The following supplement accompanies the article

Changes in bacterial diversity in response to dissolved organic matter supply in a continuous culture experiment

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Supplement. The supplement contains 5 tables each providing a detailed description of the taxonomy of the sequences obtained for the initial community (Table S1) and the continuous cultures (Tables S2 to S5)

Table S1. Description of the initial bacterial community, prior to incubation in the continuous cultures. Percentages of the total sequences belonging to each considered phylogenetic group are given. Phylogenetic affiliation was done using the RDP classifier against the Greengenes database. 'Other' refers to pooled assemblages of groups with low sequence numbers or that were not assigned

Phylum	Class	Order	Family	% of total sequences
Proteobacteria				77.87
	Alphaproteobacteria			58.37
		Rhodospirillales	*Rhodospirillaceae*	6.00
		Rickettsiales		48.51
			Pelagibacteraceae	32.73
			Other	15.78
		Other		3.87
	Betaproteobacteria			0.73
	Deltaproteobacteria			3.75
		Sva0853		3.48
		Other		0.27
	Gammaproteobacteria			14.43
		Alteromonadales		0.88
			Alteromonadaceae	0.41
			Other	0.47
		Chromatiales		1.46
		HTCC2188		2.02
		Oceanospirillales		8.58
			Alcanivoracaceae	0.15
			Halomonadaceae	8.08
			Thiohalorhabdaceae	0.26
			Other	0.49
		Other		1.5
	Other			0.59
Bacteroidetes				0.56
	Flavobacteria			0.47
		Flavobacteriales		0.38
			Flavobacteriaceae	0.29
			Other	0.09
	Other			0.09
	Sphingobacteria	*Sphingobacteriales*		0.09
Actinobacteria				1.90
	Acidimicrobiia	*Acidimicrobiales*		1.70
			OCS155	1.32
			ZA3409c	0.26
			Other	0.12
	Actinobacteria	*Actinomycetales*		0.20
Cyanobacteria	*Synechococcophycideae*	*Synechococcales*	*Synechococcaceae*	13.26
SAR406	AB16			3.28
		Arctic96B-7	A714017	3.10
		Other		0.18
Verrucomicrobia				0.69
	Pedosphaerae	Arctic97B		0.15
	Opitutae			0.18
		Pelagicoccales	*Pelagicoccaceae*	0.03
		Puniceicoccales	*Puniceicoccaceae*	0.15
	Verrucomicrobiae	*Verrucomicrobiales*	*Verrucomicrobiaceae*	0.36
			Other	0.18
Other				2.46

Table S2. Percentage of sequences belonging to phylogenetic groups within *Gammaproteobacteria* after 3 and 5 generations in the control treatment and the replicate +DOM treatments. Phylogenetic affiliation was done using the RDP classifier against the Greengenes database. 'Other' refers to pooled assemblages of groups with low sequence numbers or that were not assigned

			3 generations			5 generations		
			Control	+DOM1	+DOM2	Control	+DOM1	+DOM2
Order	Family	Genus	% of total sequences					
	Sum of *Gammaproteobacteria*		98.54	92.68	91.01	94.82	89.17	86.50
Alteromonadales			21.55	42.33	62.79	53.16	76.99	80.30
	Alteromonadaceae		20.08	37.12	55.62	52.87	75.64	78.86
		Alteromonas	13.93	10.30	16.86	0.06	0.94	1.35
		BD2-13	0	0.03	0.15	0	0	0
		Glaciecola	0.12	0.88	1.46	0.06	0.67	1.90
		HTCC2207	0	0	0	0	0.03	0.09
		Marinobacter	0.20	0	0	0.03	0.03	0.03
		Umboniibacter	0	0.20	0.15	0	0	0.09
		ZD0117	0.06	0.06	0.23	0.03	0	0.26
		Other	5.77	25.65	36.77	52.7	73.97	75.15
	Colwelliaceae		0	0.09	0.09	0	0	0
		Colwellia	0	0	0.03	0	0	0
		Other	0	0.09	0.06	0	0	0
	J115		1.26	0.88	1.26	0.12	0.26	0.23
	OM60		0	0	0	0	0.15	0.06
	Pseudoalteromonadaceae		0.18	3.98	5.21	0.03	0.91	0.97
		Pseudoalteromonas	0.18	3.95	5.18	0.03	0.91	0.97
		Other	0	0.03	0.03	0	0	0
	Shewanellaceae		0	0.09	0.03	0	0	0
	Other		0.03	0.18	0.59	0.15	0.03	0.18
Chromatiales			0	0	0	0.12	0.06	0.03
Enterobacteriales	*Enterobacteriaceae*		0	0	0	0	0	0.06
HTCC2188			0.41	1.76	1.23	1.32	0.38	1.46
	HTCC2089		0	0.09	0.26	0.12	0	0.70
	HTCC2188		0.41	1.67	0.97	1.20	0.35	0.76
	Other		0	0	0	0	0.03	0
Oceanospirillales			72.04	41.86	7.64	36.50	9.48	1.08
	Alcanivoracaceae		52.37	27.87	4.54	0.64	0.64	0.32
		Alcanivorax	52.37	27.87	4.54	0.59	0.64	0.32
		Other	0	0	0	0.06	0	0
	OM182		0	0.03	0	0	0.12	0.06
	Oceanospirillaceae		16.69	9.81	1.43	33.23	8.55	0.53
		Marinomonas	0	0.03	0.03	0	0	0
		Oleibacter	1.61	6.18	0.29	0	0	0
		Oleispira	2.37	0	0	0	0	0
		Neptuniibacter	9.31	1.80	0.79	32.69	0	0.32
		Other	3.39	1.80	0.32	0.54	8.55	0.21
	Oleiphilaceae		0.18	0.09	0.06	0	0	0
	Other		2.81	4.07	1.61	2.63	0.18	0.18
Thiotrichales	*Piscirickettsiaceae*		3.28	5.83	14.14	2.96	1.96	3.37
		Cycloclasticus	0	0	0	0.09	0	0.09
		Methylophaga	3.28	5.83	14.02	2.87	1.96	3.16
		Other	0	0	0.12	0	0	0.12
Vibrionales	*Vibrionaceae*		0	0.41	4.77	0	0	0
		Vibriofortis	0	0.03	0	0	0	0
		Other	0	0.38	4.77	0	0	0
Xanthomonadales	*Sinobacteraceae*		0	0	0	0.09	0	0
Other			1.26	0.50	0.44	0.67	0.29	0.20

Table S3. Percentage of sequences belonging to phylogenetic groups within *Alphaproteobacteria* after 3 and 5 generations in the control treatment and the replicate +DOM treatments. Phylogenetic affiliation was done using the RDP classifier against the Greengenes database. 'Other' refers to pooled assemblages of groups with low sequence numbers or that were not assigned

Order	Family	Genus	3 generations			5 generations		
			Control	+DOM1	+DOM2	Control	+DOM1	+DOM2
			% of total sequences					
	Sum of *Alphaproteobacteria*		1.23	3.10	5.24	3.19	5.50	8.05
Kiloniellales			0	0	0	0.03	0	0.64
Rhizobiales			0	0.23	0.47	0.03	0.41	0.44
	Hyphomicrobiaceae		0	0.03	0	0.03	0.09	0.09
	Other		0	0.20	0.47	0	0.32	0.35
Rhodobacterales			1.08	2.25	3.86	2.75	2.08	5.09
	Hyphomonadaceae		0	0.03	0.03	0.23	0	0.12
		Hyphomonas	0	0	0.03	0.06	0	0
		Maricaulis	0	0	0	0	0	0.09
		Oceanicaulis	0	0	0	0	0	0.03
		Other	0	0.03	0	0.18	0	0
	Rhodobacteraceae		1.08	2.22	3.83	2.52	2.08	4.98
		Anaerospora	0.44	0.53	0.91	1.64	0.41	2.17
		Loktanella	0	0.03	0.03	0	0	0
		Octadecabacter	0	0	0.03	0	0	0
		Phaeobacter	0.47	0.70	0.85	0.41	0.97	1.58
		Thalassobius	0	0	0	0	0	0.03
		Other	0.17	0.97	2.02	0.47	0.70	1.20
Rhodospirillales	*Rhodospirillaceae*		0	0	0.06	0	1.93	1.05
Rickettsiales			0.15	0.56	0.64	0.38	0.32	0.56
	AEGEAN 112		0	0	0.03	0	0	0
	Pelagibacteraceae		0.15	0.26	0.47	0.15	0.15	0.41
	Other		0	0.29	0.15	0.23	0.18	0.15
Sphingo-monadales			0	0	0.12	0	0	0
	Sphingomonadaceae		0	0	0.06	0	0	0
		Sphingopyxis	0	0	0.06	0	0	0
		Other	0	0	0.06	0	0	0
	Other		0	0	0.06	0	0	0
Other			0	0.06	0.09	0	0.76	0.26

Table S4. Percentage of sequences belonging to phylogenetic groups within *Bacteroidetes* after 3 and 5 generations in the control treatment and the replicate +DOM treatments. Phylogenetic affiliation was done using the RDP classifier against the Greengenes database. 'Other' refers to pooled assemblages of groups with low sequence numbers or that were not assigned

Class	Order	Family	Genus	3 generations			5 generations		
				Control	+DOM1	+DOM2	Control	+DOM1	+DOM2
				% of total sequences					
Sum of *Bacteroidetes*				0.20	3.25	2.28	0.38	1.52	1.05
Bacteroidia	*Bacteroidales*	*Prevotellaceae*	*Prevotella*	0	0	0	0	0.03	0
Flavobacteria				0.20	3.22	2.20	0.38	0.76	0.76
	Flavo-bacteriales			0.20	2.96	2.05	0.35	0.44	0.64
		Cryomorphaceae		0	0.35	0.06	0	0	0
		Flavo-bacteriaceae		0.20	2.58	1.87	0.29	0.44	0.59
			Leeuwenhoekiella	0	0	0.18	0	0	0
			Polaribacter	0	0.06	0	0	0	0
			Sediminicola	0	0.06	0.32	0	0	0.35
			Tenacibaculum	0	0.15	0.06	0	0	0
			Other	0.20	2.31	1.32	0.29	0.44	0.23
		Other		0	0.03	0.12	0.06	0	0.06
	Other			0	0.26	0.15	0.03	0.32	0.12
Sphingo-bacteria	*Sphingo-bacteriales*			0	0.03	0.09	0	0.70	0.26
		Balneolaceae		0	0	0.09	0	0.15	0.06
		Ekhidnaceae		0	0	0	0	0	0.15
		Saprospiraceae		0	0.03	0	0	0.56	0
			Aureispira	0	0.03	0	0	0.53	0
			Other	0	0	0	0	0.03	0
		Other		0	0	0	0	0	0.06
Other				0	0	0	0	0.03	0.03

Table S5. Percentage of sequences belonging to phylogenetic groups within *Betaproteobacteria*, *Deltaproteobacteria*, *Epsilonproteobacteria*, *Verrucomicrobia* and *Cyanobacteria* after 3 and 5 generations in the control treatment and the replicate +DOM treatments. Phylogenetic affiliation was done using the RDP classifier against the Greengenes database. 'Other' refers to pooled assemblages of groups with low sequence numbers or that were not assigned, except for the sequences not assigned at the phylum level

Class	Order	Family	Genus	3 generations			5 generations		
				Control	+DOM1	+DOM2	Control	+DOM1	+DOM2
				% of total sequences					
Other *Proteobacteria*				0	0.21	0.09	1.47	3.46	3.71
Betaproteobacteria	*Methylo philales*	*Methylophilaceae*		0	0	0	0	0.12	0
			Methylotenera	0	0	0	0	0.03	0
			Other	0	0	0	0	0.09	0
Deltaproteobacteria				0	0.12	0	1.35	3.34	3.48
	Bdello-vibrionales	*Bacterio-voracaceae*	*Bacteriovorax*	0	0	0	0	0.03	0.09
	Myxococcales	OM27		0	0.12	0	1.35	3.31	2.61
	Other			0	0	0	0	0	0.79
Epsilon-proteobacteria	*Campylo-bacterales*	*Campylo-bacteraceae*	*Arcobacter*	0	0.03	0	0	0	0
Other				0	0.06	0.09	0.12	0	0.23
Verrucomicrobia				0	0.50	0.88	0	0.09	0.50
Opitutae				0	0	0	0	0	0.33
	Pelagicoccales	*Pelagicoccaceae*	*Pelagicoccus*	0	0	0	0	0	0.18
	Other			0	0	0	0	0	0.15
Verrucomicrobiae	*Verruco-microbiales*	*Verruco microbiaceae*		0	0.50	0.88	0	0.09	0.32
Cyanobacteria				0	0.09	0.20	0	0.12	0
Synecho-coccophycideae	Synechococcales	Synechococcaceae	*Prochlorococcus*	0	0.09	0.20	0	0.12	0
Other				0.03	0.06	0.26	0.15	0.06	0.06
Not assigned				0	0.12	0.03	0	0.09	0.12