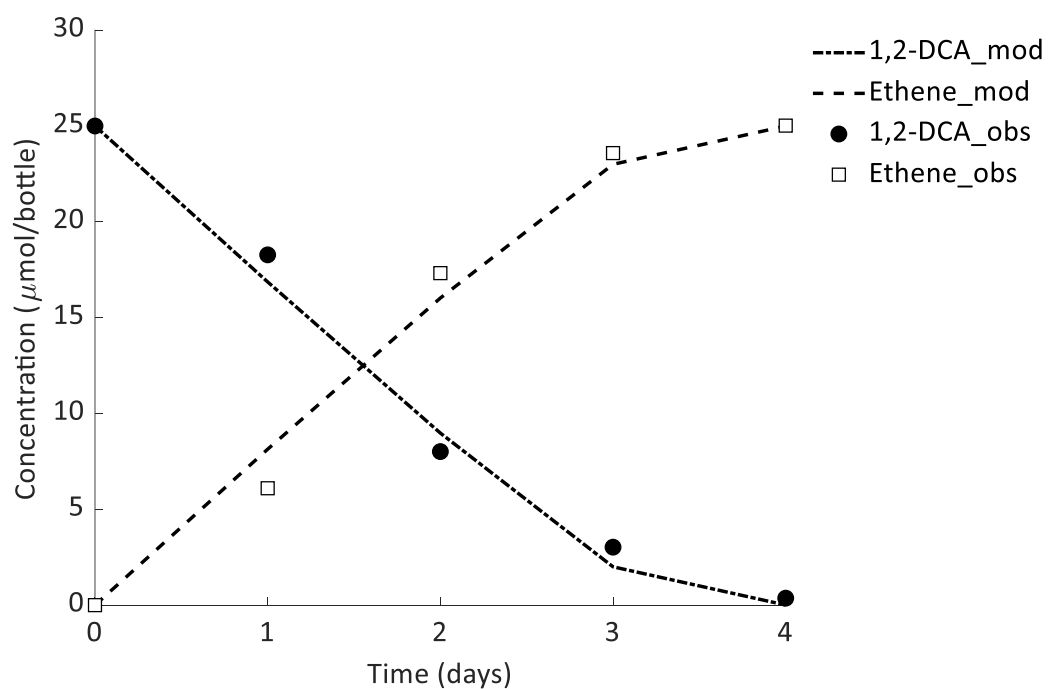


Fig. S18: Modeled (mod) and observed (obs) concentrations in culture EA-T8_B.

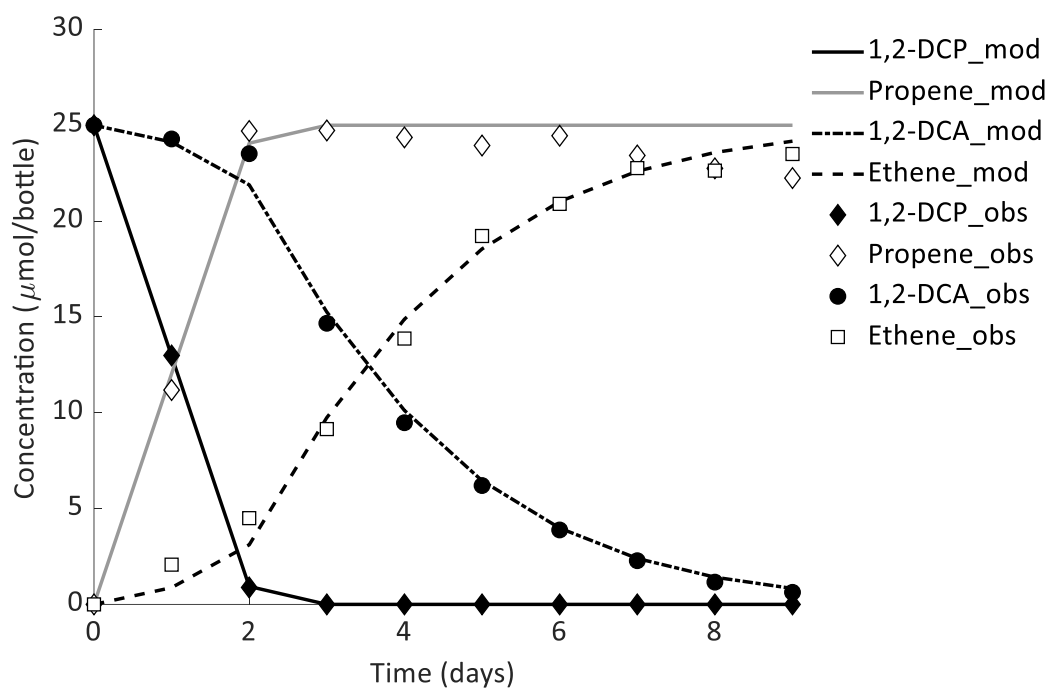


Fig. S19: Modeled (mod) and observed (obs) concentrations in culture EA-T9_A.

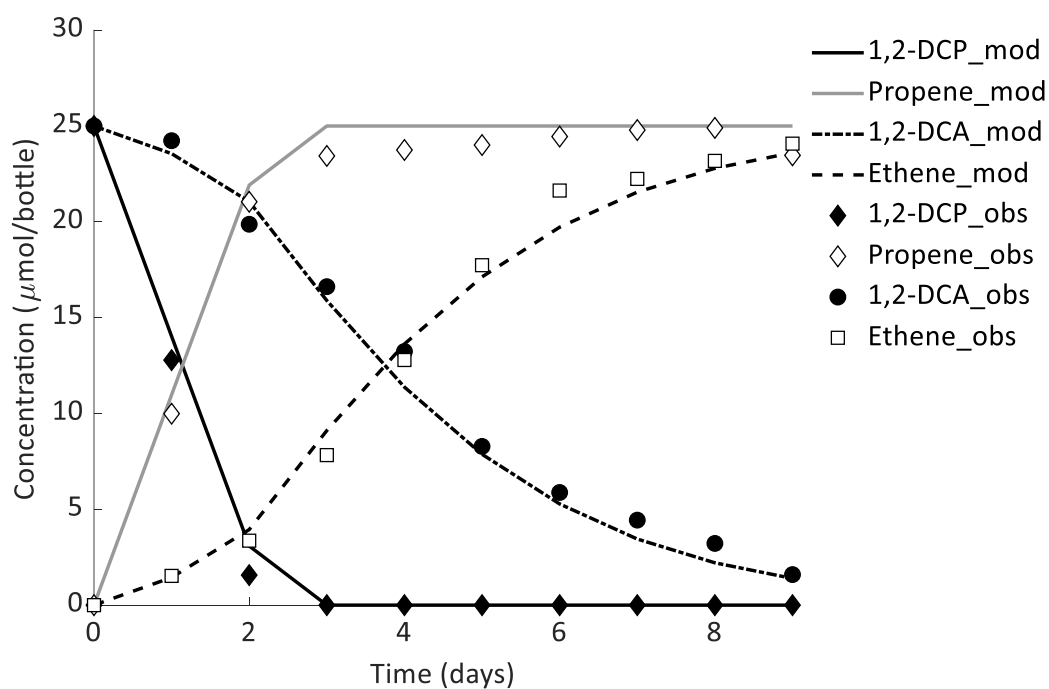


Fig. S20: Modeled (mod) and observed (obs) concentrations in culture EA-T9_B.

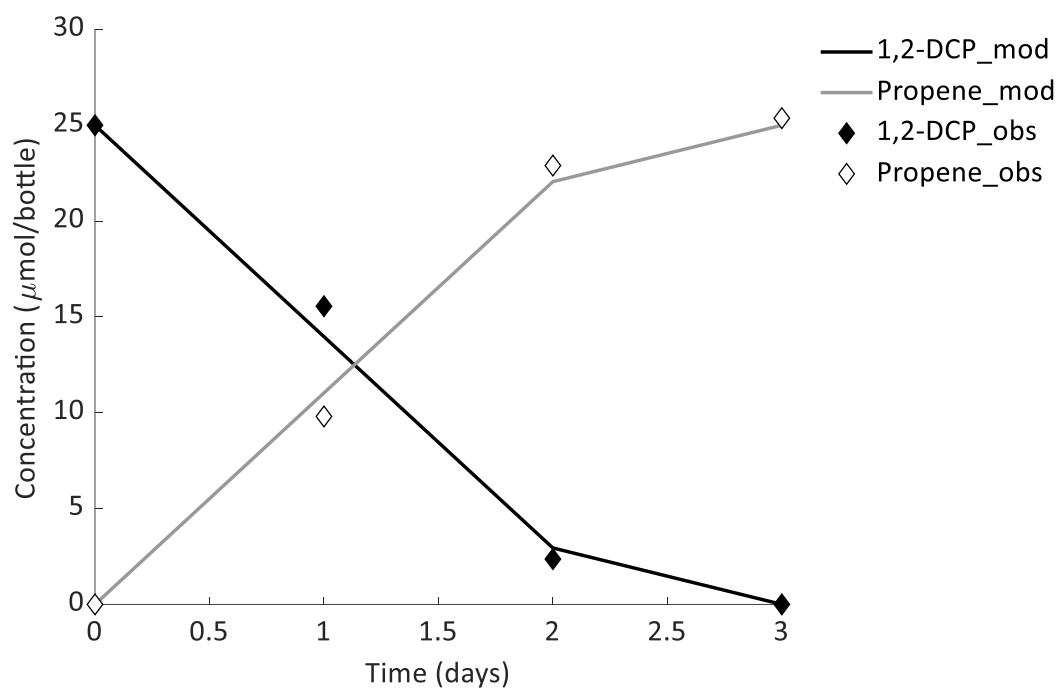


Fig. S21: Modeled (mod) and observed (obs) concentrations in culture EA-T10_A.

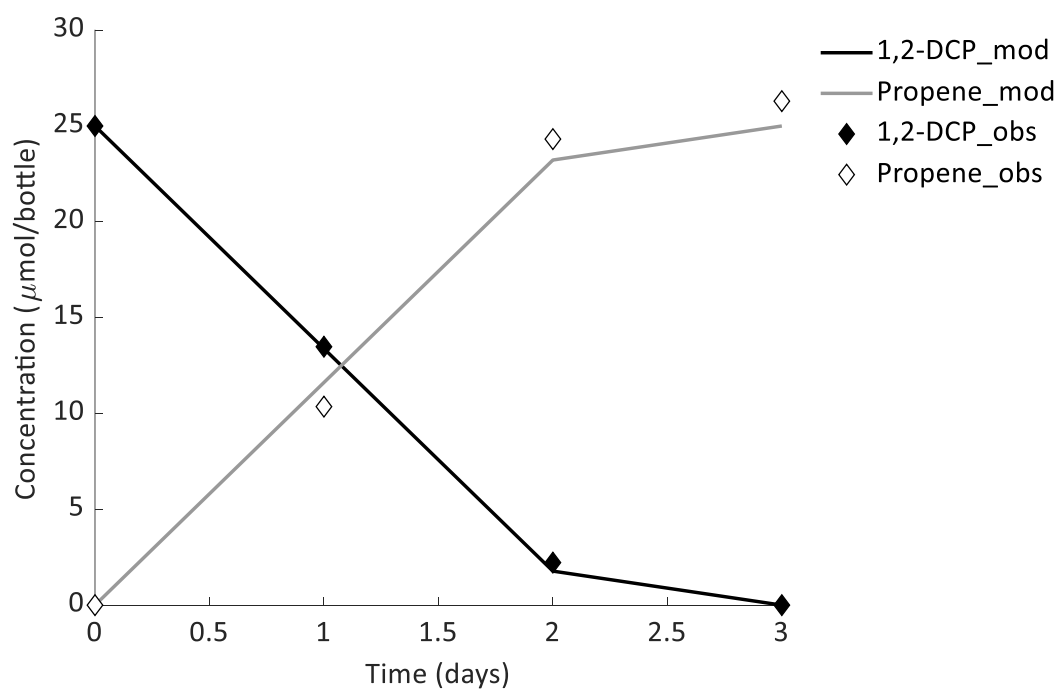


Fig. S22: Modeled (mod) and observed (obs) concentrations in culture EA-T10_B.

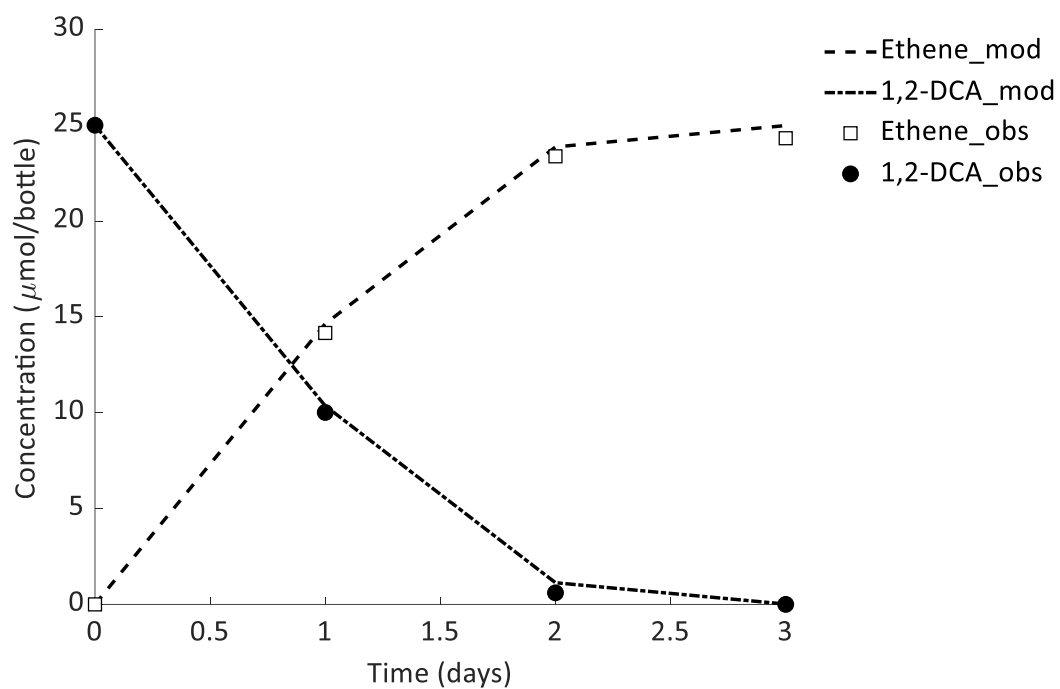


Fig. S23: Modeled (mod) and observed (obs) concentrations in culture EB-T1_A.

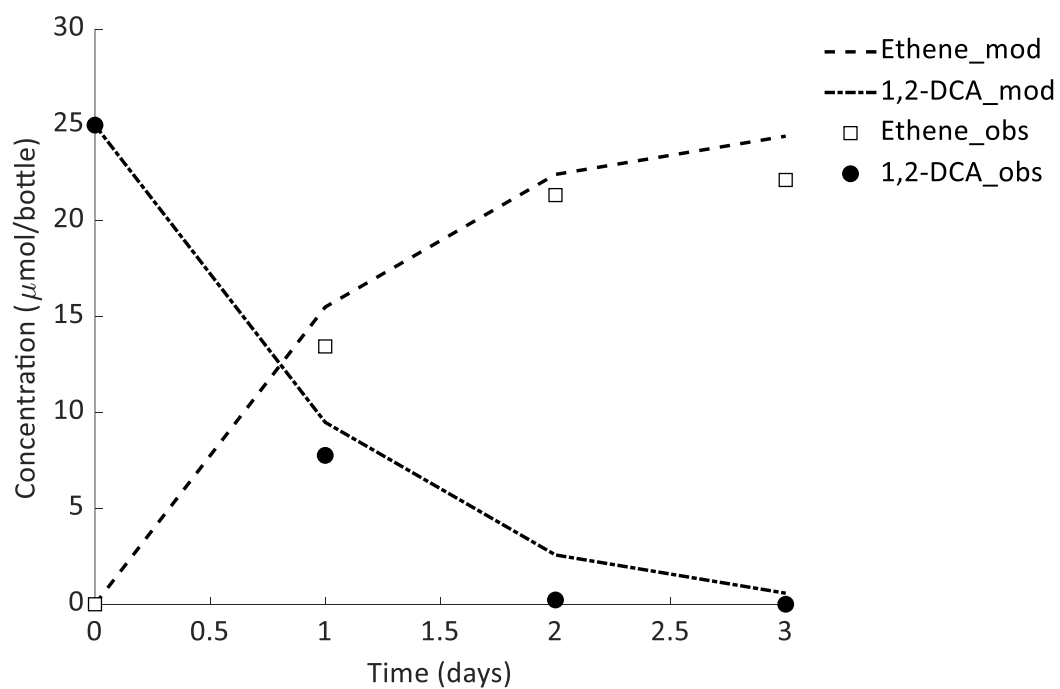


Fig. S24: Modeled (mod) and observed (obs) concentrations in culture EB-T1_B.

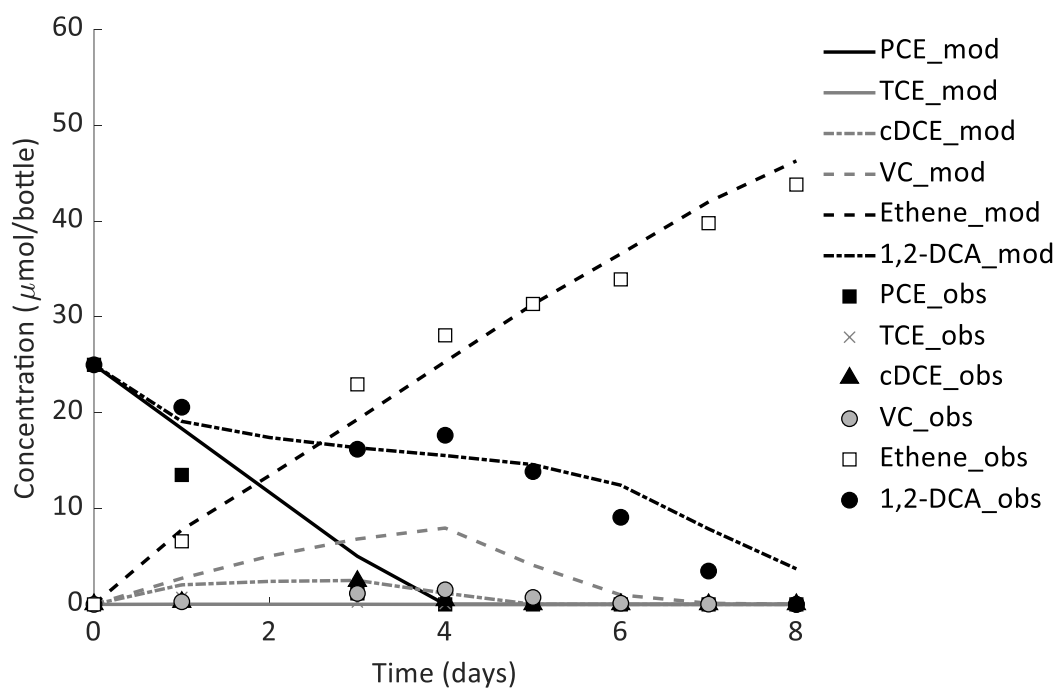


Fig. S25: Modeled (mod) and observed (obs) concentrations in culture EB-T2_A.

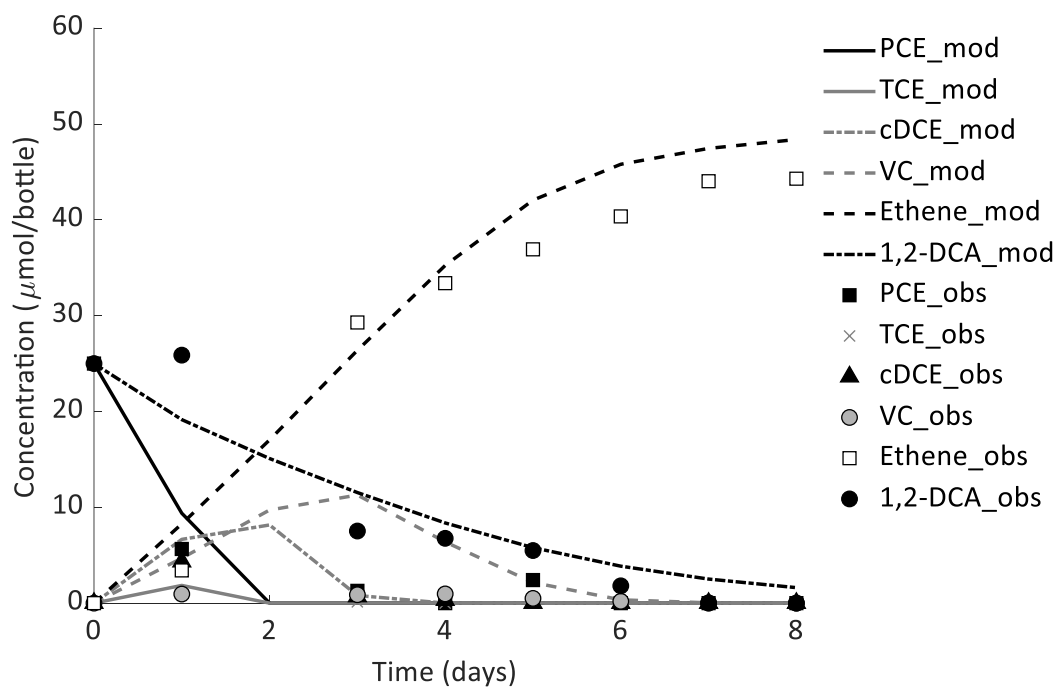


Fig. S26: Modeled (mod) and observed (obs) concentrations in culture EB-T2_B.

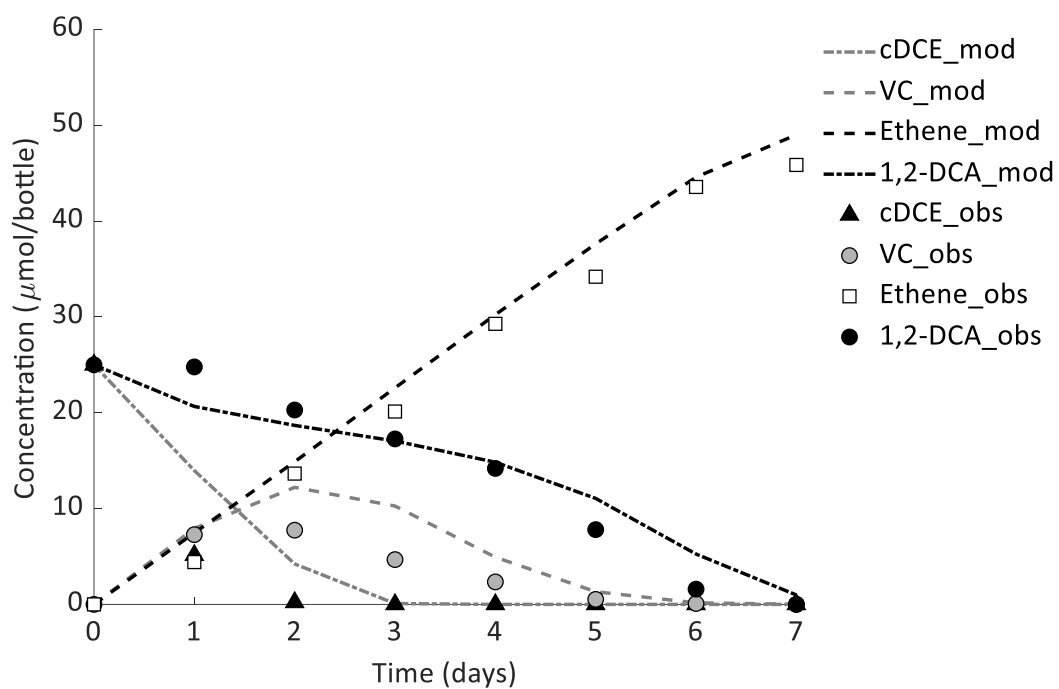


Fig. S27: Modeled (mod) and observed (obs) concentrations in culture EB-T3_A.

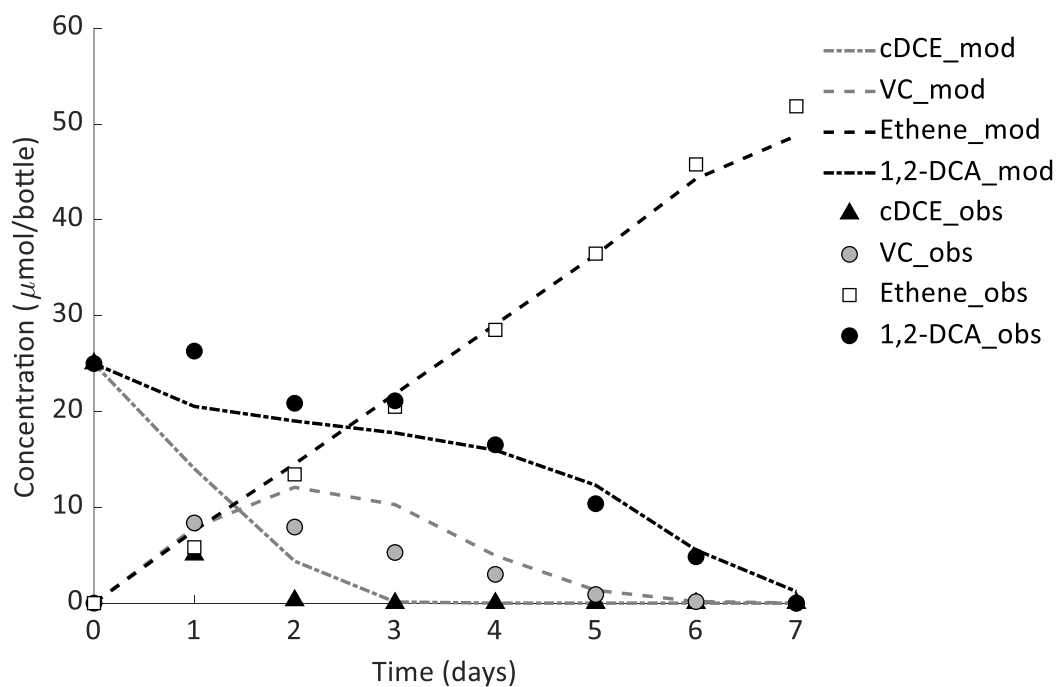


Fig. S28: Modeled (mod) and observed (obs) concentrations in culture EB-T3_B.

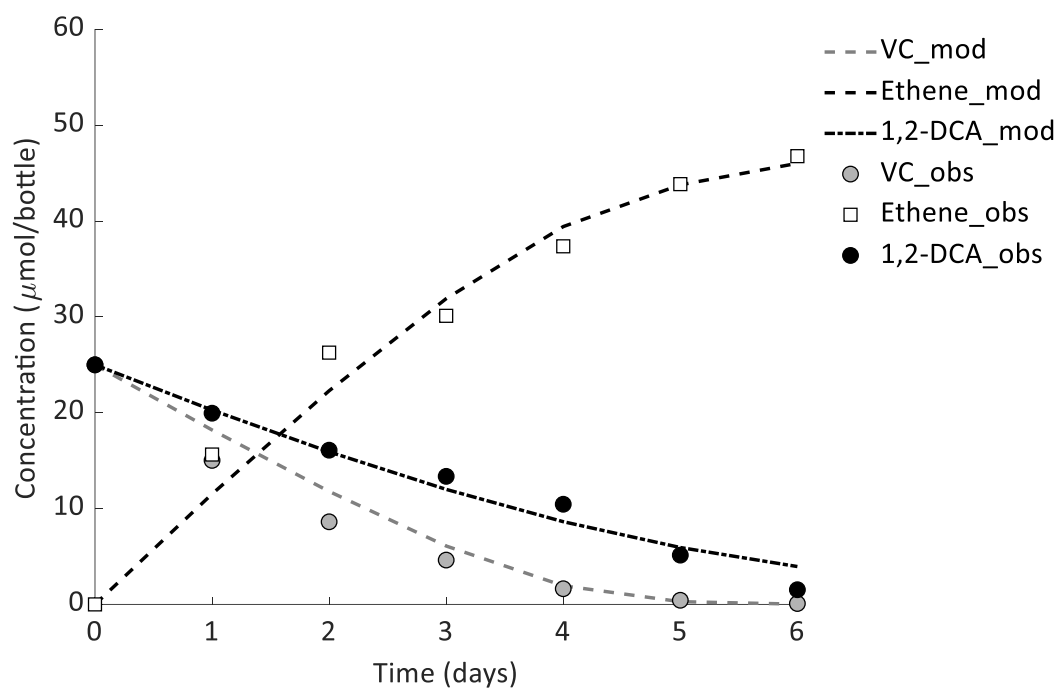


Fig. S29: Modeled (mod) and observed (obs) concentrations in culture EB-T4_A.

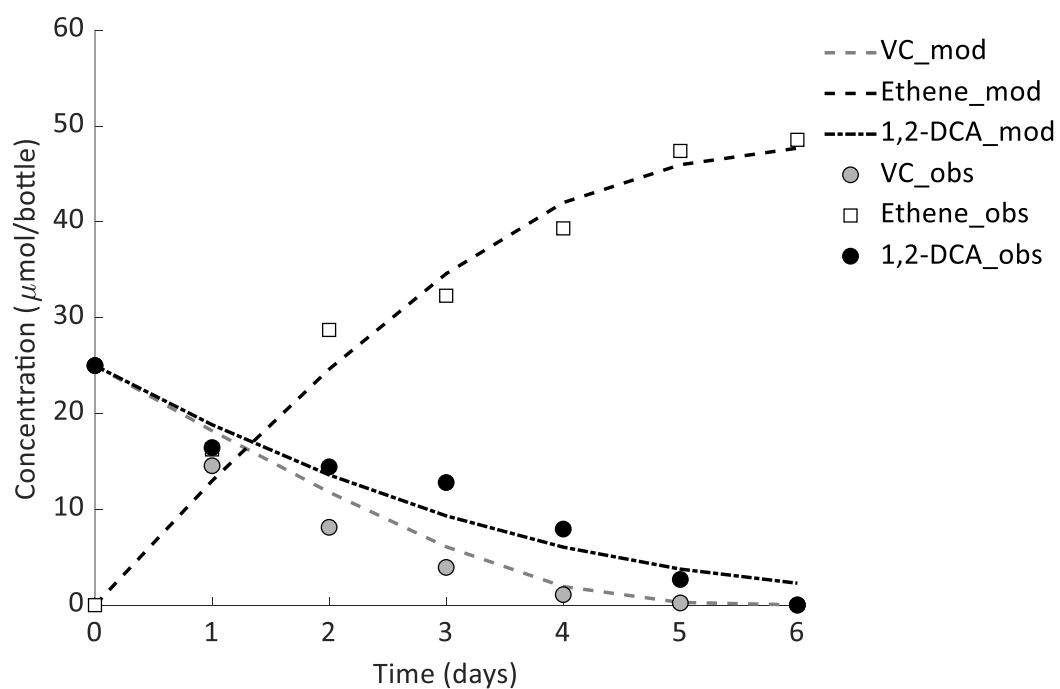


Fig. S30: Modeled (mod) and observed (obs) concentrations in culture EB-T4_B.

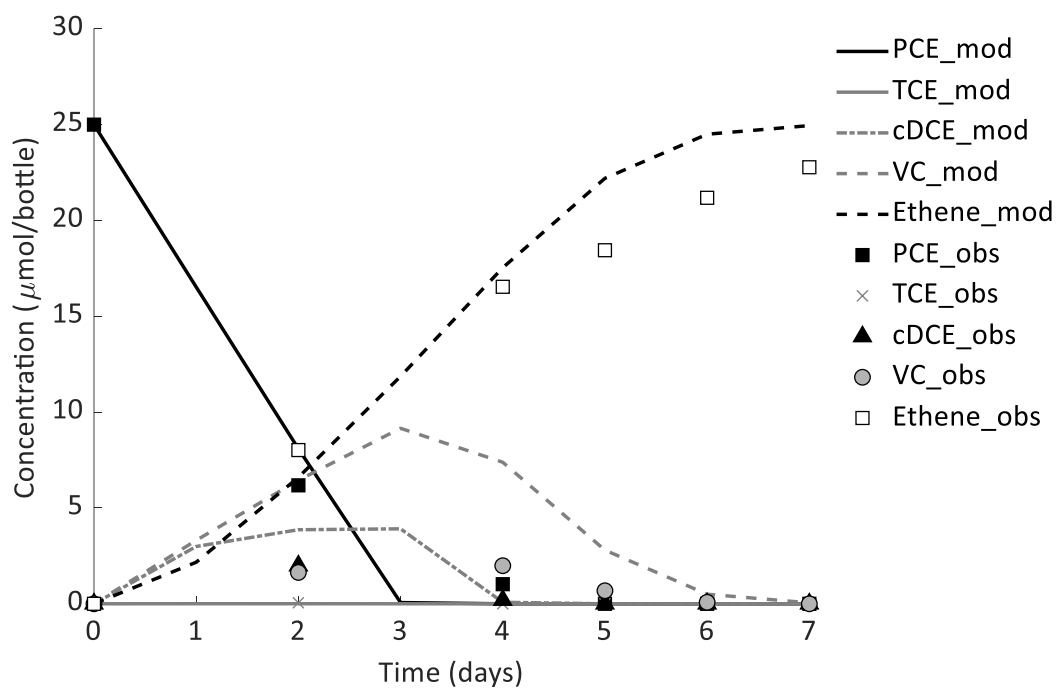


Fig. S31: Modeled (mod) and observed (obs) concentrations in culture EB-T5_A.

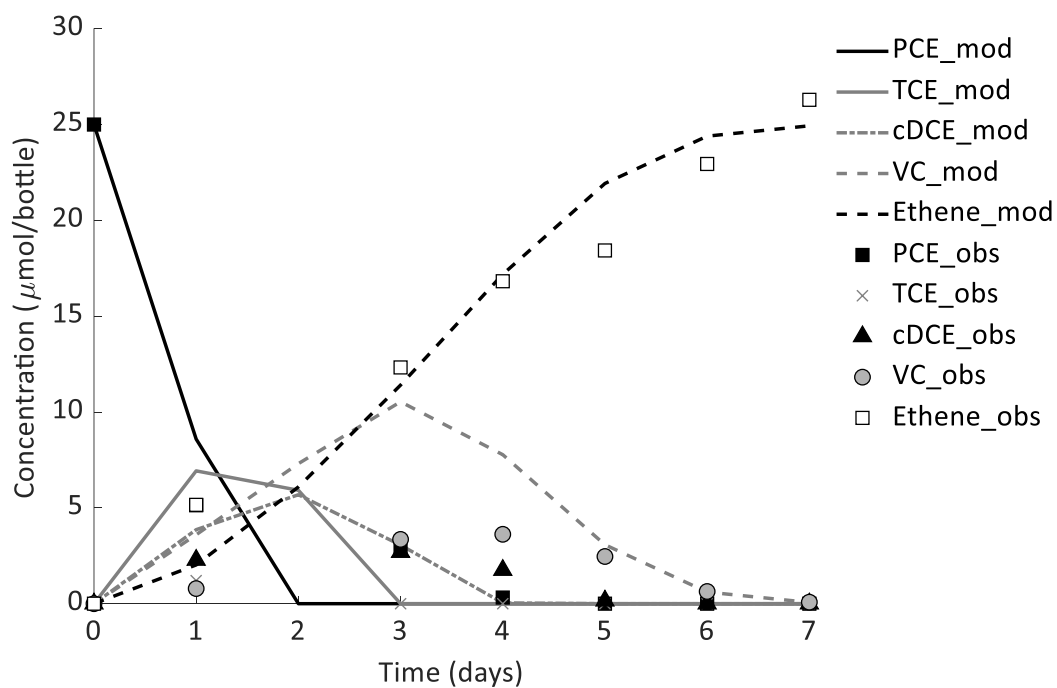


Fig. S32: Modeled (mod) and observed (obs) concentrations in culture EB-T5_B.

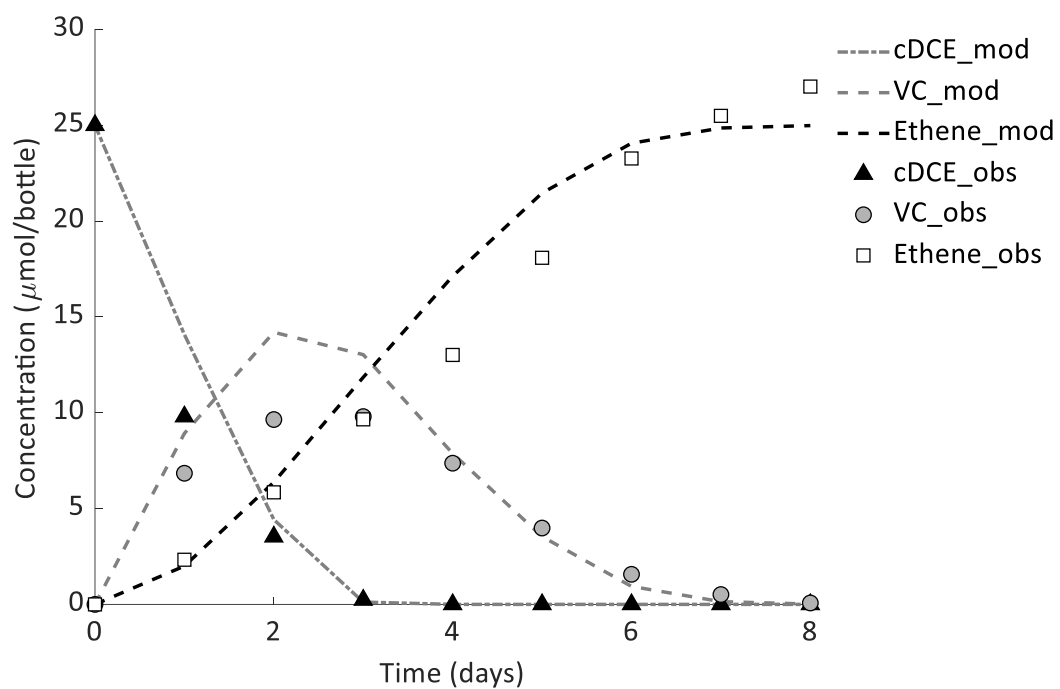


Fig. S33: Modeled (mod) and observed (obs) concentrations in culture EB-T6_A.

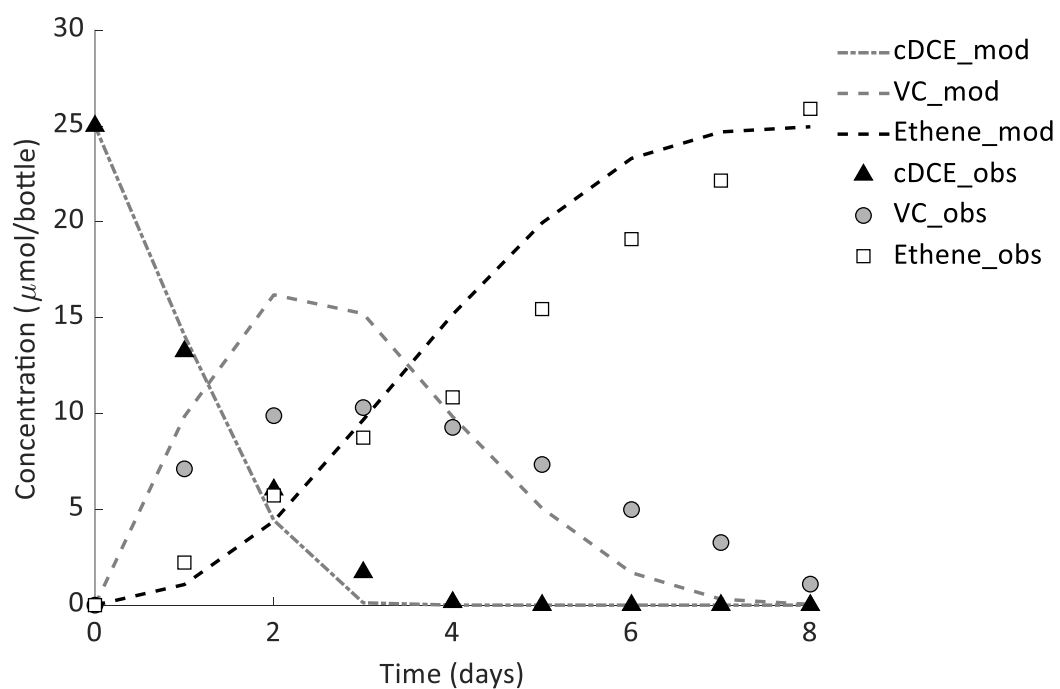


Fig. S34: Modeled (mod) and observed (obs) concentrations in culture EB-T6_B.

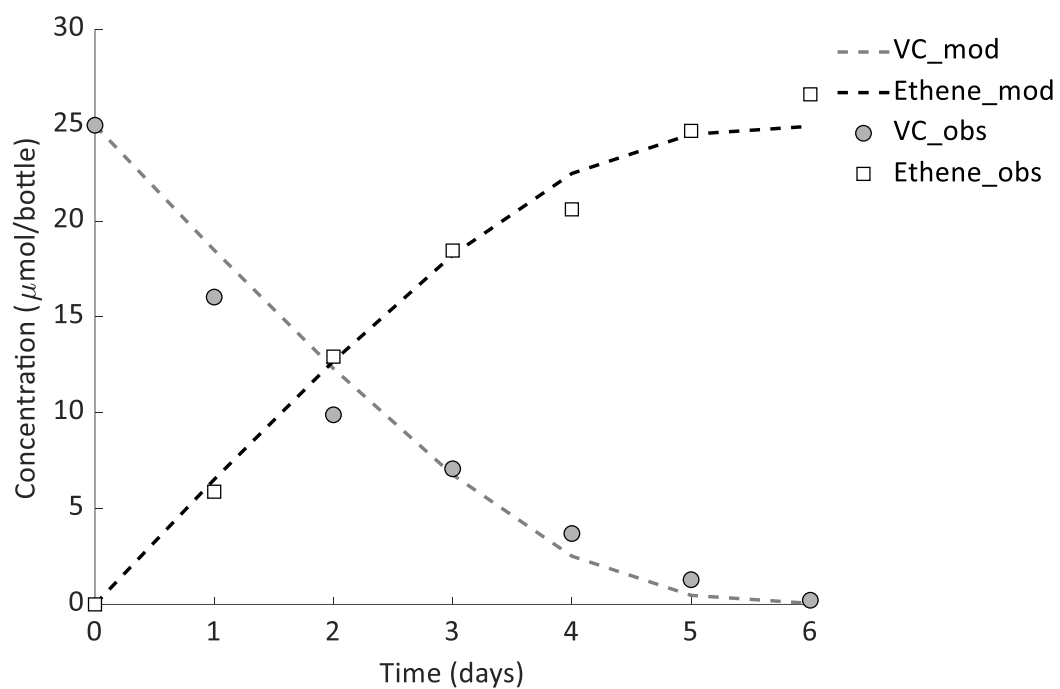


Fig. S35: Modeled (mod) and observed (obs) concentrations in culture EB-T7_A.

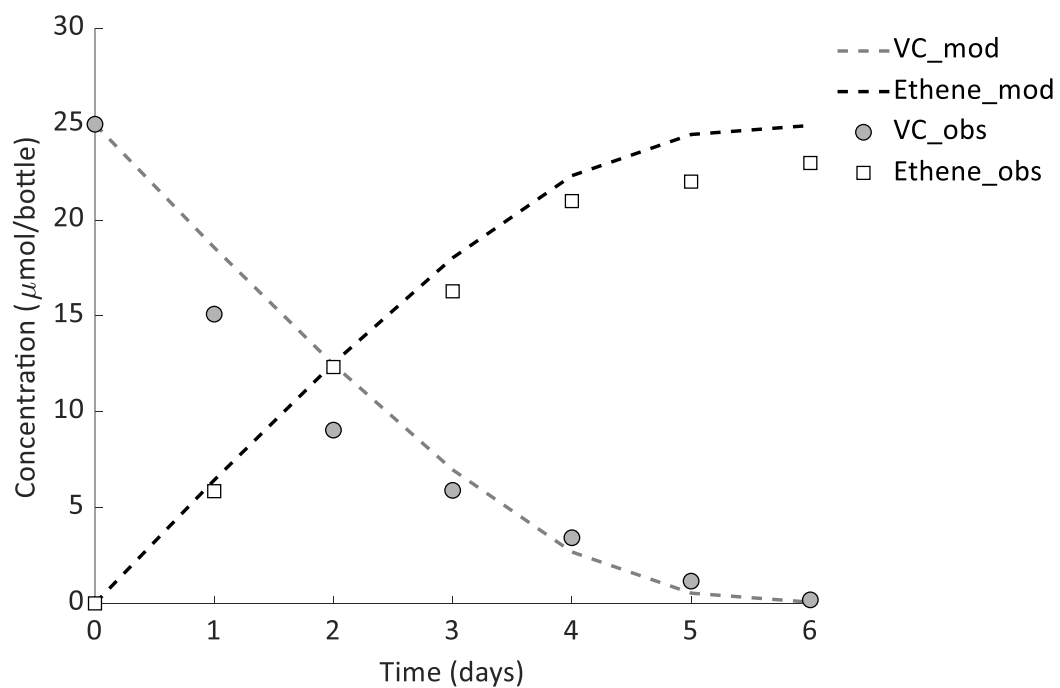


Fig. S36: Modeled (mod) and observed (obs) concentrations in culture EB-T7_B.

Table S1: Primers and amplification programs used for qPCR in this study

Target	Name ^a	Oligonucleotide sequence (5' – 3')	Reference for primer	Reference for qPCR program
Total bacteria	Eub341F Eub534R	CCTACGGGAGGCAGCAG ATTACCGCGGCTGCTGGC	(Muyzer et al. 1993)	(Atashgahi et al. 2013)
<i>Dehalogenimonas</i>	BL-DC-1243F BL-DC-1351R	GGYACAATGGGTTGCCACCGG AACGCGCTATGCTGACACGCGT	(Chen et al. 2014)	(Chen et al. 2014) ^b
<i>Desulfitobacterium</i>	Dsb406F Dsb619R	GTACGACGAAGGCCTTCGGGT CCCAGGGTTGAGCCCTAGGT	(Smits et al. 2004)	(Smits et al. 2004)
<i>Dehalococcoides</i>	Dco728F Dco944R	AAGGCGGTTTTCTAGGTTGTCAC CTTCATGCATGTCAAAT	(Smits et al. 2004)	(Atashgahi et al. 2013)
<i>Dehalobacter</i>	Dre441F Dre645R	GTTAGGGAAGAACGGCATCTGT CCTCTCCTGTCCTCAAGCCATA	(Smits et al. 2004)	(Atashgahi et al. 2013)
<i>Geobacter</i>	Geo196F Geo535R	GAATATGCTCCTGATTC TAAATCCGAACAACGCTT	(Amos et al. 2007)	(Azizian et al. 2010)
<i>Sulfurospirillum</i>	Sulfuro114F Sulfuro421R	GCTAACCTGCCCTTTAGTGG GTTTACACACCGAAATGCGT	(Sutton et al. 2015)	(Sutton et al. 2015)

^a Primer names may not correspond to the original publication

^b The qPCR program was modified as 98°C for 5 min, followed by 40 cycles of 98°C for 15 s, 68.2°C for 45 s. Melting curves were included from 55°C to 95°C with increments of 0.5°C and 10 s at each step

Table S2 can be found at: <https://github.com/mibwurrepo/Peng-et-al-2019>

References

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