

Supplementary Tables

Table S1. Horseradish peroxidase (HRP)-labelled oligonucleotide probes used for CARD-FISH. Helper and competitor oligonucleotides were not labelled.

Probe	Specificity	Sequence (5'-3')	FA (%)	Reference
EUB I-III	most Bacteria	GCWGCCWCCCGTAGGWT	35	Amann <i>et al.</i> (1990) Daims <i>et al.</i> (1999)
NON338	Negative control	ACTCCTACGGGAGGCAGC		Wallner <i>et al.</i> (1993)
GAM42a*	most <i>Gammaproteobacteria</i>	GCCTTCCCACATCGTTT	35	Manz <i>et al.</i> (1992)
ROS537	<i>Roseobacter</i> -clade bacteria (RCB)	CAACGCTAACCCCTCC	35	Eilers <i>et al.</i> (2000)
DSS658	many marine <i>Desulfobacteraceae</i> including the <i>Desulfosarcina</i> / <i>Desulfococcus</i> -group	TCCACTTCCCTCTCCAT	50	Manz <i>et al.</i> (1998)
DSB706	many marine <i>Desulfobulbaceae</i>	ACCGGTATTCCTCCCGAT	40	Loy <i>et al.</i> (2002)
Delta495 a-c*	most <i>Deltaproteobacteria</i>	AGTTAGCCGGTGCTTCCT AGTTAGCCGGCGCTTCCT AATTAGCCGGTGCTTCCT	35	Lücker <i>et al.</i> (2007)
DSS1431*	subgroup of Sva0081-MBG	GGTTTGCCCAACGACTTC	30	This study
cDSS1431a [†]	Competitor to probe DSS1431	GGTTTGCCCAACAACCTTC	30	This study
cDSS1431b [†]	Competitor to probe DSS1431	GGTTAGCCCAACAACCTTC	30	This study
cDSS1431c [†]	Competitor to probe DSS1431	GGTTGCGCCACCAACCTTC	30	This study
cDSS1431d [†]	Competitor to probe DSS1431	AGTTTGCCCAACAACCTTC	30	This study
cDSS1431e [†]	Competitor to probe DSS1431	GGTTGCGCCCAACAACCTTC	30	This study
DSS1431us [‡]	Helper to probe DSS1431	TGGTACAACCAACTCTCATGG	30	This study
DSS1431us [‡]	Helper to probe DSS1431	TTAGGCGCCTGCATCCCCGAA	30	This study
DSS1431us [‡]	Helper to probe DSS1431	TTAGGCGCCTGCATCCTGTAAA	30	This study

FA, formamide; * probes were used with published competitors; [†] competitor oligonucleotide; [‡] helper oligonucleotide

Table S2. Relative abundances of ^{14}C -acetate-assimilating cells as determined by microautoradiography and DAPI staining or hybridization with specific CARD-FISH probes in duplicate whole sediment cores incubated with ^{14}C -acetate.

Sorted population	% of all MAR-positive cells (core A/B)	% MAR-positive of hybridized cells (core A/B)
<i>Gammaproteobacteria</i>	59/61	19/19
<i>Roseobacter</i> -clade bacteria (RCB)	6/8	48/32
<i>Deltaproteobacteria</i>	8/4	9/7

Table S3. Average cell-specific ^{14}C -acetate assimilation rates of flow-sorted populations from duplicate whole core and slurry incubations. Cells were either labelled by CARD-FISH (16S rRNA) or by Nile Red-staining (polyhydroxyalkanoate, PHA).

Sample type	Cell-specific assimilation rates (fg C cell ⁻¹ d ⁻¹)						PHA* (min-max)
	<i>Bacteria</i>	<i>Gamma-proteob.</i>	RCB	<i>Desulfobacteraceae</i> Sva0081	<i>Desulfo- bulbaceae</i>		
core incubations A/B:							
0-1 cm	3.8/1.3	5.5/3.9	9.7/7.8	3.3/2.5	n.d.	4.9/7.1	
2-3 cm	0.2/0.3	0.6/0.8	0.1/1.3	0.9/0.6	n.d.	1.3/3.0	
6-7 cm	0.2/0.2	0.3/0.2	0.4/0.5	0.3/0.2	n.d.	0.8/1.6	
slurry incubations A/B:							
oxic	3.5/5.8	11.9/17.6	3.8/5.3	1.1/1.2	2.7/2.8	2.5/3.0	1-26
anoxic	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	1-20

n.d., not determined; * polyhydroxyalkanoates stained with Nile red

References:

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