Biogeosciences, 11, 3353–3368, 2014
www.biogeosciences.net/11/3353/2014/
doi:10.5194/bg-11-3353-2014

Biogeosciences Open Access

Competitive interactions between methane- and ammonia-oxidizing bacteria modulate carbon and nitrogen cycling in paddy soil

Y. Zheng[1,2], R. Huang[1], B. Z. Wang[1], P. L. E. Bodelier[3], and Z. J. Jia[1]

[1]State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing, 210008, Jiangsu Province, China
[2]University of Chinese Academy of Sciences, Beijing, 100049, China
[3]Netherlands Institute of Ecology (NIOO-KNAW), Department of Microbial Ecology, Droevendaalsesteeg 10, 6708 PB, Wageningen, the Netherlands

Correspondence to: Z. J. Jia (jia@issas.ac.cn)

Received: 19 February 2014 – Published in Biogeosciences Discuss.: 7 March 2014
Revised: 4 May 2014 – Accepted: 7 May 2014 – Published: 24 June 2014

Abstract. Pure culture studies have demonstrated that methanotrophs and ammonia oxidizers can both carry out the oxidation of methane and ammonia. However, the expected interactions resulting from these similarities are poorly understood, especially in complex, natural environments. Using DNA-based stable isotope probing and pyrosequencing of 16S rRNA and functional genes, we report on biogeochemical and molecular evidence for growth stimulation of methanotrophic communities by ammonium fertilization, and that methane modulates nitrogen cycling by competitive inhibition of nitrifying communities in a rice paddy soil. Pairwise comparison between microcosms amended with CH_4, CH_4+Urea, and Urea indicated that urea fertilization stimulated methane oxidation activity 6-fold during a 19-day incubation period, while ammonia oxidation activity was significantly suppressed in the presence of CH_4. Pyrosequencing of the total 16S rRNA genes revealed that urea amendment resulted in rapid growth of *Methylosarcina*-like MOB, and nitrifying communities appeared to be partially inhibited by methane. High-throughput sequencing of the ^{13}C-labeled DNA further revealed that methane amendment resulted in clear growth of *Methylosarcina*-related MOB while methane plus urea led to an equal increase in *Methylosarcina* and *Methylobacter*-related type Ia MOB, indicating the differential growth requirements of representatives of these genera. An increase in ^{13}C assimilation by microorganisms related to methanol oxidizers clearly indicated carbon transfer from methane oxidation to other soil microbes, which was enhanced by urea addition. The active growth of type Ia methanotrops was significantly stimulated by urea amendment, and the pronounced growth of methanol-oxidizing bacteria occurred in CH_4-treated microcosms only upon urea amendment. Methane addition partially inhibited the growth of *Nitrosospira* and *Nitrosomonas* in urea-amended microcosms, as well as growth of nitrite-oxidizing bacteria. These results suggest that type I methanotrophs can outcompete type II methane oxidizers in nitrogen-rich environments, rendering the interactions among methane and ammonia oxidizers more complicated than previously appreciated.

1 Introduction

The intensive use of nitrogenous fertilizers in rice agriculture is a prerequisite for meeting the growing demand for food, especially since this crop feeds more than half of world's population (Galloway et al., 2008). The tight coupling between nitrogen fertilization and methane emission from rice paddy ecosystems in combination with the significant contribution of these systems to the global methane emission, 15 to 25 % (Bodelier, 2011), has evoked numerous studies focusing on this topic. Recent meta-analysis indicates that the increasing rice biomass by nitrogen fertilization may result in the elevated supply of readily available carbon in support of methanogenesis, stimulating methane emission in paddy fields (Banger et al., 2012). However, opposed to this is a strong body of evidence demonstrating stimulation of methane oxidation by ammonium-based fertilizers in rice

soil, leading to reduced methane flux (Bodelier et al., 2000b). The vast number of studies following these observations as well as possible underlying mechanisms for nitrogen regulation of methane oxidation in soils and sediments has been reviewed (Bodelier, 2011; Bodelier and Laanbroek, 2004). However, the role of interactions between methanotrophs and ammonia oxidizers and the consequences for interactions between carbon and nitrogen cycling has rarely been investigated in natural complex ecosystems (Stein et al., 2012).

Aerobic methane-oxidizing bacteria (MOB) belong to two phyla: *Proteobacteria* and *Verrucomicrobia* (Stein et al., 2012). While proteobacterial MOB are widespread, *Verrucomicrobia* seem to be restricted to extreme environments (Dunfield et al., 2007). Aerobic proteobacterial MOB can be divided into two major groups mainly based on phylogeny type I (*Gammaproteobacteria*) and type II (*Alphaproteobacteria*). This group assignment used to be supported by differences in biochemical, physiological and morphological properties. Based on congruent 16S rRNA and *pmoA* phylogeny, type I MOB harboring the family *Methylococcaceae* can be further divided into type Ia (including genera *Methylosarcina*, *Methylobacter*, *Methylomonas*, *Methylomicrobium*, *Methylosoma*, *Methylosphaera* and *Methylovulum*) and type Ib (including genera *Methylococcus*, *Methylocaldum*, *Methylogaea*, *Methylohalobius* and *Methylothermus*). Type II MOB include the family *Methylocystaceae* (including genera *Methylocystis* and *Methylosinus*) and *Beijerinckiaceaea* (including genera *Methylocella*, *Methylocapsa* and *Methyloferula*). The methane monooxygenase (MMO) exist either as a particulate (pMMO) or a soluble (sMMO) form. All known methanotrophs contain pMMO except *Methylocella* and *Methyloferula*, while sMMO is only found in a subset of MOB (Hanson and Hanson, 1996; Lipscomb, 1994; Stein et al., 2012). Methanotrophs convert CH_4 into methanol, which can be utilized by methanol-oxidizing bacteria as a carbon and energy source. The known soil-retrieved methanol-oxidizing bacteria are quite diverse; however, most of them are facultative methylotrophic, indicating the capability to utilize alternative carbon substrate (Kolb, 2009). The family *Methylophilaceae* is the known obligate methylotrophs that use methanol as the sole source of carbon and energy (Bratina et al., 1992; Devries et al., 1990; Kolb, 2009). Nitrifying bacteria use ammonia monooxygenase (AMO) for oxidation of their primary growth substrate. Though the AMO gene was thought to be unique to ammonia-oxidizing bacteria (AOB), the discovery of ammonia-oxidizing archaea (AOA) has suggested an important role of archaeal nitrification in the global nitrogen cycle (Könneke et al., 2005; Prosser and Nicol, 2012). However, until now the relative contribution of AOB and AOA to ammonia oxidation in agricultural soil is still unclear (Jia and Conrad, 2009; Pratscher et al., 2011; Zhang et al., 2010). 16S rRNA and *amoA* gene analyses of AOB revealed that physiological groups are confined to monophyletic lineages within the β and γ subclasses of *Proteobacteria*. The genera *Nitrosospira* and*Nitrosomonas* form a grouping within the β subclass and the genus *Nitrosococcus* is affiliated with the γ subclass (Purkhold et al., 2000, 2003). AOA are much more diverse than AOB based on the 16S rRNA and *amoA* gene and four major lineages have been suggested, including the *Nitrososphaera* cluster, the *Nitrosopumilus* cluster, the *Nitrosotalea* cluster, and the *Nitrosocaldus* cluster (Pester et al., 2012; Stahl and de la Torre, 2012). The conversion of nitrite into nitrate is catalyzed by nitrite-oxidizing bacteria (NOB). NOB comprise four genera, including *Nitrobacter*, *Nitrococcus*, *Nitrospina* and *Nitrospira*, which were assigned to the α-proteobacteria, γ-proteobacteria, δ-proteobacteria and phylum *Nitrospirae*, respectively (Bock and Wagner, 2006).

The key enzymes, methane monooxygenase (MMO) in methanotrophs and ammonia monooxygenase in ammonia oxidizers are evolutionarily linked (Holmes et al., 1995), leading to functional similarities enabling both methanotrophs and ammonia oxidizers to oxidize both methane and ammonia (Jones and Morita, 1983; O'Neill and Wilkinson, 1977). Pure culture studies demonstrated that methane can act as a competitive inhibitor for ammonia oxidizers, and ammonia inhibits the growth and activity of methanotrophs (Bedard and Knowles, 1989; Stein et al., 2012). Next to this, both MOB as well as AOB have to deal with toxic intermediates (hydroxylamine in the case of MOB and methanol in the case of AOB) (Stein et al., 2012). At the microbial community level, however, the growth of methanotrophs might be nitrogen-limited and nitrogen fertilization might relieve methane oxidizers from nutrient limitation (Bodelier et al., 2000b). At the same time ammonia oxidizers and subsequent nitrification may be inhibited by the methanotrophic N assimilation. However, the research efforts focusing on methane effects on nitrification in natural complex ecosystems is very limited, which is in sharp contrast to a large number of studies executed to elucidate the effect of nitrogenous fertilizers on methane oxidation. Moreover, the lack of knowledge on this topic is even more evident taking the yet unknown role of AOA in interactions with MOB into account. DNA-based stable isotope probing (DNA-SIP) is generally used to link the metabolisms of ^{13}C-labeled substrates with growing microbial communities in the environment. DNA-SIP has been employed to identify the active methanotrophs (Morris et al., 2002) and ammonia oxidizers in soils (Jia and Conrad, 2009). The combined use of stable isotope labeling and high-throughput pyrosequencing is a powerful combination of approaches that offers great opportunities in elucidating the interaction between MOB and AOB/AOA, because both groups can easily and specifically be labeled using $^{13}CH_4$ (Bodelier et al., 2012, 2013) and $^{13}CO_2$ (Jia and Conrad, 2009). However, studies that assessed both functional groups in interaction with each other are missing.

The interactions between methane and ammonia oxidizers are linked to methane–nitrogen cycling in light of climate change. Elucidating these interactions may offer solutions for the effects of nitrogen on methane oxidation, which

are complicated and often contradictory. Therefore, the microbial populations and functional dynamics of methane and ammonia oxidizers were investigated in paddy soil microcosms incubated with CH_4, urea and CH_4+Urea using culture-independent techniques.

2 Materials and methods

2.1 Site description and soil sampling

The paddy soil was collected from Yangzhou City (119°42′0″ E, 32°35′5″ N) of Jiangsu Province, one of the major regions for rice production in China. The soil was silt clay and classified as Calcaric Glevsols. The field has a history of rice cultivation for more than 50 years. Soil sampling was performed at 0–15 cm depth by steel cores with three replicates. Soil maximum water holding capacity (WHC) was 55 %, and the soil samples were homogenized by passing through a 2 mm meshed sieve. The resulting soil samples were kept at 40 % maximum water holding capacity in a fridge until use. Soil characteristics are as follows: 15 g total organic C kg^{-1}, 1.59 g total N kg^{-1}, 1.23 g total P kg^{-1} and pH 7.4 determined with a water to soil ratio at 2.5.

2.2 DNA-SIP microcosms

Four treatments were performed including ^{13}C–CH_4-labeled microcosms (incubated with ^{13}C–CH_4), ^{13}C–Urea-labeled microcosms (incubated with ^{13}C–Urea and ^{13}C–CO_2), ^{13}C–CH_4+Urea-labeled microcosms (incubated with ^{13}C–CH_4, ^{13}C–Urea and ^{13}C–CO_2) and ^{12}C–CH_4+Urea control microcosm (incubated with ^{12}C–CH_4, ^{12}C–Urea and ^{12}C–CO_2). The hydrolysis of ^{13}C-labeled urea was employed to generate ammonia and ^{13}C–CO_2 in support of autotrophic nitrifying communities in soil as previously reported (Lu and Jia, 2013). Pairwise comparison among the treatments of ^{13}C–CH_4, ^{13}C–CH_4+Urea, and ^{13}C–Urea was used to assess the effect of urea fertilization on methane oxidation activity and MOB community composition, and the role of methane on ammonia oxidation activity and AOB/AOA community composition. The soil microcosm with ^{12}C–CH_4+Urea amendment was performed as control treatment for the labeled SIP microcosms.

Microcosms for stable-isotope probing incubations were constructed in triplicate by adding approximately 7.30 g fresh soil (equivalent to 6.0 g dry weight of soil, i.e., d.w.s.) to 120 mL serum bottles capped with black butyl stoppers for incubation at 28° in the dark for 19 days. To increase the labeling efficiency of targeted microorganisms, the pre-incubation of soil at 40 % maximum water-holding capacity (WHC) was performed for 14 days to reduce the amount of soil-respired ^{12}C–CO_2 (Jia and Conrad, 2009; Xia et al., 2011). The ^{13}C–CH_4-labeled microcosms and ^{13}C–CH_4+Urea-labeled microcosms were injected with $^{13}CH_4$ (99 atom %^{13}C, Sigma-Aldrich Co., St Louis, MO, USA) to reach 9000 ppmv (Supplement Table S1). Meanwhile, ^{13}C–Urea fertilization of 100 µg urea–N g^{-1} d.w.s. with 5 % $^{13}CO_2$ (99 atoms %^{13}C, Sigma-Aldrich Co., St Louis, MO, USA) was performed for ^{13}C–Urea-labeled microcosms and for ^{13}C–CH_4+Urea-labeled microcosms as previously described (Jia and Conrad, 2009). As for ^{13}C–CH_4-labeled microcosms, the distilled water instead of urea was added. SIP control microcosms were established in triplicate by addition of the unlabeled CH_4, urea and CO_2 instead of ^{13}C substrate. CH_4 and CO_2 concentrations were measured every few hours depending on the rate of methane consumption by gas chromatography (Shimadzu GC12-A, Japan) as previously described (Zhu et al., 2010). After more than 90 % of CH_4 was consumed, the headspace was flushed with pressurized synthetic air (20 % O_2, 80 % N_2) for 1 min to maintain oxic conditions before ^{13}C-labeled or unlabeled substrate was renewed, to reach about 10 000 ppmv CH_4 and/or 100 µg urea–N g^{-1} d.w.s. plus 5 % CO_2. Due to strong methane oxidation in microcosms amended with ^{13}C–CH_4+Urea treatment (Supplement Fig. S1), methane addition was regularly repeated, in addition to urea and CO_2 substrates. The scenario of SIP microcosm construction was detailed in Supplement Table S1. The destructive sampling was performed in triplicate after incubation of SIP microcosms for 0, 5 and 19 days. Soil samples were immediately frozen at −20° until further use. For SIP microcosm amended with urea, approximately 3 g of fresh soil was removed from each of triplicate microcosms. The rest of the soil was homogenized with 15 mL of 2M KCl by shaking at 200 rpm for 60 min and then passed through filter paper for determination of NH_4^+–N and NO_3^-–N using a Skalar SAN Plus segmented flow analyzer (Skalar, Inc., Breda, Netherlands).

2.3 DNA extraction and Isopycnic centrifugation

The total DNA from 0.5 g soil (fresh weight) of each microcosm was extracted using the FastDNA spin kit for soil (MP Biomedicals, Cleveland, OH, USA), according to the manufacturer's instructions. Soil DNA quality and quantity were observed by a Nanodrop ND-1000UV-Vis Spectrophotometer (NanoDropTechnoloqies, Wilmington, DE, USA), and soil DNA was stored at −20°.

For each treatment, density gradient centrifugation of total DNA was performed to separate the ^{13}C-labeled DNA from ^{12}C DNA as previously described in detail (Jia and Conrad, 2009; Xia et al., 2011). In brief, approximately 2.0 µg DNA was mixed well with CsCl stock solution to achieve an initial CsCl buoyant density of 1.725 g mL^{-1} using gradient buffer (pH 8.0; 100 mM Tris-HCl; 100 mM KCl; 1.0 mM EDTA). The mixture was ultra-centrifuged in a 5.1 mL Beckman polyallomer ultracentrifuge tube by using a Vti65.2 vertical rotor (Beckman Coulter, Inc., Palo Alto, CA, USA) at 177 000 g for 44 h at 20 °C. A NE-1000 single syringe pump (New Era Pump Systems, Inc., Farmingdale, NY, USA) with a precisely controlled flow rate of 0.38 mL min^{-1} was used

to fractionate DNA by displacing the gradient medium with sterile water from the top. Fourteen or fifteen DNA fractions were obtained with equal volumes of about 340 µL, and a 65 µL aliquot was used for refractive index measurement using an AR200 digital hand-held refractometer (Reichert Inc., Buffalo, NY, USA). The CsCl medium was removed by PEG precipitation (polyethylene glycol 6000), and the DNA pellet was further purified with 70 % ethanol. The fractionated DNA was then dissolved in 30 µL sterile water for downstream analysis.

2.4 Real-time quantitative PCR of total and fractionated DNA

Real-time quantitative analysis of the *pmoA* gene in total DNA and in each buoyant density of DNA gradient fraction was performed to determine the growth and efficiency of ^{13}C incorporation into the genomic DNA of MOB communities on a CFX96 Optical Real-Time Detection System (Bio-Rad, Laboratories Inc., Hercules, CA, USA), respectively. The growth and labeling of AOB and AOA communities was assessed by real-time quantitative PCR of bacterial and archaeal *amoA* genes, respectively (Lu and Jia, 2013). The primers and PCR conditions were described in Supplement Table S2. The reactions was performed in a 20 µL mixture containing 10.0 µL SYBR Premix Ex Taq (Takara, Dalian), 0.5 µM each primer, and 1 µL of DNA template. The amplification efficiencies were 93–103 % obtained with R^2 values of 99.1–99.9 %.

2.5 Pyrosequencing of 16S rRNA genes at the whole community level

Pyrosequencing of the total 16S rRNA genes was performed in triplicate microcosms (Supplement Table S3) and in the fractionated DNA from fractions 3 to 13 of each treatment (Supplement Table S4) using the universal primers 515F/907R with primer adaptors, key sequence, and tag sequence as previously described (Lu and Jia, 2013). Tag sequences were used to barcode the PCR amplicons, and PCR conditions and primers were described in Supplement Table S2. 50 µL PCR reaction mixture containing 45 µL Platinum PCR SuperMix (Invitrogen, Shanghai, China), a 200 nM final concentration of each primer, and 2 µL template DNA was performed and the amplicons were purified and visualized on 1.8 % agarose gels. The purified PCR products were determined by a Nanodrop ND-1000 UV-Vis Spectrophotometer. Pyrosequencing was performed on a Roche 454 GS FLX Titanium sequencer (Roche Diagnostics Corporation, Branford, CT, USA). The read was trimmed to generate high-quality sequences using the mothur software (Schloss et al., 2009). Taxonomic assignment of the high-quality sequence reads were obtained by RDP Multi Classifier with a confidence threshold of 50 % (Wang et al., 2007). The MOB and AOB-like 16S rRNA gene sequences were extracted and clustered into operational taxonomic unit (OTU) at 97 % sequence identify cut-off using the mothur software package. One representative sequence of each OTU was then used for phylogenetic analysis.

2.6 Pyrosequencing of *amoA* and *pmoA* genes from total DNA and ^{13}C-labeled DNA

The *pmoA* gene for MOB and bacterial *amoA* gene for AOB were also analyzed using high-throughput pyrosequencing of the total DNA and the ^{13}C-labeled DNA in the ^{13}C-labeled microcosms on day 0 and day 19 (Supplement Table S5). PCR primer pairs were A189F/mb661r for *pmoA* gene (Costello and Lidstrom, 1999; Holmes et al., 1995), and amoA-1F/amoA-2R for bacterial *amoA* gene (Rotthauwe et al., 1997), respectively (Supplement Table S2). The functional genes were amplified using total DNA extract from triplicate microcosms for each treatment. The "heavy" DNA fraction showed the highest relative abundance of AOB and MOB 16S rRNA genes was used as the ^{13}C DNA for pyrosequencing of functional genes. PCR was performed in a 50 µL PCR reaction mixture containing 45 µL L^{-1} Platinum PCR SuperMix (Invitrogen, Shanghai, China), a 200 nM final concentration of each primer, and 2 µL template. PCR products were gel purified and sent for pyrosequencing on a Roche 454 GS FLX Titanium sequencer (Roche Diagnostics Corporation, Branford, CT, USA). Raw sequences were imported into the mothur software (Schloss et al., 2009) for quality check, alignment and phylogenetic tree construction. High-quality sequences (read length longer than 200 bp, average quality score more than 25, without ambiguous base calls) were extracted for further analysis. Pyrosequencing of *pmoA* gene yield about 47 000 high-quality sequence reads with an average length of 482 bp, while about 47 000 bacterial *amoA* gene sequence reads were generated with an average length of 469 bp (Supplement Table S5). *pmoA* gene sequences and bacterial *amoA* gene sequences were clustered into operational taxonomic unit (OTU) at 87 % (Degelmann et al., 2010) and 97 % sequence identity cut-off, respectively. One representative sequence was then used from each OTU for phylogenetic analysis.

2.7 Statistical analysis

Effect of urea or CH_4 on measured parameters was tested using one-way analysis of variance analysis (ANOVA). Prior to ANOVA analysis these data were tested for normality (plots of SD versus means) and for homogeneity of variances (Levene's test). All analyses were performed using SPSS Statistics soft package version 16.0.

2.8 Accession number of nucleotide sequences

The pyrosequencing reads have been deposited at the DNA Data Bank of Japan (DDBJ) with accession numbers

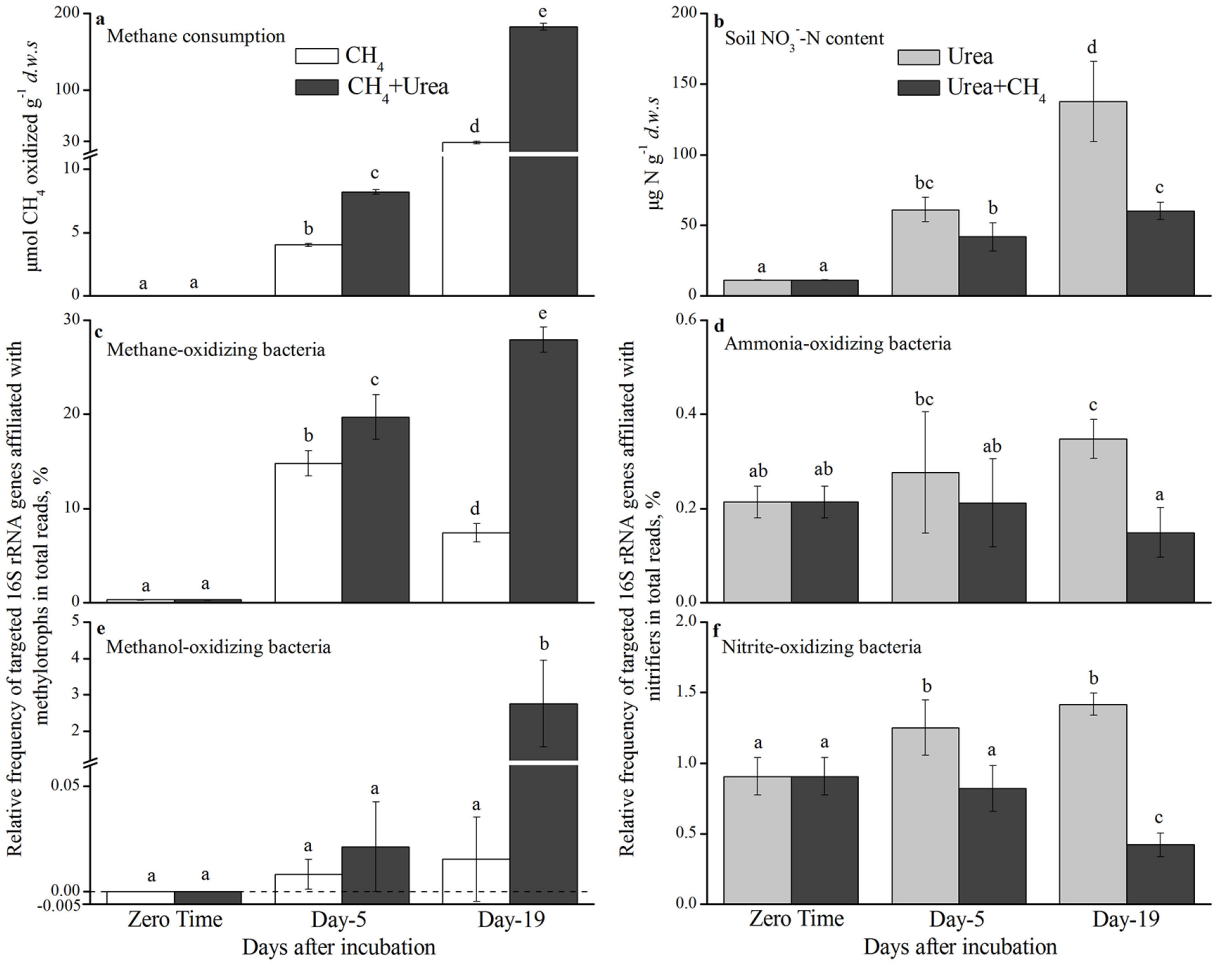

Figure 1. Interactions between microbial methane and ammonia oxidation in a paddy soil. The left panel shows urea effect on methane oxidation activity **(a)**, methane-oxidizing bacteria **(c)** and methanol-oxidizing bacteria **(e)**. The right panel refers to methane effect on ammonia oxidation activity **(b)**, ammonia-oxidizing bacteria **(d)** and nitrite-oxidizing bacteria **(f)** in soil microcosms after incubation for 5 and 19 days. The amount of methane consumed was used to assess methane oxidation activity and soil nitrate production was used to evaluate ammonia oxidation activity. The total microbial communities were pyrosequenced using universal primers of the 16S rRNA gene. The relative frequency is expressed as the percentage of the targeted 16S rRNA genes to the total 16S rRNA reads for each soil sample. The error bars represent standard deviations of the triplicate microcosms, while for the CH_4+Urea treatment 6 replicates were used including both ^{12}C-control and ^{13}C-labeled treatments. The different letters above the columns indicate a significant difference ($P < 0.05$) using analysis of variance.

DRA001245 and DRA001247 for the 16S rRNA genes and functional genes (bacterial *amoA* and *pmoA*), respectively.

3 Results

3.1 Microbial oxidation of methane and ammonia

Methane oxidation activity was assessed by determining the amount of methane consumed in soil microcosms over the incubation time of 19 days and displayed a strong capacity of methane consumption in the paddy soil tested (Supplement Fig. S1). It is estimated that 4.01 and 32.4 μmol CH_4 g^{-1} d.w.s. were oxidized in soil microcosms after incubation with CH_4 for 5 and 19 days, respectively (Fig. 1a). Urea fertilization significantly stimulated methane oxidation activity by 2- and 6-fold on days 5 and 19, respectively (Fig. 1a). Soil nitrification activity was determined as the increase in soil nitrate concentrations during incubation of microcosms for 19 days. Soil nitrate content significantly increased from 11.1 μg NO_3^-–N g^{-1} d.w.s. in urea-amended microcosms on day 0, to 61.0 and 137.6 μg NO_3^-–N g^{-1} d.w.s. on days 5 and 19, respectively (Fig. 1b, Supplement Fig. S2). The presence of CH_4 in the headspace of urea-amended microcosms significantly suppressed production of soil nitrate on day 19, although statistically significant differences were not observed on day 5 (Fig. 1b, Supplement Fig. S2).

High-throughput fingerprinting of the total microbial communities was performed by pyrosequencing of the total 16S rRNA genes in SIP microcosms over the 19 days incubation period (Supplement Table S3). About 346 000 high-quality sequence reads were obtained with an average length of 377 bp in the V3–V4 region, while about 337 000 sequences were affiliated with bacteria. Relative abundance of bacterial 16S rRNA genes ranged from 95.3 to 98.8 % in these microcosms, which was much higher than that of archaeal 16S rRNA genes (Supplement Table S3). Pyrosequencing data provided the information about relative abundance of targeted microbial 16S rRNA gene sequences in the total microbial community. Methanotrophic 16S rRNA genes comprised only 0.28 % of total microbial community in the paddy soil tested (Fig. 1c). However, methane oxidation led to a remarkable increase in MOB-like 16S rRNA genes up to 27.9 % of the total microbial community during SIP microcosm incubations (Fig. 1c). Interestingly, methanotrophic proportions appeared to show a decreasing trend with prolonged incubation of microcosms amended only with CH_4 from 14.8 % on day 5 to 7.42 % on day 19. Nonetheless, urea addition resulted in a higher abundance of methanotroph-like 16S rRNA gene sequences up to 19.8 and 27.9 % on day 5 and day 19, respectively, representing 1.3- and 4-fold increases relative to CH_4-amended microcosms (Fig. 1c). The population size of MOB community determined by real-time PCR of *pmoA* genes (Supplement Fig. S3a) showed similar results to 16S rRNA pyrosequencing analysis. The copy number of *pmoA* genes increased significantly from 4.44×10^8 copies g^{-1} d.w.s. on day 0 to 1.45×10^9copies g^{-1} d.w.s. and 1.16×10^9 copies g^{-1} d.w.s. in the microcosms incubated with CH_4 for 5 and 19 days, respectively. Urea addition led to 1.35 and 3.16 times more *pmoA* genes than that in only CH_4-incubated microcosms on day 5 and day 19, respectively. The family *Methylophilaceae*, using methanol as sole source of carbon and energy (Bratina et al., 1992; Devries et al.,1990; Kolb, 2009), was methanol-oxidizing bacteria analyzed in our study. Similar trend was observed for 16S rRNA gene sequences affiliated with methanol-oxidizing bacteria (Fig. 1e), the relative abundance of which was 150-fold higher in soil microcosms with CH_4+Urea treatment (2.76 %) than that in CH_4-amended microcosms (0.02 %) on day 19.

AOB 16S rRNA gene sequences comprised only a tiny fraction of the total microbial community during a 19-day incubation period (Fig. 1d). The relative abundance increased significantly in urea-amended microcosms from 0.21 % on day 0 to 0.35 % on day 19. The presence of CH_4 significantly suppressed the proportional increase in AOB-like 16S rRNA gene reads leading to a relative frequency down to 0.15 % on day 19 (Fig. 1d). The copies of bacterial *amoA* gene detected by real-time PCR increased from 4.08×10^7 copies g^{-1} d.w.s. on day 0 to 1.06×10^8 copies g^{-1} d.w.s. on day 19 in the microcosms incubated with urea (Supplement Fig. S3b). The increase was also observed in the Urea+CH_4 treatment; however, the presence of CH_4 resulted in a 1.33-fold decrease relative to urea-amended microcosms only after incubation for 19 days. This indicated that CH_4 partially inhibited the growth of AOB. Similar results were observed for soil nitrite-oxidizing bacteria (NOB). For instance, the relative abundance of NOB 16S rRNA gene sequences in total microbial community increased significantly from 0.91 % on day 0 to 1.42 % on day 19 in the urea-amended microcosms, while soil microcosms with Urea+CH_4 displayed a relative abundance as low as 0.42 % on day 19 (Fig. 1f). As for AOA, there was no significant change in relative abundances upon urea fertilization during SIP microcosm incubation, although a decreasing trend was observed in the presence of CH_4 (Supplement Fig. S4). A similar result was also observed by the real-time PCR of archaeal *amoA* gene (Supplement Fig. S3c).

3.2 High-throughput fingerprinting of functional guilds against the total community

The 16S rRNA genes affiliated with MOB and AOB were selected for phylogenetic analysis from the total pyrosequencing reads in soil microcosms, after incubation for 5 and 19 days, following the additions of methane and/or urea. Phylogenetic analysis revealed a remarkable shift of MOB community structure based on both the 16S rRNA (Supplement Fig. S5a) and *pmoA* gene (Supplement Fig. S5b). Although type II methanotrophs dominate the MOB community in original soil on day 0, the consumption of CH_4 in soil microcosms led to a drastic increase in relative abundance of type Ia methanotrophic 16S rRNA gene sequences in the total 16S rRNA gene sequences from 0.09 % on day 0 to 14.4 % on day 5 (Fig. 2a). Interestingly, type II methanotroph-like 16S rRNA genes stayed at very low proportions in the total microbial community during the entire incubation period, whereas significant increase was observed from 0.12 % on day 0 to 0.55 % on day 19. Urea fertilization further stimulated the relative abundance of type Ia methanotrophs reaching 1.3 and 4 times higher in the CH_4+Urea-amended microcosms than that in the microcosms amended only with CH_4 on day 5 and day 19, respectively. However, urea nitrogen appeared to have no effect on the relative abundance of type II methanotrophs. Similar results were obtained by pyrosequencing analysis of *pmoA* genes (Supplement Fig. S5b). Phylogenetic analysis of *pmoA* genes indicated that type Ia *pmoA* sequences were stimulated from 7.4 % on day 0 to 69.8 % of total methanotrophic community after incubation with CH_4 for 19 days. Urea addition further stimulated the proportion of type Ia methanotroph *pmoA* gene sequences to 85.0 %.

The AOB community was exclusively dominated by *Nitrosospira*-like 16S rRNA gene sequences on day 0, and none of 16S rRNA gene sequences could be assigned to the genus *Nitrosomonas* (Supplement Fig. S6a). However, the relative abundance of *Nitrosomonas*-like 16S rRNA genes

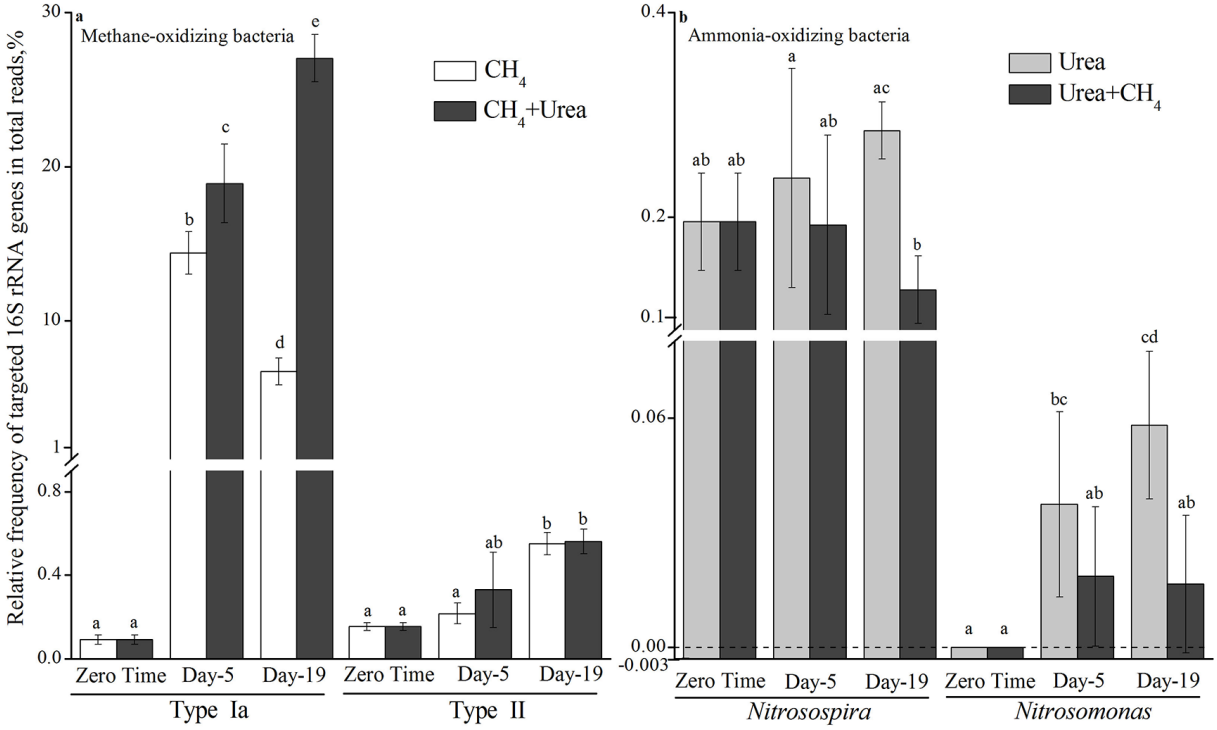

Figure 2. Change in relative abundance of methane-oxidizing bacteria **(a)** and ammonia-oxidizing bacteria **(b)** in soil microcosms incubated for 5 and 19 days. The relative abundance of type Ia, type II methanotrophs, *Nitrosospira* and *Nitrosomonas* are expressed as the targeted 16S rRNA gene to total 16S rRNA gene reads in soil microcosms incubated with CH_4, urea and CH_4+Urea. The error bars represent standard deviation of the triplicate microcosms, while for the CH_4+Urea treatment 6 replicates were used including both ^{12}C-control and ^{13}C-labeled treatments. The different letters above the columns indicate a significant difference ($P < 0.05$) using analysis of variance.

rose to 0.04 % and 0.06 % of the total microbial community in urea-amended microcosms after incubation for days 5 and 19, respectively (Fig. 2b). CH_4 addition resulted in lower abundance of *Nitrosomonas*-like 16S rRNA genes in the total microbial community on day 5 and day 19, representing 2- and 3-fold decreases relative to that in urea-amended microcosms (Fig. 2b). The relative abundance of *Nitrosospira*-like AOB was stimulated by urea fertilization, but suppressed in the presence of CH_4 (Fig. 2b). These results were further verified by phylogenetic analysis of the *amoA* pyrosequencing reads (Supplement Fig. S6b). For instance, none of *amoA* gene sequences was affiliated with *Nitrosomonas* in the original soil on day 0, whereas 6.6 % of *amoA* gene sequences were affiliated with *Nitrosomonas* on day 19 in the urea-amended microcosms.

3.3 Stable isotope probing of active methanotrophs and ammonia oxidizers

The incorporation of the ^{13}C label into nucleic acid of active microbial communities in complex soil was analyzed by isopycnic centrifugation of total DNA extracted from SIP microcosms. The fractionated DNA over the entire density range of a given gradient was further assessed by pyrosequencing of the total 16S rRNA gene. About 418 000 high-quality reads were generated with an average length of 356 bp in the V3–V4 region of the 16S rRNA gene (Supplement Table S4), while about 409 000 sequences were affiliated with bacteria. Relative abundances of microbial guilds as a function of the buoyant density of the DNA gradient indicated that MOB and AOB were ^{13}C-labeled to different extents. The relative abundance of 16S rRNA gene sequences of methanotrophs was exceptionally high, up to 90 % of the total 16S rRNA gene sequences in the "heavy" DNA fractions from the labeled microcosms, suggesting strong labeling of the methanotrophic community after incubation for 5 (Fig. 3a) and 19 days (Fig. 3b). This was further supported by quantitative analysis of *pmoA* gene copies reaching the peak in the "heavy" DNA fractions from the labeled microcosms, while the highest number was observed in the "light" DNA fractions for the ^{12}C-control treatment (Supplement Fig. S7). In addition, the relative abundance of 16S rRNA gene sequences affiliated with methanol-oxidizing bacteria was apparently higher in the "heavy" DNA fractions from the labeled microcosms (^{13}C–CH_4 and ^{13}C–CH_4+Urea) than those in the control treatments (^{12}C–CH_4+Urea), despite the relatively low proportion of ~ 0.20 % on day 5 (Fig. 3c). The prolonged incubation for 19 days increased the proportion of methanol-oxidizing bacteria significantly up to 11.0 % of the

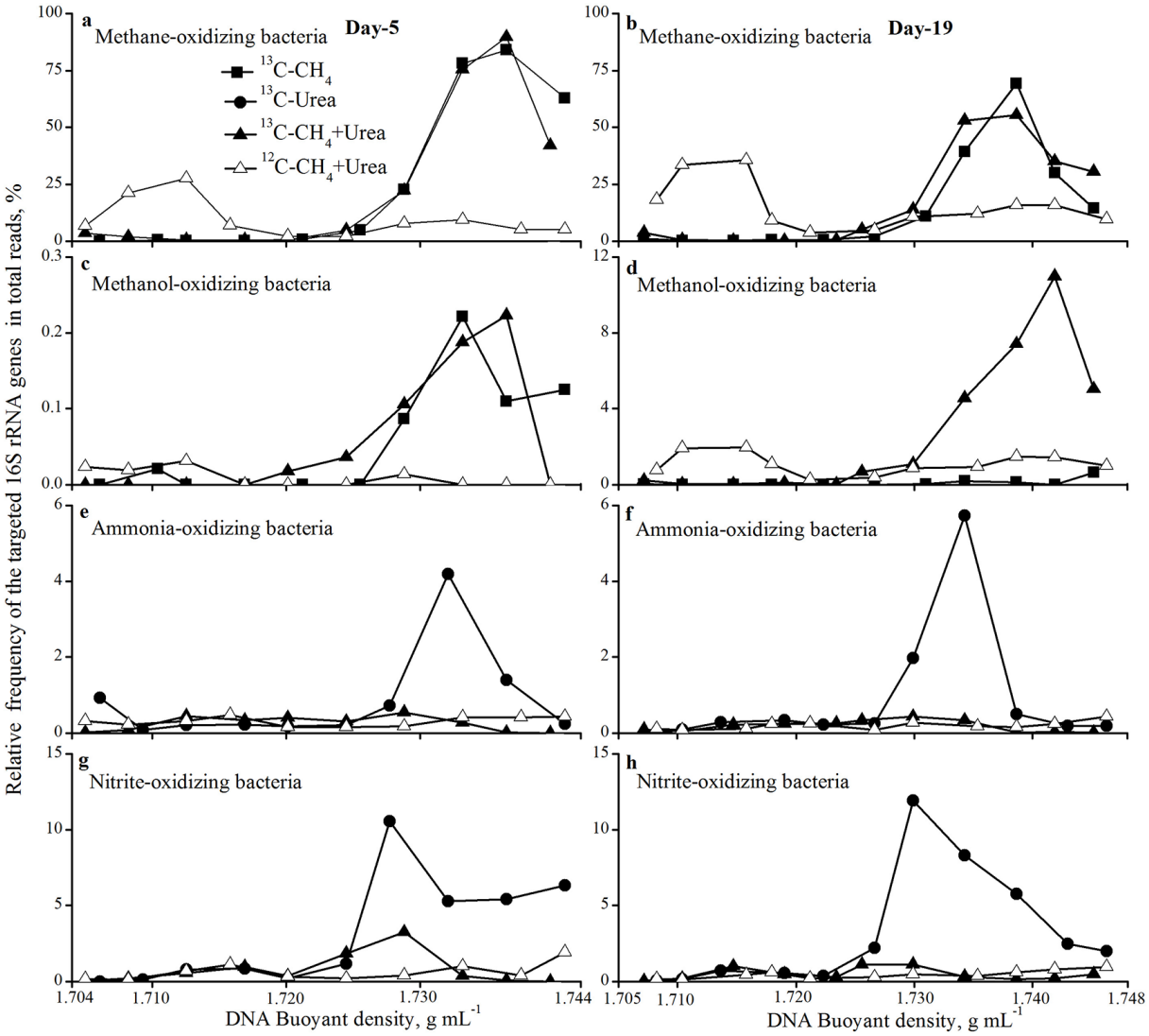

Figure 3. Relative frequency of the 16S rRNA gene sequences affiliated with methane-oxidizing bacteria **(a, b)**, methanol-oxidizing bacteria **(c, d)**, ammonia-oxidizing bacteria **(e, f)** and nitrite-oxidizing bacteria **(g, h)** across the buoyant density gradient of DNA fractions from the ^{13}C-labeled and ^{12}C-control microcosms after incubation for 5 and 19 days. ^{13}C–CH$_4$ refers to microcosm incubation with ^{13}CH$_4$ for labeling of methane-metabolizing communities, and ^{13}C–Urea represents incubation with ^{13}C–Urea plus ^{13}CO$_2$ for labeling of nitrifying communities. The relative frequency is expressed as the percentage of the targeted 16S rRNA genes to total 16S rRNA reads in each DNA gradient fraction.

total 16S rRNA gene sequences in the ^{13}C DNA from the labeled soil microcosms amended both with CH$_4$ and Urea, but not in the labeled microcosms that received only CH$_4$ (Fig. 3d).

The 16S rRNA gene sequences of AOB were highly enriched in "heavy" DNA fractions from the labeled microcosm amended only with urea on day 5 (Fig. 3e) and day 19 (Fig. 3f), but not the CH$_4$+Urea treatment during the 19-day incubation period. For instance, up to 5.73 % of total 16S rRNA gene sequences in the "heavy" DNA fractions could be assigned to AOB for ^{13}C–Urea treatment, while only 0.33 % of the total 16S rRNA gene sequences in the ^{13}C–Urea+CH$_4$ treatments were related to AOB on day 19 (Fig. 3f). Similar results were obtained for nitrite-oxidizing bacteria (Fig. 3g and h). The relative abundance of NOB in the "heavy" DNA fractions was significantly higher in microcosms with ^{13}C–Urea than ^{13}C–Urea+CH$_4$ treatment, implying a much greater degree of labeling of NOB cells in ^{13}C–Urea treatments during active nitrification. Furthermore, it is noteworthy that no significant enrichment of archaeal 16S rRNA gene sequences occurred in the "heavy" DNA fractions from the labeled microcosms (Supplement Fig. S8).

Phylogenetic analysis of the ^{13}C-labeled 16S rRNA genes demonstrated that active MOB were affiliated with

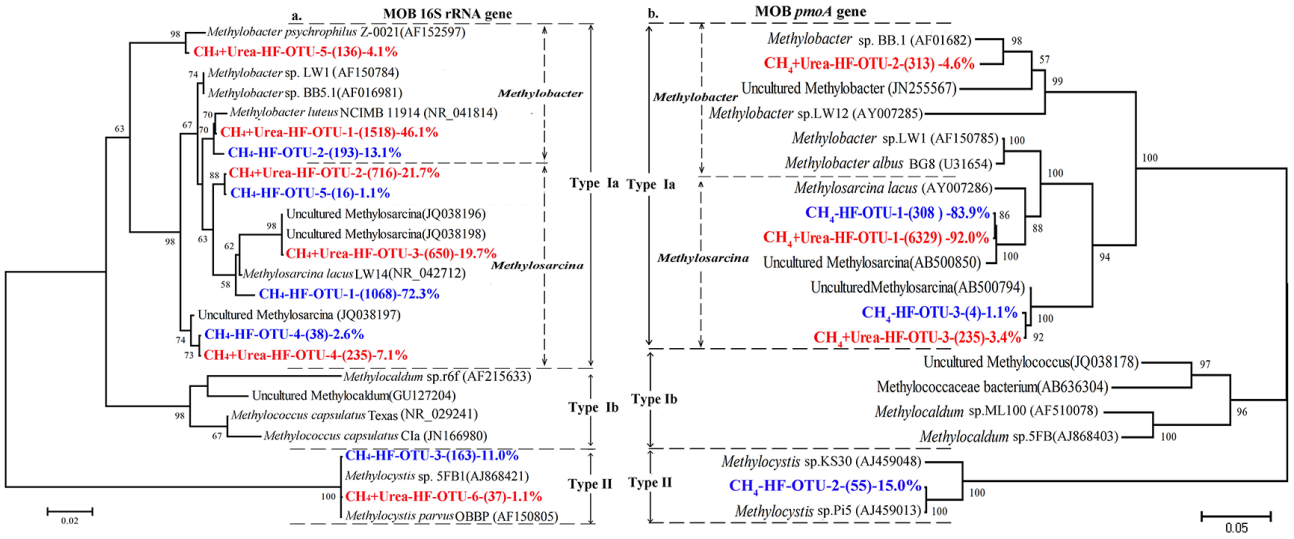

Figure 4. Phylogenetic tree of the ^{13}C-labeled 16S rRNA genes affiliated with methane-oxidizing bacteria **(a)** and *pmoA* genes **(b)** from the labeled microcosm after incubation for 19 days. The designations of CH_4 represent soil microcosms incubated with ^{13}C–CH_4, and the designation of CH_4+Urea denotes incubation with ^{13}C–CH_4 and ^{13}C–Urea plus ^{13}C–CO_2. CH_4-HF-OTU-1-(1068)-72.3 % indicates that OTU-1 contained 1068 reads with sequence identity of > 97 %, accounting for 72.3 % of the total methanotroph-like 16S rRNA genes in the "heavy" DNA fraction from the labeled microcosms. One representative sequence was extracted using the mothur software package for tree construction. The scale bar represents nucleotide acid substitution percentage.

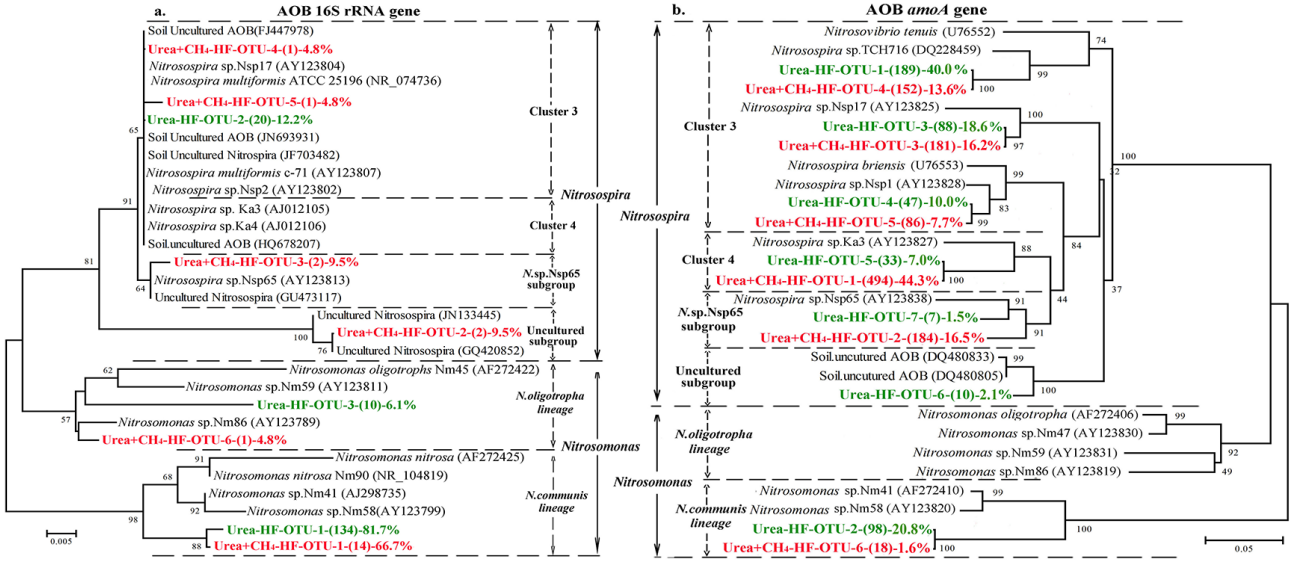

Figure 5. Phylogenetic tree of the ^{13}C-labeled 16S rRNA genes affiliated with ammonia-oxidizing bacteria **(a)** and bacteria *amoA* genes **(b)** from the labeled microcosm after incubation for 19 days. The designations of Urea represent soil microcosms incubated with ^{13}C–Urea plus ^{13}C–CO_2, and the designation of Urea+CH_4 denotes incubation with ^{13}C–CH_4 and ^{13}C–Urea plus ^{13}C–CO_2. Urea-HF-OTU-1-(134)-81.7 % indicates that OTU-1 contained 134 reads with sequence identity of > 97 %, accounting for 81.7 % of the total AOB-like 16S rRNA genes in the "heavy" DNA fraction from the labeled microcosms. One representative sequence was extracted using the mothur software package for tree construction. The scale bar represents nucleotide acid substitution percentage.

Type Ia (*Methylobacter*- and *Methylosarcina-like*) and *Methylocystis*-related type II methanotrophs, while type Ib methanotrophic sequences were not detected during active methane oxidation (Fig. 4a). Active ammonia oxidizers were phylogenetically assigned to distinctly different phylotypes including the *Nitrosospira* cluster and the *Nitrosomonas communis* lineage on the basis of ^{13}C-16S rRNA gene analysis (Fig. 5a). DNA-SIP demonstrated remarkable community

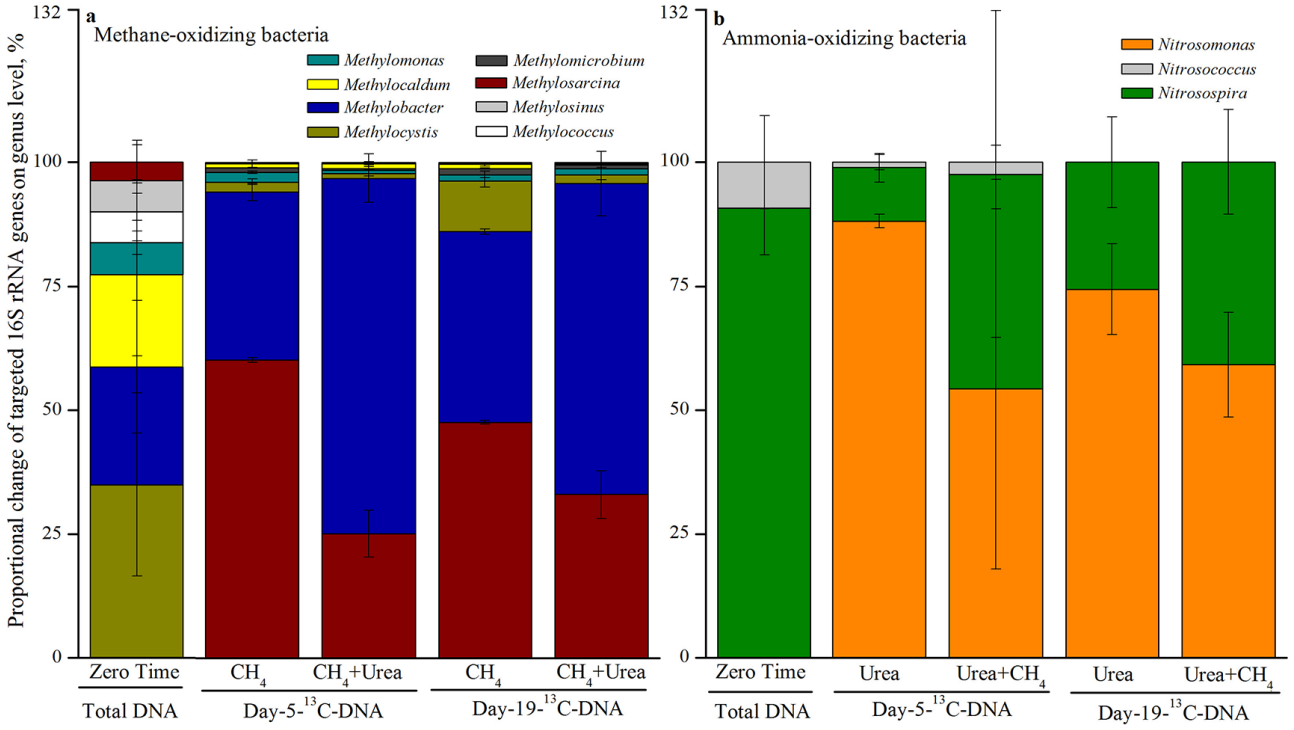

Figure 6. Percent changes of bacterial phylotypes affiliated with methane-oxidizing bacteria **(a)** and ammonia-oxidizing bacteria **(b)** in the ^{13}C DNA fractions from the labeled microcosm after incubation for 5 and 19 days. The designation of CH_4+Urea represents soil microcosms incubated with ^{13}C–CH_4 and ^{13}C–Urea plus ^{13}C–CO_2, and the designation of Day-5 ^{13}C DNA denotes the ^{13}C-labeled methanotrophic communities in the "heavy" DNA fractions after isopycnic centrifugation of the total DNA extracted from microcosms after incubation with the labeled substrates for 5 days. The percentage of different phylotypes is expressed as the targeted 16S rRNA gene reads to the total 16S rRNA gene reads affiliated with methane-oxidizing bacteria and ammonia-oxidizing bacteria in duplicate.

shifts of methanotrophs and ammonia oxidizers during the 19-day incubation period (Fig. 6). Type Ia-like MOB accounted for 89.7 % of the ^{13}C-labeled methanotrophic 16S rRNA sequences in CH_4-amended microcosms on day 19, while up to 98.1 % of the active methanotrophs could be assigned to Type Ia MOB in soil microcosms amended with both CH_4 and urea (Fig. 6a). This was further supported by pyrosequencing analysis of *pmoA* genes in the ^{13}C DNA (Fig. 4b). For instance, 85.0 % of *pmoA* genes were affiliated to type Ia MOB in CH_4-amended microcosms on day 19, whereas all *pmoA* sequences were detected exclusively as type Ia MOB in the microcosms amended with both CH_4 and urea. As for ammonia oxidizers, the relative abundance of *Nitrosomonas*-like 16S rRNA genes was as high as 88.2 % of the ^{13}C-labeled AOB communities in microcosms after incubation with urea for 5 days (Fig. 6b). However, the presence of CH_4 resulted in lower proportions of *Nitrosomonas*-like 16S rRNA genes, represented by 1.6 and 1.3 times lower than that in urea-amended microcosms on day 5 and day 19, respectively. Pyrosequencing of *amoA* genes in the ^{13}C DNA lend further support for the suppression of *Nitrosomonas*-like AOB since it decreased from 20.8 % to 1.6 % of the active AOB community upon CH_4 addition (Fig. 5b).

4 Discussion

The interaction between methane and nitrogen has been identified as one of the major gaps in carbon–nitrogen cycle interactions (Gardenas et al., 2011; Stein et al., 2012). There are many possible feedbacks to climate change through effects on methane and N_2O emissions and eutrophication of soils and sediments as a consequence of interactions between methane and ammonia oxidizers. The inhibition of mineral nitrogen on methane consumption has been demonstrated from numerous studies; however, ammonium-based fertilization was observed to stimulate methane consumption in rice paddies (Bodelier and Laanbroek, 2004). Mechanistically, there is still a poor understanding of nitrogen effects on methane cycling and vice versa. Elucidation of these mechanisms is of utmost importance to obtain comprehensive understanding of the nature of the effects of, e.g., climate change on the release of major greenhouse gases from various ecosystems.

Due to the enzymatic similarity of methane and ammonia monooxygenase, methane and ammonia oxidizers can oxidize methane as well as ammonia (Bodelier and Frenzel, 1999; O'Neill and Wilkinson, 1977; Stein et al., 2012). However, methane oxidizers do not gain energy out of the

oxidation of ammonia while ammonia oxidizers do not grow on methane (Stein et al., 2012). Moreover, mineral nitrogen is essential for biomass formation, especially for those methanotrophs lacking the ability to fix molecular nitrogen (Semrau et al., 2010). The latter indicates that next to direct enzymatic effects, interactions at the level of competition for N will play an important role in this matter, especially in high-methane environments where ammonia oxidizers will face enzymatic as well as competitive stress, with respect to which sparse information is available.

The pre-incubation was performed to increase the labeling efficiency of targeted microorganisms because the dilution of $^{13}CO_2$ by soil-respired $^{12}CO_2$ could be decreased significantly by pre-incubation as reported previously (Jia and Conrad, 2009, Xia et al., 2011). No apparent change of the ammonia oxidizer community was observed during a 4-week pre-incubation without ammonium fertilization, whereas a significant shift in the AOB community occurred in the ammonium-amended soils (Jia and Conrad, 2009). The nitrogenous fertilization of paddy soil in this study is about 250 kg N ha^{-1}, which is equivalent to 107 µg N g^{-1} d.w.s., assuming an effective soil depth of 20 cm. In addition, methane concentrations of 900–15 000 ppmv were generally detected in paddy soil during rice-growing season (Nouchi et al., 1990, 1994). Therefore, the microcosms were incubated with 100 µg urea–N g^{-1} d.w.s. and 10 000 ppmv methane to extrapolate the microbial interactions between methane and ammonia oxidation under field conditions. This suggests that microcosms might represent largely what is occurring under in situ conditions, although it could not entirely reproduce the physiochemical and biological conditions in field. For instance, it has also been reported that the results of microcosm incubations remained largely consistent with population dynamics of methanotrophic communities in the field (Eller et al., 2005).

In our study, it is demonstrated that urea fertilization significantly stimulated methane oxidation activity and growth of MOB. Growth and activity of ammonia oxidizers was partially inhibited in the presence of CH_4. It is obvious that competitive inhibition of the methane monooxygenase did not occur in our microcosms. The ratio of N–CH_4 is approximately 0.11 (assuming all urea is converted to ammonium). In other studies ratios of up to 200 (Bodelier et al., 2000b) did not lead to inhibition. Hence, it is safe to conclude that the ammonium formed out of urea or the subsequently produced nitrate acted as a nitrogen source for biomass generation of MOB. The decreased NH_4^+–N concentrations corresponded to the increased NO_3^-–N concentrations via nitrification only in the microcosms without methane amendment. Addition of methane to microcosms led to lower recovery of mineral N (Table 1), despite the equal addition of urea (Supplement Table S1), suggesting that part of the consumed ammonia was not oxidized to nitrate via nitrification or that part of the nitrate disappeared. We deduce that the consumed ammonia, which was not involved in ammonia oxidation, may be assimilated as a nitrogen nutrient for cell growth of MOB. Assuming that for oxidation of every mol CH_4–C, 0.25 mol N has to be assimilated by MOB (Bodelier and Laanbroek, 2004), the amount of N assimilated can be calculated using a 70 : 30 ratio of respiration of CH_4 vs. assimilation. This calculation shows that of the total amount of urea added 69 % was assimilated by MOB, while 20 % was nitrified (Supplement Table S6). However, the fate of unaccounted remaining nitrogen (11 %) needs to be verified by further experimentation.

Our results even demonstrate the dependence of the MOB on sufficient N availability. The relative abundance of both 16S rRNA and *pmoA* genes decreased when incubating with methane only, demonstrating loss of activity and of growth potential when N is limiting. A similar result was obtained in microcosms planted with rice (Bodelier et al., 2000a), where MOB even lost their potential for oxidizing methane. However, adding ammonium to these inactive communities led to immediate re-activation of oxidation (Bodelier et al., 2000a), indicating that N limitation is not only inhibiting growth but also regulated methane consumption enzyme machinery. This inactivation and rapid re-activation of methane oxidation has even been demonstrated on a field scale in rice paddies (Dan et al., 2001; Kruger and Frenzel, 2003). It has been proposed that nitrogen fixation may deplete reducing equivalents leading to lowering and even cessation of methane oxidation (Bodelier and Laanbroek, 2004; Dan et al., 2001). The available inorganic nitrogen source was indeed almost depleted after incubation in CH_4-amended microcosms, decreasing from 11.6 µg g^{-1} d.w.s. on day 0, to 1.37 and 1.19 µg g^{-1} d.w.s. on day 5 and day 19, respectively (Table 1). This suggests that under conditions of high-methane and low-nitrogen availability, there is a niche for methanotrophy outcompeting nitrifying communities. Nitrifiers can operate in the absence of competition with MOB when the latter are inactive due to energy depletion as the result of N_2 fixation. Hence, this points to niche differentiation or avoidance strategies of the nitrifiers.

It is obvious that only a subset of the MOB profit substantially from the combined addition of methane and urea–N. Although type II MOB increase in relative abundance of 16S rRNA gene sequences in total microbial community with the addition of methane they do not profit from the addition of urea, but are also not affected by it. Addition of ammonium to rice soil has been demonstrated to inhibit type II MOB (Mohanty et al., 2006). This is obviously not the case in our study, where the rapid growth of type Ia MOB keeps ammonium N low. The growth of type II MOB is apparently independent of the N availability, suggesting that they can rely on N_2 fixation only. ^{13}C-labeled methanotrophic 16S rRNA gene sequences are closely affiliated with *Methylocystis parvus* OBBP, which possesses nitrogenase and are capable of nitrogen fixing (Murrell and Dalton, 1983). This suggested that these *Methylocystis parvus*-like type II may respond under

Table 1. Changes in pH, moisture content, NH_4^+–N and NO_3^-–N content in soil microcosms over the course of 19 days of incubation.

Treatments	pH[a]	Moisture (%)[b]	NH_4^+–N ($\mu g\,g^{-1}$ d.w.s.)[c]	NO_3^-–N ($\mu g\,g^{-1}$ d.w.s.)[c]
Zero time	7.39 ± 0.04	19.4 ± 0.42	0.51 ± 0.10	11.1 ± 0.31
Day-5 CH_4	7.53 ± 0.01	26.1 ± 0.16	0.47 ± 0.33	0.90 ± 0.35
Day-5 Urea	7.35 ± 0.06	25.5 ± 0.51	16.1 ± 3.81	61.0 ± 8.62
Day-5 CH_4 + Urea	7.37 ± 0.12	24.8 ± 1.31	8.01 ± 4.66	41.6 ± 9.87
Day-19 CH_4	7.54 ± 0.03	28.3 ± 1.89	0.78 ± 0.12	0.41 ± 0.49
Day-19 Urea	7.27 ± 0.30	30.5 ± 1.85	44.8 ± 6.69	137.6 ± 28.3
Day-19 CH_4 + Urea	6.85 ± 0.09	28.6 ± 2.03	3.66 ± 1.56	59.9 ± 6.01

[a] pH was determined using a ratio of H_2O to soil as 2.5 (v/w). The mean ± standard deviation of triplicate microcosms was given for each treatment. [b] The mean ± standard deviation of triplicate microcosms was given for each treatment. [c] The mean ± standard deviation of triplicate microcosms was given for each treatment, while for the CH_4+Urea treatment 6 replicates were used including both ^{12}C-control and ^{13}C-labeled treatments.

N-limited conditions in our study. Next to this, the presence of highly active type I MOB did not prevent the growth of type II. However, significant growth of type II MOB only occurs after 19 days of incubation suggesting that they either have lower growth rates than type I or type II MOB depend on the activity of type I. The former is indeed the case as was demonstrated in wetland soil microcosms (Steenbergh et al., 2010) while the latter maybe the result from the fact that type II MOB may use CO_2 (Yang et al., 2013) as their main C source for assimilation (Matsen et al., 2013). Labeled CO_2 in the microcosms can only be formed by methane oxidation carried by type Ia in the early stages of the experiment. Another explanation may be succession of MOB, with type II MOB increasing in number when type I MOB is limited by N (Krause et al., 2010).

The strong stimulation of type Ia MOB upon methane application alone and in combination with urea–N application has been observed frequently in rice soils but also in other environments, reflecting their competitive life strategy as being reviewed and synthesized (Ho et al., 2013). The most responsive MOB species in high-methane habitats seem to be *Methylobacter* species (Krause et al., 2012). Our experiments show that *Methylosarcina* species are clearly the most responsive without addition of urea. This is in contrast with the niche differentiation observed at high spatial resolution in rice soil microcosms (Reim et al., 2012). The presence of *Methylosarcina*-related MOB in the surface layer of thin-layer microcosms and not in the methane–oxygen interface implies that *Methylosarcina* thrives under low-methane ("oligotrophic") conditions, in contrast to *Methylobacter*, which dominates the zone of high-methane flux. However, remarkably, in our experiments *Methylosarcina* clearly is dominant at high-methane supply, but is replaced partly by *Methylobacter* when urea–N is added. This might be attributed to competition for methane, nitrogen, or even oxygen. A similar result was observed in SIP analyses of lake sediment microcosms using a metagenomic approach (Beck et al., 2013). Hence, we speculate that the observations by Reim et al. (2012) may also be explained by weak competitive abilities of *Methylosarcina* instead of being restricted to low-methane habitats. A comparison of 16S rRNA gene and *pmoA* gene sequences revealed that *Methylobacter* was detected in a higher proportion in the MOB-16S rRNA gene phylogenetic tree than in the *pmoA* gene phylogenetic tree. The incongruence might result from the bias associated with the different coverage of *pmoA* and 16S rRNA gene primers as reported previously (Costello and Lidstrom, 1999).

The significant increase in obligate methanol oxidizer *Methylophilaceae* was observed in the microcosms incubated with CH_4 plus urea. The occurrence 16S rRNA of these sequences in the "heavy" DNA fractions indicates that these *Methylophilaceae* assimilated methane-derived carbon. Cross-feeding of methylotrophs by methanotrophs releasing methanol has been demonstrated before (Antony et al., 2010; Beck et al., 2013; He et al., 2012; Noll et al., 2008). The direct mechanism for this cross-feeding and what compound actually is exchanged have not been elucidated yet. We can add another component to this body of unsolved mechanisms, which is the strong stimulation of methylotrophs upon urea fertilization, thereby linking the nitrogen and the carbon cycles. It is very likely that the enhanced methane consumption and growth of methanotrophs leads to a higher availability of methanol. However, we can not exclude the possibility that urea has stimulatory effect on the methylotrophs directly. We also speculate that the active removal of methanol by the methylotrophs is beneficial to methanotrophs given the toxic nature of the compound. However, this would be the subject of further study. This link between nitrogen and cross-feeding of methanotrophic metabolites by other microorganism is interesting, possibly creating novel niches, e.g., a more methane-driven carbon substrate, a lower-toxic environment for methylotrophs in soil.

Our results revealed that the presence of CH_4 in microcosms partially inhibited the nitrification activity in the paddy soil tested. Physiologically, the enzymatic similarity of ammonia oxidizers and MOB may result in ammonia

oxidation by MOB (Bodelier and Frenzel, 1999), leading to reduced availability of ammonia for ammonia oxidizers. However, previous studies showed that MOB had lower affinity for ammonia than for CH_4 (Banger et al., 2012; Bedard and Knowles, 1989; Yang et al., 2011). Moreover, it has been proposed that ammonia oxidation by MOB occurred only when the ratio of ammonia to CH_4 is higher than 30 in soils (Banger et al., 2012; Bodelier and Laanbroek, 2004; Yang et al., 2011). The molecular ratio of ammonia to CH_4 was about 0.11 in our study, thus the suppression of ammonia oxidizers growth and activity in the presence of CH_4 may not be explained by ammonia oxidation by MOB. Furthermore, a large part of the applied N disappeared in the presence of CH_4, and presumably assimilated by MOB. This explanation seems plausible for the suppression of methane on ammonia oxidation and the growth of ammonia oxidizers. In the meantime, the toxic effect of metabolic intermediates of methane oxidation on nitrifying communities remains elusive. For example, methanol may inhibit the growth of AOA and AOB communities and we detected no archaeal *amoA* genes and 16S rRNA genes. The possibility of heterotrophic AOA lifestyle could also not be excluded (Ingalls et al., 2006; Stahl and de la Torre, 2012).

The genus *Nitrosospira* was the dominant AOB in the native soil, being consistent with general observations that *Nitrosospira* are ubiquitous in upland soils as important members of nitrifying communities (Hastings et al., 1997; Stephen et al., 1996). In our study, the apparent growth of *Nitrosospira* was observed in the microcosms amended with urea–N, and cluster 3 was the dominant active *Nitrosospira* group. It has been reported that *Nitrosospira* cluster 3 was the dominant AOB group in a number of neutral soil receiving nitrogen fertilization (Bruns et al., 1999; Mendum et al., 1999). Intriguingly, methane addition suppressed the growth of *Nitrosospira*, and AOB within the cluster 3 appeared to be inhibited to a greater extent than those of cluster 4. It has been proposed that reduced ammonia supply may select for cluster 4 AOB (Kowalchuk and Stephen, 2001). In the presence of methane, the growth of methanotrophs was significantly stimulated and methanotrophic N assimilation likely led to the depletion of ammonium in support of nitrification activity. It was noteworthy that none of 16S rRNA and *amoA* genes were affiliated with *Nitrosomonas* in the native soil on day 0. The growth of *Nitrosomonas* was stimulated to a much greater extent than that of *Nitrosospira* in urea-amended microcosms, but *Nitrosomonas* appeared to be suppressed more than *Nitrosospira*. This might be explained by the fact that *Nitrosomonas* species are markedly responsive to ammonia input (Hastings et al., 1997). Similar to methanotrophic communities, the proportion of *Nitrosospira* in AOB community detected by 16S rRNA gene sequences was lower than that detected by *amoA* gene. It could be in part attributed to the variation of *amoA* copy numbers among different AOB. For instance, the species *N. briensis* and *N. europaea* have two copies of *amoA* genes and *N. tenuis* contained three identical *amoA* genes (Norton et al., 1996; Sayavedra-Soto et al., 1998).

The abilities to catalyze the hydrolysis of urea to yield ammonia can be observed in a wide range of microorganisms possessing urease activity (Mobley and Hausinger, 1989). Some methanotrophs have been identified with the ability of urea hydrolysis (Boden et al., 2011; Khmelenina et al., 2013); however, the ^{13}C-labeled active methanotrophs on the basis of the 16S rRNA gene (Fig. 4a) and the *pmoA* gene (Fig. 4b) were phylogenetically distinctly different from the known ureolytic methanotrophs. However, the ^{13}C-labeled AOB showed high sequence similarity to ureolytic *Nitrosomonas nitrosa* and *Nitrosomonas oligotrophs* (Fig. 5a). This indicates the potential of hydrolyzing urea in these active ammonia-oxidizing bacteria. It was estimated that 30–50 % of ammonia could be released from hydrolysis of urea by AOB in a batch culture (Pommerening-Roser and Koops, 2005). This suggests that ammonia oxidizers may have to compete for the ammonia released into the environment with other ammonia-utilizing microorganisms such as methanotrophs, intensifying the competition for nitrogen between AOB and MOB. It is noteworthy that there was no report about the ureolytic activity of AOA in non-acid soils.

Taken together, the results of this study demonstrate the stimulation of methane consumption and growth of MOB by urea and the subsequent suppression of nitrifier growth and activity. Only a sub-set of the MOB profited from the urea addition, with *Methylobacter* species responding the most vigorous, showing that urea addition gives rise to niche differentiation in MOB communities. In addition, our results revealed the cross-feeding of methane-derived carbon in the soil system upon urea fertilization, indicating urea might play an important role in carbon cycle through the microbial food web processing carbon from methane oxidation in paddy soil. Assimilation of N by MOB is the most likely mechanism for inhibition of ammonia oxidizers by methane addition. Therefore, we speculated that competition for nitrogen between methane and ammonia oxidizers play a dominant role in microbial interactions in our study, which is of help toward predictive understandings of carbon and nitrogen cycle in complex environments.

The Supplement related to this article is available online at doi:10.5194/bg-11-3353-2014-supplement.

Acknowledgements. This work was financially supported by the National Science Foundation of China (41090281), the Ministry of Science and Technology of China (2010DFA22770), and the Distinguished Young Scholar Program of Jiangsu Province (BK2012048). The authors thank our lab colleagues for helpful discussions.

Edited by: K. Küsel

References

Antony, C. P., Kumaresan, D., Ferrando, L., Boden, R., Moussard, H., Fernandez Scavino, A., Shouche, Y. S., and Murrell, J. C.: Active methylotrophs in the sediments of Lonar Lake, a saline and alkaline ecosystem formed by meteor impact, ISME J., 4, 1470–1480, 2010.

Banger, K., Tian, H., and Lu, C.: Do nitrogen fertilizers stimulate or inhibit methane emissions from rice fields?, Glob. Change Biol., 18, 3259–3267, 2012.

Beck, D. A. C., Kalyuzhnaya, M. G., Malfatti, S., Tringe, S. G., Glavina Del Rio, T., Ivanova, N., Lidstrom, M. E., and Chistoserdova, L.: A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the Methylococcaceae and the Methylophilaceae, Peer J., 1, e23, doi:10.7717/peerj.23, 2013.

Bedard, C. and Knowles, R.: Physiology, biochemistry, and specific inhibitors of CH_4, NH_4^+, and CO oxidation by methanotrophs and nitrifiers, Microbiol. Rev., 53, 68–84, 1989.

Bock, E. and Wagner, M.: Oxidation of inorganic nitrogen compounds as an energy source, edited by: Dworkin, M. and Falkow, S., The Prokaryotes, Springer Verlag, New York, 457–495, 2006.

Bodelier, P. L. E.: Interactions between nitrogenous fertilizers and methane cycling in wetland and upland soils, Curr. Opin. Environ. Sustainability, 3, 379–388, 2011.

Bodelier, P. L. E. and Frenzel, P.: Contribution of methanotrophic and nitrifying bacteria to CH_4 and NH_4^+ oxidation in the rhizosphere of rice plants as determined by new methods of discrimination, Appl. Environ. Microb., 65, 1826–1833, 1999.

Bodelier P. L. E. and Laanbroek, H. J.: Nitrogen as a regulatory factor of methane oxidation in soils and sediments, FEMS Microbiol. Ecol., 47, 265–277, 2004.

Bodelier, P. L. E., Hahn, A. P., Arth, I. R., and Frenzel, P.: Effects of ammonium-based fertilisation on microbial processes involved in methane emission from soils planted with rice, Biogeochemistry, 51, 225–257, 2000a.

Bodelier, P. L. E., Roslev, P., Henckel, T., and Frenzel, P.: Stimulation by ammonium-based fertilizers of methane oxidation in soil around rice roots, Nature, 403, 421–424, 2000b.

Bodelier, P. L. E., Bär-Gilissen, M.-J., Meima-Franke, M., and Hordijk, K.: Structural and functional response of methane-consuming microbial communities to different flooding regimes in riparian soils, Ecol. Evol., 2, 106–127, 2012.

Bodelier, P. L. E., Meima-Franke, M., Hordijk, C. A., Steenbergh, A. K., Hefting, M. M., Bodrossy, L., von Bergen, M., and Seifert, J.: Microbial minorities modulate methane consumption through niche partitioning, ISME J., 7, 2214–2228, 2013.

Boden, R., Cunliffe, M., Scanlan, J., Moussard, H., Kits, K. D., Klotz, M. G., Jetten, M. S. M., Vuilleumier, S., Han, J., Peter, L., Mikhailova, N., Teshima, H., Tapia, R., Kyrpides, N., Ivanova, N., Pagani, I., Cheng, J. F., Goodwin, L., Han, C., Hauser, L., Land, M. L., Lapidus, A., Lucas, S., Piluck, S., Woyke, T., Stein, L., and Murrell, J. C.: Complete Genome Sequence of the Aerobic Marine Methanotroph *Methylomonas methanica* MC09, J. Bacteriol., 193, 7001–7002, 2011.

Bratina, B. J., Brusseau, G. A., and Hanson, R. S: Use of 16S ribosomal-RNA analysis to investigate phylogeny of methylotrophic bacteria, Int. J. Syst. Bacteriol., 42, 645–648, 1992.

Bruns, M. A., Stephen, J. R., Kowalchuk, G. A., Prosser, J. I., and Paul, E. A.: Comparative diversity of ammonia oxidizer 16S rRNA gene sequences in native, tilled, and successional soils, Appl. Environ. Microb., 65, 2994–3000, 1999.

Costello, A. M. and Lidstrom, M. E.: Molecular characterization of functional and phylogenetic genes from natural populations of methanotrophs in lake sediments, Appl. Environ. Microb., 65, 5066–5074, 1999.

Dan, J. G., Kruger, M., Frenzel, P., and Conrad, R.: Effect of a late season urea fertilization on methane emission from a rice field in Italy, Agr. Ecosyst. Environ., 83, 191–199, 2001.

Degelmann, D. M., Borken, W., Drake, H. L., and Kolb, S.: Different atmospheric methane-oxidizing communities in European beech and Norway spruce soils, Appl. Environ. Microb., 76, 3228–3235, 2010.

Devries, G. E., Kues, U., and Stahl, U.: Physiology and genetics of methylotrophic bacteria, FEMS Microbiol. Rev., 75, 57–101, 1990.

Dunfield, P. F., Yuryev, A., Senin, P., Smirnova, A. V., Stott, M. B., Hou, S., Ly, B., Saw, J. H., Zhou, Z., Ren, Y., Wang, J., Mountain, B. W., Crowe, M. A., Weatherby, T. M., Bodelier, P. L. E., Liesack, W., Feng, L., Wang, L., and Alam, M.: Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia, Nature, 450, 879–882, 2007.

Eller, G., Kruger, M., and Frenze, P.: Comparing field and microcosm experiments: a case study on methano- and methylotrophic bacteria in paddy soil, FEMS Microbiol. Ecol., 51, 279–291, 2005.

Galloway, J. N., Townsend, A. R., Erisman, J. W., Bekunda, M., Cai, Z., Freney, J. R., Martinelli, L. A., Seitzinger, S. P., and Sutton, M. A.: Transformation of the nitrogen cycle: Recent trends, questions, and potential solutions, Science, 320, 889–892, 2008.

Gardenas, A. I., Agren, G. I., Bird, J. A., Clarholm, M., Hallin, S., Ineson, P., Katterer, T., Knicker, H., Nilsson, S. I., Nasholm, T., Ogle, S., Paustian, K., Persson, T., and Stendahl, J.: Knowledge gaps in soil carbon and nitrogen interactions-From molecular to global scale, Soil Biol. Biochem., 43, 702–717, 2011.

Hanson, R. S., and Hanson, T. E.: Methanotrophic bacteria, Microbiol. Rev., 60, 439–471, 1996.

Hastings, R. C., Ceccherini, M. T., Miclaus, N., Saunders, J. R., Bazzicalupo, M., and McCarthy, A. J.: Direct molecular biological analysis of ammonia oxidising bacteria populations in cultivated soil plots treated with swine manure, FEMS Microbiol. Ecol., 23, 45–54, 1997.

Ho, A., Kerckhof, F.-M., Luke, C., Reim, A., Krause, S., Boon, N., and Bodelier, P. L. E.: Conceptualizing functional traits and ecological characteristics of methane-oxidizing bacteria as life strategies, Environ. Microbiol. Rep., 5, 335–345, 2013.

Holmes, A. J., Costello, A., Lidstrom, M. E., and Murrell, J. C.: Evidence that particulate methane monoxygenase and ammonia monooxygenase may be evolutionarily related, FEMS Microbiol. Lett., 132, 203–208, 1995.

Ingalls, A. E., Shah, S. R., Hansman, R. L., Aluwihare, L. I., Santos, G. M., Druffel, E. R., and Pearson, A.: Quantifying archaeal community autotrophy in the mesopelagic ocean using natural radiocarbon, P. Natl. Acad. Sci. USA, 103, 6442–6447, 2006.

Jia, Z. and Conrad, R.: Bacteria rather than Archaea dominate microbial ammonia oxidation in an agricultural soil, Environ. Microbiol., 11, 1658–1671, 2009.

Jones, R. D. and Morita, R. Y.: Methane Oxidation by *Nitrosococcus oceanus* and *Nitrosomonas europaea*, Appl. Environ. Microb., 45, 401–410, 1983.

Khmelenina, V. N., Beck, D.A.C., Munk, C., Davenport, K., Daligault, H., Erkkila, T., Goodwin, L., Gu, W., Lo, C. C., Scholz, M., Teshima, H., Xu, Y., Chain, P., Bringel, F., Vuilleumier, S., Dispirito, A., Dunfield, P., Jetten, M. S. M., Klotz, M. G., Knief, C., Murrell, J. C., Opdencamp, H. J. M., Sakai, Y., Semrau, J., Svenning, M., Stein, L., Trotsenko, Y. A., and Kaylyuzhnaya, M. G.: Draft Genome Sequence of *Methylomicrobium buryatense* Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium, Genome announcements, 4, 2169–8287, 2013.

Kolb, S.: Aerobic methanol-oxidizing bacteria in soil, FEMS Microbiol. Lett., 300, 1–10, 2009.

Könneke, M., Bernhard, A. E., de la Torre, J. R., Walker, C. B., Waterbury, J. B., and Stahl, D. A.: Isolation of an autotrophic ammonia-oxidizing marine archaeon, Nature, 437, 543–546, 2005.

Kowalchuk, G. A. and Stephen, J. R.: Ammonia-oxidizing bacteria: a model for molecular microbial ecology, Annu. Rev. Microbiol., 55, 485–529, 2001.

Krause, S., Lueke, C., and Frenzel, P.: Succession of methanotrophs in oxygen-methane counter-gradients of flooded rice paddies, ISME J., 4, 1603–1607, 2010.

Krause, S., Lueke, C., and Frenzel, P.: Methane source strength and energy flow shape methanotrophic communities in oxygen-methane counter-gradients, Environ. Microbiol. Rep., 4, 203–208, 2012.

Kruger, M. and Frenzel, P.: Effects of N-fertilisation on CH_4 oxidation and production, and consequences for CH4 emissions from microcosms and rice fields, Glob. Change Biol., 9, 773–784, 2003.

Lipscomb, J. D.: Biochemistry of the soluble methane monooxygenase, Annu. Rev. Microbiol., 48, 371–399, 1994.

Lu, L. and Jia, Z.: Urease gene-containing Archaea dominate autotrophic ammonia oxidation in two acid soils, Environ. Microbiol., 15, 1795–1809, 2013.

Matsen, J. B., Yang, S., Stein, L. Y., Beck, D., and Kalyuzhnaya, M. G.: Global Molecular Analyses of Methane Metabolism in Methanotrophic Alphaproteobacterium, *Methylosinus trichosporium* OB3b. Part I: Transcriptomic Study, Front. Microbiol., 4, 40–40, 2013.

Mendum, T. A., Sockett, R. E., and Hirsch, P. R.: Use of molecular and isotopic techniques to monitor the response of autotrophic ammonia-oxidizing populations of the beta subdivision of the class Proteobacteria in arable soils to nitrogen fertilizer, Appl. Environ. Microb., 65, 4155–4162, 1999.

Mobley, H. L. and Hausinger, R. P.: Microbial ureases: significance, regulation, and molecular characterization, Microbiol. Res., 53, 85–108, 1989.

Mohanty, S. R., Bodelier, P. L. E., Floris, V., and Conrad, R.: Differential effects of nitrogenous fertilizers on methane-consuming microbes in rice field and forest soils, Appl. Environ. Microb., 72, 1346–1354, 2006.

Morris, S. A., Radajewski, S., Willison, T. W., and Murrell, J. C.: Identification of the functionally active methanotroph population in a peat soil microcosm by Stable-Isotope Probing, Appl. Environ. Microb., 68, 1446–1453, 2002.

Murrell, J. C. and Dalton, H.: Nitrogen-fixation in obligate methanotrophs, J. Gen. Microbiol., 129, 3481–3486, 1983.

Noll, M., Frenzel, P., and Conrad, R.: Selective stimulation of type I methanotrophs in a rice paddy soil by urea fertilization revealed by RNA-based stable isotope probing, FEMS Microbiol. Ecol., 65, 125–132, 2008.

Nouchi, I., Mariko, S., and Aoki, K.: Mechanism of methane transport from the rhizosphere to the atmosphere through rice plants, Plant Physiol., 94, 59–66, 1990.

Nouchi, I., Hosono, T., Aoki, K., and Minami, K.: Seasonal-variation in methane flux from rice paddies associated with methane concentration in soil-water, rice biomass and temperature, and its modeling, Plant Soil, 161, 195–208, 1994.

Norton, J. M., Low, J. M., and Martin, G.: The gene encoding ammonia monooxygenase subunit A exists in three nearly identical copies in *Nitrosospira* sp. NpAV, FEMS Microbiol. Lett., 139, 181–188, 1996.

O'Neill, G. G. and Wilkinson, J. F.: Oxidation of ammonia by methane-oxidizing bacteria and the effects of ammonia on methane oxidation, J. Gen. Microbiol., 100, 407–412, 1977.

Pester, M., Rattei, T., Flechl, S., Grongroft, A., Richter, A., Overmann, J., Reinhold-Hurek, B., and Loy, A.: *amoA*-based consensus phylogeny of ammonia-oxidizing archaea and deep sequencing of *amoA* genes from soils of four different geographic regions. Environ. Microbiol., 14, 525–539, 2012.

Pommerening-Roser, A., and Koops, H. P.: Environmental pH as an important factor for the distribution of urease positive ammonia-oxidizing bacteria, Microbiol. Res., 160, 27–35, 2005.

Pratscher, J., Dumont, M. G., and Conrad, R.: Ammonia oxidation coupled to CO_2 fixation by archaea and bacteria in an agricultural soil, P. Natl. Acad. Sci. USA, 108, 4170–4175, 2011.

Purkhold, U., Pommerening-Roser, A., Juretschko, S., Schmid, M. C., Koops, H. P., and Wagner, M.: Phylogeny of all recognized species of ammonia oxidizers based on comparative 16S rRNA and *amoA* sequence analysis: Implications for molecular diversity surveys, Appl. Environ. Microb., 66, 5368–5382, 2000.

Purkhold, U., Wagner, M., Timmermann, G., Pommerening-Roser, A., and Koops, H. P.: 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, Int. J. Syst. Evol. Micr., 53, 1485–1494, 2003.

Prosser, J. I. and Nicol, G. W.: Archaeal and bacterial ammonia-oxidisers in soil: the quest for niche specialisation and differentiation, Trends Microbiol., 20, 523–531, 2012.

Reim, A., Lueke, C., Krause, S., Pratscher, J., and Frenzel, P.: One millimetre makes the difference: high-resolution analysis of methane-oxidizing bacteria and their specific activity at the oxic-anoxic interface in a flooded paddy soil, ISME J., 6, 2128–2139, 2012.

Rotthauwe, J. H., Witzel, K. P., and Liesack, W.: The ammonia monooxygenase structural gene *amoA* as a functional marker: Molecular fine-scale analysis of natural ammonia-oxidizing populations, Appl. Environ. Microb., 63, 4704–4712, 1997.

Sayavedra-Soto, L. A., Hommes, N. G., Alzerreca, J. J., Arp, D. J., Norton, J. M., and Klotz, M. G.: Transcription of the *amoC*, *amoA* and *amoB* genes in *Nitrosomonas europaea* and *Nitrosospira* sp. NpAV, FEMS Microbiol. Lett., 167, 81–88, 1998.

Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., Lesniewski, R. A., Oakley, B. B., Parks, D.

H., Robinson, C. J., Sahl, J. W., Stres, B., Thallinger, G. G., Van Horn, D. J., and Weber, C. F.: Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities, Appl. Environ. Microb., 75, 7537–7541, 2009.

Semrau, J. D., DiSpirito, A. A., and Yoon, S.: Methanotrophs and copper, FEMS Microbiol. Rev., 34, 496–531, 2010.

Stahl, D. A. and de la Torre, J. R.: Physiology and diversity of ammonia-oxidizing archaea, Annu. Rev. Microbiol., 66, 83–101, 2012.

Steenbergh, A. K., Meima, M. M., Kamst, M., and Bodelier, P. L. E.: Biphasic kinetics of a methanotrophic community is a combination of growth and increased activity per cell, FEMS Microbiol. Ecol., 71, 12–22, 2010.

Stein, L. Y., Roy, R., and Dunfield, P. F.: Aerobic methanotrophy and nitrification: processes and connections, in: Encyclopedia of life sciences (eLS.), John Wiley & Sons Ltd, Chichester, 1–11, 2012.

Stephen, J. R., McCaig, A. E., Smith, Z., Prosser, J. I., and Embley, T. M.: Molecular diversity of soil and marine 16S rRNA gene sequences related to beta-subgroup ammonia-oxidizing bacteria, Appl. Environ. Microb., 62, 4147–4154, 1996.

Wang, Q., Garrity, G. M., Tiedje, J. M., and Cole, J. R.: Naive bayesian classifier for rapid assignment of rrna sequences into the new bacterial taxonomy, Appl. Environ. Microb., 73, 5261–5267, 2007.

Xia, W., Zhang, C., Zeng, X., Feng, Y., Weng, J., Lin, X., Zhu, J., Xiong, Z., Xu, J., Cai, Z., and Jia, Z.: Autotrophic growth of nitrifying community in an agricultural soil, ISME J., 5, 1226–1236, 2011.

Yang, N., Lu, F., He, P., and Shao, L.: Response of methanotrophs and methane oxidation on ammonium application in landfill soils, Appl. Microbiol. Biot., 92, 1073–1082, 2011.

Yang, S., Matsen, J. B., Konopka, M., Green-Saxena, A., Clubb, J., Sadilek, M., Orphan, V. J., Beck, D., and Kalyuzhanaya, M. G.: Global moelcuar analyses of methane metabolism in methanotrophic alphaprotebacterium, *Methylosinus Trichosporium* OB3b. Part II. Metabolomics and ^{13}C-labelling study, Front. Microbiol., 4, 70, doi:10.3389/fmicb.2013.00070, 2013.

Zhang, L. M., Offre, P. R., He, J. Z., Verhamme, D. T., Nicol, G. W., and Prosser, J. I.: Autotrophic ammonia oxidation by soil thaumarchaea, P. Natl. Acad. Sci. USA, 107, 17240–17245, 2010.

Zhu, R. B., Liu, Y. S., Xu, H., Huang, T., Sun, J. J., Ma, E. D., and Sun, L. G.: Carbon dioxide and methane fluxes in the littoral zones of two lakes, east Antarctica, Atmos. Environ., 44, 304–311, 2010.