

The following supplement accompanies the article

Effects of finfish aquaculture on biogeochemistry and bacterial communities associated with sulfur cycles in highly sulfidic sediments

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Table S1. Bacterial community structure and number of clones in farm and reference sites. Numbers in parentheses represent percentage of each clone number.

Phylogenetic group	Farm		Reference	
	0-1 cm	1-2 cm	0-1 cm	1-2 cm
<i>Proteobacteria</i> Alpha	6 (6.1)	2 (2.2)	11 (10.4)	5 (5.7)
Beta	0 (0.0)	0 (0.0)	1 (0.9)	0 (0.0)
Gamma	27 (27.6)	8 (8.7)	26 (24.5)	11 (12.5)
Delta	17 (17.3)	8 (8.7)	18 (17.0)	26 (29.5)
Epsilon	8 (8.2)	57 (62.0)	9 (8.5)	7 (7.9)
<i>Acidobacteria</i>	10 (10.2)	2 (2.2)	13 (12.3)	10 (11.4)
<i>Actinobacteria</i>	0 (0.0)	0 (0.0)	2 (1.9)	0 (0.0)
<i>Armatimonadetes</i>	1 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>Bacterioidetes</i>	8 (8.2)	0 (0.0)	6 (5.7)	0 (0.0)
<i>Chloroflexi</i>	1 (1.0)	1 (1.1)	1 (0.9)	3 (3.4)
<i>Cyanobacteria</i>	1 (1.0)	2 (2.2)	0 (0.0)	0 (0.0)
<i>Deferribacteres</i>	1 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>Deinococcus</i>	0 (0.0)	0 (0.0)	0 (0.0)	1 (1.1)
<i>Firmicutes</i>	2 (2.0)	1 (1.1)	0 (0.0)	2 (2.3)
<i>Fusobacteria</i>	0 (0.0)	1 (1.1)	0 (0.0)	0 (0.0)
<i>Latescibacteria</i>	0 (0.0)	0 (0.0)	1 (0.9)	2 (2.3)
<i>Parcubacteria</i>	1 (1.0)	0 (0.0)	0 (0.0)	0 (0.0)
<i>Planctomycetes</i>	2 (2.0)	0 (0.0)	4 (3.8)	0 (0.0)
<i>Verrucomicrobia</i>	2 (2.0)	0 (0.0)	1 (0.9)	0 (0.0)
Unclassified	12 (11.2)	10 (10.9)	16 (12.3)	21 (23.9)
No. of clones	98	92	106	88
No. of OTUs	87	38	96	81
Good's coverage (%)	11.2	58.7	9.4	8.0

Table S2. The *dsrA* gene clone library data for the farm and reference sites. Numbers in parentheses represent the relative abundance of each clone.

Group affiliation ^a	No. of clones		Nearest match by BLASTIN search (accession no.)	Similarity	Phylogenetic affiliation	Ref.	
	Farm	Reference					
I	1(1.5)	1(2.0)	Aarhus Bay clone A04 (JQ304763)	95	<i>Desulfobacteraceae</i>	(1)	
	1(1.5)	0	Gas hydrate-bearing sediment clone dsr-137(EU496887)	96	<i>Desulfobacteraceae</i>	-	
	1(1.5)	0	<i>Desulfococcus multivorans</i> strain DSM2059 (CP019913)	97	<i>Desulfobacteraceae</i>	-	
	1(1.5)	0	Sediment contaminated by petroleum clone Ebext-10 (FM212289)	95	<i>Desulfobacteraceae</i>	(2)	
	0	1(2.0)	Aarhus Bay sediment clone DSRI-7 (AM408827)	96	<i>Desulfobacteraceae</i>	(3)	
	1(1.5)	0	Ulleung Basin sediment clone UBM1D80.73 (JN798936)	96	<i>Desulfobacteraceae</i>	(4)	
	1(1.5)	0	Arctic marine sediment clone AH4_1 (KF896973)	98	n. d.	-	
	1(1.5)	1(2.0)	Arctic marine sediment clone AH4_26 (KF896976)	98	n. d.	-	
II	0	3(6.1)	Harbor sediment clone VHS057 (DQ112190)	96-98	<i>Desulfobulbaceae</i>	(5)	
	0	1(2.0)	Salt marsh sediment clone AA_JR_04 (KP992730)	90	<i>Desulfobulbaceae</i>	(6)	
III	33(50.8)	23(46.9)	Aarhus Bay clone B02 (JQ304781)	95-99	<i>Syntrophobacteraceae</i>	(1)	
	4(6.2)	3(6.1)	Aarhus Bay clone A18 (JQ304763)	95-98	<i>Syntrophobacteraceae</i>		
IV	1(1.5)	0	Puget sound sediment clone T1Adsr_G01 (DQ996890)	99	n. d.	(7)	
	5(7.7)	0	Arctic marine sediment clone J5-3 (KF896911)	96-97	n. d.	-	
V	1(1.5)	0	Nankai Trough deep-sea sediment clone NTd-V07 (AB263178)	98	Unknown	(8)	
	1(1.5)	0	Aarhus Bay clone A19 (JQ304765)	98	Unknown	(1)	
	5(7.7)	1(2.0)	Arctic marine sediment clone AH1_13 (KF896963)	94-98	n. d.	-	
	2(3.1)	0	Intertidal sand flat clone fosws7f8 (CT025836)	90	Unknown	(9)	
	0	2(4.1)	Guaymas Basin hydrothermal vent sediment clone B04P004 (AY197450)	92	Unknown	(10)	
	0	2(4.1)	Sulfate reduction zone sediment slurry incubated with 13C-aceate clone 12CSRZ_DSRPort4 (FN424347)	94	Unknown	(11)	
	4(6.2)	3(6.1)	Pearl River Estuary sediment clone MidDsr71 (FJ748842)	88-96	Unknown	(12)	
	1(1.5)	0	Pearl River Estuary sediment clone BotDsr73 (FJ748843)	98	Unknown		
	1(1.5)	1(2.0)	Pearl River Estuary sediment clone TopDsr59 (FJ748835)	90	Unknown		
	0	2(4.1)	Pearl River Estuary sediment clone TopDsr2 (FJ748839)	87	Unknown		
	0	4(8.2)	Pearl River Estuary sediment clone TopDsr78 (FJ748838)	96	Unknown		
	0	1(2.0)	Pearl River Estuary sediment clone TopDsr35 (FJ748832)	98	Unknown		
No. of clones	65	49					
No. of OTUs	42	28					
Good's Coverage (%) ^b	35	43					

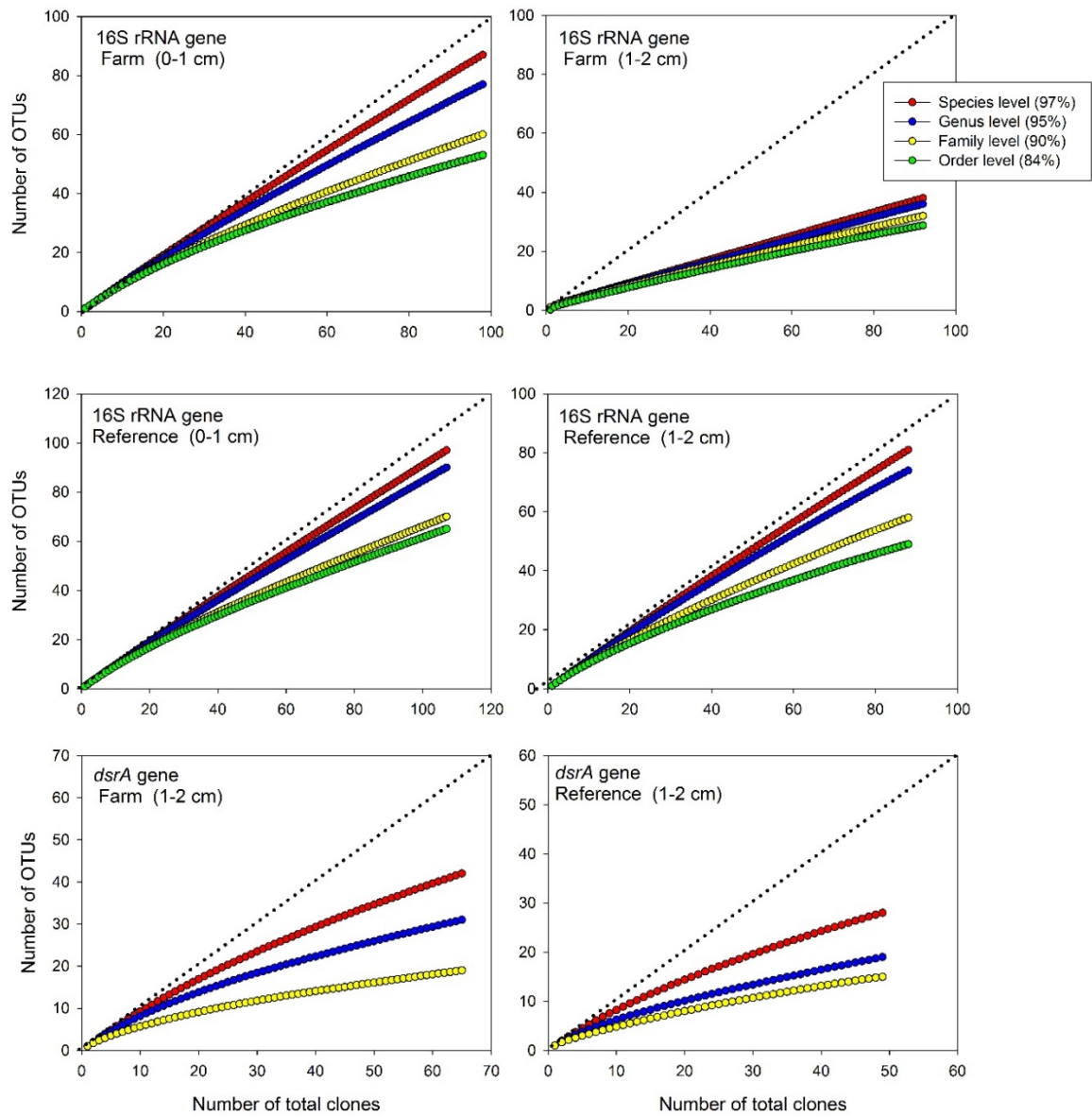
(1) de Reznde et al (2013); (2) Giloteaux et al (2010); (3) Leloup et al (2009); (4) Cho et al (2017); (5) Zhang et al (2008); (6) Angermeyer et al (2016); (7) Tiquia et al (2008); (8) Kaneko et al (2007); (9) Mussmann et al (2005); (10) Dhillon et al (2003); (11) Webster et al (2010); (12) Jiang et al (2009)

n.d.= no data

^a Affiliation of *dsrA* clones as inferred from Fig.4

^b Good's coverage (%) = $[1-(n/N)] \times 100$ (n, the number of OTUs; N, the total number of clones)

Fig. S1. Rarefaction curves showing the relationship between number of sequences and OTUs observed. Rarefaction curve for individual bacterial 16S rRNA gene and *dsrA* gene clone libraries from the farm and reference sediments. The values in brackets (97%, 95%, 90% and 84%) represent 3%, 5%, 10% and 16% 16S rRNA gene and *dsrA* gene sequences variation using MOTHUR program.



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