

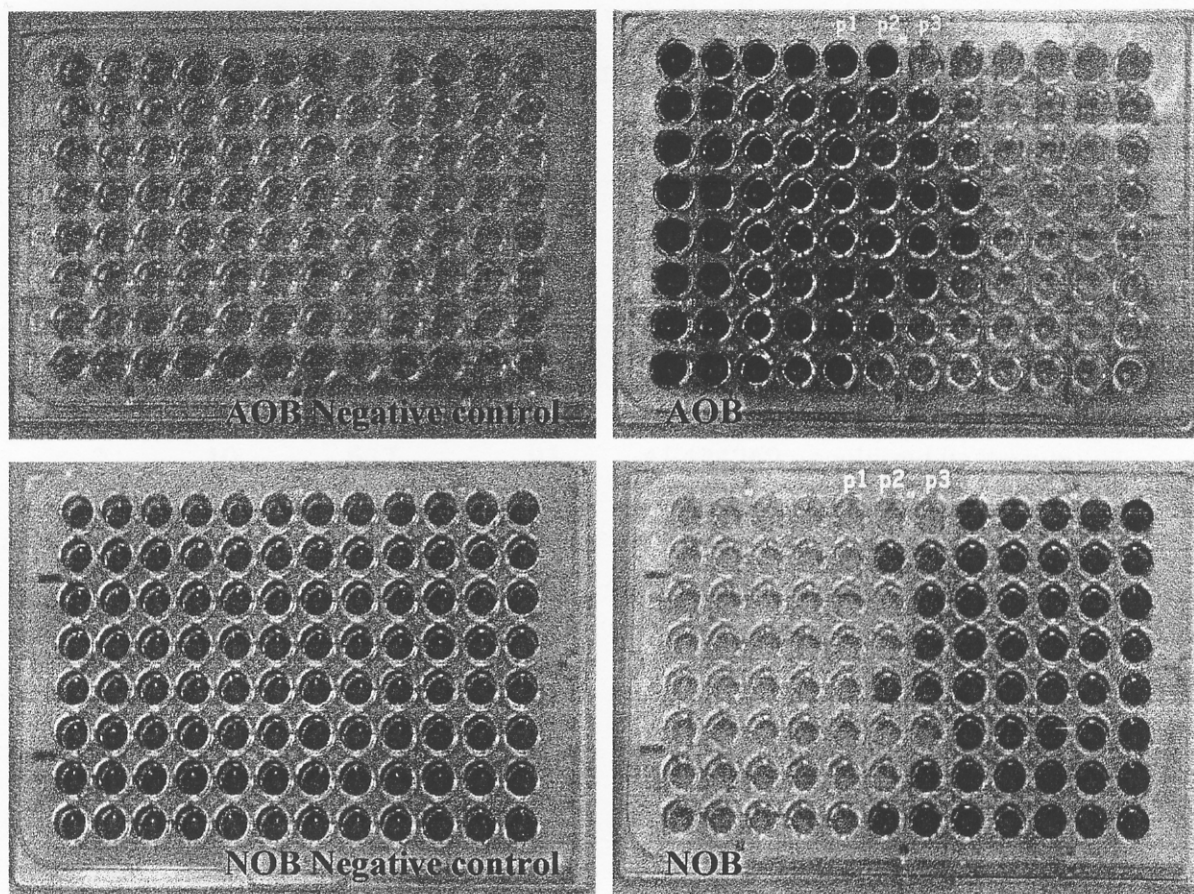
Appendix 1.1. MPN table

$p_1$	$p_2$	$p_3$	MPN	Standard error	$p_1$	$p_2$	$p_3$	MPN	Standard error
1	0	0	0.037	1.000	6	1	4	0.570	0.311
2	0	0	0.077	0.706	6	1	5	0.635	0.299
2	0	1	0.117	0.578	6	2	0	0.397	0.361
2	1	0	0.118	0.578	6	2	1	0.455	0.342
2	1	1	0.160	0.501	6	2	2	0.515	0.328
3	0	0	0.121	0.579	6	2	3	0.579	0.312
3	0	1	0.163	0.502	6	2	4	0.645	0.300
3	0	2	0.206	0.449	6	2	5	0.715	0.289
3	1	0	0.165	0.502	6	3	0	0.462	0.342
3	1	1	0.208	0.499	6	3	1	0.524	0.326
3	1	2	0.253	0.411	6	3	2	0.589	0.312
3	2	0	0.210	0.450	6	3	3	0.657	0.301
3	2	1	0.256	0.411	6	3	4	0.728	0.290
3	2	2	0.302	0.381	6	3	5	0.803	0.281
4	0	0	0.168	0.502	6	4	0	0.533	0.327
4	0	1	0.213	0.450	6	4	1	0.599	0.313
4	0	2	0.259	0.411	6	4	2	0.668	0.301
4	0	3	0.306	0.382	6	4	3	0.742	0.291
4	1	0	0.216	0.450	6	4	4	0.818	0.282
4	1	1	0.262	0.412	6	4	5	0.901	0.275
4	1	2	0.310	0.382	6	5	0	0.608	0.314
4	1	3	0.360	0.358	6	5	1	0.680	0.302
4	2	0	0.265	0.412	6	5	2	0.755	0.292
4	2	1	0.314	0.382	6	5	3	0.835	0.283
4	2	2	0.365	0.358	6	5	4	0.919	0.276
4	2	3	0.416	0.338	6	5	5	0.101	0.289
4	3	0	0.318	0.382	7	0	0	0.347	0.386
4	3	1	0.369	0.358	7	0	1	0.404	0.362
4	3	2	0.422	0.339	7	0	2	0.463	0.343
4	3	3	0.477	0.322	7	0	3	0.525	0.327
5	0	0	0.221	0.451	7	1	0	0.410	0.363
5	0	1	0.269	0.412	7	1	1	0.470	0.343
5	0	2	0.319	0.383	7	1	2	0.534	0.327
5	0	3	0.370	0.359	7	1	3	0.601	0.314
5	0	4	0.423	0.339	7	1	4	0.671	0.302
5	1	0	0.272	0.413	7	1	5	0.746	0.292
5	1	1	0.323	0.383	7	2	0	0.478	0.343
5	1	2	0.375	0.359	7	2	1	0.543	0.328
5	1	3	0.429	0.340	7	2	2	0.612	0.315
5	1	4	0.484	0.323	7	2	3	0.684	0.303
5	2	0	0.327	0.383	7	2	4	0.760	0.293
5	2	1	0.380	0.360	7	2	5	0.841	0.284
5	2	2	0.435	0.340	7	2	6	0.926	0.277
5	2	3	0.492	0.323	7	3	0	0.552	0.329
5	2	4	0.550	0.309	7	3	1	0.623	0.315
5	3	0	0.385	0.360	7	3	2	0.696	0.304
5	3	1	0.441	0.340	7	3	3	0.775	0.294
5	3	2	0.499	0.324	7	3	4	0.858	0.286
5	3	3	0.559	0.310	7	3	5	0.947	0.278
5	3	4	0.622	0.298	7	3	6	1.042	0.272
5	4	0	0.447	0.341	7	4	0	0.634	0.316
5	4	1	0.507	0.324	7	4	1	0.710	0.305
5	4	2	0.568	0.310	7	4	2	0.790	0.296
5	4	3	0.632	0.298	7	4	3	0.877	0.287
5	4	4	0.699	0.288	7	4	4	0.969	0.280
6	0	0	0.280	0.414	7	4	5	1.068	0.273
6	0	1	0.332	0.384	7	4	6	1.176	0.268
6	0	2	0.386	0.360	7	5	0	0.724	0.306
6	0	3	0.442	0.341	7	5	1	0.808	0.296
6	0	4	0.500	0.324	7	5	2	0.896	0.288
6	1	0	0.336	0.384	7	5	3	0.992	0.281
6	1	1	0.391	0.361	7	5	4	1.096	0.275
6	1	2	0.449	0.341	7	5	5	1.209	0.270
6	1	3	0.508	0.325	7	5	6	1.332	0.266

## Appendix 1.1. MPN table (continued)

$p_1$	$p_2$	$p_3$	MPN	Standard error	$p_1$	$p_2$	$p_3$	MPN	Standard error
7	6	0	0.825	0.298	8	4	3	1.054	0.287
7	6	1	0.917	0.290	8	4	4	1.171	0.282
7	6	2	1.018	0.283	8	4	5	1.301	0.278
7	6	3	1.126	0.278	8	4	6	1.444	0.274
7	6	4	1.244	0.273	8	4	7	1.607	0.272
7	6	5	1.376	0.269	8	5	0	0.870	0.302
7	6	6	1.523	0.266	8	5	1	0.972	0.295
8	1	0	0.495	0.346	8	5	2	1.085	0.289
8	1	1	0.564	0.330	8	5	3	1.208	0.284
8	1	2	0.637	0.317	8	5	4	1.346	0.281
8	1	3	0.714	0.306	8	5	5	1.500	0.278
8	1	4	0.796	0.296	8	5	6	1.679	0.277
8	2	0	0.574	0.331	8	5	7	1.886	0.277
8	2	1	0.648	0.318	8	6	0	0.999	0.297
8	2	2	0.728	0.307	8	6	1	1.117	0.292
8	2	3	0.812	0.297	8	6	2	1.248	0.288
8	2	4	0.903	0.289	8	6	3	1.396	0.285
8	2	5	1.001	0.283	8	6	4	1.565	0.283
8	2	6	1.106	0.277	8	6	5	1.760	0.283
8	3	0	0.662	0.319	8	6	6	1.993	0.285
8	3	1	0.744	0.308	8	6	7	2.279	0.288
8	3	2	0.831	0.299	8	7	0	1.153	0.295
8	3	3	0.925	0.291	8	7	1	1.293	0.291
8	3	4	1.027	0.285	8	7	2	1.452	0.289
8	3	5	1.138	0.279	8	7	3	1.636	0.289
8	3	6	1.259	0.275	8	7	4	1.855	0.291
8	3	7	1.395	0.271	8	7	5	2.124	0.294
8	4	0	0.759	0.310	8	7	6	2.465	0.301
8	4	1	0.850	0.301	8	7	7	2.921	0.312
8	4	2	0.947	0.293					

## Appendix 1.2. MPN determination



A typical test result of enumerating AOB and NOB in a sample is depicted above. Microwells containing dark-colored solutions are positive tests for AOB enumeration according to the presence of nitrate-nitrite. While colorless wells are positive for NOB enumeration because of the absence of nitrite. Values for  $p_1$ ,  $p_2$  and  $p_3$  are determined as follows:  $p_1$  is the number of positive wells in the least-concentrated dilution in which either all the wells are positive or the greatest number are positive, and  $p_2$  and  $p_3$  are the number of positive wells in the next two higher dilutions, respectively.

**Appendix 2.** A table describing the BLAST identity according to partial 16S rDNA sequence, percent sequence similarity with closest BLAST match and the affiliation with the bacterial phylum based on BLAST and phylogeny for the clones of the Bacterial clone library.

OTU	No. of Clone	No. of nucleotides	BLAST %	BLAST Identity; Phylum
1	15	451	93	AJ296578 <i>Cytophaga</i> sp; Bacteroidetes
2	10	637	93	AF424269 uncultured bacterium; Alphaproteobacteria
3	9	732	92	AF314421 uncultured bacterium; Bacteroidetes
4	7	691	92	AF139997 <i>Xanthomonas</i> group; Gammaproteobacteria
5	6	777	94	AF502216 <i>Rhodobacter</i> ; Alphaproteobacteria
6	6	801	91	AF186698 uncultured bacterium; Alphaproteobacteria
7	5	670	98	AB026946 <i>Marinobacter</i> sp. NK-1; Gammaproteobacteria
8	5	739	86	M58789 <i>Flexibacter</i> ; Bacteroidetes
9	5	634	98	AB008511 uncultured bacterium; Actinobacteria
10	4	431	93	AY094492 uncultured microbacterium; Actinobacteria

## Appendix 2. (continued)

Clone group	No. of Clone	No. of nucleotides	BLAST%	BLAST Identity; Phylum
11	4	792	90	X84482 uncultured bacterium; OP10
12	3	728	99	AF082798 <i>Hyphomonas</i> group; Alphaproteobacteria
13	3	682	91	AY027805 <i>Flavobacteria</i> ; Bacteroidetes
14	2	780	93	AY007683 unknown marine bacterium; Alphaproteobacteria
15	2	469	98	AY055797 <i>Nitrobacter</i> sp.; Alphaproteobacteria
16	2	687	96	AF272419 <i>Nitrosomonas</i> sp.; Betaproteobacteria
17	2	673	88	AF050546 uncultured bacterium; Chlorobi
18	1	665	99	AF368759 <i>Pseudomonas</i> sp.; Gammaproteobacteria
19	1	665	91	AF424110 uncultured bacterium; Gammaproteobacteria
20	1	451	93	AJ296578 <i>Sphingomonas</i> ; Alphaproteobacteria
21	1	684	96	AF156710 <i>Mesorhizobium</i> ; Alphaproteobacteria

**Appendix 2. (continued)**

Clone group	No. of Clone	No. of nucleotides	BLAST%	BLAST Identity; Phylum
22	1	614	99	AF487431 <i>Rhodopseudomonas</i> ; Alphaproteobacteria
23	1	514	96	AB049763 <i>Rhodocyclus</i> ; Betaproteobacteria
24	1	599	90	AF146230 <i>Acedobacteria</i> ; Fibrobacter
25	1	819	93	AJ277687 uncultured bacterium; Actinobacteria
26	1	730	92	X80625 <i>Rhodococcus</i> and <i>Nocardia</i> ; Actinobacteria
27	1	657	95	AF280849 <i>Bacillus/Clostridium</i> group; Firmicutes

**Appendix 3.** A table describing the BLAST identity according to partial 16S rDNA sequence, percent sequence similarity with closest BLAST match and the affiliation with the bacterial phylum based on BLAST and phylogeny for the clones of the AOB clone library.

OTU	No. of Clone	No. of nucleotides	BLAST %	BLAST Identity; Phylum
1	3	614	96	AF272419 <i>Nitrosomonas</i> sp. NM 33; Betaproteobacteria
2	1	339	98	AF272419 <i>Nitrosomonas</i> sp. NM 33; Betaproteobacteria
3	12	714	98	AF272419 <i>Nitrosomonas</i> sp. NM 33; Betaproteobacteria

**Appendix 4.** A table describing the BLAST identity according to partial 16S rDNA sequence, percent sequence similarity with closest BLAST match and the affiliation with the bacterial phylum based on BLAST and phylogeny for the clones of the LNOBSBR clone library.

OTU	No. of Clone	No. of nucleotides	BLAST %	BLAST Identity; Phylum
1	7	490	97	AY117620 <i>Mesorhizobium</i> sp. PRF86 Alphaproteobacteria
2	6	851	90	X84482; uncultured bacterium SBR1039; candidate division OP10
3	4	1020	97	AY124342 Uncultured actinobacterium clone CS1Bacteria; Actinobacteria
4	4	482	97	AF461159 <i>Paracoccus</i> sp.; Alphaproteobacteria
5	4	525	97	AF069958 <i>Nitrobacter alkalicus</i> strain AN4Proteobacteria; Alphaproteobacteria
6	4	1048	99	AJ244716. <i>Erythrobacter</i> -like sp. V4.BO.03; Alphaproteobacteria
8	3	390	97	AB098586 <i>Mesorhizobium</i> sp. TUT1018; Alphaproteobacteria
9	3	1037	97	AY124342, Uncultured actinobacterium clone CS1Bacteria; Actinobacteria
10	3	543	94	AF530158; <i>Cytophaga</i> sp. MGP- 14AN; Bacteroidetes



**Appendix 4. (continued)**

Clone group	No. of Clone	No. of nucleotides	BLAST %	BLAST Identity; Phylum
13	3	420	95	AY205564 <i>Exiguobacterium</i> sp. BTAH1; Firmicutes
14	2	954	94	AF035212; <i>Azomonas</i> <i>macrocytogenes</i> ; Gammaproteobacteria
30	1	416	91	AJ296579; Uncultured bacterium GR-Sh1-209; unaffiliated

**Appendix 5.** A table describing the BLAST identity according to full 16S rDNA sequence for clone group 1 except that partial sequence, percent sequence similarity with closest BLAST match and the affiliation with the bacterial phylum based on BLAST and phylogeny for the clones of the HNOBSBR library

OTU	No. of Clone	No. of nucleotides	BLAST %	BLAST Identity; Phylum
1	12	1455	99	AY135357 Nitrite-oxidizing bacterium MPN2; Alphaproteobacteria
2	10	1032	97	AF097803 Unidentified bacterium clone; Gammaproteobacteria
3	9	911	97	AB055207 <i>Alcanivorax</i> sp. TE-9; Gammaproteobacteria
4	7	981	98	AY135357 Nitrite-oxidizing bacterium MPN2; Alphaproteobacteria
5	7	885	91	AB073564 <i>Cytophaga</i> sp.; Bacteroidetes

**Appendix 6.** A table describing the BLAST identity according to partial 16S rDNA sequence, percent sequence similarity with closest BLAST match and the affiliation with the bacterial phylum based on BLAST and phylogeny for the clones of the nNFSBR, nLNOBSBR and nHNOBSBR clone libraries

OTU	Clone library	No. of Clones	BLAST %	BLAST identity; phylum
1	NFSBR	1	0	Not significant match
	LNOBSBR	13	0	Not significant match
	HNOBSBR	33	0	Not significant match
2	NFSBR	2	0	Not significant match
	LNOBSBR	5	85	AL 162756 <i>Neisseria meningitides</i> ; betaproteobacteria
	HNOBSBR	14	0	Not significant match
3	NFSBR	1	-	
	LNOBSBR	3	82	AP00598 <i>Bradyrhizobium japonicum</i> ; Alphaproteobacteria
	HNOBSBR	2	-	
4	NFSBR	2	91	AF523995 Uncultured bacterium clone; unaffiliated
	HNOBSBR	3	0	Not significant match

**Appendix 6. (continued)**

OTU	Clone library	No. of Clones	BLAST %	BLAST identity; phylum
5	NFSBR	1	97	Not significant match
	LNOBSBR	1	-	
	HNOBSBR	1	97	<i>Marinobacter exelentus</i> AY180101; Gammaproteobacteria
6	NFSBR	1	0	Not significant match
	HNOBSBR	1		
7	HNOBSBR	1	-	
8	NFSBR	1	0	Not significant match
9	NFSBR	1	80	AP00598 <i>Bradyrhizobium japonicum</i> ; Alphaproteobacteria
10	NFSBR	1	0	Not significant match

- = not successfully sequenced

**Appendix 7. Full 16S rDNA sequence for the Clone Bact0442, Bact0471 (affiliated with AOB) and Bact0193 (affiliated with NOB) of Bacterial clone library**

>Bact0442clone\_1,460 bp

ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGGGC  
 AACCTGGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGTGTCATAAA  
 GAGGGGGATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGA  
 AAGCAGGGGATCGCAAGACCTTGCCTTTTTGAGCGGCCGATGCCTGATTAGCTA  
 GTTGGTAAGGTAAGGCTTACCAAGGCAACGATCAGTAGCTGGTCTGAGAGGAC  
 GACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGT  
 GGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAA  
 GAAGGCCTTCGGGTTGTAAAGCTCTTTCGGTCGGGAAGAAATAGTTGTGGCTAAT  
 ATCCACAATGAATGACGGTACCGACATAAGAAGCACCGGCTAACTACGTGCCAG  
 CAGCCGCGTAATACGTAGGGTGCAAGCGTTAATCGGAATTATTGGGCGTAAAG  
 GGTGCGCAGGCGGTTGTATAAGTCAGATGTGAAAGCCCTGGGCTTAACCTAGGA  
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 GTAGCAGTGAATGCGTAGAGATGTGGAAGAACACCGATGGCGAAGGCAGCTCC  
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 TACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTCGGATCTATTTAAA  
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 AGATTA AAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGG  
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 GCAGAGATGTGAAAGTGCCCGAAAGGGAATCGAGACACAGGTGCTGCATGGCTG  
 TCGTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCAGCAACGAGCGCAACCCTT  
 GTCATAATTGCCATCATTTAGTTGGGCACTTTAGTGAGACTGCCGGTGACAAAC  
 CGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGGGCTTC  
 ACACGTAATAACAATGGCGCGTACAGAGGGTTGCCAACCTGCGAAGGGGAGCTAA  
 TCTCATAAAGCGCGTTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGTGAAGT  
 CGGAATCGCTAGTAATCGCGGATCAGCATGTGCGCGTGAATACGTTCCCGGGTCT  
 TGTACACACCCCGCTCACACCATGGGAGTAATTTTACCAGAAGCAAATAGTCT  
 AACCGCAAGGAGGGCGTTTGCACGGTGAGAGTTATGACTGGGGTG

>Bact0471clone\_1,123 bp

CGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCACGGGGGCAACCCT  
 GGTGGCGAGTGGCGAACGGGTGAGTAATACATCGGAACGTGTCATAAAGAGGGG  
 GATAACGCATCGAAAGATGTGCTAATACCGCATATTCTCTAAGGAGGAAAGCAG  
 GGGATCGCAAGACCTTGCCTTTTTGAGCGGCCGATGCCTGATTAGCTAGTTGGT  
 AAGGTAAGGCTTACCAAGGCAACGATCAGTAGCTGGTCTGAGAGGACGACCAG  
 CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAA  
 TTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGAGTGAAGAAGGC  
 CTTTCGGGTTGTAAAGCTCTTTCGGTTCGGGAAGAAATAGTTGTGGCTAATATCCAC  
 AATGAATGACGGTACCGACATAAGAAGCACCGGCTAACTACGTGCCAGCAGCCG  
 CGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTATTGGGCGTAAAGGGTGGC  
 CAGGCGGTTGTATAAGTCAGATGTGAAAGCCCTGGGCTTAACCTAGGAATTGCGT  
 TTGAAACTATATGACTAGAGTGTGACAGAGGGGAGTGGAATCCATGTGTAGCA  
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 GGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTCGGATCTATTTAAAGATTAG  
 GTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGAAGTACGGTCGCAAGATTA  
 AAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATTATGTGGATTAAT

TCGATGCAACGCGAAAAACCTTACCTACCCCTTGACATGCTCGAAATTTTCGCAGAG  
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 GCTCGTGTCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCT  
 AATTGCCATCATTAGTTGGGCACCTTAGTGAGACTG

>Bact0193clone\_1,149 bp

TTTGATCCTGGCTCAGAGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTCGAA  
 CGGGCGTAGCAATACGTCAGTgCAGACGGGTGAGTAACCGCTGGGAACGTACC  
 TTTTGGTTCGGAACAACCCAGGGAAACTTGGGCTAATACCGGATAAGCCCTTACG  
 GGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCTGATTAGCTTGTGGTGAGG  
 TAACGGCTCACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCAC  
 ATTGGGACTGAGACACGGCCCAAACCTCCTACGGGAGGCAGCAGTGGGGAATATT  
 GGACAATGGGCGCAAGCCTGATCCAGCCATGCCCGCTGAGTGATGAAGGCCCTA  
 GGGTTGTAAGCTCTTTTGTGCGGGAAGATAATGACGGTACCGCAAGAATAAGC  
 CCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTC  
 GGAATTACTGGGCGTAAAGGGTGCCTAGGCCGGTCTTTAAGTCAGGGGTGAAAT  
 CCTGGAGCTCAACTCCAGAACTGCCTTTGATACTGAGGATCTTGAGTTCGGGAGA  
 GGTGAGTGGAAGTGCAGTGTAGAGGTGAAATTCGTAGATATTGCAAGAACAC  
 CAGTGGCGAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAGCGTG  
 GGGAGCAAACAGGATTAGATAACCCTGGTAGTCCACGCCGTAACCGATGAATgCC  
 AGCCGTTAGTGGGTACTCACTAGTGGCGCAGCTAACGCTTTAAGCATiCCGCCT  
 GGGGAGTACGGTCGCAAGATTA AAACTCAAAGGAATTGACGGGGGCCCGACAA  
 GCGGTGGAGCATGTGGTTAATTCGACGCAACGCGCAGAACCTTACCAGCCCTTG  
 ACATGTCCATGACCGGTGCGCAGAGATGTGACCTTCTCTTCGGAGCATGGAGACA  
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 ACGAGCGCAACCCCGTCCTTAGTTGCTACCATTTAGTTGAGCACTCTAAGGAGA  
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 GGTGACCCCTAGCAAATCTCAAAAACCGTCTCAGTTCGGATTGGGCTCTGCAAC  
 CCGAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCATGCCACGGTGA  
 ATACGTTCCCGGGCCTTGACACACCGCCCGTACACCATGGGAGTTGGTTTTAC  
 CTGAAGGCAGTGCCTAACC CGCAAGGGAGGCAGCCGACCACGGTAGGGTCagC  
 GACTGGGGTGAAGTCGTAACAAGGTAGCCGTA

**Appendix 8.** Full 16S rDNA sequence for the Clone AOB025, AOBclone030  
and AOB012 of AOB clone libraries

>AOB025\_1,293 bp

GGAGAAAAGCAGGGGATCGCAAGACCTTGCCTTTTTGAGCGGCCGATGCCTGA  
TTAGCTAGTTGGTAAGGTAAGGCTTACCAAGGCAACGATCAGTAGCTGGTCTGA  
GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC  
AGCAGTGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG  
AGTGAAGAAGGCCTTCGGTTGTAAAGCTCTTTCGGTCGGGAAGAAATAGTTGTG  
GCTAATATCCACAATGAATGACGGTACCGACATAAGAAGCACCCGGCTAACTACG  
TGCCAGCAGCCGCGGTAATACGTAGGGTGAAGCGTTAATCGGAATTATTGGGC  
GTAAAGGGTGCGCAGGCGGTTGTATAAGTCAGATGTGAAAGCCCTGGGCTTAAC  
CTAGGAATTGCGTTTTGAACTATATGACTAGAGTGTGACAGAGGGGAGTGGAAT  
TCCATGTGTAGCAGTGAATGCGTAGAGATGTGGAAGAACACCGATGGCGAAGG  
CAGCTCCCTGGGTTAACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAG  
GATTAGATACCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTCGGATCT  
ATTTAAAGATTAGGTAACGTAGTTAACGCGTGAAGTTGACCGCCTGGGAAGTACG  
GTCGCAAGATTAATACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATT  
ATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGCTCGA  
AATTTTCGACAGAGATGTGAAAGTGCCCGAAAGGGAATCGAGACACAGGTGCTGCA  
TGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA  
ACCCTTGTCACTAATTGCCATCATTTAGTTGGGCACCTTGTGAGACTGCCGGTGA  
CAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAGG  
GCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCTGCGAAGGGGA  
GCTAATCTCATAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCGT  
GAAGTCGGAATCGCTAGTAATCGCGGATCAGCATGTGCGCGGTGAATACGTTCCCG  
GGTCTTGTACACACCGCCCGTCACACCATGGGAGTAATTTTACCAGAAGCAAAT  
AGTCTAACCGCAAGGAGGGCGTTTCCACGGTGAGAGTTA

>AOB030\_1,293 bp

TGATTAAGCAGGGGATCGCAAGACCATGCGCTTTTTGAGCGGCCGATGCCTGAT  
TAGCTAGTTGGTAAGGTAAGGCTTACCAAGGCAACGATCAGTAGCTGGTCTGA  
GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC  
AGCAGTGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG  
AGTGAAGAAGGCCTTCGGTTGTAAAGCTCTTTCGGTCGGGAAGAAATAGTTGTG  
GCTAATATCCACAATGAATGACGGTACCGACATAAGAAGCACCCGGCTAACTACG  
TGCCAGCAGCCGCGGTAATACGTAGGGTGAAGCGTTAATCGGAATTATTGGGC  
GTAAAGGGTGCGCAGGCGGTTGTATAAGTCAGATGTGAAAGCCCTGGGCTTAAC  
CTAGGAATTGCGTTTTGAACTATATGACTAGAGTGTGACAGAGGGGAGTGGAAT  
TCCATGTGTAGCAGTGAATGCGTAGAGATGTGGAAGAACACCGATGGCGAAGG  
CAGCTCCCTGGGTTAACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAG  
GATTAGATACCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTCGGGTCT  
ATTTAAAGATTAGGTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGAAGTAC  
GGTCGCAAGATTAATACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAT  
TATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGCTCG  
AAATTTTCGACAGAGATGTGAAAGTGCCCGAAAGGGAATCGAGACACAGGTGCTGC  
ATGGCTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGC  
AACCTTGTACTAATTGCCATCATTTAGTTGGGCACCTTAGCGAGACTGCCGGT  
GACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTA  
GGGCTTCACACGTAATACAATGGCGCGTACAGAGGGTTGCCAACCTGCGAAGGG  
GAGCTAATCTCATAAAGCGCGTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCC  
GTGAAGTCGGAATCGCTAGTAATCGCGGGTCAGCATGTGCGCGGTGAATACGTTTC

CGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTAATTTTCACCAGAAGCAA  
ATAGTCTAACCGCAAGGAGGGCGTTTGCCACGGTGAGAGTTA

>AOB012\_1,304 bp

GGAGAAAAGCAGGGGATCGCAAGACCTTGCGCTTTTTGAGCGGCCGATGCCTGA  
TTAGCTAGTTGGTAAGGTAAGGCTTACCAAGGCAACGATCAGTAGCTGGTCTGA  
GAGGACGACCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC  
AGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCCACGCCGCGTG  
AGTGAAGAAGGCCTTCGGGTTGTAAAGCTCTTTCGGTTCGGGAAGAAATAGTTGTG  
GCTAATATCCACAATGAATGACGGTACCGACATAAGAAGCACCGGCTAACTACG  
TGCCAGCAGCCGCGGTAATACGTAGGGTGCAAGCGTTAATCGGAATTATTGGGC  
GTAAAGGGTGCGCAGGCGGTTGTATAAGTCAGATGTGAAAGCCCTGGGCTTAAC  
CTAGGAATTGCGTTTGAAACTATATGACTAGAGTGTGACAGAGGGGAGTGGAAT  
TCCATGTGTAGCAGTGAATGCGTAGAGATGTGGAAGAACACCGATGGCGAAGG  
CAGCTCCCTGGGTTAACTGACGCTCATGCGCGAAAGCGCGGGGAGCAAACAG  
GATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTAGTTGTTCGGATCT  
ATTTAAAGATTAGGTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGAAGTAC  
GGTCGCAAGATTA AAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAT  
TATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGCTCG  
AAATTTTCGAGAGATGTGAAAGTGCCTGAAAGGGAATCGAGACACAGGTGCTGC  
ATGGCTGTTCGTCAGCTCGTGTTCGTGAGATGTTGGGTAAAGTCCCAGCAACGAGCGC  
AACCTTGTCACTAATTGCCATCATTAGTTGGGCACTTTAGTGAGACTGCCGGTG  
ACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCCTCATGGCCCTTATGGGTAG  
GGCTTCACACGTAATAACAATGGCGCGTACAGAGGGTTGCCAACCTGCGAAGGGG  
AGCTAATCTCATAAAGCGCGTTCGTAGTCCGGATCGGAGTCTGCAACTCGACTCCG  
TGAAGTCGGAATCGCTAGTAATCGCGGATCAGCATGTTCGCGGTGAATACGTTCCC  
GGGTCTTGTACACACCGCCCGTCACACCACGGGAGTAATTTTCACCAGAAGCAA  
TAGTCTAACCGCAAGGAGGGCGTTTGCCACGGTGAGAGTTATGACTGGGGTG



**Appendix 9. Nearly full 16S rDNA sequence for the Clone LNOBSBR078 of LNOBSBR clone library affiliated with NOB**

>LNOBSBR078clone\_1,086 bp

ACCAATGTGCGTGTTCGTGGCTATTCTTGGGGCGTAWTAGKGTGCGKTAGGCGRGT  
CTTTAAGTCAGKRGTGARATCCTGGWGCTCAACTCCAGAACTGCCTTTGATACTG  
WKGATCTTGAGTTCGGGAGMGSTTGAGTGGWACTGCGAGTGTAGARGTGAAATT  
CGTAGATATTCGCAAGAACACCAGTGGCGAAGGCGGCTCACTGGCCCGATACTG  
ACGCTGAGRCACGWAWGCGTGGRGAGCAAACARGATTAGATACCCTGGTAGTCC  
ACGCCGTAACGATGRATGGCCASCCGTTAGTGRGTTTACTCACTAGTGGCGCAG  
CTAWCGCTTTAAGCAYTCCGCCTGGGGAGTACGGTCGCAAGATTA AAAACTCAA  
GGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTTAATTCGACGCAA  
CGCGCAGAACCTTACCAGCCCTTGACATGTCCATGACCGGTCGCAGAGATGTGAC  
CTTCTCTTCGGAGCATGGAGCACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCG  
TGAGATGTTGGGTYAAGTCCC GCAACGAGCGCAACCCCCGTCCTTAGTTGCTACC  
ATTTAGTTGAGCACTCTAAGGAGACTGCCGGTGATAAGCCGCGAGGAAGAGTGG  
GGATGACGTCAAGTCCTCATGGCCCTTACGGGCTGGRCTACACACGTGCTACAAT  
GGCGGTGACAATGGGAAGCAAAGGGGTGACCCCTAGCAAATCTCAAAAAACCGT  
CTCAGTTCGGATTGGGCTCTGCAACCCGAGCCCATGAAGTTGGAATCGCTAGTAA  
TCGTGGATCAGCATGCCACGGTGAATACGTTTCCCGGGCCCTTGTRCACACCCGC  
CGTCACACCATGGGAGTTGGGTTTTACCTGAARGCRGTGCGCTAACCCGCAAGGG  
AGGCAGCCGACCAGGTAGGGTCAGCGACTGGGGTGAAAGTCCTTACAAGGTAC  
CCGTAATCACTAGTGAATTCCCGGCCGCCTGCAGGTCGACATATGGGAGAGCTC  
CCAAACGCGTGGATGCATAGCTTGAGTTTCTATAGTGTACCTAAATAAC

**Appendix 10.** Full 16S rDNA sequence of the 2 Clones alignment; HNOBSBR025 and HNOBSBR015, of the HNOBSBR clone library affiliated with AY135357 Nitrite-oxidizing bacterium MPN2

>HNOBSBRclone\_1,455 bp

GAGTTTGATCCTGGCTCAGAGCGAACGCTGGCGGCAGGCTTAACACATGCAAGTC  
 GAACGGGCGTAGyAATACGTCAGTGGCAGACGGGTGAGTAACGCGTGGGAACGT  
 ACCTTTTGGTTTCGGAACAACCCAGGGAACTTGGGCTAATACCGGATAAGCTmCT  
 TACGGGGAAAGATTTATCGCCGAAAGATCGGCCCGCGTCTGATTAGCTTGTGGT  
 GAGGTAACGGCTCACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAG  
 CCACATTGGGACCGAGACACGGCCAAACTCCTACGGGAGGCGGCAGTGGGGAA  
 TATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGC  
 CCTAGGGTTGTAAGCTCTTTTktGCGGGAAGATAATGACGGTACCGCAAGAATA  
 AGCCCCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTT  
 GCTCGGAATTACTGGGCGTAAAGGGTGCCTTAGGCGGGTCTTTAAGTCAGGGGTG  
 AAATCCTGGAGCTCAACTCCAGAAGTGCCTTTGATACTGAGGATCTTGAGTTCGG  
 GAGAGGTGAGTGGAACTGCGAGTGTAGAGGTGAAATTCGTAGATATTCGCAAGA  
 ACACCAGTGGCGAAGGCGGCTCACTGGCCCGATACTGACGCTGAGGCACGAAAG  
 CGTGGGGAGCAAACAGGATTAGATAACCCTGGTAGTCCACGCCGTAACCGATGAA  
 TGCCAGCCGTTAGTGGGTTTACTCACTAGTGGCGCAGCTAACGCTTTAAGCATT  
 CGCCTGGGGAGTACGGTCGCAACGATTA AAACTCAAAGGAATTGACGGGGGCC  
 GCACAAGCGGTGGAGCATGTGGTTTAATTCGACGCAACGCGCAGAACCCTACCA  
 GCCCTTGACATGTCCATGACCGGTGCGAGAGATGTGACCTTCTCTTCGGAGCATG  
 GAGCACAGGTGCTGCATGGCTGTCGTACGCTCGTGTGAGATGTTGGGTCAAG  
 TCCGCAACGAGCGCAACCCCGTCTTAGTTGCTACCATTTAGTTGAGCACTCT  
 AAGGAGACTGCCGGTGATAAGCCGCGAGGAAGGTGGGGATGACGTCAAGTCCTC  
 ATGGCCCTTACGGGCTGGGCTACACACGTGCTACAATGGCGGTGACAATGGGAA  
 GCAAAGGGGTGACCCCTAGCAAATCTCAAAAACCGTCTCAGTTCCGGATTGGGCT  
 CTGCAACCCGAGCCCATGAAGTTGGAATCGCTAGTAATCGTGGATCAGCATGCCA  
 CGGTGAATACGTTCCCGGGCCTTGTGCACACCGCCCGTCACACCATGGGAGTTGG  
 TTTTACCTGAAGGCAGTGCCTAACCCGCAAGGGAGGCAGCCGACCACGGTAGG  
 GTCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCGTAA

**Appendix 11. Full 16S rDNA sequence for the OTU1**

> OTU1\_718 bp

AGAGTTTGATCCTGGCTCAGGTTTTTACCCAGTAACAAATACCGGTTTGAATYCC  
GCCACAAAGCCTGCTGGTAAATAATCCGGCCCGTATATAAGGGGCCTCCGATAA  
AAGGTTTTTGAACAAAGAAGGAATGGACTTCCAGGTCTTTTGATAAAAATCATA  
CCTTTGATAATCCATAACTCCGGCTTCATTTTCTATGAAGAAATAGTATTTAGAAG  
AATCCGCTACTTTAGGATTGGGTAAAGAAAAGACCGCTCTGCTGCTGTTGAATC  
TTTCATGGCCAATTCATCCGTAATAGATATGGCATCTGTTAATGAAGTGTCATGGT  
TGCAATTGCAAGACGTTAAACMTGACAAGCAGAACAAAAATAAAAGCTGGAATC  
CGTTTTTCATAAATAAAAAAGTGATAAACTTCCATACAATATTATTAATTTTATC  
TTTGCAACGATAAATAATGGTCACAATGAAACAAATGGTATATCTGATGTTGCTG  
GCAGGACTKTYKTGMCTKTGTTTTCATCAAAGAAGTATGAGACCTTGCAGCGGC  
GATATCAATCCACGGACCGCGGTTGGCAGAAATGCAAAAAACACGGAATTCC  
AGGAACAGACCATTGCTGACCTCAGACAGCGCATACTGATCCTGGAGGATCTCCG  
GAAAGAATTAGCTGCTACAAAGGAAAAATTTGCTGCCCTGCAGGGCAGCAATGA  
ACAGC

### Publications

- Paungfoo, C., Prasertsan, P., Intrasungkha, N., Blackall, L. L. and Bhamidimarri, R. 2003. Enrichment of nitrifying microbial communities from shrimp farms and commercial inocula. *Wat. Sci. Tech.* 48(8): 143-150.
- Paungfoo, C , Prasertsan, P., Burrell, P, Intrasungkha, N., Blackall, L. 2003. Investigation of Nitrifying Bacterial Communities in an Aquaculture Wastewater Treatment System Using Fluorescence *in Situ* Hybridization (FISH), 16S rRNA Gene Cloning and Phylogenetic Analysis. *Wat. Sci. Tech.* (submitted).
- Paungfoo, C., Burrell, P., Prasertsan, P., Intrasungkha, N., Blackall, L. Who is responsible for nitrite- oxidation in aquaculture systems? (manuscript).

### Presentations

- Paungfoo, C., Burrell, P., Prasertsan, P., Intrasungkha, N., Blackall, L. 2004. Who is responsible for nitrite- oxidation in aquaculture systems? The 3<sup>rd</sup> National Environmental Conference. January 28-30, 2004, Songkhla, Thailand.
- Paungfoo, C , Prasertsan, P., Burrell, P, Intrasungkha, N., Blackall, L. 2003. Investigation of Nitrifying Bacterial Communities in an Aquaculture Wastewater Treatment System Using Fluorescence *in Situ* Hybridization (FISH), 16S rRNA Gene Cloning and Phylogenetic Analysis. *Asian WaterQual2003 Conference*. October 20-23, 2003, Bangkok, Thailand.
- Paungfoo C, Prasertsan P, Intrasungkha N, Blackall L.L. and Bhamidimarri R. 2002. Enrichment of Nitrifying Microbial Communities from Shrimp Farms and Commercial Inocula. Environmental Biotechnology Conference. April 15-17, 2002, Massey University, Palmerston North, New Zealand.

Paungfoo, C., O-Thong, S., Rokaerd, S., Prasertsan, P., Intrasungkha, N and Bhamidimarri, R. 2001. Comparison between Ammonia Removal Efficiencies of Natural and Commercial Nitrifying Bacteria in Saline Wastewater by Sequencing Batch Reactor (SBR). BioThailand 2001. November 7-10, 2001, Queen Sirikit National Convention Center, Bangkok, Thailand.

Paungfoo, C., O-Thong, S., Prasertsan, P., Intrasungkha, N and Bhamidimarri, R. 2001. Ammonia Removal from Saline Wastewater by Nitrifying Bacteria in Sequencing Batch Reactor (SBR). The 27<sup>th</sup> Congress on Science and Technology of Thailand (27<sup>th</sup> STT). October 16-18, 2001, Hat Yai, Songkhla, Thailand.

## VITAE

Name Miss Chanyarat Paungfoo

Birth Date 9 August, 1976

### Education Attainment

Degree	Name of Institution	Year of graduation
Bachelor of Science (Biotechnology, Second Class Honors)	Prince of Songkla University	1999

Field of interest: Environmental Biotechnology

### Prizes and Grants:

1999-2003 Royal Golden Jubilee Ph.D. Grant, TRF

1999-2003 Graduate School Research Grant, PSU

2001-2002 Basic Research Grant, TRF

1998 High Distinction in Study Award, Faculty of Science, PSU

### Professional Development:

Training in Fluorescence *In Situ* Hybridization Course at Stradbroke Island, Australia, organized by Advanced Wastewater Management Centre (AWMC), The University of Queensland, during December 2-6, 2001.

Certified in achievement of Hyper Course on Bioinformatics at Thailand's National Science and Technology Development Agency (NSTDA) organized by Thailand Graduate Institute of Science and Technology (TGIST) during October 24-28, 2000.

Training course in "The Use of Molecular and Chemical Techniques in Microbial Diversity and Environmental Biotechnology" at Faculty of Science, Mahidol University, Thailand, organized by The National

Center for Genetic Engineering and Biotechnology (BIOTEC), Society for General Microbiology, and Faculty of Science, Mahidol University, during November 1-5, 1999.