16S rRNA and amoA-based phylogeny of 12 novel betaproteobacterial ammonia-oxidizing isolates: extension of the dataset and proposal of a new lineage within the nitrosomonads

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The phylogenetic relationship of 12 ammonia-oxidizing isolates (eight nitrosospiras and four nitrosomonads), for which no gene sequence information was available previously, was investigated based on their genes encoding 16S rRNA and the active site subunit of ammonia monooxygenase (AmoA). Almost full-length 16S rRNA gene sequences were determined for the 12 isolates. In addition, 16S rRNA gene sequences of 15 ammonia-oxidizing bacteria (AOB) published previously were completed to allow for a more reliable phylogeny inference of members of this guild. Moreover, sequences of 453 bp fragments of the amoA gene were determined from 15 AOB, including the 12 isolates, and completed for 10 additional AOB. 16S rRNA gene and amoA-based analyses, including all available sequences of AOB pure cultures, were performed to determine the position of the newly retrieved sequences within the established phylogenetic framework. The resulting 16S rRNA gene and amoA tree topologies were similar but not identical and demonstrated a superior resolution of 16S rRNA versus amoA analysis. While 11 of the 12 isolates could be assigned to different phylogenetic groups recognized within the betaproteobacterial AOB, the estuarine isolate Nitrosomonas sp. Nm143 formed a separate lineage together with three other marine isolates whose 16S rRNA sequences have not been published but have been deposited in public databases. In addition, 17 environmentally retrieved 16S rRNA gene sequences not assigned previously and all originating exclusively from marine or estuarine sites clearly belong to this lineage.

INTRODUCTION

Chemolithoautotrophic ammonia-oxidizing bacteria (AOB) are capable of gaining energy via conversion of ammonia to nitrite and are thus of considerable importance in the global nitrogen cycle. Almost all aerobic environments in which organic matter is mineralized are possible habitats for AOB (Bock & Wagner, 2001). They have been detected in a variety of soil, marine, estuarine and freshwater systems and are crucial for the removal of nitrogen compounds in wastewater treatment plants (Painter, 1986), thus contributing to the impairment of anthropogenic damage to the environment. On the other hand, AOB activity causes deterioration of natural building stones (Bock & Sand, 1993) and enhances nitrogen fertilizer loss from arable soil (MacDonald, 1986). Due to their importance in natural and engineered systems, significant efforts have been made to characterize the diversity, distribution patterns and ecophysiology of AOB (for reviews see Koops & Pommerening-Röser, 2001; Kowalchuk & Stephen, 2001; Koops et al., 2003).

The first isolation of AOB was reported in 1890 (Frankland & Frankland, 1890; Winogradsky, 1890) and since then a considerable number of AOB isolates was obtained from various environments, leading to the description of 16 AOB species (reviewed by Koops et al., 2003). Comparative 16S rRNA gene sequence analyses of these species showed that ‘Nitrosococcus halophilus’ and Nitrosococcus oceani belong to the class ‘Gammaproteobacteria’, while the remaining 14
species form a monophyletic lineage within the class ‘Betaproteobacteria’ (Head et al., 1993; Pommerening-Röser et al., 1996; Purkhold et al., 2000; Stehr et al., 1995a; Teske et al., 1994; Woese et al., 1984, 1985). Betaproteobacterial AOB encompass the genera Nitrosomonas (including ‘Nitrosococcus mobilis’) and Nitrosospira (including Nitrosolobus and ‘Nitrosovibrio’; Head et al., 1993). Cultured nitrosomonads can be subdivided further into five phylogenetically well-defined lineages (Pommerening-Röser et al., 1996; Purkhold et al., 2000; Stephen et al., 1996). A similar subdivision system has been suggested also for nitrosospiras and was used to assign cultured nitrosospiras into four ‘clusters’ (Pommerening-Röser et al., 1996; Purkhold et al., 2000; Stephen et al., 1996). However, due to the close phylogenetic relationship of all known nitrosospiras with each other, their subdivision is not well supported by phylogeny inference methods (Purkhold et al., 2000; Koops et al., 2003). The current perception of AOB phylogeny established by comparative 16S rRNA sequence analysis could be confirmed independently by exploiting the gene amoA, which encodes the active site subunit of the enzyme ammonia monoxygenase (AmoA), as an alternative phylogenetic marker (Klotz & Norton, 1995; McTavish et al., 1993; Purkhold et al., 2000; Rothhauwe et al., 1995). Generally, 16S rRNA and amoA-based trees possess congruent topologies, although the fragment of the latter gene, which is usually used for phylogeny inference, provides less resolution (Koops et al., 2003).

Cultivation-dependent analysis of environmental AOB diversity is time consuming and tedious due to the slow growth rates of these microorganisms. Furthermore, the enrichment and isolation strategies currently applied might fail to recover the entire diversity of this guild. Triggered by these limitations, the last decade saw an enormous increase in molecular, cultivation-independent diversity surveys of AOB. 16S rRNA gene sequences retrieved directly from environmental samples revealed that, with the exception of two lineages within the nitrosomonads (Stephen et al., 1996; de Bie et al., 2001) and one cluster within the nitrosospiras (Stephen et al., 1996), most sequences retrieved environmentally are closely related to cultured AOB (reviewed by Purkhold et al., 2000). Similar findings were obtained by phylogenetic analysis of environmental amoA gene fragments (Casciotti & Ward, 2001; Hommes et al., 1998; Klotz & Norton, 1995; McTavish et al., 1993; Purkhold et al., 2000; Rothhauwe et al., 1997; Yamagata et al., 1999).

In the present study, we extended the current 16S rRNA and amoA gene databases of AOB by (i) determining the respective sequences of 12 novel AOB isolates and (ii) improving the length and/or quality of several sequences of other AOB published previously. Based on these data, a thorough phylogenetic analysis of betaproteobacterial AOB was performed to obtain a phylogenetic framework, which is required for the design and specificity evaluation of PCR primers and probes and which allows the assignment of environmentally retrieved sequences. Based on the findings obtained, we propose a new lineage within the nitrosomonads which also encompasses many 16S rRNA gene clones from marine systems that were not assigned previously.

**METHODS**

**Pure cultures of AOB.** Table 1 summarizes the strains investigated in this study. AOB were cultured using the media and conditions described previously (Koops et al., 1991).

**DNA–DNA hybridization.** DNA similarities were estimated by photometric determination of thermal renaturation rates, as described by Koops & Harms (1985).

**DNA extraction for PCR.** AOB were harvested from 10 l of exponentially growing cultures by continuous flow centrifugation (20 000 g, 400 ml min−1). Total genomic DNA was extracted according to the following protocol: a 0.25 g pellet (wet wt) of each sample was resuspended in a 2 ml polypropylene tube containing glass beads (Fast DNA Spin kit for soil; BIO 101) with 500 µl AE buffer (20 mM sodium acetate, 1 mM EDTA, pH 5.5, adjusted with acetic acid), 50 µl 25% SDS and 600 µl phenol/chloroform/isoamyl alcohol (25:24:1, by vol.). Cells were lysed in a BeadBeater (BIO 101; 2 x 15 s, speed setting 4-5) and the mixture was then centrifuged (10 min, 10,000 g, 4 °C). The aqueous phase was transferred carefully to a fresh tube, mixed with 600 µl chloroform/isoamyl alcohol (24:1, v/v) and centrifuged (10 min, 10,000 g). The aqueous phase was transferred to a fresh tube and, after the addition of 0.1 vol. 3 M sodium acetate, nucleic acids were precipitated by incubation with 0.6 vol. 2-propanol and 5 µl glycerol (5 mg ml−1) for 1 h at −20 °C and subsequently pelleted by centrifugation (20 min, 10,000 g, 4 °C). Pellets were washed with 1 ml ice-cold 70% ethanol, dried and resuspended in 30–50 µl elution buffer (10 mM Tris/HCl, pH 8:5).

**PCR amplification of 16S rDNA.** Amplification of 16S rRNA genes was performed as specified by Juretschko et al. (1998) and Purkhold et al. (2000) using the primers 616F and 630R.

**PCR amplification of the amoA gene fragment.** A 453 bp fragment (without primers) of the amoA gene was amplified from 100 ng DNA using the optimized (Stephen et al., 1999) primers amoA1F and amoA2R (Rothhauwe et al., 1997) for PCR with a Primus cycler (MWG Biotech). Reaction mixtures containing 50 pM of each primer were prepared in a total volume of 50 µl using 20 mM MgCl2 reaction buffer and 1 U Taq polymerase (Promega). Thermal cycling was carried out by an initial denaturation step at 94 °C for 1 min, followed by 30 cycles of denaturation at 94 °C for 20 s, annealing at 50 °C for 20 s and elongation at 72 °C for 40 s. Cycling was completed by a final elongation step at 72 °C for 5 min.

**Cloning, sequencing and phylogeny inference.** The amplified 16S rRNA and amoA gene fragments were cloned according to the manufacturer’s instructions into pCR2.1 TOPO TA vectors (Invitrogen). After plasmid purification (Qiagen), sequences were determined using a Thermo Sequenase Cycle sequencing kit (Amersham), infrared-labelled (IRD 800) primers and an automated DNA sequencer (Li-Cor). 16S rRNA and amoA gene sequences were added to the respective database using the ARB program package (http://www.arb-home.de). Sequences were aligned using the package’s implemented tools and corrected by visual inspection. Phylogenetic analyses were performed based on nucleic acid (16S rRNA, amoA) and amino acid (AmoA) sequences applying distance-matrix (PHYLIP and FITCH), maximum-parsimony and maximum-likelihood methods using the respective tools in the program package. Since the betaproteobacterial AOB encompass a closely related group of microorganisms, no conservation filters were applied and all sequence
positions were considered in the calculations. For a more detailed description of the phylogeny inference methods applied, see Purkhold et al. (2000).

**RESULTS AND DISCUSSION**

**AOB phylogeny inferred from 16S rRNA**

To establish an encompassing high-quality 16S rRNA gene database for AOB, we resequenced the respective genes of several AOB isolates for which only incomplete sequences were available. In detail, 16S rRNA gene sequences (nt 1496–1498) were completed for *Nitrosomonas* spp. Nm58, Nm84 and Nm86, which represent isolates from the River Elbe (Stehr et al., 1995a). In addition, ambiguities and errors in the 16S rRNA gene sequences of *Nitrosospira* spp. Nsp1, Nsp2, Nsp17, Nv6 (all Aakra et al., 2001b), Ka3 (Aakra et al., 1999b), III7 (Utaker & Nes, 1998) and L115 (Utaker et al., 1995) and *Nitrosospiro briensis* Nsp10 (Aakra et al., 2001b), *Nitrosomonas eutropha* Nm57 (Aakra et al., 2001b; Head et al., 1993), ‘*Nitrosovibrio tenuis* Nv1’ (Head et al., 1993) and *Nitrosolobus multiiformis* NL13 (Teske et al., 1994) were corrected and the sequences were extended by 23–290 bp to almost full-length (nt 1497–1498).

Furthermore, we determined almost full-length 16S rRNA gene sequences (nt 1494–1501) for the following 12 AOB isolates, which were not characterized at this level previously: *Nitrosomonas* spp. Nm47, Nm59, Nm143 and Nm148 and *Nitrosospira* spp. Nsp5, Nsp40, Nsp41, Nsp57, Nsp58, Nsp62, Nsp65 and NL5.

As expected, all 16S rRNA gene sequences determined showed highest similarities (96–7–100 %) to sequences of AOB belonging to the class ‘Betaproteobacteria’ (available as supplementary data in IJSEM Online). Phylogenetic inference based on 16S rRNA gene sequences of AOB included distance-matrix, maximum-parsimony and maximum-likelihood methods and only considered sequences of more than 1000 nucleotides in length. All AOB analysed formed a

**Table 1. Pure cultures of AOB used in this study**

AOB were obtained from the culture collection of the Institut für Allgemeine Botanik, Abteilung Mikrobiologie, Universität Hamburg, Germany.

<table>
<thead>
<tr>
<th>Organism</th>
<th>Reference</th>
<th>Origin</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Nitrosomonas</em> sp. Nm47</td>
<td>H.-P. Koops (unpublished)</td>
<td>Wastewater treatment plant, Germany</td>
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<td><em>Nitrosomonas eutropha</em> Nm57&lt;sup&gt;T&lt;/sup&gt;</td>
<td>Koops &amp; Harms (1985)</td>
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<td><em>Nitrosomonas</em> sp. Nm58</td>
<td>Stehr et al. (1995a)</td>
<td>Sediment, River Elbe, Germany</td>
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<td>S. Sowitzki (unpublished)*</td>
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<td><em>Nitrosomonas</em> sp. Nm84</td>
<td>Stehr et al. (1995a)</td>
<td>Suspended particulate matter, River Elbe, Germany</td>
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<td>Stehr et al. (1995a)</td>
<td>River Elbe, Germany</td>
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<td>H.-P. Koops (unpublished)</td>
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<tr>
<td><em>Nitrosomonas</em> sp. Nm148</td>
<td>H.-P. Koops (unpublished)</td>
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<td>Soil, Germany</td>
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<td><em>Nitrosospira</em> sp. Nsp5</td>
<td>Koops &amp; Harms (1985)</td>
<td>Freshwater cave lake, Sardinia, Italy</td>
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<td>Koops &amp; Harms (1985)</td>
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<td>Koops &amp; Harms (1985)</td>
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<td>Soil, India</td>
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<td>Utaker et al. (1995)</td>
<td>Peat bog, Finland</td>
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<td><em>Nitrosospira</em> sp. III7</td>
<td>Utaker &amp; Nes (1998)</td>
<td>Spruce forest, Norway</td>
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<td><em>Nitrosospira</em> sp. Ka3</td>
<td>Aakra et al. (1999b)</td>
<td>Soil, Norway</td>
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*University of Hamburg, Germany.
monophyletic group within the class ‘Betaproteobacteria’. Within this group, ‘Nitrosomonas cryotolerans’ forms an independent lineage. In addition, five stable subgroupings (lineages Nitrosomonas oligotropha, Nitrosomonas marina, Nitrosomonas europaea/‘Nitrosococcus mobilis’, Nitrosomonas communis and Nitrosospira; Stephen et al.,
Phylogenetic relationship of the newly analysed
nitrosomonads. *Nitrosomonas* isolates Nm47, Nm59, Nm84 and Nm86 are related most closely to organisms within the *Nitrosomonas oligotropha* lineage (97–0–97.5 %). As have many other members of this group, these isolates have been isolated from either freshwater or wastewater habitats and are characterized by remarkably low affinity constants for ammonia (Koops & Pommerening-Röser, 2001; Pommerening-Röser et al., 1996; Stehr et al., 1995a; Suwa et al., 1994). Moreover, *Nitrosomonas* sp. Nm84 has been shown to produce significant amounts of exopolymeric substances, especially under conditions of limited ammonia (Stehr et al., 1995b); this property has also been observed for other members of this lineage (H.-P. Koops, unpublished results).

*Nitrosomonas* spp. Nm58 and Nm148 can both be assigned unambiguously to the *Nitrosomonas communis* lineage (maximum sequence similarities 99.6 and 98.3 %, respectively; Fig. 1). *Nitrosomonas* sp. Nm148 has been isolated from a hot spring and is a strain of the species *Nitrosomonas nitrosa* (82 % DNA–DNA homology), which has been obtained from activated sludge of a wastewater treatment plant connected to chemical processing facilities (Koops et al., 1991). The 16S rRNA gene sequence of *Nitrosomonas* sp. Nm58 is almost identical to the sequence of the soil isolate *Nitrosomonas* sp. Nm41 (99.6 %). The close relationship between both isolates is also reflected by their high DNA–DNA homology (71 %). In contrast to the *Nitrosomonas oligotropha* lineage, the *Nitrosomonas communis* lineage exhibits a high heterogeneity considering the ecophysiological traits of its members (Koops & Pommerening-Röser, 2001; Pommerening-Röser et al., 1996).

The only 16S rRNA gene sequence obtained in this study that was not related directly to a published sequence from an AOB isolate was extracted from the estuarine isolate *Nitrosomonas* sp. Nm143. Considering only described species, the 16S rRNA gene of this organism shows highest sequence similarity to ‘*Nitrosomonas cryotolerans*’ (96.7 %). Together with the marine strains C-17, TT140-098-2 and TT140-89A, isolated from sediment samples at the Galapagos Islands and the Washington coast (GenBank accession nos AF338202, AF338209 and AF338208; maximum sequence similarity 99.0 %; Ward, 1982; Ward & Carlucci, 1985), *Nitrosomonas* sp. Nm143 forms a novel lineage within the betaproteobacterial AOB. This lineage is recovered with all treeing methods and is highly supported by bootstrapping. It comprises not only sequences of isolated strains but also harbours 17 16S rRNA gene sequences directly retrieved from different marine habitats (accession nos U09545–U09547, Z69090, AJ132050, AJ132056, AY114346, AY114347, AF489686–AF489689, Z69127, Z69134, Z69136, Z69141 and Z69143; de Bie et al., 2001; McCaig et al., 1994; Nicolaïsen & Ramsing, 2002; Stephen et al., 1996; Freitag & Prosser, 2003). In accordance with the current classification schemes (Pommerening-Röser et al., 1996; Purkhold et al., 2000; Stephen et al., 1996), we propose to designate the new lineage as *Nitrosomonas* sp. Nm143 lineage. All isolates and sequences within this group originate from a total of eight distinct estuarine or marine habitats. Within these environments, members of the *Nitrosomonas* sp. Nm143 lineage seem to be distributed widely, since the sampling sites range from coastal surface water (McCaig et al., 1994) to polluted (Stephen et al., 1996) or even anoxic sediments (Freitag & Prosser, 2003). Nitrogen load and oxygen concentration at the various sampling sites differ significantly [polluted and non-polluted fish farm sediments (Stephen et al., 1996), an eutrophic estuary (Nicolaïsen & Ramsing, 2002) and estuarine sampling sites with ammonium concentrations below 15 mM (de Bie et al., 2001) as well as anoxic sediments (Freitag & Prosser, 2003) and estuarine sites with oxygen saturation levels around 40 % (de Bie et al., 2001)]. A common feature among the sites investigated are salinity values above 10 p.p.t. Interestingly, however, members of this lineage were not yet detected in the open sea (Bano & Hollibaugh, 2000; Phillips et al., 1999; Hollibaugh et al., 2002).

**Fig. 1.** 16S rRNA-based phylogenetic tree of the nitrosomonads. The tree includes all isolates for which 16S rRNA gene sequences longer than 1000 nucleotides are available. Species whose sequences have been determined in this study are depicted in bold. Maximum-likelihood, maximum-parsimony and neighbour-joining trees were calculated and merged. Filled and empty circles indicate parsimony bootstrap values (100 resamplings) above 90 and 70 %, respectively. The phylogenetic affiliation of the 12 AOB isolates newly sequenced is summarized below.

Phylogenetic relationship among the newly analysed *Nitrosospira*. As expected, *Nitrosospira* isolates NL5, Nsp5, Nsp40, Nsp41, Nsp57, Nsp58, Nsp62 and Nsp65 show the highest 16S rRNA gene similarities to sequences within the *Nitrosospira* lineage (98.6–100 %). *Nitrosospira*...
isolates Nsp57 and Nsp58, which, according to DNA–
DNA hybridization data, are members of the same species
(63 % DNA–DNA homology; note that AOB strains having more than
60 % DNA–DNA homology are considered as members of
the same species; Koops et al., 2003) group together but
ca be assigned neither to one of the clusters within
the cultured nitrosospiras nor to the Nitrosospi ra cluster 1,
which is composed entirely of environmentally retrieved
sequences (Stephen et al., 1996). Similarly Nitrosospi ra sp.
Nsp65 forms an independent branch in the Nitrosospi ra
lineage and currently represents the deepest branch within
this evolutionary lineage. In contrast, isolate Nsp5 groups
with cluster 0 and isolates Nsp 62, Nsp 41, Nsp 40 and
NL5 are related most closely to members of the
Nitrosospi ra cluster 3, which contains the three described
species of this genus (Fig. 2). Although three of the 12
Nitrosospi ra-related isolates investigated cannot be assigned
to previously suggested clusters of this lineage (Purkhold
et al., 2000; Stephen et al., 1996), we refrain from propos-
ing two novel clusters for these AOB because it has been
noted that subdivision of nitrosospiras is not well sup-
ported by bootstrap analysis (Fig. 2; Purkhold et al., 2000).
The failure to recover stable clusters within the nitro-
sopiras reflects that 16S rRNA sequence similarities within
the entire Nitrosospi ra lineage are higher (> 96.1 %) than
those found within each of the Nitrosomonas lineages
described. Furthermore, according to DNA–DNA hybridi-
ization data of available strains, Nitrosospi ra clusters 0 and
2 each currently encompass only strains from a single
species. Within cluster 0, Nitrosospi ra spp. II12, 40K1,
Nsp12 and Nsp5 possess DNA–DNA homology values
with each other above 67 %. Within cluster 2, Nitrosospi ra
spp. II7 and B6 share 76 % DNA–DNA homology. These
values indicate that for both groupings of strains, the
proposal of additional taxonomic units (clusters 0 and 2)
is not justified at this time.

AOB phylogeny inferred from amoA

During the past few years, the gene encoding the active
site subunit of amoA has been exploited increasingly as a
marker molecule for AOB diversity research in natural and
engineered systems (Baribeau et al., 2000; Gieseke et al.,
2001; Horz. et al., 2000; Rotthauwe et al., 1997). Initially,
amoA gene fragment sequences published previously of
Nitrosospi ra spp. Nsp1, Nsp2, Nsp12, Nsp17, Nv6, Ka3, II17
and L115, Nitrosospi ra briensis Nsp10 and ‘Nitroso-
 vibrio tenuis Nv1’ (Aakra et al., 2001a) were extended by 39 bp
each to 453 bp, which represents the complete fragment
obtained after PCR amplification using the modified
(Stephen et al., 1999) primer set of Rotthauwe et al.
(1997). In addition, 453 bp long amoA sequences were
determined for the 12 novel AOB isolates Nitrosospi ra spp.
Nm47, Nm59, Nm143 and Nm148 and Nitrosospi ra spp.
Nsp5, Nsp40, Nsp41, Nsp57, Nsp58, Nsp62, NL5 and
Nsp65. In addition, the amoA gene fragment sequences of
the River Elbe isolates, Nitrosospi ra spp. Nm58, Nm84 and
Nm86, were determined.

All amoA/AmoA sequences determined showed the highest
similarity (83.2–99.3 % and 90.7–100 %, respectively) to
sequences of AOB belonging to the class ‘Betaproteobacteria’
(available as supplementary data in IJSEM Online). Phyl-
ogenic trees for amoA/AmoA were calculated from the
nucleotide and amino acid datasets by distance-matrix,
maximum-parsimony and maximum-likelihood methods.
In general, topologies of amoA/AmoA- and 16S rRNA-based
trees were very similar (Figs 1 and 3). The monophyly of the
Nitrosospi ra lineage, the Nitrosomonas marina lineage and
the Nitrosomonas europaea/’Nitrosooccus mobilis’ lineage
was recovered by all methods, although the bootstrap
support for these lineages was considerably lower than
that found for 16S rRNA gene trees. In contrast to 16S
rRNA trees, the Nitrosomonas oligotropha lineage and the
Nitrosomonas communis lineage are not always retrieved
in amoA/AmoA trees as monophyletic assemblages (Purkhold
et al., 2000).

For all AOB strains for which the amoA/AmoA sequence was
newly determined in this study, consistent affiliations were
found in the 16S rRNA gene- and amoA/AmoA-based trees
(Figs 1 and 3). However, the amoA/AmoA sequences of the
nitrosospiras analysed offer insufficient resolution for
inferring details on the phylogenetic substructure of this
lineage. The clusters proposed previously within the nitro-
sopiras are not always monophyletic in amoA/AmoA trees
(dependent on the treeing method used) and the bootstrap
support of the clusters is very low (data not shown). As
expected, the amoA/AmoA sequence of Nitrosomonas sp.
Nm143, the organism representing the novel lineage in the
16S rRNA AOB tree, is not closely related to amoA/AmoA
sequences of cultured AOB in the database. However, some,
but not all, treeing methods suggest a weak affiliation of the
amoA/AmoA sequence of Nitrosomonas sp. Nm143 with
members of the Nitrosomonas marina and/or Nitrosomonas
oligotropha lineages.

With the extending dataset and an increasing number of
closely related amoA/AmoA sequences, the limitation of
the amoA/AmoA approach as applied now becomes more
apparent. Although using the amoA approach, AOB pure
cultures or AOB in environmental samples can be assigned
rapidly to some phylogenetic subgroups within this guild
(see above), the amoA/AmoA fragment analysed does provide
less resolution compared to the 16S rRNA, since it is
relatively short (453 nt and 151 aa positions, respectively)
and highly conserved (224/93 positions have an identical
nucleotide/amino acid in at least 98 % of the betaproteo-
bacterial AOB). This limitation might be solved in future
studies by application of primers that allow the amplifica-
tion of a longer amoA fragment (Norton et al., 2002).

Inconsistencies between determined sequences
and published database entries

To improve the respective databases, we resequenced in this
study several 16S rRNA and amoA sequences of defined
isolates. Comparison of the newly determined sequences
Fig. 2. 16S rRNA-based phylogenetic tree of the highly related genera *Nitrosospira*, *Nitrosolobus* and 'Nitrosovibrio' forming the *Nitrosospira* lineage (Head *et al.*, 1993). The tree includes all isolates for which 16S rRNA gene sequences longer than 1000 nucleotides are available. Species whose sequences have been determined in this study are depicted in bold. Maximum-likelihood, maximum-parsimony and neighbour-joining trees were calculated and merged. Multifurcations connect branches for which a relative order cannot be determined unambiguously by applying different treeing methods. Filled and empty circles indicate parsimony bootstrap values (100 resamplings) above 90 and 70%, respectively. Sequences included in the analysis were published by Aakra *et al.* (1999a, b, 2001b), Head *et al.* (1993), Teske *et al.* (1994), Tokuyama *et al.* (1997) and Uta˚ker *et al.* (1995). Sequences of strains GS833, E12, NRS527, NpAV, RY6A, RY6C, TCH716 and PJA1 are unpublished but are available at GenBank. Scale bar represents 10% estimated sequence divergence.
with those sequences published previously by others revealed several inconsistencies that could not be explained by simple sequencing errors.

Firstly, differences in the amoA/AmoA sequences (97·6 and 99·2 %, respectively) of *Nitrosospira* sp. III7 determined in this study and those published by Aakra *et al.* (2001a) were detected. However, both sequences show the same phylogeny and, therefore, probably represent two different gene copies. The existence of more than one *amoA* gene copy is common among betaproteobacterial AOB and up to four copies have been reported to occur within the genomes of some nitrosospiras (Bock & Wagner, 2001).

Secondly, we came across published sequences that were obviously retrieved from a contaminant and have not been extracted from the indicated AOB. The 16S rRNA gene sequence of *Nitrosospira* sp. Nv1 published by Aakra *et al.* (2001b) differs significantly (sequence similarity 98·6 %) from the sequences determined in this study (accession no. AY123803) and by Head *et al.* (1993) (accession no. M96404) and which are almost identical (99·9 %) to each
other. It seems likely that the latter two sequences are correct also because the close association of *Nitrosospira* sp. Nv1 with *Nitrosospira* sp. Nv12 (accession no. M96405, 99.8%; Head et al., 1993) is not supported by DNA–DNA hybridization data, which demonstrate that the two organisms belong to different species (Pommerening-Röser, 1993). Furthermore, the *amoA* fragment of *Nitrosospira* sp. L115 (Aakra et al., 2001a) shows significant sequence differences to the respective sequence determined in this study (nucleic acid, 88-9%; amino acid, 94-6%). We claim our sequence to be correct since (in contrast to the sequence of Aakra and co-workers) the results of its phylogenetic analysis are in accordance with the respective 16S rRNA phylogeny (Fig. 2).

**Conclusion**

This study extended significantly the current 16S rRNA and *amoA* databases for AOB. For several AOB isolates, previously published sequences of both marker molecules were improved in quality and length. Furthermore, gene sequences of both macromolecules were determined for 12 novel AOB isolates. Based on these data, a thorough phylogenetic analysis was performed, which led to the description of a new 16S rRNA gene lineage within the nitrosomonads. This lineage also contains 17 previously unassigned environmental clones, demonstrating that at least one of the new AOB lineages discovered during the past few years by molecular diversity surveys harbours AOB species that can be cultured by traditional techniques.

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