A novel marine nitrite-oxidizing *Nitrospira* species from Dutch coastal North Sea water

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**Introduction**

The ocean is the largest reservoir of fixed nitrogen on Earth containing about five times more fixed nitrogen than terrestrial systems (Gruber, 2008) which renders marine systems of major importance to global nitrogen cycling. Nitrogen, as the bioavailable forms of ammonium and nitrate, is one of the key nutrients in marine waters and may limit primary production especially in coastal systems (Downing, 1997; Wollast, 1998; Zehr and Kudela, 2011). Most of the fixed organic nitrogen in the ocean is converted to nitrate by remineralization consisting of ammonification and nitrification (Gruber, 2008). In the two-step process of nitrification, ammonia is oxidized first to nitrite by aerobic ammonia-oxidizing microorganisms and then to nitrate by aerobic nitrite-oxidizing microorganisms.

The microbial mediators of nitrification have intrigued scientists ever since the hallmark publication by Winogradsky (1890) in which not only the ability of nitrifying organisms to withdraw energy from mineral substances was reported but it was also concluded that these microorganisms assimilate carbon from carbon dioxide. At present, after 120 years of research efforts, many nitrifying microorganisms are available in culture, and therefore amenable to physiological characterization, but marine species are underrepresented. For instance, when evaluating the phylogeny of β-proteobacterial ammonia-oxidizing bacteria (AOB) Akra et al. (2001) examined no less than 38 isolates of which only five had a marine origin. In the review by Koops and Pommerehn-Röser (2001) on the distribution and ecophysiology of nitrifying bacteria the phylogenetic relationship of 19 cultured AOB species is shown and for only five of those species a preference for a marine habitat is indicated. In marine ecosystems ammonia-oxidizing archaea (AOA) species have been shown to outnumber their bacterial counterparts based on direct cell counts and gene (16S rRNA and amoA) copy numbers (Francis et al., 2003; Wuchter et al., 2006; Mincer et al., 2007). Currently, however, the only two cultured AOA species with a marine or estuarine origin are *Nitropumilus*

**Keywords:** marine nitrification, enrichment, *Nitrospira*, *Nitrosomonas*, *Nitrospira*, fluorescence in situ hybridization, transmission electron microscopy, 16S rRNA

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Marine species have been found in four of the recognized nitrite-oxidizing bacterial genera (Nitrospina, Nitrospira, Nitro bacter, and Nitrococcus; Ward and Carlucci, 1985). For the genus Nitrospira (Alawi et al., 2007) no marine species are presently known. The recently described nitrite oxidizer Nitromonarchus hollandicus (Sorokin et al., 2012), which in contrast to the previously known proteobacterial nitrite oxidizers belongs to the Chloroflexi phylum, was isolated from a reactor treating sewage plant digester effluent and no data on its salt tolerance or environmental distribution is yet available.

Within the process of nitrification ammonia oxidation to nitrite is the rate-limiting step and nitrite rarely accumulates in the process of nitrification (Philips et al., 2002; Arp, 2009). This may explain why nitrite-oxidizing bacteria (NOB) are often overlooked in marine environmental studies concerning nitrification. Recent findings in the Namibian oxygen minimum zone (OMZ) by Füssel et al. (2011), however, indicate that nitrite oxidation rates may even exceed ammonia oxidation rates. Marine Nitrospira species have been isolated from a surface water sample of the Gulf of Maine (Watson et al., 1986) as well as from marine recirculation aquaculture system biofilters (Keuter et al., 2011; Brown et al., 2013). In addition they have been described as inhabitants of marine sponges (Hoffmann et al., 2009; Off et al., 2010). Nitrospina species have been detected in both coastal and open ocean habitats (Suzuki et al., 2004; DeLong et al., 2006; Berman et al., 2010) based on 16S rRNA gene sequences. Moreover, co-variation of archaeal amoA and 16S rDNA genes with Nitrospina-like 16S rDNA genes has been observed which suggests that Nitrospina NOB may be natural nitrite-oxidizing partners of marine AOA (Minorio et al., 2007; Santoro et al., 2010). Fluorescence in situ hybridization (FISH) analyses using probes targeting all nitrite-oxidizing genera known at that time by Füssel et al. (2011) on Namibian OMZ samples demonstrated the presence of only Nitrospina and Nitrococcus NOB in equal abundance.

The elucidation of the ecophysiology of marine nitrite oxidizers in part is complicated by the difficulties in combining molecular data (e.g., presence and abundance of particular genes or species) with cultivation-derived parameters (e.g., proof of physiological capabilities, affinities, growth rates, salt tolerance). Increasing the availability of cultured species and ultimately determining their key physiological traits is helpful because it will aid in designing directed environmental research. Knowledge of physiological constraints of different strains and species, for instance, enables making informed guesses about which particular strain or species inhabits a certain habitat. To increase the number of cultivated marine nitrite oxidizers, a bioreactor set-up was used in the present study to first enrich a marine assemblage of aerobic ammonia oxidizers and nitrite oxidizers and ultimately solely the nitrite oxidizers from North Sea coastal water. The microbial community composition was evaluated by FISH analyses and the phylogenetic position of the enriched aerobic ammonia oxidizers and nitrite oxidizers determined by 16S rDNA gene sequence [polymerase chain reaction (PCR) and metagenome data] based analyses. The cell plan of the enriched nitrite-oxidizing Nitrospina species was visualized with transmission electron microscopy (TEM) and, using a newly designed primer pair targeting Nitrospina species, its presence was detected in a time series (Wucher et al., 2006; Pitcher et al., 2011) of high molecular weight DNA isolated from the same coastal sampling site.

MATERIALS AND METHODS

INOCULUM DESCRIPTION AND REACTOR SET-UP

Water representative of Dutch coastal North Sea water (Pitcher et al., 2011) was collected in February 2007 at high tide at the jetty of the Royal Netherlands Institute for Sea Research situated on the island Texel (53°09′25″ N, 4°78′27″ E). An aliquot of 48 L of North Sea water was filtered using a HAWP05 polysulfone capillary artificial Kidney/Hemofilter (Fresenius Medical Care Nederland BV, Nieuwkuijk, the Netherlands). This resulted in 2 L of 24-fold concentrated biomass suspension and a cleared solution (filtrate) devoid of particles. The collected biomass suspension was incubated in a sterile glass and stainless steel reactor (adaptive, 2 L working volume). Heat-sterilized (20 min, 120°C, 15 kPa) filtrate supplemented with ammonium or nitrite (from 1 M sterile stocks of NH₄Cl and NaNO₂) was used as a medium. Oxygen and pH were monitored online using Applikon (Applikon Biotechnology BV, Schiedam, the Netherlands) sensors. Nitrite concentrations were determined offline in liquid samples withdrawn daily from the reactor using Merckquant test strips (Merck BV, Schiphol-Rijk, the Netherlands) and ammonium as well as nitrite concentration weekly using colorimetric methods (see below). The reactor was kept at a pH 7.8 with solutions of sterile 1 M NaHCO₃ and 0.6 M HCl, operated at room temperature 22 ± 2°C, stirred at 150 rpm, and supplied with an air flow of 80 ml/min.

ENRICHMENT WITH AMMONIA AS THE SUBSTRATE

The culture was amended with 300 μM NH₄Cl and incubated for 19 days as a batch and then for another 2 days after addition of 400 μM NH₄Cl. To avoid nitrite toxicity, the reactor system was thereafter switched to a continuous mode of operation using medium containing 750 μM NH₄Cl at a dilution rate of 0.25 day⁻¹. When nitrite disappeared from the culture, indicating activity of nitrite oxidizers, the ammonium concentration was subsequently increased to 1.5 mM after 3 months, and further to 2, 3, and finally 10 mM after 4, 4.5, and 5.5 months, respectively. The reactor was switched to nitrite as the sole substrate after 7 months.

ENRICHMENT WITH NITRITE AS THE SUBSTRATE

To stimulate growth of the nitrite oxidizers, a batch mode of operation was adopted by adding 750 μM NaN₃O₂ as the substrate. Whenever nitrite was depleted, it was restored to 750 μM. In this manner, a total of 43 mmol of nitrite were supplied in the first month of operation with nitrite as the sole substrate. Wall growth was suspended and the biomass diluted fourfold by replacement of reactor content with medium respectively, 1 week and 1 month after the switch to nitrite. After 1 month, a feed-batch mode of operation was adopted by adding medium containing 30 mM NaN₃O₂ at a flow rate starting at 40 ml per day. The pump rate
of the influent was increased manually in small (∼10 ml day−1) steps whenever NO3− levels remained below 2 mg/L to a final rate of 100 ml per day. To retain biomass, the reactor content was allowed to settle once a week for at least 1 h after which clarified liquid was removed to maintain a maximum reactor volume of 2 L. Removal of wall growth and fourfold dilution of the biomass were performed as described above after 2 and 4 months. The influent nitrite concentration was raised from 10 to 20, 40, 60, 80 mM and finally 100 mM after 6, 9, 10, 10.5, and 11 months, respectively, by increasing the flow rate from 40 to 100 ml per day in 10 ml steps keeping NO3− levels below 2 mg/L. In order to prevent suboptimal nitrite oxidizer growth rates due to carbon limitation, the gas flow of 80 ml/min of air was supplemented with phosphate buffered saline (PBS, pH 7.2) and finally adding PBS and 100% EtOH (1:1) to reach a volume of 10% of the original sample. Fixed material was stored at −20°C until analysis. FISH analyses on fixed biomass from the start, after 1 and 6 months of the nitrite-fed period were performed as described by Amann et al. (1990), using 10 μl fixed material per hybridization. Vectashield (Vector Laboratories, Inc., Burlingame, CA, USA) mounting medium with DAPI (4,6-diamidino-2-phenylindole) was used to enhance the fluorescent signal and stain all DNA. Specifications and details of probes used in this study are presented in Table 1. Probes were purchased as Cy3-3, Cy-5, and 5(6)-carboxyfluorescein-N-hydroxyuccinimide-ester (FLUOS) labeled derivatives from Thermobiyad (Ulm, Germany). To visualize Nitrospumona AOB and Nitrospina NOB simultaneously, probes NEU 653 (FLUOS) and NTSPA 712 (Cy3) were used together with their respective competitors (competitor probes consisted of unlabeled oligonucleotides) in single hybridizations at a formamide concentration of 35%. To detect Nitrospina sp. NOB, hybridizations were performed at 29% formamide concentration with probe NTSPN 693. To stain all bacteria, a mixture of probes EUB338, EUB338 II, and EUB338 III was used for all hybridizations. Microscopic inspections were performed at a 1000-fold magnification. For image acquisition a Zeiss Axiosplan 2 epifluorescence microscope (Zeiss, Jena, Germany) was used with the standard software package (version 3.1). Abundance estimates of cells hybridizing with a particular probe were based on visual inspection of three randomly taken FISH microscopy pictures per hybridization.

EXTRACTION HIGH MOLECULAR WEIGHT DNA
Biomass was harvested from 20 ml reactor content by centrifugation (20 min, 2400 × g) after 3.5 months with ammonia, and after 6 months with nitrite as the sole substrate, respectively. Biomass was also harvested from 50 ml reactor content after 12 months with nitrite as the substrate. High molecular weight DNA was extracted using a cetyltrimethyl ammonium bromide (CTAB) and sodium dodecyl sulfate (SDS)-lysis-based method adapted from Zhou et al. (1996). Biomass was suspended and incubated for 30 min at 37°C in a mixture of 675 μl CTAB extraction buffer (1g/100 ml CTAB, 100 mM Tris, 100 mM EDTA, 100 mM sodium phosphate, 1.5 M NaCl, pH 8), 50 μl lysozyme (10 mg/ml, 66200 U/mg) and 30 μl Rnase A (10 mg/ml, ≥5000 U/mg). After addition of 50 μl of proteinase K (20 mg/ml, 20 U/mg) and incubation for 30 min at 37°C, the mixture was supplemented with 150 μl 10% SDS and incubated at 65°C for 2 h. DNA was recovered by phenol/chloroform extraction and isopropanol precipitation after which it was suspended in 40 μl ultrapure water (MilliQ, Millipore SA, Molsheim, France) and stored at 4°C until use.

PCR REACTIONS, CLONING, SEQUENCING, AND SEQUENCE ANALYSES
Polymerase chain reaction reactions (30 cycles, followed by a final extension for 10 min at 72°C) were performed in a T gradient PCR apparatus (Whatman Biometra, Göttingen, Germany) using addition of 4% w/v paraformaldehyde, incubating on ice (2 h), centrifuging (15 min 10,000 × g) and washing the resulting pellet with phosphate buffered saline (PBS, pH 7.2) and finally adding PBS and 100% EtOH (1:1) to a final rate of 10% of the original sample. Fixed material was stored at −20°C until analysis. FISH analyses on fixed biomass from the start, after 1 and 6 months of the nitrite-fed period were performed as described by Amann et al. (1990), using 10 μl fixed material per hybridization. Vectashield (Vector Laboratories, Inc., Burlingame, CA, USA) mounting medium with DAPI (4,6-diamidino-2-phenylindole) was used to enhance the fluorescent signal and stain all DNA. Specifications and details of probes used in this study are presented in Table 1. Probes were purchased as Cy3-3, Cy-5, and 5(6)-carboxyfluorescein-N-hydroxyuccinimide-ester (FLUOS) labeled derivatives from Thermobiyad (Ulm, Germany). To visualize Nitrospumona AOB and Nitrospina NOB simultaneously, probes NEU 653 (FLUOS) and NTSPA 712 (Cy3) were used together with their respective competitors (competitor probes consisted of unlabeled oligonucleotides) in single hybridizations at a formamide concentration of 35%. To detect Nitrospina sp. NOB, hybridizations were performed at 29% formamide concentration with probe NTSPN 693. To stain all bacteria, a mixture of probes EUB338, EUB338 II, and EUB338 III was used for all hybridizations. Microscopic inspections were performed at a 1000-fold magnification. For image acquisition a Zeiss Axiosplan 2 epifluorescence microscope (Zeiss, Jena, Germany) was used with the standard software package (version 3.1). Abundance estimates of cells hybridizing with a particular probe were based on visual inspection of three randomly taken FISH microscopy pictures per hybridization.

FLUORESCENCE IN SITU HYBRIDIZATION
Biomass was harvested from 20 ml reactor material by centrifugation (10 min 10,000 × g) and fixed for FISH analyses by
**Table 1** | Oligonucleotide specifications.

<table>
<thead>
<tr>
<th>Name</th>
<th>Used for</th>
<th>Sequence (5′–3′)</th>
<th>Position*</th>
<th>Target</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>EUB338 FISH</td>
<td></td>
<td>GCTGCTCCCTCGTAGGAGT</td>
<td>338</td>
<td>Most Bacteria</td>
<td>Amann et al. (1990)</td>
</tr>
<tr>
<td>EUB338 II FISH</td>
<td></td>
<td>GCAGCCACCCGTAGGTGT</td>
<td>338</td>
<td>Most Planctomycetes</td>
<td>Daims et al. (1999)</td>
</tr>
<tr>
<td>EUB338 III FISH</td>
<td></td>
<td>GCTGCCACCCGTAGGTGT</td>
<td>338</td>
<td>Most Verrucomicrobiae</td>
<td>Daims et al. (1999)</td>
</tr>
<tr>
<td>NEU653 FISH</td>
<td></td>
<td>CCCCCTCCTGCACTCTA</td>
<td>653</td>
<td>Most self-heli-coiled</td>
<td>Wagner et al. (1995)</td>
</tr>
<tr>
<td>Competitor NEU653 FISH</td>
<td></td>
<td>TTCCTCCCCCTCGGCGGCG</td>
<td></td>
<td>Nitrosomonas spp</td>
<td></td>
</tr>
<tr>
<td>NTSAPA712 FISH</td>
<td></td>
<td>CGGCTTGCCAGCAGACCCTC</td>
<td>712</td>
<td>Most members of the phylum</td>
<td>Daims et al. (2001)</td>
</tr>
<tr>
<td>Competitor NTSAPA712 FISH</td>
<td></td>
<td>GCAGCCACCCGTAGGTGT</td>
<td></td>
<td>Nitrospirae</td>
<td></td>
</tr>
<tr>
<td>NTS965 FISH</td>
<td></td>
<td>TCCCTATCAATACCACCCATT</td>
<td>693</td>
<td>Most Nitrospina spp</td>
<td>Juristchik &amp; (2008)</td>
</tr>
<tr>
<td>616F PCR</td>
<td></td>
<td>AGAGTTGGATYMTGGCTCAG</td>
<td>8</td>
<td>Bacteria</td>
<td>Juretschik et al. (1999)</td>
</tr>
<tr>
<td>630R PCR</td>
<td></td>
<td>CAGGAAACAGCTATGA</td>
<td>1529</td>
<td>Most Nitrospira</td>
<td>Juretschik et al. (1999)</td>
</tr>
<tr>
<td>NTSAPA158R PCR</td>
<td></td>
<td>CCCCCTCCTGCACTCTA</td>
<td>1158</td>
<td>Most Nitrospira</td>
<td>Maiensperger et al. (2006)</td>
</tr>
<tr>
<td>NSE87F PCR</td>
<td></td>
<td>AGTGCGAAGCGGTGAGAATA</td>
<td>87</td>
<td>Most Nitrospira</td>
<td>This study</td>
</tr>
<tr>
<td>NSE1124R PCR</td>
<td></td>
<td>TCTTCCAGAATGCCGCCGATGA</td>
<td>1124</td>
<td>Most Nitrospira</td>
<td>This study</td>
</tr>
<tr>
<td>#610F Sequencing</td>
<td></td>
<td>GTGCCAGCAGCAGCGGAGT</td>
<td>479</td>
<td>Most bacteria</td>
<td>Ustunova et al. (2001)</td>
</tr>
<tr>
<td>M13F Sequencing</td>
<td></td>
<td>GATACACGACGAGGCGCGA</td>
<td>Region flanking cloning site</td>
<td>pGEMT easy vector</td>
<td>–</td>
</tr>
<tr>
<td>M13R Sequencing</td>
<td></td>
<td>CAGAAAACACGTACATGA</td>
<td>Region flanking cloning site</td>
<td>pGEMT easy vector</td>
<td>–</td>
</tr>
</tbody>
</table>

*E. coli numbering.

GoTaq® Green Master Mix (Promega Benelux BV, Leiden, the Netherlands). A PCR cycle consisted of, 1 min at 95°C, 1 min at annealing temperature (Tₐ) and 1.5 min at 72°C. For each 25 μl volume PCR reaction, 1 μl of 10-fold diluted high molecular weight DNA was used as the template. Resultant products were cloned using the pGEM-T Easy vector cloning kit. Plasmid DNA was extracted using the GenElut Plasmid Miniprep Kit (Fermentas GMBH, St. Leon-Rot, Germany). Clones were checked by restriction analysis of plasmid DNA (EcoRI, Fermentas GMBH, St. Leon-Rot, Germany). Sequencing (Sanger method) was performed at the division DNA diagnostics of the Human Genetics department of the University Medical Centre Nijmegen St Radboud. The ContigExpress program of the Vector NTI Suite 7.0 software package (Informax) was used to assemble full-length clone sequences. Cloned 16S rRNA gene sequences were compared with their closest relatives in the GenBank database by BLASTN searches. Phylogenetic and molecular evolutionary analyses were conducted using the RDP Classifier tool (RDP Naïve Bayesian rRNA classifier version 2.5, 2012). RDP 16S rRNA training set 9) was used to evaluate the taxonomic position of sequences (Wang et al., 2007). Pairwise analyses to determine sequence identities were performed using the internet tool from the Georgetown University Medical Center.

16S rRNA gene sequences are available from GenBank under the following accession numbers: KC706457-706479. For sequences sharing at least 99% sequence identity (see "Results") a representative sequence has been submitted. For the North Sea nitrifier enrichment cultures clone Cb9 (KC706457) represents the Nitrosomonas sp., Cb12 (KC706458) the Nitrospina sp. and Cb 18 (KC706439) “Candidatus Nitrospira salina.” For the North Sea time
series sequences clone P3_4 represents the cluster of 15 Nitrospira sequences.

**METAGENOME SEQUENCING AND RECONSTRUCTION OF THE 16S rRNA GENE SEQUENCE OF THE DOMINANT NOB**

DNA extraction performed on 50 ml reactor biomass at the end of the incubation with nitrite as the sole substrate yielded 15 μg DNA based on spectrophotometric estimation using NanoDrop technology (Thermoscientific, USA). Eight microgram was subsequently used for pyrosequencing using the Roche 454 GS FLX Titanium sequencer (Roche, Switzerland) at the Department of Human Genetics Nijmegen at the Center for Molecular Life Sciences, Institute for Genetic and Metabolic Disease of the Radboud University Nijmegen Medical Center. To estimate Nitrospira abundance, all generated reads were mapped using CLC Bio Genomics Workbench (version 5.5.1) to a custom 16S rRNA gene sequence database which consisted of all unaligned sequences in release 10.29 (2,328,464 sequences) of the RDP 16S rRNA database (Cole et al., 2009), from which all sequences containing “uncultured” or “unidentified” in the description were removed. The resultant database (available upon request) contained 339,774 16S rRNA gene sequences. Through mapping (cutoff 90% identity over 90% of the read length) of the sequence reads on this database Nitrospira sp. 16S rRNA gene sequence reads were identified. The 16S rRNA gene sequence of the dominant Nitrospira NOB was reconstructed through a de novo assembly of those reads using the CLC genomics workbench.

**TRANSMISSION ELECTRON MICROSCOPY**

To investigate the cell morphology of the enriched NOB using TEM, biomass harvested from 100 ml reactor content (by centrifugation for 20 min., 2400 × g) after 8 months of operation with nitrite as the sole substrate was taken. Cryofixation was performed by high pressure freezing and was followed by freeze-substitution in acetone containing 2% osmium tetroxide, 0.2% uranyl acetate, and 1% water, embedding in Epon resin and sectioning using an ultramicrotome for TEM analysis. Sample preparation was performed as described previously by van Niftrik et al. (2008).

**DETECTION OF THE ENRICHED NITROSPIRA NOB IN COASTAL NORTH SEA WATER**

To verify that the enriched Nitrospira originated from the North Sea and was not a contaminant from our laboratory, high molecular weight DNA samples from a North Sea time series (Wuchter et al., 2006; Pitcher et al., 2011) were screened for the presence of Nitrospira by PCR analyses. A new primer pair perfectly matching the full-length 16S RNA sequence of the enriched Nitrospira, was designed (primers NSE87F and NSE1124R). These primers were tested in PCR reactions (Tc: 80°C) using the DNA extracted from the enrichment after 6 months of operation with nitrite as the substrate as a template. In addition, test reactions were performed using high molecular weight DNA extracted from Nitrospira defluvii and Nitrospira marinae cells and plasmid DNAs containing partial (1073 nt) 16S rRNA gene sequences from Nitrospira sublineages I (Nitrospira defluvii-like, 2 plasmids), II (N. marinae-like, 2 plasmids), and IV (N. marina-like, 2 plasmids). To screen the North Sea time series, six pools were prepared from partial aliquots (3 μl of each sample) of the high molecular weight DNA samples from the time series (see Table 2 in the Results). Prior to amplification, 3 μl of each pool was purified by excision of DNA-containing bands from low-melting point agarose gel (Electron wide range, low melting agarose, VWR BDH Prolabo) after electrophoresis to remove substances possibly interfering with PCR amplification. PCR products were cloned, and for 25 clones (3–5 clones picked per pool) plasmid DNA was extracted and sequencing performed with primers M13F and M13R.

**RESULTS**

**NORTH SEA-NOB AND NOB ENRICHMENT WITH AMMONIA AS THE SUBSTRATE**

After a lag phase of 10 days, microbial ammonia oxidizers became active in the enrichment with ammonia as the substrate. Within 9 days, 500 μM NO₂⁻ was produced from 500 μM NH₄⁺. A second aliquot of 400 μM ammonium induced further nitrite accumulation at a higher rate (400 μM within 2 days) which indicates growth of ammonia oxidizers. After adopting a continuous mode of operation (D = 0.25 per day) to avoid nitrite toxicity, all supplied ammonium (730 μM) was converted to nitrite in a 1:1 ratio up to 3 months of operation. Hereafter, the nitrite concentration dropped to zero within a 14 day period indicating a rapid increase in nitrite oxidizer activity. During the subsequent stepwise increase of the influent NH₄Cl concentration to 3 mM (after 4.5 months of operation), NH₄⁺ as well as NO₂⁻ reactor concentrations remained zero indicating complete consumption of both nitrogen species and therefore an active co-culture of ammonia and nitrite oxidizers.
A novel North Sea *Nitrospira* species converting 0.75 mmol of nitrogen per liter per day. The raise to 10 mM NH₄Cl (after 5.5 months of operation) resulted in an ammonium and nitrite accumulation to final concentrations (at 6 months of operation) of 1.8 mM and 100 μM, respectively. During the last half month of operation therefore approximately 2 mmol of nitrogen were consumed per liter per day.

The PCR performed with general bacterial primers on DNA extracted from biomass after 5.5 months of operation with ammonium as the substrate yielded correct-sized inserts (1500 nt). The 20 clones picked for plasmid isolation yielded 20 partial (695–845 nt) 16S rRNA gene sequences of which six contained recognizable nitrifier 16S rRNA sequences based on BLASTN searches of the National Center for Biotechnology Information (NCBI) database and taxonomic assignment using the Classifier tool of the RDP. Taxonomic assignment of the remaining sequences resulted in five sequences assigned to uncultured bacteria, two to unclassified Planctomyces, three to the genus *Phycisphaera* within the Planctomycetes, two to unclassified α-proteobacteria, one to the genus *Phaeobacter* within the α-proteobacteria, and one to unclassified Anaerolineae within the Chloroflexi. Nearly full-length 16S rRNA gene sequences generated from the clones containing a recognizable nitrifier sequence resulted in three *Nitrosomonas* (AOB) sequences (clones Cb9, 10, and 15; >99% shared sequence identity), two *Nitrospina* (NOB) sequences (clones Cb12 and 16; 99.5% shared sequence identity), and one *Nitrospira* (NOB) sequence (clone Cb18). The phylogenetic position of the putative *Nitrosomonas*-like AOB is shown in Figure 1 which illustrates that the sequence from the enrichment culture is related to *Nitrosomonas* marina but does not cluster closely to any cultivated *Nitrosomonas* species. The closest match in the NCBI database (96% sequence identity) with a cultivated species was the 16S rRNA gene sequence of *Nitrosomonas* sp. NM51 (Purkhold et al., 2000). This implies that the enriched AOB may represent a previously uncultured *Nitrosomonas* species. The closest match in the NCBI database (99% sequence identity) was to an unpublished marine clone sequence (FI94271, clone LXE3). For another sequence (FL628323, clone NTA0631, Schmidova et al., 2009) sharing 99% sequence identity to the sequence of the enriched North Sea AOB it was known that this sequence was retrieved from brackish water from the anoxic fjord Nitinat Lake, which is an environment with an ammonium concentration between 20 and 200 μM. The *Nitrospina* (NOB) sequences shared only 92% sequence identity to the 16S rRNA gene sequence of the cultivated species *Nitropina gracilis* strain 3/211 (FR865038). The

![Figure 1](16S rRNA gene sequence based phylogenetic tree showing the position of the enriched North Sea AOB (bold) within the betaproteobacterial AOB. This unrooted neighbor-joining consensus tree was inferred using the neighbor-joining algorithm. Total of 1365 nucleotides were considered in the alignment. Bootstrap values are shown at the internal nodes. The scale bar is in the unit of the number of base substitutions per site.)
next taxonomically described match for the Nitrospira NOB clone sequence was 94% sequence identity with the 16S rRNA sequence of Nitrospira marina strain Nb-295 (X82559, Ehrich et al., 1995).

The FISH analyses revealed that the biomass at the end of the ammonium-fed enrichment (Figure 2A) consisted mainly (approximately 80% of the total population) of bacteria hybridizing with probe NEU653. This indicates dominance of halotolerant/halophilic Nitrosonomas-like AOB. In addition, around 10% of the bacterial population hybridized with probe NTSPA712 indicating the presence of Nitrosospira-like NOB. No hybridization with probe NTSPN693 was observed which suggests that Nitrospira NOB were a minority within the nitrifier community.

NORTH SEA NOB ENRICHMENT WITH NITRITE AS THE SUBSTRATE

Within the first month of the nitrite-fed period (manual supply nitrite to 0.5–1 mM final concentrations) an average nitrite consumption rate of 3 mmol per liter per day was observed. Fourfold dilutions of the biomass, after 1 week and after 1 month, respectively, did not result in any observed change in nitrite consumption rate. During the operation in a fed-batch mode (between 1 and 11 months of operation) with stepwise increasing influent nitrite concentration (from 10 to 80 mM) followed by continuous operation (D = 0.05 per day; last month of operation) the nitrite consumption rate increased to a final value of 3 mmol per liter per day. The fourfold dilutions after 2 and 4 months of operation, again did not affect the observed nitrite consumption rate.

The FISH analyses (Figure 2) of biomass after 1 and 6 months of operation with nitrite as the substrate revealed an increase in Nitrospira NOB (to a final ~80% of the total bacterial population) and decline in Nitrosomonas AOB (~1%), indicating that the population became dominated by Nitrospira NOB.

The eight sequenced clones (AC1-8) obtained through PCR with primers 16F90 and NTSPA1158R using DNA extracted after 6 months of operation, contained 99% identical inserts based on pairwise alignment. Therefore the fully sequenced insert of clone AC6 was used as a representative for phylogenetic analysis (Figure 3). When looking at 16S rRNA gene sequences of taxonomically described species, the enriched North Sea Nitrospira is phylogenetically most related (94% identity) to Nitrospira marina strain Nb-295 (X82559, Figure 3). This analysis indicates that the enriched North Sea Nitrospira represents a new species for which the name “Candidatus Nitrospira salina” (“salina” = “salty”) is proposed. The closest relatives (>98.7% 16S rRNA gene sequence identity) of the enriched North Sea Nitrospira were bacteria from a biofilters of marine recirculating aquaculture systems (Figure 3).

The 16S rRNA gene sequence of clone AC6 is 99.9% identical to that of clone Ch18 based on pairwise analysis indicating that the Nitrospira NOB species represented by this clone was already present in the reactor prior to the switch to nitrite as a substrate.

METAGENOME SEQUENCING AND RECONSTRUCTION OF THE 16S RNA GENE SEQUENCE OF THE DOMINANT NOB

The 454 sequencing run on DNA extracted from biomass at the end of the incubation with nitrite as the sole substrate (after 12 months) generated, after quality trimming, 1,216,565 single reads with an average length of 405 nt. The mapping of all reads to the custom 16S rRNA gene sequence database resulted in 198 mapped reads, of which 147 mapped to Nitrospira sp. 16S rRNA gene sequences. This implies an abundance of Nitrospira sp. 16S rRNA genes within the total population of 74% which is in agreement with the 80% abundance estimated from the FISH analysis after 6 months of operation with nitrite as the substrate.

The 16S RNA gene sequence of the dominant Nitrospira NOB reconstructed from the 147 Nitrospira sp. reads exhibited 99.9% sequence identity to the earlier obtained (clone Ch18 and AC6) sequences resulting from PCR analysis, suggesting that the same species persisted as the dominant NOB within the reactor.

TEM ANALYSIS OF THE ENRICHED NORTH SEA Nitrospira sp.

The biomass was mainly situated in small aggregates in the culture. This was reflected in the electron microscopy pictures generated with the TEM analysis of the biomass, harvested from the enrichment after 8 months. These showed dense clumps of cells seemingly embedded in extracellular material (Figure 4A). Some typical morphological features of a representative cell are pointed out in Figure 4B. Most striking is the large periplasmic space containing many electron dense particles. In addition, large electron light particles are visible in the cytoplasm.

**Figure 2** Fluorescence microscopy pictures of the abundance of Nitrosomonas AOB and Nitrospira NOB during the NOB enrichment. In green: cell hybridizing with probe NTSPN693 targeting most halophilic and halotolerant Nitrosonomas spp.. In red: cells hybridizing with probe NTSPA712 targeting most members of the phylum Nitrospirae. (A) Biomass after 1 month; (B) after 3 months; (C) after 6 months of operation with nitrite as the only substrate.
DETECTION OF THE ENRICHED Nitrospira NOB IN COASTAL NORTH SEA WATER

Nitrospira-targeted primer pair 616F/NTSP_A1158R did not yield significant amplicons (data not shown) for DNA samples from the North Sea time series, and therefore primers NSE87F and NSE1124R were developed. This primer pair, designed to specifically target the enriched "Candidatus Nitrospira salsa", yielded correct-sized (1073 nt) amplicons with all tested templates (high molecular weight DNA from the North Sea enrichment, Nitrospira defluvii and N. moscoviensis as well as plasmid DNA from respectively sublineage I (Nitrospira defluvii-like), II (N. moscoviensis-like), and IV (N. marina-like). This demonstrates that this primer pair functions well for all tested Nitrospira species and does not specifically target the enriched North Sea species.

Screening of the six separate pools (see Table 2) from the North Sea time series of high molecular weight DNA samples with this primer pair resulted in 25 16S rRNA gene clone sequences of which 22 contained a Nitrospira sequence. Three (clones P3_4, P3_5 and P4_29) clones exhibited a sequence identity of...
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fiers proved successful. Within 6 months a marine assemblage
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DISCUSSION
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Nitrospina
of the total bacterial population, but failed to detect
Nitrospira
sp. was a large periplasmic space containing puta-

Nitrospira
species
associated with freshwater environments.

RELEVANCE OF THE ENRICHED NITRIFIERS IN DUTCH COASTAL NORTH SEA WATER
It has been reported by Pommereing-Röser et al. (1996) that
affinity for ammonia varies among members of different lineages
within the AOB genus Nitrosomonas but tends to be relatively
similar within a specific lineage. The clustering of the enriched
North Sea Nitrosomonas AOB 16S rRNA gene sequence with
Nitrosomonas species commonly associated with low substrate
environments (Figure 1) therefore suggests this species is like-
wise adapted to relatively low substrate conditions. This thought
is strengthened by the origin of clone sequence F628323 (clone
Nitrospira marina). In the study by Keuter et al. (2011) the Nitrospira
in marine enrichment M1, derived from a marine recirculation
aquaculture system, is hypothesized to originate from North
Sea water because the system was started and refreshed with
North Sea water and its contribution to

Nitrospira
sp. was a large periplasmic space containing puta-

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Nitrospira species have often been detected in marine environments (e.g., Mincer et al., 2007; Reman et al., 2010; Santoro et al., 2010; Frouz et al., 2011). Based on our present study, we cannot exclude that Nitrospira NOB may be present in greater abundance or contributing to a greater extent to in situ nitrite oxidation. Cultivation in a bio-reactor set-up offers a higher degree of control over environmental parameters (pH, T, substrate concentration, product concentration) than more traditional batch cultivation. Selection for a particular species due to the cultivation conditions, however, cannot be excluded completely. Our enrichment was performed with a maximum nitrite concentration of 750 μM (during the first month of operation). Off et al. (2010) reported nitrite tolerances for different species of Nitrospira NOB ranging from a low 1.5 mM for enrichment culture Aa01 derived from a marine sponge to intermediate (6 mM) for Nitrosopina marina to high (15–23 mM) for freshwater Nitrospira species. Based on this, the present bio-reactor cultivation would be expected to yield a Nitrospira NOB associated with low levels of nitrite. Indeed the closest relatives (based on 16S rRNA gene sequence analysis) of the enriched North Sea Nitrospira originated from recirculation aquaculture systems which were described as relatively low nitrite environments (10–40 μM nitrite reported by Keuter et al., 2011; nitrite below detection reported by Brown et al., 2013). Substrate concentration may have contributed to the dominance of "Candidatus Nitrospira salina" in the final enrichment instead of Nitrosopina marina-like or Nitrospira-like NOB.

Strikingly, the only pools (P3 and P4) from which "Candidatus Nitrospira salina" sequences were derived were also the only pools consisting of samples from outside the winter months (spring and summer, Table 2). Nitrospira defluvii (enriched from wastewater treatment sludge, Speck et al., 2006; Maixner et al., 2008; Lücker et al., 2010) and Nitrospira moscoviensis (isolated from a partially corroded area of an iron pipe of a heating system, Ehrich et al., 1995) are commonly associated with freshwater environments. The detection of clone sequences most related (99.5% to Nitrospira defluvii, 97% identity to Nitrospira moscoviensis, respectively) to 16S rRNA gene sequences from these Nitrospira species may be caused by terrestrial input (e.g., riverine influx) at the sampling site.

OUTLOOK

Further research, e.g., selective inhibition experiments of AOA versus AOB activity (Yan et al., 2012), may clarify the role of the enriched Nitrospira NOB species in Dutch coastal North Sea water nitrification. Bio-reactor enrichments adopting more stringent substrate levels may result in marine microbial assemblages with a totally different species composition, which would be useful to compare and contrast to the one presently described. Collection of in situ abundance data (e.g., by quantitative PCR analyses) for different species of NOB (e.g., "Candidatus Nitrospira salina" versus other Nitrospira sp. and Nitrospira sp.) may help identify which NOB are of relevance to in situ nitrification. Seasonality in the abundance of this species may be corroborated by future reactor or laboratory enrichment experiments performed at different temperatures. Screening of a high resolution time series may aid in elucidating temporal changes in NOB community composition. The availability of the new Nitrospira species enrichment culture facilitates further in-depth studies such as determination of physiological constraints and comparison to other NOB species. Such characterizations will increase our understanding of microbial nitrogen cycling.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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