

***Burkholderiales* participating in pentachlorophenol biodegradation in iron-reducing  
paddy soil as identified by stable isotope probing**

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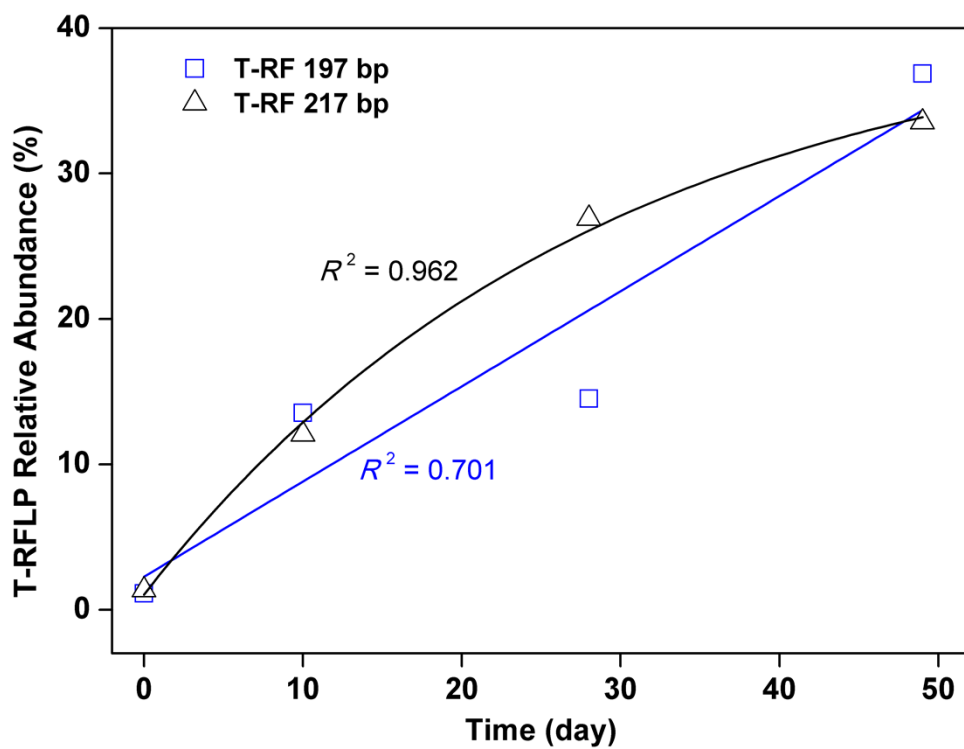
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Number of figures: 1

Number of tables: 2

**Figure S1** The relative abundance of T-RFs in the  $^{13}\text{C}$ -DNA heavy fractions. The solid line is the model-fitted relative abundance using the pseudo-first-order kinetic model.



**Table S1.** Phylogenetic affiliation of two (A and B) 16S *rRNA* clone in PCP degrading microcosms.

A

<sup>12</sup> C-Heavy fraction of clones	Phylum	Class	Order	Family	Genus
8	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacteriales</i>	<i>Enterobacteriaceae</i>	<i>Escherichia/Shigella</i>
7	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	Unclassified		
4	<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Planctomycetales</i>	<i>Planctomycetaceae</i>	<i>Unclassified</i>
3	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacteriales</i>	<i>Enterobacteriaceae</i>	Unclassified
2	<i>Acidobacteria</i>	<i>Acidobacteria_Gp10</i>			<i>Gp10</i>
2	<i>Acidobacteria</i>	Unclassified			
2	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfuromonadales</i>	Unclassified	
2	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Nannocystineae</i>	Unclassified	
1	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>Peptococcaceae</i>	Unclassified
1	<i>Acidobacteria</i>	<i>Acidobacteria_Gp3</i>			Unclassified
1	<i>Acidobacteria</i>	<i>Acidobacteria_Gp1</i>			<i>Gp1</i>
1	<i>Acidobacteria</i>	<i>Acidobacteria_Gp23</i>			<i>Gp23</i>
1	<i>Acidobacteria</i>	<i>Acidobacteria_Gp6</i>			<i>Gp6</i>
1	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidimicrobiales</i>	<i>Acidimicrobineae</i>	Unclassified
1	<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Planctomycetales</i>	<i>Planctomycetaceae</i>	<i>Isosphaera</i>
1	<i>Planctomycetes</i>	<i>Planctomycetacia</i>	<i>Planctomycetales</i>	<i>Planctomycetaceae</i>	<i>Singulisphaera</i>
1	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodospirillales</i>	<i>Rhodospirillaceae</i>	<i>Azospirillum</i>
1	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodospirillales</i>	<i>Acetobacteraceae</i>	Unclassified
1	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodospirillales</i>	Unclassified	
1	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	Unclassified	
1	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Syntrophobacterales</i>	<i>Syntrophaceae</i>	<i>Syntrophus</i>
1	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Syntrophobacterales</i>	<i>Syntrophaceae</i>	Unclassified
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Stenotrophomonas</i>
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Dyella</i>
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	Unclassified
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	Unclassified		
1	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Delftia</i>
1	<i>Proteobacteria</i>	Unclassified			
5	Unclassified				

B

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<sup>13</sup>C-Heavy fraction

of clones	Phylum	Class	Order	Family	Genus
8	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacteriales</i>	<i>Enterobacteriaceae</i>	Unclassified
6	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Alcaligenaceae</i>	<i>Achromobacter</i>
5	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	Unclassified		
4	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Stenotrophomonas</i>
3	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacteriales</i>	<i>Enterobacteriaceae</i>	<i>Escherichia/Shigella</i>
4	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Moraxellaceae</i>	<i>Acinetobacter</i>
4	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Comamonas</i>
3	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Alcaligenaceae</i>	<i>Bordetella</i>
2	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>Ruminococcaceae</i>	Unclassified
2	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfuromonadales</i>	<i>Geobacteraceae</i>	<i>Geobacter</i>
2	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	Unclassified	
1	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Propionibacteriaceae</i>	<i>Propionibacterium</i>
1	<i>Cyanobacteria</i>	<i>Chloroplast</i>	<i>Chloroplast</i>	<i>Chloroplast</i>	Unclassified
1	<i>Acidobacteria</i>	<i>Acidobacteria_GpI</i>			<i>GpI</i>
1	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	<i>Peptococcaceae 2</i>	Unclassified
1	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	Unclassified		
1	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Syntrophobacterales</i>	<i>Syntrophobacteraceae</i>	<i>Desulforhabdus</i>
1	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Syntrophobacterales</i>	<i>Syntrophobacteraceae</i>	Unclassified
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	Unclassified
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Enterobacteriales</i>	<i>Enterobacteriaceae</i>	<i>Serratia</i>
1	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	Unclassified		
1	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>	<i>Duganella</i>
1	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Hydrogenophilales</i>	<i>Hydrogenophilaceae</i>	<i>Thiobacillus</i>
1	Unclassified				

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**Table S2.** Comparison of dominant T-RF fragments (bp) of 16S *rRNA* in heavy fraction to predicted fragment with clone library sequences.

	<i>Hae</i> III	<i>Alu</i> I	<i>Hha</i> I	<i>Rsa</i> I
affiliated sequence				
T-RF (bp)	197	236	209	475
clones	202	234	212	476
affiliated sequence				
T-RF (bp)	217	155	570	475
clones	221	157	571	475