Table 1 Comparison of n-damo bacteria enrichments available in the literature

Source	Origin of inoculum	Scale (L)	CH_4 supply	Anaerobic control	T (°C)	pH	Stir	Medium supply	Headspace-CH_4
Hu et al. (2009)	Mixture of sediments from freshwater lake, anaerobic digester sludge+return sludge from WWTP	2 (1.6 L liquid)	headspace was flushed periodically with mixed gas (N_2, CH_4 and CO_2)	……	22 35 45[4]	….	…	Nitrate added periodically	1.1–1.3 atm; He injected for confirming no gas leakage
Hu et al. (2011)	Parent culture from Hu et al. (2009) [Culture A (320 ml) + Culture B (160 ml) inocula]	2; (1.6 L liquid)	5%N_2+90%CH_4+5%CO2 to flush headspace regularly with a P_{CH4}(0.5-1 atm)	N2 sparged into medium, then placed in an anaerobic chamber for 24 hours before it was used	35	7.0-7.5	200 rpm	20 min settling; 400 ml fresh medium exchanged /4 weeks[NO_3^-: 1-10mM; NO_2^-: 1ml/72min-daily]	+80ml He into for increasing P > 1.2 atm after each flushing
Ettwig et al. (2008)	Biomass (1.5 liters) from an enrichment culture in Raghoebarsing et al. (2006)[7]	16; SBR (13 L liquid)	CH_4-CO_2 95:5%; 10 ml/min	Ar-CO_2 95:5% (Continuously sparged in reactor and medium)	30	7.3-7.6	200 rpm	Continuous supply; 0.2-0.8 L/day with nitrite conc. 3-15 mM(keep NO_2^+: 0-1 mM)	……
	Biomass After 13 months enrichment from the above[2]	0.3 (0.22 liquid)	…….	Ar-CO_2 95:5%	30	….	Stirrer	……..	6% (2.5% when measuring)
Ettwig et al. (2009)	Mixture sludge (2 liters) from four ditches draining agricultural land (upper 5 cm);	16; SBR (10-13 L liquid)	CH_4-CO_2 95:5%; 10 ml/min[1]	6 cycles of vacuuming and subsequent gassing with Ar-CO_2 95:5, then 5 min of Ar-CO_2, leaving 0.5 10^5 overpressure (100 ml/min)	30	6.9-7.5	100 rpm Gently	0.3-1 L/day (pending on nitrite conc.: 0.2-1.5 mM)	Final conc.: 2.5 to 10%
	Biomass After 230 days enrichment from the above	Batch study according to Ettwig et al. (2008)							
Luesken et al. (2011b)	Enriched biomass from the bellow 15 L bioreactor	3; SBR	CH_4-CO_2 95:5%; 10 ml/min	Ar-CO_2 95:5% (Continuously sparged in reactor and medium)	------	6.8-7.3	100 rpm	23.2 h/day; 0.3-1 L/day pending on nitrite conc.; (To maintain nitrite: 0.1-1 mM)	0.3 L; 4% (5.3%, 4.8% when measured on day 308,315)
	WWTP in Lieshout	15; SBR							
Luesken et al. (2011a)	N-damo culture from Ettwig et al. (2009) (1 liter)	3; SBR	CH_4-CO_2 95:5%; 12 ml/min (Continuously flushed)	Ar-CO_2 95:5% 10 ml/min (Vessel flushed)	30	7.3-7.6	200 rpm	Synthetic medium from Ettwig et al. (2009)	…….
Zhu et al. (2011)	500 mL Anammox granules from WWTP (van der Star et al. 2007)	2 liquid; SBR	>60 days, CH_4 10 ml/min[1] supplied with NO_2^+	SBR operated according to Luesken et al. (2011a)	Room temp.	7.2	…	Nitrite: ammonium=4:3	Always above 20% (255 µM)

Ref.	Nitrite reduction /Test time (Operating days)	Methane oxidation /Test time	Detection /Sample volume	FISH detection after X time	Observed stoichiometry
Hu et al. (2009)	0.065 mmol NO_3^- /day (day 220-260) 3.2 mmol NO_3^- /day (day 283-312)[8] **……..(320 days in total)**	0.038 mmol/day (day 220-260) 2.4 mmol/day (day 283-312) ……	GC/MS for 13C-SIP	270 day: no archaea 15% NC10 297 d: 40% archaea 50% NC10 ….	Consuming 16.7% more methane than predicted
Hu et al. (2011)	1.97 mmol/day for A (NO_2^- only, day 90-94) 0.062 mmol NO_3^-/day for B (NO_3^- only, day 50-105) **(150 days in total)**	A: close to calculated value B: 0.045 mmol/day	Test strip nitrite limit control daily FIA for NH_4^+ NO_2^- NO_3^-(1ml) GC-40 °C for CH_4, N_2; 90 °C for He	Archaea disappeared after day 100 in A	B: 13.3% > stoichiometrical predicted: 0.039 mmol CH_4/day
Ettwig et al. (2008)	Around 3.5(mmol/day) for 13 months Only increased (≈9) till 450 ml new source added after 17, 19 months(**22 months in total**) 3.7 nmol /min/mg protein after 22 m	1.7 nmol /min/mg protein after 22 m; Test length: 36 h	Merckoquant test strip: NO_2^-, NO_3^- GC: 65 °C-- N_2; 120 °C--CH_4; BCA assay: total protein 100 µl gas; 1 ml liquid collected HPLC-UV: NO_2^-:NO_3^-;10µl used GC: CH4;	Monthly, >70% NC10 all the time Archaea disappear from 10 to12 month	8:3.6=Consumption of NO_2^-:CH_4 (? 8:3 Stated by Ettwig et al, 2009) 5:1=NO_2^-:NO_3^- (21 h)
Ettwig et al. (2009)	Max=33.5 (mmol/day); 217(**243 days in total**) 4.7to5.1(nmol /min/mg protein^{-1}; red/ grey stopper) Day 136-142 3.4to5.6(nmol /min/mg protein); 2 months period with 4.75 protein	1.6to2.2(nmol /min/mg protein; red/grey stopper); Day 136-142 with bioreactor stop; tested in batches; Test length: 32 h	The same to the above except: 50 µl gas GC/MS-80 ℃ for N_2 (5 min)	5 m-can be used 6 m-be dominant[6] 7 m-70% n-damo	8:3.5=Consumption of NO_2^-:CH_4
Luesken et al. (2011b)	After 70 d, activity increased (**308 d in total**) 0.4 mmol/day (day 112); 1.1 after day 175; 0.9 (nmol /min/mg protein) on day 308,315; 1.2 after day 315 2.1 (nmol NO_2^- /**h**/mg protein); 9.2 (nmol NO_3^- /**h**/mg protein); Denitrifying activity decresed	0.3 (nmol /min/mg protein) on day 308,315; 0.5 after day 315 Test length: 10 h 1.7 (nmol /**h**/mg protein)	Routine nitrite analysis daily Batch exp. On day 308, 315 and Analysis according to Ettwig et al, 2008	64 days-detected 2-3%; 308 days-60-70% n-damo No n-damo detected	9.8NO_2^-:3CH_4 (day 308,315) 10.1NO_2^-:3CH_4 (day 308,315) …….
Luesken et al. (2011a)	8.1 (nmol /min/mg protein) on 49 d; 17.2 mmol/day after day151 (?No data shown) 15.4 (nmol /min/mg protein) on day 142 (with anammox); 5.0 after 3 h when ammonium depleted (its rate was 9.0) [**161 days in total**]	3.1 (nmol /min/mg protein) on 49 d (then NH_4^+ added); Coculture with anammox, (responsible for 77% NO_2^+↓ and constituted 50%	Analysis according to Ettwig et al. (2008)	45 days-80% n-damo no anammox; 108 days- 5% anammox 151 days, 50% of each	8.1NO_2^-:3CH_4 (day 49)

Ref.	Nitrite reduction /Test time (Operating days)	Methane oxidation /Test time	Detection /Sample volume	FISH detection after X time	Observed stoichiometry
Zhu et al. (2011)	21.8 mmol/day after 2 months**[1 year in total]** 13.9 mmol/l per day after 1 year; 8.4 for ammonium (Coculture with anammox,)	1.6 (nmol /min/mg protein)[0.7 mmol/l per day] after 1 year Test length: 100 min	……..	1 year is necessary	$8NO_2^-$:$3CH_4$ (1 year later)

Notes:

1 3-7days supply+1-2 h settling+ 30-60 min pumping out liquid. As activity increased, after 6 months the cycle was shortened to 22.5h of supply of medium, 1 h of settling, and 30 min of drawing off of liquid.

2 After being made anoxic by thorough flushing with a mixture of Ar/CO_2 (95:5), culture liquid from the enrichment culture was being pumped through at a flow rate of 17.5 ml/min; After c. 24 h (accounting for at least 110 volume changes) it was disconnected from the main culture vessel by closing the influent and effluent tubes.

3 23.2 h supply+20 min settling+ 30 min pumping out liquid.

4 Stopped on day 90 as no denitrification was detected after day 40.

5 The use of black butyl rubber stoppers caused total inhibition of the activity of methane oxidation. Anoxic handling of the biomass, in contrast, was not crucial; exposure to oxygen during transfer to the bottles did not lead to lower activity.

6 Even though NC10 phylum bacteria already accounted for more than 50% of the population in the enrichment culture, they were not detected in a clone library (31 clones) obtained after 6 months with general 16S rRNA gene primers (primers 8F and 1545R). Instead, this library was dominated by uncultured *Acidobacteria* (11 clones) and *Chloroflexi* (10 clones) (data not shown).

7 FISH showed that upon inoculation the population was dominated by a bacterium affiliated with the phylum NC10 (approximately 80%) and an archaeon of the order *Methanosarcinales* (approximately 10%)

8 Decreased to 0.3 mmol NO_3—N/day in 40 days; Increased after 220d to 2.0 on day 312 (35 °C); 0.14 without methane supply; 0.11 for day 50-260 (22 °C)

Table 2 A summary of 16S rDNA PCR primers currently used for detecting n-damo bacteria from environmental samples

Primer	Froward/ Reverse	Position	Sequence (5'-3')	Speciality	References
202F	Froward	202-230	GAC CAA AGG GGG CGA GCG	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)
NC10-202Fdeg	Froward	202-230	RAC CAA AGG RGG CGA GCG	*M. oxyfera* 16S rDNA	Deutzmann and Schink (2011)
1492R	Reverse	1510-1529	GGT TAC CTT GTT ACG ACT T	Bacterial 16S rDNA	Lane (1991)
8F	Froward	8-27	AGA GTT TGA TYM TGG CTC AG	Bacterial 16S rDNA	Juretschko et al. (1998)
1043R	Reverse	1042-1060	TCT CCA CGT TCC CTT GCG	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)
1043Rb	Reverse	1042-1060	TCT CCA CGC TCC CTT GCG	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)
NC10-1043Rdeg	Reverse	1042-1060	TCT CCR CGY TCC CTT GCG	*M. oxyfera* 16S rDNA	Deutzmann and Schink (2011)
1545R	Reverse	1529-1545	CAK AAA GGA GGT GAT CC	Bacterial 16S rDNA	Juretschko et al. (1998)
qP1F	Froward	1001-1024	GGG CTT GAC ATC CCA CGA ACC TG	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)
qP1R	Reverse	1180-1201	CGC CTT CCT CCA GCT TGA CGC	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)
qP2F	Froward	1169-1189	GGG GAA CTG CCA GCG TCA AG	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)
qP2R	Reverse	1440-1460	CTC AGC GAC TTC GAG TAC AG	*M. oxyfera* 16S rDNA	Ettwig et al. (2009)

Table 3 A summary of *pmoA* gene-based PCR primers specific for n-damo bacteria currently used

primer	Froward/ Reverse	Position	Sequence (5'-3')	GC%	Tm (ºC)	Test 1	Test 2	Test 3	Test 4	References
A189_b	Forward	121-138	GGN GAC TGG GAC TT**Y** TGG	55.6	64.5-69.4	+*	+	+	+	Luesken et al. (2011c)
cmo682	Reverse	637-654	AAA **Y**CC GGC **R**AA GAA CGA	44.4	61-65.8	-	-	+	+	Luesken et al. (2011c)
cmo182	Forward	167-184	TCA CGT TGA CGC CGA TCC	61.1	66.5	-	+	+	+	Luesken et al. (2011c)
cmo568	Reverse	537-556	GCA CAT AC***T*** CCA TCC CCA TC	55.0	63.9	-	-	+	+	Luesken et al. (2011c)
NA638Rdeg	Reverse	593-612	RAA TGT TCG RAG CGT VCC BC	45.0	59.5-70.0	+	+	+	+	Deutzmann and Schink (2011)
NA720R	Reverse	675-694	TCC CCA TCC ACA CCC ACC AG	65.0	69.6	-	-	+	+	Deutzmann and Schink (2011)
682_NC10	Reverse	637-654	AAA **T**CC GGC **G**AA GAA CGA	50.0	63.0	-	-	+	+	Kojima et al. (2012)
HP3F1	Forward	209-233	CCC AGT ACT TCA TGT GGG ARA ARA T	40.0	59.3-61.8	+	+	+	+	Han and Gu (2013)
HP3R1	Reverse	463-484	GGG GGC CAG CCA NRY CCA RTT	57.1	68.1-78.0	+	+	+	+	Han and Gu (2013)

* Test 1: Hairpins; Test 2: Self complementarity; Test 3: False priming in target group (FP565575 *M. oxyfera*); Test 4 False priming in excluded group (DQ119048 *Methylosinus sporium*); "+" means observed while "-" means not;

** A189f (general *pmoA* primer; 5'-3'): GGN GAC TGG GAC TT**C** TGG (Holmes et al. 1995); key differences within the same priming site are highlighted in bold.

Table 4 A summary and analysis of n-damo bacteria from different habitats based on *pmoA* gene sequences*

Source/Environment	N-damo related clone	OTU	Shannon-Wiener	Chao1	Type	Accession number in GenBank	Reference**
CF5S	21	2	0.6365	1	M/R	KJ023443, KJ023450	Chen et al. (2014)
CF5B	4	1	0	1	M/R	KJ023444	Chen et al. (2014)
E201S	8	2	0.3768	1	M/R	KJ023445-KJ023446	Chen et al. (2014)
E407S	6	2	0.4506	1	M/R	KJ023447-KJ023449	Chen et al. (2014)
E407B	24	2	0.3768	1	M/R	KJ023451, KJ023455	Chen et al. (2014)
E510S	16	2	0.2338	1	M/R	KJ023452, KJ023456	Chen et al. (2014)
E525S	24	1	0	1	M/R	KJ023453	Chen et al. (2014)
E525B	1	1	--	--	M/R	KJ023454	Chen et al. (2014)
						KF528962-KF528968	
SCS E704S	24	3	1.0055	1	M	KF528973-KF528984	Chen et al. (2015)
						KF742451-KF742455	
						KF528961	
SCS E401	13	3	0.9110	1	M	KF528969-KF528972	Chen et al. (2015)
						KF742444-KF742450	
Lake Constance	15	6	1.4878	10.5	F	HQ906565-HQ906579	Deutzmann and Schink (2011)
Lake Biwa	21	1	0	1	F	AB661605-AB661625	Kojima et al. (2012)
Reed bed	12	1	0	1	F	JX898463-JX898474	Han and Gu (2013)
Reservoir	9	7	1.8892	13.2500	F	JX898486-JX898494	Han and Gu (2013)
WWTP^	10	7	1.8344	19.5	E	JX898495-JX898504	Han and Gu (2013)
Paddy soil	11	2	0.3046	1	F	JX898475-JX898485	Han and Gu (2013)
Paddy soil	14	1	0	1	F	JN704402-JN704415	Wang et al. (2012)
Paddy field	20	2	0.1985	1	F	KC341611-KC341630	Zhu et al. (2015)
Jingshan paddy field	27	1	0	1	F	KC905857-KC905883	Hu et al. (2014)

Source/Environment	N-damo related clone	OTU	Shannon-Wiener	Chao1	Type	Accession number in GenBank	Reference**
Xixi wetland	21	3	0.3805	1	F	KC905884-KC905904	Hu et al. (2014)
XZ wetland	4	1	0	1	F	KC905905-KC905908	Hu et al. (2014)
FreshwaterWetlands (Jingshan Paddy; Xixi wetland; XZ wetland)	52	5	1.0575	1	F	KC905857-KC905908	Hu et al. (2014)
Baiyangdian Lake	24	1	0	1	F	KC341248-KC341271	Zhu et al. (2015)
Bosten Lake	16	2	0.4826	1	F	KC341301-KC341316	Zhu et al. (2015)
Chaohu Lake	19	6	1.1513	1	F	KC341317-KC341335	Zhu et al. (2015)
Dongting Lake	21	2	0.6920	1	F	KC341336-KC341356	Zhu et al. (2015)
Jiaxing C. wetland-winter	13	8	1.8393	26	F	KC341375-KC341387	Zhu et al. (2015)
Jiaxing Constructed wetland-summer	11	8	2.0198	12.1667	F	KC341388-KC341398	Zhu et al. (2015)
Subsurface North canal	18	2	0.6870	1	U	KC341272-KC341289	Zhu et al. (2015)
North canal-12 m	3	1	0	1	U	KC341298-KC341300	Zhu et al. (2015)
North canal-15 m	8	1	0	1	U	KC341290-KC341297	Zhu et al. (2015)
Panjin swamp	21	1	0	1	F	KC341437-KC341457	Zhu et al. (2015)
Peat land China	23	6	1.3944	8	F	KC341414-KC341436	Zhu et al. (2015)
Poyang Lake	21	2	0.5983	1	F	KC341458-KC341478	Zhu et al. (2015)
Shahe River	18	5	1.2094	1	F	KC341479-KC341496	Zhu et al. (2015)
Songhuajiang River	18	7	1.6715	9.25	F	KC341497-KC341514	Zhu et al. (2015)
Tarim River	19	2	0.6918	1	F	KC341515-KC341533	Zhu et al. (2015)
Tiaoxi River	20	3	0.9973	1	F	KC341534-KC341553	Zhu et al. (2015)
Tibetan Lake	10	1	0	1	S/R	JQ429431-JQ429432	Yang et al. (2012)
Tulufan River	18	3	0.8487	3	F	KC341357-KC341374	Zhu et al. (2015)
Wuliangshuhai Lake	24	4	0.9366	4.5	F	KC341554-KC341577	Zhu et al. (2015)

Source/Environment	N-damo related clone	OTU	Shannon-Wiener	Chao1	Type	Accession number in GenBank	Reference**
Yellow River	15	1	0	1	F	KC341399-KC341413	Zhu et al. (2015)
Yuanmingyuan Lake	12	3	0.7215	3.5	F	KC341698-KC341709	Zhu et al. (2015)
Pearl River-winter	20	5	1.0098	6	F	KC341578-KC341597	Zhu et al. (2015)
Pearl River-summer	13	2	0.6172	1	F	KC341598-KC341610	Zhu et al. (2015)
Donghu Lake	15	3	0.8033	1	F	KC341631-KC341645	Zhu et al. (2015)
Honghaitan Tidal Land	17	4	1.1151	4.5	C	KC341646-KC341662	Zhu et al. (2015)
Shangqiu Reservoir	17	7	1.6100	8.5	F	KC341663-KC341679	Zhu et al. (2015)
Tianchi Lake	18	9	1.8121	18	F	KC341680-KC341697	Zhu et al. (2015)
WWTP^	128	3	0.8487	1	U	KC700842-KC700715	Gao et al. (2013)
Soils^	40	3	0.3813	1	U	KC700675-KC700714	Gao et al. (2013)
Qiantang River	50	16	2.1437	29.5	F	KC503613-KC503662	Shen et al. (2014)
West Lake	24	8	1.5359	12	F	JX531974-JX531997	Zhu et al. (2013)
Jiaojiang estuary	80	20	2.3787	30.1250	C	KC512302-KC512381	Li-Dong et al. (2014)
Freshwater habitats (Alpine peat bog WWTPs^ Drainage ditch Contaminated aquifer^)	12	9	NA	NA	F/R	HQ698926-HQ698937	Luesken et al. (2011c)
WWTPs^	19	10	NA	NA	F/R	JF706214-JF706196	Luesken et al. (2011b)
SBR co-enrichment with anammox^	7	3	NA	NA	E/R	JN006731-JN006737	Luesken et al. (2011a)
Sewage treatment plants^	12	8	NA	NA	E/R	KC112371-KC112382	Ho et al. (2013)
Minerotrophic peatland^	3	3	NA	NA	E/R	JX262153-JX262155	Zhu et al. (2012)
Lab scale reactor^	13	3	1.0579	1	E/?	AB767281-AB767293	Masashi et al. (2013)

*Abbreviations: NA, not applicable; M, marine; F, freshwater; S, saline lake; C, coastal; U, unknown; E, enrichment; R, representative sequences available in the GenBank database only;

**Unpublished reference indicates that the related DNA sequences have already been released in the database without a published journal paper until 17-April-2014 when the information was accessed; OTU, Shannon-Wiener and Chao1 were recalculated using Fastgroup II (Yu et al. 2006) with the cutoff of 5%.

^Isolation sources/environments are not sedimen

References

Chen J, Jiang XW, Gu J-D (2015) Existence of Novel Phylotypes of Nitrite-Dependent Anaerobic Methane-Oxidizing Bacteria in Surface and Subsurface Sediments of the South China Sea. Geomicrobiol J 32: 1-9

Chen J, Zhou ZC, Gu J-D (2014) Occurrence and Diversity of Nitrite-dependent Anaerobic Methane Oxidation Bacteria in the Sediments of the South China Sea Revealed by Amplification of both 16S rRNA and pmoA Genes. Appl Microbiol Biotechnol 98: 5685-5696

Deutzmann JS, Schink B (2011) Anaerobic Oxidation of Methane in Sediments of Lake Constance, an Oligotrophic Freshwater Lake. Appl Environ Microbiol 77: 4429-4436

Ettwig KF, Shima S, van de Pas-Schoonen KT, Kahnt J, Medema MH, op den Camp HJM, Jetten MSM, Strous M (2008) Denitrifying bacteria anaerobically oxidize methane in the absence of Archaea. Environ Microbiol 10: 3164-3173

Ettwig KF, van Alen T, van de Pas-Schoonen KT, Jetten MSM, Strous M (2009) Enrichment and Molecular Detection of Denitrifying Methanotrophic Bacteria of the NC10 Phylum. Appl Environ Microbiol 75: 3656-3662

Gao J, Luo X, Wu G, Peng Y (2013) Occurrence of nitrite-dependent anaerobic methane oxidizing bacteria from different soil and wastewater sludge. NCBI Genbank web http://wwwncbinlmnihgov/nuccore/ Accessed 17 April 2014

Han P, Gu J-D (2013) A newly designed degenerate PCR primer based on pmoA gene for detection of nitrite-dependent anaerobic methane-oxidizing bacteria from different ecological niches. Appl Microbiol Biotechnol 97: 10155-10162

Ho A, Vlaeminck SE, Ettwig KF, Schneider B, Frenzel P, Boon N (2013) Revisiting methanotrophic communities in sewage treatment plants. Appl Environ Microbiol 79: 2841-2846

Holmes AJ, Costello A, Lidstrom ME, Murrell JC (1995) Evidence that particulate methane monooxygenase and ammonia monooxygenase may be evolutionarily related. FEMS Microbiol Lett 132: 203-208

Hu BL, Shen LD, Lian X, Zhu Q, Liu S, Huang Q, He ZF, Geng S, Cheng DQ, Lou LP, Xu XY, Zheng P, He YF (2014) Evidence for nitrite-dependent anaerobic methane oxidation as a previously overlooked microbial methane sink in wetlands. Proc Natl Acad Sci U S A 111: 4495-4500

Hu SH, Zeng RJ, Burow LC, Lant P, Keller J, Yuan ZG (2009) Enrichment of denitrifying anaerobic methane oxidizing microorganisms. Env Microbiol Rep 1: 377-384

Hu SH, Zeng RJ, Keller J, Lant PA, Yuan ZG (2011) Effect of nitrate and nitrite on the selection of microorganisms in the denitrifying anaerobic methane oxidation process. Env Microbiol Rep 3: 315-319

Juretschko S, Timmermann G, Schmid M, Schleifer KH, Pommerening-Roser A, Koops HP, Wagner M (1998) Combined molecular and conventional analyses of nitrifying bacterium diversity in activated sludge: Nitrosococcus mobilis and Nitrospira-like bacteria as dominant populations. Appl Environ Microbiol 64: 3042-3051

Kojima H, Tsutsumi M, Ishikawa K, Iwata T, Mussmann M, Fukui M (2012) Distribution of putative denitrifying methane oxidizing bacteria in sediment of a freshwater lake, Lake Biwa. Syst Appl Microbiol 35: 233-238

Lane DJ (1991) 16S/23S rRNA sequencing. In E. Stackebrandt and M. Goodfellow (ed). Nuleic acid techniques in bacterial systematics. John Weiley & Sons, New York, NY: 115-175

Li-Dong S, Qun Z, Shuai L, Ping D, Jiang-Ning Z, Dong-Qing C, Xiang-Yang X, Ping Z, Bao-Lan H (2014) Molecular evidence for nitrite-dependent anaerobic methane-oxidising bacteria in the Jiaojiang Estuary of the East Sea (China). Appl Microbiol Biotechnol

Luesken FA, Sanchez J, van Alen TA, Sanabria J, Op den Camp HJM, Jetten MSM, Kartal B (2011a) Simultaneous Nitrite-Dependent Anaerobic Methane and Ammonium Oxidation Processes. Appl Environ

Microbiol 77: 6802-6807

Luesken FA, van Alen TA, van der Biezen E, Frijters C, Toonen G, Kampman C, Hendrickx TL, Zeeman G, Temmink H, Strous M, Op den Camp HJ, Jetten MS (2011b) Diversity and enrichment of nitrite-dependent anaerobic methane oxidizing bacteria from wastewater sludge. Appl Microbiol Biotechnol 92: 845-854

Luesken FA, Zhu BL, van Alen TA, Butler MK, Diaz MR, Song B, den Camp HJMO, Jetten MSM, Ettwig KF (2011c) pmoA Primers for Detection of Anaerobic Methanotrophs. Appl Environ Microbiol 77: 3877-3880

Masashi H, Masafumi K, Masato K, Takashi Y (2013) Enrichment of denitrifying anaerobic methane oxidizing microorganisms using nitrate or nitrite as electron acceptor. NCBI Genbank web http://wwwncbinlmnihgov/nuccore/ Accessed 17 April 2014

Raghoebarsing AA, Pol A, van de Pas-Schoonen KT, Smolders AJP, Ettwig KF, Rijpstra WIC, Schouten S, Damste JSS, Op den Camp HJM, Jetten MSM, Strous M (2006) A microbial consortium couples anaerobic methane oxidation to denitrification. Nature 440: 918-921

Shen LD, Zhu Q, Liu S, Du P, Zeng JN, Cheng DQ, Xu XY, Zheng P, Hu BL (2014) Molecular evidence for nitrite-dependent anaerobic methane-oxidising bacteria in the Jiaojiang Estuary of the East Sea (China). Appl Microbiol Biotechnol 98: 5029-5038

van der Star WRL, Abma WR, Blommers D, Mulder JW, Tokutomi T, Strous M, Picioreanu C, Van Loosdrecht MCM (2007) Startup of reactors for anoxic ammonium oxidation: Experiences from the first full-scale anammox reactor in Rotterdam. Water Res 41: 4149-4163

Wang Y, Zhu G, Harhangi HR, Zhu B, Jetten MS, Yin C, Op den Camp HJ (2012) Co-occurrence and distribution of nitrite-dependent anaerobic ammonium and methane oxidizing bacteria in a paddy soil. FEMS Microbiol Lett 336: 79-88

Yang J, Jiang HC, Wu G, Hou WG, Sun YJ, Lai ZP, Dong HL (2012) Co-occurrence of nitrite-dependent

anaerobic methane oxidizing and anaerobic ammonia oxidizing bacteria in two Qinghai-Tibetan saline lakes. Front Earth Sci 6: 383-391

Yu YN, Breitbart M, McNairnie P, Rohwer F (2006) FastGroupII: A web-based bioinformatics platform for analyses of large 16S rDNA libraries. Bmc Bioinformatics 7: 57

Zhu B, Sanchez J, van Alen TA, Sanabria J, Jetten MS, Ettwig KF, Kartal B (2011) Combined anaerobic ammonium and methane oxidation for nitrogen and methane removal. Biochem Soc Trans 39: 1822-1825

Zhu BL, van Dijk G, Fritz C, Smolders AJP, Pol A, Jetten MSM, Ettwig KF (2012) Anaerobic Oxidization of Methane in a Minerotrophic Peatland: Enrichment of Nitrite-Dependent Methane-Oxidizing Bacteria. Appl Environ Microbiol 78: 8657-8665

Zhu G, Zhou L, Wang Y, Wang S, Guo J, Long XE, Sun X, Jiang B, Hou Q, Jetten MS, Yin C (2015) Biogeographical distribution of denitrifying anaerobic methane oxidizing bacteria in Chinese wetland ecosystems. Environ Microbiol Rep 7: 128-138

Zhu Q, Shen LD, Hu BL, Lou LP, Cheng DQ (2013) Molecular detection of denitrifying anaerobic oxidizing bacteria in the sediment of West Lake, Hangzhou. Acta Scientiae Circumstantiae 33: 1321-1325