Adaptability as the key to success for the ubiquitous marine nitrite oxidizer *Nitrooccus*

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Nitrite-oxidizing bacteria (NOB) have conventionally been regarded as a highly specialized functional group responsible for the production of nitrate in the environment. However, recent culture-based studies suggest that they have the capacity to lead alternative lifestyles, but direct environmental evidence for the contribution of marine nitrite oxidizers to other processes has been lacking to date. We report on the alternative biogeochemical functions, worldwide distribution, and sometimes high abundance of the marine NOB *Nitrooccus*. These largely overlooked bacteria are capable of not only oxidizing nitrite but also reducing nitrate and producing nitrous oxide, an ozone-depleting agent and greenhouse gas. Furthermore, *Nitrooccus* can aerobically oxidize sulfide, thereby also engaging in the sulfur cycle. In the currently fast-changing global oceans, these findings highlight the potential functional switches these ubiquitous bacteria can perform in various biogeochemical cycles, each with distinct or even contrasting consequences.

INTRODUCTION

Nitrite oxidation is the major pathway that generates nitrate, the dominant form of biologically available nitrogen and often a limiting nutrient to biological production in surface oceans. The prevalence of nitrite below surface, however, attests to the substantial occurrence of nitrite oxidation in the ocean interior, which represents a key conduit to resupply nitrogen to the surface ocean and is thus essential to the global nitrogen cycle (1). Nevertheless, current knowledge of the physiology of marine nitrite-oxidizing bacteria (NOB) remains poor, with only a few species described to date that belong to the genera *Nitrobacter, Nitrospira, Nitrospina, Candidatus Nitromaritima*, or *Nitrococcus* (2, 3). Although several studies have challenged the conventional understanding of nitrate production as the only relevant contribution of NOB to global biogeochemical cycling (4–7), no direct environmental evidence of marine NOB participating in elemental cycles other than nitrogen and carbon has been reported to date.

Most recent research on marine nitrite oxidizers has been heavily biased toward *Nitrospina*, which can be found in a wide range of habitats, including open ocean (8), sediments (9, 10), and suboxic water columns (11, 12). Experimental and genome analyses of the two cultured *Nitrospina* strains, *Nitrospina gracilis* and *Nitrospina watsonii*, strongly suggest that these organisms are chemolithoautotrophs dependent on nitrite oxidation for energy conservation (13–15). In comparison, *Nitrooccus*, with only one species known to date, *Nitrooccus mobilis*, has had its presence reported only twice in the 1980s in the Pacific (16, 17) and once in a high-salinity pond (18) since its first isolation (13); its presence has not been reported again until its recently recorded abundance in the Namibian oxygen minimum zone (OMZ) where they even outnumbered *Nitrospina* (11). In that study, *Nitrooccus* and *Nitrospina* were the only NOB genera detectable via catalyzed reporter deposition fluorescence in situ hybridization (CARD-FISH) and together comprised almost 10% of the total microbial community. Although *Nitrospina* use a putatively high-affinity *cbp*-type terminal oxidase, which should allow them to catalyze nitrite oxidation even under hypoxic conditions (14), the adaptation strategy of *Nitrooccus* to oxygen-deficient conditions remains unclear. *Nitrospina* preferred residing in the oxycline and the upper OMZ, whereas *Nitrooccus*, in contrast, became more abundant in the lower OMZ (4.9% of total microbial abundance) where oxygen levels were minimal (11). Here, a similar trend was again observed for October 2011, with *Nitrospina* contributing up to 1.3% of total microbial community in the upper OMZ (65 m, 95 μM O2), whereas *Nitrooccus* displayed maximal abundance (1.3%) at 119 m (16 μM O2) (Fig. 1A). Overall, *Nitrooccus* showed a moderate yet significant negative correlation with oxygen (Spearman correlation = 0.44, P < 0.01) and was undetectable at oxygen concentrations >20 μM (Fig. S1A).

To investigate whether *Nitrooccus* is restricted to certain environmental conditions, we searched for *Nitrooccus*-like sequences in publicly available databases. Three novel *Nitrooccus*-like phytophotes, in addition to *N. mobilis*, were identified in the SILVA 16S ribosomal RNA (rRNA) database (19, 20), sharing 97.8 to 99.2%, 96.5 to 97.8%, and 96.6 to 97.3% sequence identities with *N. mobilis* (fig. S2 and table S1). Subsequent searches for all phytophotes’ 16S rRNA genes in marine amnicon and metagenomic data sets from the MetaGenome Rapid Annotation using Subsystems Technology (MG-RAST) server (21), Ocean Sampling Day 2014 (OSD) (22), and Taraceans (23) revealed the presence of *N. mobilis* and *Nitrooccus*-like phytophotes in 69% of all data sets examined. Among the data sets that carry geographical information, *N. mobilis* and *Nitrooccus*-like phytophotes were found to be globally distributed from coastal upwelling regions to oligotrophic open oceans, from tropical to temperate and polar latitudes, and from epipelagic (surface sunlit layer, ~0 to 100 m) to mesopelagic (twilight zone, ~100 to 1000 m) ocean waters (Fig. 1B and tables S2 and S3). Considering only metagenomic data sets (table S2) and excluding the more bias-prone amnicon sequencing data (table S3), higher contributions of *N. mobilis* and *Nitrooccus*-like phytophotes to total microbial community (>5%, up to 17%) were nearly exclusively associated with highly productive environments, such as the...
Peruvian OMZ and Guanabara Bay or with hypersaline lagoons, indicating an ecological advantage for them under these conditions (Fig. 1B and table S2). On the basis of Tara Oceans metagenomic data alone, which is currently the most comprehensive data set with consistent sequencing depths and covering the widest geographic range of global oceans to date, 16S rRNA genes affiliated with Nitrooccus were present in all samples and represented 1.2 to 5.1% (mean, 2.3%) of the microbial community (table S2).

We analyzed the genome of N. mobilis Nb-231 to identify potential functional roles Nitrooccus may play in such diverse environments. The resulting genome-derived hypotheses were tested in incubation experiments with both the pure culture isolate N. mobilis Nb-231 and Namibian OMZ seawater samples. Nitrooccus only encodes a putative low-affinity aa3-type cytochrome c oxidase (Fig. 2 and table S4), thus ruling out a specialization on microaerobic respiration as suggested for Nitrospira (14). Instead, its abundance in OMZ waters indicates the utilization of alternative anaerobic metabolisms. In agreement with this hypothesis, Nitrooccus was abundant even in waters where no nitrite oxidation was detectable in the Namibian OMZ, and no correlation with nitrite oxidation rates was observed (Spearman correlation = 0.05, P > 0.05, n = 35) (Fig. 1A and fig. S1B). These findings suggest that NOB other than Nitrooccus, such as Nitrospira, were responsible for most of the nitrite oxidation detected in the Namibian OMZ (Fig. 1A).

On the other hand, Nitrooccus abundance was significantly correlated with nitrate reduction rates (fig. S1C) (Spearman correlation = 0.54, P < 0.05), suggesting a contribution to this anaerobic process. The key enzyme for nitrite oxidation, nitrite oxidoreductase (NXR), is reversibly, and nitrate reduction activities have previously been observed in Nitrobacter (24, 25) and Nitrospira (6). When the N. mobilis pure culture was subjected to anoxic conditions in the presence of formate and acetate, substrates that have previously been reported to support mixotrophic or heterotrophic growth in NOB (6, 25), NO3− was reduced at a rate of 3.66 ± 0.32 fmol per cell per day (±SD) within the first 230 hours of incubation (Fig. 3A). Because the N. mobilis genome does not encode any other known nitrate-reducing enzyme, the NXR of Nitrooccus is most likely the candidate for nitrate reduction (Fig. 2). Furthermore, N. mobilis encodes duplicated versions of NXR alpha subunit (NxrA), the substrate-binding catalytic subunit of the enzyme complex (fig. S3) (26, 27). NxrA1 is encoded in one genomic region together with genes for the NXR beta, delta, and gamma subunits. The duplicated subunit NxrA2 (fig. S3), with an amino acid identity of 89% to NxrA1, is not clustered with any other genes known to be involved in nitrite oxidation. This duplication of the catalytic NxrA subunit alone has also been observed in all sequenced Nitrobacter genomes and in Nitrolacea hollandica (28, 29). It is tempting to speculate that Nitrooccus uses one NxrA paralog for nitrite oxidation and the other for the reduction of nitrate, but biochemical verification will be necessary.

The observed switch to NO3− reduction with formate and acetate indicates that Nitrooccus can use organic matter as energy and carbon source. Although whether this truly translates to growth remains to be empirically verified, chemoorganoheterotrophic and autotrophic potentials of Nitrooccus are corroborated by the presence of all genes for the oxidative TCA (tricarboxylic acid) cycle, glycolysis, PPP (pentose phosphate pathway), and the Calvin-Benson-Bassham cycle in the genome (Fig. 2 and table S4). Genome annotation also revealed genes for respiratory complexes I to V (Fig. 2 and table S4). Complexes I to III are not required for energy conservation during nitrite oxidation, unlike during the oxidation of organic substrates, but they do mediate the reverse electron flow from nitrite to NAD+ during chemolithoautotrophic growth. An ETF (electron-transport flavoprotein) complex and an ETF/quinone oxidoreductase probably couple β-oxidation of fatty acids to the respiratory chain.

Fig. 1. Occurrence and distribution of Nitrooccus in a marine OMZ and the global oceans. (A) Water column chemistry and nitrogen cycling rates in the Namibian OMZ. Left: Vertical distribution of oxygen, NO3−, NH4+, and NO2− at station 2. Middle: Nitrite oxidation rates, NO3− production rates, and cellular abundance of Nitrooccus and Nitrospira. Right: Rates of ammonia oxidation, nitrate reduction, and anammox measured with 15N-labeling experiments. Error bars show SDs derived from linear regression analyses. (B) Worldwide distribution of Nitrooccus mobilis and Nitrooccus-like phylotypes in the oceans. Combined abundance of all four phylotypes in different metagenomic data sets is denoted in orange (MG-RAST), turquoise (OSD), and blue (Tara Oceans). Circle size indicates percentage of 16S rRNA gene reads relative to all bacterial and archaeal 16S rRNA gene reads within each sample.
rapid remineralization of $^{13}$C-DOM by other organisms followed by lithoautotrophic uptake of $^{13}$C-HCO$_3^-$ by *Nitrococcus* can be largely excluded, as no detectable $^{13}$C enrichment was observed in *Nitrococcus* cells in parallel anoxic incubations with $^{13}$C-HCO$_3^-$ and NO$_2^-$ (Fig. 3C).

The high $^{13}$C enrichment in combination with our findings from genome analyses and pure culture experiments strongly indicate a chemooorganoheterotrophic potential of *Nitrococcus* under NO$_3^-$ reducing conditions. The broad range of $^{13}$C enrichment observed in our incubations (table S5) can likely be attributed to the presence of different *Nitrococcus* phylotypes or phenotypic heterogeneity of individual cells within a population (31).

When exposed to elevated nitrite levels (~200 μM), pure cultures of *N. mobilis* continuously produced small but significant amounts of N$_2$O during anoxic incubations [3.2 (±0.48) × 10$^{-3}$ fmol per cell per day during the first 230 hours] (Fig. 3B and fig. S4). No organic substrates were amended in these incubations, and denitrification was likely driven by the oxidation of dissolved organic carbon present in the sterilized seawater used for medium preparation (table S6) and/or the oxidation of intracellular storage compounds such as glycogen (Fig. 2) (13). *N. mobilis* encodes a copper-containing nitrite reductase (NirK) (table S4), likely facilitating nitrite reduction to nitric oxide (NO). None of the enzymes known to be responsible for the reduction of NO to N$_2$O—cytochrome c or quinone-dependent nitric oxide reductase (cNOR or qNOR, respectively)—were identified in the genome. However, the Nb-231 genome carries the genes for a two-subunit oxidase that belongs to a distinct phylogenetic cluster within the haem-copper oxidase family (table S4 and fig. S5). This enzyme group is designated the sNOR family and likely functions as NO reductases to detoxify NO.
targeted by CARD-FISH among other microbial cells (blue). Middle:32S/12C of the yet to be confirmed. Although we can exclude strictly abiotic N2O production from 13C-labeled bicarbonate under hypoxic conditions. Left: Fig. 3. Denitrifying potential of Nitrococcus mobilis Nb-231. (A) Anaerobic nitrogen dissimilation under (left) organoheterotrophic conditions (500 µM 15NO3−, 250 µM acetate, and 250 µM formate, anoxic) and (right) without the addition of electron donor (200 µM 15NO3−, anoxic). See the main text for more details. Error bars indicate SD of three biological replicates. (B) FISH-SIMS analyses of single Nitrococcus cells in Namibian OMZ bottom water samples (1.20 m above seafloor), incubated with (top) 13C-labeled dissolved organic matter (DOM) or (bottom) 13C-labeled bicarbonate under hypoxic conditions. Left: Nitrococcus cells (green) targeted by CARDFISH among other microbial cells (blue). Middle: 32S/12C of the corresponding cells. Right: 16C/13C ratio. Scale bars, 1 µm.

intermediates produced in the periplasm, as proposed for ammonia-oxidizing bacteria (32). To our knowledge, this is the first time that partial denitrification (NO3− or NO2− reduction to N2O) has been shown for an organism apparently containing this type of NOR only, thus giving indirect evidence that this enzyme family functions as NOR and might be used for energy conservation under denitrifying conditions. It should, however, be noted that the N. mobilis Nb-231 genome is not closed such that the definite absence of a canonical NOR is yet to be confirmed. Although we can exclude strictly abiotic N2O production based on our abiotic control incubation (fig. S4), we cannot rule out abiotic-biotic hybrid N2O formation, in which the NO formed from NirK-mediated NO2− reduction may react abiotically with medium components to give N2O. This has recently been reported to be the main N2O production pathway by ammonia-oxidizing archaea that also lack a known NOR (33). A nitrous oxide reductase (for reduction of N2O to N2) has not been identified in the genome, which is consistent with the lack of detectable N2 production in our pure-culture experiments.

OMZs are a major global source of oceanic N2O (25 to 59%) (34), a potent greenhouse gas and ozone-depleting agent that has usually been attributed to denitrifying and ammonia-oxidizing microorganisms (35, 36). In the Namibian OMZ, N2O production (~17 nM day−1) was detected particularly in the bottom waters where Nitrococcus abundance was maximal and nitrite oxidation was minimal (Fig. 1A), strongly indicating a contribution from Nitrococcus. Considering the worldwide distribution and high abundance of N. mobilis and Nitrococcus-like phylotypes especially within productive coastal ecosystems, Nitrococcus might represent a previously overlooked yet significant source of oceanic N2O. Because OMZs are expanding and intensifying globally (37), Nitrococcus may switch from a nitrogen-preserving (NO2−-oxidizing) mode to one that facilitates nitrogen loss (NO2−/NO3− reduction to N2O).

Apart from their importance in nitrogen cycling, Nitrococcus may also affect sulfur cycling. The N. mobilis genome harbors several key sulfur-metabolizing enzymes, including a sulfide/quinone oxidoreductase (sqr) that might oxidize hydrogen sulfide (H2S) to elemental sulfur or polysulfide (S0) in the periplasmic space with concomitant reduction of quinone (Fig. 2 and table S4). In addition, a periplasmic sulfite dehydrogenase (sor) may oxidize sulfite to sulfite and transfer the electrons onto cytochrome c. Last, a cytoplasmic type 3b bidirectional hydrogenase (38) is present (Fig. 2 and table S4). This so-called sulfhydrogenase can catalyze the reversible oxidation of H2 with NAD(P)H (39) and has been shown to reduce S0 to H2S in the hyperthermophilic archaeon Pyrococcus furiosus (40).

The ability of Nitrococcus to catalyze sulfide oxidation in the presence of O2 was confirmed with N. mobilis pure cultures, which consumed sulfide at a rate of 43 nmol S per microgram of protein per day, whereas the disappearance of sulfide in the abiotic control was negligible even during 5 hours of incubation (Fig. 4B). To our knowledge, this is the first time that capability for sulfur oxidation has ever been reported in association with nitrifying organisms, adding another remarkable facet to the versatile metabolic repertoire already known in NOB.

Among 20 screened marine environmental metagenomes, 50% were found to contain sqr genes with high sequence identities to the N. mobilis sequence, indicating the prevalent potential of Nitrococcus to oxidize reduced S-compounds in the oceans. More than half of the metagenomes from mesopelagic habitats contain N. mobilis-like sqr, but none do from the deep chlorophyll maxima and epipelagic ocean (fig. S6 and table S7). Hence, sulfide-oxidizing capacity seems to present an ecological advantage for Nitrococcus in subsurface waters: This could mean a direct coupling with growth, or facilitation of sulfide detoxification and/or preservation of biologically available sulfur (41, 42).

The prevalence of this functional trait of Nitrococcus in the mesopelagic is consistent with the recently reported widespread occurrence of sulfide-oxidizing enzyme complexes in the mesopelagic ocean and within the Global Ocean Sampling (GOS) metagenomic data sets, despite the apparent lack of detectable sulfide (42–44). On the basis of the 138 Tara Oceans data sets that distinguish mesopelagic from surface and deep chlorophyll maximum (DCM) samples, N. mobilis and Nitrococcus-like phylotypes appeared to be particularly abundant in the mesopelagic ocean (mean, 3.3%, versus 2 and 2.1% for surface and DCM, respectively) (table S2). Particulate organic matter, both sinking and suspended, serves as a major carbon source for heterotrophic communities in the mesopelagic ocean. Although Nitrococcus does not necessarily rely on these particles for their carbon demand, active remineralization by other microbes may create oxygen-deficient microniches and facilitate anaerobic processes within marine snow (45–47). Moreover, remineralization processes release inorganic and organic nutrients, including reduced sulfur compounds, proteins, or osmolytes such as...
dimethylsulfoniopropionate that may further be metabolized to release sulfide (42, 43). *Nitrooccus*, sometimes found enriched on particles (11), could then use these reduced sulfur compounds to support sulfide oxidation. The actual occurrence and ecological significance, however, remain to be determined in situ.

In coastal OMZs associated with highly productive upwelling areas, such as the Namibian and Peruvian OMZs, sulfide sometimes accumulates to levels that are detrimental to marine life and fisheries. Previous studies have shown that sulfide-oxidizing bacteria affiliated with Gammaproteobacteria and Epsilonproteobacteria participate in detoxifying the harmful sulfide in these oxygen-deficient zones (48, 49). The relatively high abundance of 16S rRNA genes affiliated with *N. mobilis* and *Nitrooccus*-like phylotypes (up to 9.2%; table S2) in Peruvian OMZ metagenomes during a sulfidic event (49) indicates that they are well adapted to such episodic sulfidic conditions and may hint toward a contribution to sulfide detoxification in these waters (48, 49).

NOB are important preservers of biologically available nitrogen in global oceans. Their significance in OMZs, specifically in counteracting nitrogen loss through anammox and denitrification, which both reduce $\text{NO}_2^-$ to $\text{N}_2$, has been increasingly recognized in recent years through direct activity measurements, molecular surveys, and natural stable isotope analyses (11, 12, 50). Thus far, nitrite oxidation is postulated to have prevented oxygen-deficient water bodies from turning into active nitrogen-loss zones (51). This nitrogen conservation role is most certainly becoming more crucial as global ocean deoxygenation continues (37).

Nonetheless, our findings of relatively high abundance of *Nitrooccus* in these waters and of the diverse alternative biogeochemical functions *Nitrooccus* may perform suggest that they may be on the verge of reversing the NOB community’s usual role to instead reduce nitrate and produce $\text{N}_2\text{O}$, thus promoting nitrogen loss and exacerbating the global greenhouse effect.

In a wider context, the remarkably versatile and sometimes contrasting functional capacities of *Nitrooccus* unveiled in our study—nitrate reduction versus conventional nitrite oxidation, heterotrophy (degradation of organic carbon releasing $\text{CO}_2$) versus autotrophy ($\text{CO}_2$ fixation into organic carbon), along with $\text{N}_2\text{O}$ production and sulfide oxidation—have conferred on these organisms appreciable adaptability and robustness toward dynamic, changing environmental conditions. Their success is shown by their widespread distribution across diverse habitats, with particular prominence in dynamic settings such as coastal upwelling, or the vast mesopelagic ocean where resources likely come in pulses. Hence, potential occurrence of any functional switches of *Nitrooccus* could extend beyond oxygen-deficient waters to the wider ocean and may substantially affect the cycling and budgets of nitrogen, carbon, oxygen, and sulfur in global oceans as a result. In the face of rapid global environmental changes, the key regulatory controls and the tipping points of contrasting biogeochemical functions associated with the ubiquitous *Nitrooccus* thus urgently need to be determined.

**MATERIALS AND METHODS**

**Sample collection**

Water sampling was conducted on board the R/V Maria S. Merian in October 2011 (MSM19/1c) over the Namibian shelf between 21°59.9′S/13°40.92′E and 28°30′S/15°45.01′E. Salinity, temperature, dissolved oxygen, and chlorophyll a fluorescence were measured with a conductivity-temperature-depth (CTD) system, equipped with an oxygen sensor and a fluorometer (Sea-Bird Electronics). Water samples were collected with 12-liter Niskin bottles attached to the CTD system. Oxygen data were calibrated against Winkler titration. The benthic boundary layer (BBL) was sampled at three depths from 30 cm to 2 m above seafloor using a bottom water sampler (52). $\text{NO}_2^-$ and $\text{NH}_4^+$ were measured on board spectrophotometrically (53) and fluorometrically (54). Water samples were frozen for later $\text{NO}_3^-$ and $\text{PO}_4^{3-}$ analyses with an autoanalyser in a shore-based laboratory (TrAacs 800, Bran & Luebbe). Detection limits for $\text{NH}_4^+$, $\text{NO}_2^-$, $\text{NO}_3^-$, and $\text{PO}_4^{3-}$ were 0.01, 0.01, 0.1, and 0.1 μM, respectively.

**Incubation experiments with environmental samples**

Incubation experiments were conducted with water collected from two stations in the Namibian OMZ, located at 22°S/13°E and 22°6′S/16°6′E. Water samples (250 ml) were collected from five to six depths with the CTD system or the bottom water sampler for samples from the BBL. Different combinations of $^{15}$N and $^{14}$N substrates were added for rate determinations of ammonia and nitrite oxidation as well as nitrate reduction (table S8). Samples were purged with helium for 15 min to eliminate any $\text{O}_2$ contamination from the CTD system (55). For $\text{NH}_3$ and $\text{NO}_2^-$ oxidation, a second set of incubation experiments without helium purging was conducted. Each $^{15}$N($^{14}$N)-amended sample was immediately transferred into five 12-ml Exetainer vials (Labco). These samples were incubated for up to 48 hours in the dark at in situ temperatures. At each time interval (approximately 0, 6, 12, 24, and 48 hours), incubation in one Exetainer was terminated by adding 100 ml of saturated mercuric chloride solution to stop biological activities. Samples were stored upside down in the dark at room temperature until further
processing in a shore-based laboratory [for a more detailed description, see the study of Holtappels et al. (56)].

**Stable isotopic analyses of N₂**

Nitrogen-stable isotopic ratios of N₂ were determined by gas chromatography–isotope ratio mass spectrometry (GC-IRMS; VG Optima). Ammonia oxidation rates and nitrate reduction rates were determined as the 15NO₂⁻ production over time from incubations amended with 15NH₄⁺/14NO₂⁻ or 14NO₃⁻/14NO₂⁻ via the conversion of NO₂⁻ by sulfamic acid (57). Nitrite oxidation rates were determined in incubations amended with 15NO₂⁻/14NO₃⁻. After the removal of residual NO₂⁻, NO₃⁻ was reduced to NO₂⁻ with cadmium and subsequently to N₂ via sulfamic acid, as previously described (11). Process rates were calculated from the slopes of linear regressions with 15N₂ production as a function of time, and only when the production was instantaneous. For anoxic incubation experiments, cultures were harvested by centrifugation and transferred into 2 liters of anaerobic marine NOB medium, including the various amendments for experiments 1 to 8 as listed (table S3). Subsequently, each experimental step was conducted in an anaerobic chamber (90% N₂/10% CO₂ atmosphere) to avoid oxygen contamination. One hundred milliliters of nitrite-free culture per incubation was harvested and washed, as described above, and resuspended in 100 ml of marine NOB medium. Ten milliliters of nitrite-free culture per incubation was transferred to 30-ml serum bottles, and 250 μM Na₂S was added. Overpressure in the bottles was ensured by adding 5-ml sterile air to each incubation. Incubations were performed in a shaking incubator at 28°C. Cell-free medium was used as a negative control. One milliliter of headspace was sampled every hour. Sulfide concentrations were determined by gas chromatography. One milliliter of approximately 557× diluted headspace samples was injected in triplicate into a gas chromatographer [Agilent 7890B, equipped with a Chrompack ML 848 glass column (2 m × 4 mm) with Carbopack B HT 100 40 to 60 mesh packing, at 80°C; Agilent Technologies] combined with a flame photometric detector (Agilent Technologies).

**N₂O and N₂ measurements**

The gas samples were injected into sterile water–filled 3-ml Exetainers, and the gas was displaced via a compensation needle. The concentration of N₂O in the headspace was measured by a gas chromatograph with a 61Ni electron capture detector (Shimadzu, GC-8A). The linear increase over time was used to calculate N₂O production rates by Nitrooccus. Nitrogen-stable isotopic ratios of N₂ (15N15N/14N14N and 15N14N/14N14N) were determined by GC-IRMS (VG Optima). Rates were calculated from the slopes of linear regressions with 29N₂/30N₂ and N₂O production as a function of time.

**NanoSIMS analyses**

During the cruise to the Namibian OMZ, 250-ml water samples were amended with either 13C-labeled DOM (13C-DOM) or 5 μM 15NO₃⁻ and 200 μM 13C-HCO₁³⁻, alongside incubations for rate measurements. After ~29 hours of incubation, samples were fixed with 1% PFA (final concentration) for 8 to 12 hours at 4°C. Subsequently, 11 ml of the sample was filtered onto gold-palladium precoated polycarbonate filters (GTTP, 0.2 μm pore size, 25 mm diameter; Millipore) and stored at −80°C until further analyses in a shore-based laboratory. Nitrooccus cells were hybridized on a filter with Nitrooccus-specific CARD-FISH probes as described previously (11) and analyzed with a NanoSIMS 50L (Cameca). To obtain a stable ion emission rate and to clean the sample from any contamination, we presputtered the area of interest with a Cs⁺ primary ion beam of 100 pA. The cells were analyzed by rastering a primary Cs⁺ ion beam with a beam current of 0.8 to 1 pA and a beam diameter of <100 nm. Secondary ion images of 13C⁺, 14C⁺, 15F⁻, 12C14N⁺, and 32S⁻ were recorded in parallel. The analyzed areas ranged from 10 × 10 μm to 20 × 20 μm with an image size of 256 × 256 pixels and a dwell time of 1 ms per pixel. Tuning of the instrument for high mass resolution (~7000 mass resolving power) reduced the interference for 13C. Data analyses were performed with the freeware Look@NanoSIMS (59).
**Genome annotation of N. mobilis**

The genome of *N. mobilis* Nb-231 was sequenced by the J. Craig Venter Institute in the framework of the Gordon and Betty Moore Foundation Marine Microbiology Initiative. The sequence was deposited in the GenBank database in 2006 and consists of 43 assembled contigs.

The draft genome of *N. mobilis* Nb-231 (GenBank project PRJNA13475) was integrated into the MicroScope annotation platform (60). After automated prediction and annotation of coding sequences (CDS), the annotation of all CDS in key pathways, including those for nitrite oxidation, respiration, and carbon fixation, was manually refined by using the respective tools of MaGe (60), as described in detail elsewhere (27).

**Phylogenetic analyses**

16S rRNA sequences classified as *Nitrococcus* were identified within the SILVA small subunit rRNA database release 119 (20). Affiliation with the genus was confirmed by phylogenetic analyses and by selecting for sequence identities ≥94.5% (61). The three *N. mobilis* 16S rRNA gene sequences (HM038001, L35510, and AAOF01000010) originate from the *N. mobilis*-type strain and the genome sequence. *Nitrococcus*-like phylotypes were defined on the basis of a 98.7% sequence identity threshold (19, 61). Only sequences ≥1300 bases were used for phylogenetic reconstruction. Shorter sequences were added to the tree using the parsimony insertion tool in ARB (62). NxrA and heme-copper oxidase (HCO) family member proteins were imported in custom-made databases.

Sequence alignments for all data sets were generated and manually refined using the sequence editor in ARB. Phylogenetic trees were calculated using RAxML version 7.0.4 (63), with 100 (NxrA and HCO) or 1000 (16S rRNA) bootstraps. To test for tree stability, other treeing methods (neighbor joining, maximum parsimony, and Bayesian inference) were used but yielded almost identical branching patterns. For 16S rRNA analyses, the GTR+GAMMA substitution model and a 50% conservation filter resulting in 1515 valid alignment positions were used. NxrA and HCO trees were calculated using the PROTMIX rate distribution and the WAG substitution model, with a 10% conservation filter for NxrA and without a conservation filter for HCO, resulting in 1198 and 1367 distinct alignment positions, respectively.

**Metagenomic data analyses**

In total, 253 metagenomic and 422 amplicon data sets of marine origin were downloaded from MG-RAST (21), 150 metagenomic and 155 amplicon data sets were obtained from OSD 2014, as detailed in https://github.com/MicroB3-IS/osd-analysis/wiki/Guide-to-OSD-2014-data, and 138 samples of 16S rDNA miTags Illumina sequence data were obtained from http://ocean-microbiome.embl.de/companion.html as fasta files from the Tara Oceans project. Metadata for the data sets are provided in table S1. All sequence reads were processed with the next-generation sequencing analysis pipeline of the SILVA project (available at www.arb-silva.de/ngs). A cutoff of (BLASTN percent query coverage + BLASTN percent alignment identity)/2 > 97% was used to assign *Nitrococcus*-like phylotypes to a read. Of the 1118 data sets, 772 were found to contain at least one *N. mobilis* or *Nitrococcus*-like phylotype (tables S1 and S2). Of these, only metagenomic data sets (Fig. 1B) were used to create a world map showing the global distribution and relative abundance of *N. mobilis* or *Nitrococcus*-like phylotypes.

Selected OSD metagenomes, Tara, and MG-RAST samples were mapped to the *N. mobilis* Nb-231 genome (accession no. gi|211606481| ref[NZ_CH672427.1] using FR-HIT version 0.7 with the following parameters: -e 0.001 -u 0 -p 8 -c 80 -m (dynamically set to 40% of average read length in a sample). Hits for nitrogen and sulfur cycling genes of interest were considered significant when the e value was <10^{-3}, and percent sequence identity was >80%. The results were evaluated on the basis of presence/absence of genes, rather than quantitatively, as the *Nitrococcus* species had rather low relative abundance in most data sets.

**Supplementary Materials**

Supplementary material for this article is available at http://advances.sciencemag.org/cgi/content/full/3/11/e1700807/DC1

**Supplementary Text**

fig. S1. Abundance of *Nitrococcus*-affiliated cells in the Namibian OMZ based on CARD-FISH counts.

fig. S2. 16S rDNA gene-based phylogenetic tree visualizing the relation of four *Nitrococcus* phylotypes.

fig. S3. Phylogenetic analysis of NxrA.

fig. S4. Incubation experiments with *N. mobilis* Nb-231.

fig. S5. Phylogenetic analysis of the sNOR.

fig. S6. Selection of Tara Oceans, MG-RAST, and OSD samples that were mapped to the *N. mobilis* Nb-231 genome.

fig. S7. Effect of reduced O₂ and enhanced iO₂ concentrations on nitrite oxidation rates.

table S1. Percent identity of 16S rRNA genes between *N. mobilis* and the newly identified *Nitrococcus*-like phylotype 1.

table S2. List of marine environmental metagenomes that contain at least one of the four *Nitrococcus* phylotypes.

table S3. List of marine amplicon sequencing data sets that contain at least one of the four *Nitrococcus* phylotypes.

S4. *N. mobilis* strain Nb-231 proteins with predicted functions in key metabolic pathways.

S5. 13C enrichment of single *Nitrococcus* cells from the Namibian OMZ.

S6. Composition of marine NOB medium used to grow *N. mobilis*.

S7. Functional genes associated with *Nitrococcus* spp. in selected Tara Oceans metagenomes.

S8. Summary of stations, sampling depths, and 15N incubation experiments conducted.

S9. NOB specific 16S rRNA-targeted oligonucleotide probes.

S10. Substrate amendments for *N. mobilis* Nb-231 incubation experiments.

**References and Notes**


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