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

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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 by 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 type Ia 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 equal increase in *Methylosarcina* and *Methylobacter*-related MOB, indicating the differential growth requirements of representatives of these genera. 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, in addition of nitrite-oxidizing bacteria. These results suggest that type I methanotrophs could likely outcompete type II methane oxidizers under nitrogen-rich environment and the competitive interactions among methane and ammonia oxidizers are complicated than previously appreciated.

Key Words:

Paddy soil, methane oxidation, ammonia oxidation, microbial interactions, high-throughput pyrosequencing, DNA-SIP

Introduction

The intensive use of nitrogenous fertilizers in rice agriculture is a perquisite to meet 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 system to the global methane emission 15 to 45% of global CH_4 budget (Bodelier, 2011) has evoked numerous studies focusing on this topic. Recent meta-analysis indicate that the increasing rice biomass by nitrogen fertilization may result in the elevated supply of readily available carbon in suport of methanogenesis, stimulating methane emission in paddy fields(Banger et al., 2012). However, opposed to this there 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 amount 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 (Bodelier, 2011).

Aerobic methane-oxidizing bacteria (MOB) belong to two phyla: *Proteobacteria* and *Verrucomicrobia* (Bodelier et al., 2009). Whereas 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 being 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, Methylobius* and *Methylothermus*). Type II MOB include the family *Methylocystaceae* (including genera *Methylocystis* and *Methylosinus*) and *Beijerinckiaceaea* (including genera *Methylocella, Methylocapsa* and *Methyloferula*) (Stein et al., 2012). 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 found only in a few species (Hanson and Hanson, 1996; Lipscomb, 1994). Methanotrophs covert CH_4 into methanol, which can be utilized by methanol-oxidizing bacteria as carbon and energy source. The known soil-retrieved methanol-oxidizing bacteria was with high diversity, 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, He et al 2012).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 important role of archaeal nitrification in the global nitrogen cycle (Lu and Jia, 2013; Venter et al., 2004). However, until now the relative contribution of AOB and AOA to ammonia oxidation in agricultural soil is still unclear (Prosser and Nicol, 2012; Xia et al., 2011). 16S rRNA and *amoA* gene analyses of AOB revealed that physiological groups are confined to monophyletic lineages within β- and γ-subclass of *Proteobacteria*. *Nitrosospira* and *Nitrosomonas* form a grouping within β-subclass and *Nitrosococcus* is affiliated with γ-subclass (Purkhold et al 2000, Purkhold et al 2003). Enormous diversity of AOA based on 16S rRNA and *amoA* gene has been suggested, and four major lineages have been displayed, including *Nitrososphaera* cluster, *Nitrosopumilus* cluster, *Nitrosotalea* cluster, and *Nitrosocaldus* cluster (Pester et al 2012, Stahl and de la Torre 2012). The conversion of nitrite into nitrate is caused by nitrite-oxidizing bacteria (NOB). NOB are composed of four genera, including *Nitrobacter, Nitrococcus, Nitrospina* and

115 *Nitrospira*, which were assigned to the α-proteobacteria, γ-proteobacteria,
116 δ-proteobacteria and phylum *Nitrospirae*, respectively (Bock and Wagner 2006).

117 The key enzymes methane monooxygenase (MMO) in methanotrophs and ammonia
118 monooxygenase in ammonia oxidizers are evolutionarily linked (Holmes et al., 1995),
119 leading to functional similarities enabling both methanotrophs and ammonia oxidizers
120 to oxidize both methane and ammonia (Jones and Morita, 1983; O'Neill and
121 Wilkinson, 1977). Pure culture studies demonstrated that methane can act as a
122 competitive inhibitor for ammonia oxidizers, and ammonia inhibits the growth and
123 activity of methanotrophs (Bedard and Knowles, 1989; Stein et al., 2012). Next to this,
124 both MOB as well as AOB have to deal with toxic intermediates (hydroxylamine in
125 case of MOB and methanol in case of AOB) (Stein et al., 2012). At the microbial
126 community level, however, the growth of methanotrophs might be nitrogen-limited
127 and nitrogen fertilization might relieve methane oxidizers from nutrient constraint
128 (Bodelier et al., 2000b). At the same time ammonia oxidizers and subsequent
129 nitrification may be inhibited by the methanotrophic N-assimilation. However, the
130 research focus of methane effect on nitrification in natural complex ecosystems is
131 poor, which is in sharp contrast with a large number of studies executed to elucidate
132 effect of nitrogenous fertilizers on methane oxidation. Moreover, the lack of
133 knowledge on this topic is even more evident taking the yet unknown role of AOA in
134 interactions with MOB into account. DNA-based stable isotope probing (DNA-SIP) is
135 generally used to link the metabolisms of ^{13}C-labeled substrates with growing
136 microbial communities in the environment. DNA-SIP has been employed to identify
137 the active methanotrophs (Dumont et al., 2011) and ammonia oxidizers in soils (Jia
138 and Conrad, 2009; Lu and Jia, 2013; Xia et al., 2011). The combined use of stable
139 isotope labeling and high throughput pyrosequencing is a powerful combination of
140 approaches that offers great opportunities in elucidating interaction between MOB
141 and AOB/AOA, because both groups can easily and specifically be labeled using
142 $^{13}CH_4$ (Bodelier et al., 2013; Bodelier et al., 2012) and $^{13}CO_2$ (Jia and Conrad, 2009).
143 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 cycle in light of climate change. However, the effects of nitrogen on methane oxidation are complicated and contradictory results are often reported. Therefore, the microbial populations and functional dynamics of methane- and ammonia oxidizers were investigated in microcosms incubated with CH_4, urea and CH_4+urea in a paddy soil using culture-independent techniques.

Materials and Methods

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 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 water to soil ratio at 2.5.

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° C in the dark for 19 days. To increase the labeling efficacy 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 (Table S1). Meanwhile, ^{13}C-Urea fertilization of 100 μg urea-N/g. *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 10000 ppmv CH_4 and/or 100 μg urea-N/g. *d.w.s.* plus 5% CO_2. Due to strong methane oxidation in microcosms amended with ^{13}C-CH_4+Urea treatment (Fig. S1), methane addition was regularly repeated, in addition to urea and CO_2 substrates. The scenario of SIP microcosm construction was detailed in supplemental 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° C 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).

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 instruction. 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 hours 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 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 30μL sterile water for downstream analysis.

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 efficacy 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 Supplementary Table S2. The reactions was performed in a 20 μL mixture containing 10.0 μL SYBR Premix Ex Taq (Takara, Dalian), 0.5μM each primer, and 1μL of DNA template. The amplification efficiencies were 93%~103% obtained with R^2 values of 99.1%~99.9%.

Pyrosequencing of 16S rRNA genes at the whole community level

Pyrosequencing of the total 16S rRNA genes was performed in triplicate microcosms (Table S3) and in the fractionated DNA from fraction-3 to 13 of each treatment (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 Supplementary Table S2. 50 μL PCR reaction mixture containing 45μL L^{-1} 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 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-like and AOB-like 16S rRNA gene sequences were

extracted and clustered into operational taxonomic unit (OTU) at 97% sequence identify cut-off using mothur software package. One representative sequence of each OTU was then used for phylogenetic analysis.

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 ^{13}C-labeled DNA in the ^{13}C-labeled microcosms at day 0 and day 19 (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 (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 45μL 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 mothur software (Schloss et al 2009) for quality check, alignment and phylogenetic tree construction. High quality sequences (read length longer than 200bp, average quality score more than 25, without ambiguous base calls) were extracted for further analysis. Pyrosequencing of *pmoA* gene yield about 36 000 high quality sequence reads with an average length of 482bp, while about 47 000 bacterial *amoA* gene sequence reads were generated with an average length of 469bp (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.

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.

Accession number of nucleotide sequences

The pyrosequencing reads have been deposited at DNA Data Bank of Japan (DDBJ) with accession numbers DRA001245 and DRA001247 for the 16S rRNA genes and functional genes (bacterial *amoA* and *pmoA*), respectively.

Results

Microbial oxidation of methane and ammonia

Methane oxidation activity was assessed by determining the amount of methane consumed in soil microcosms over the incubation course of 19 days, and the strong capacity of methane oxidation was observed in the paddy soil tested (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 at day 5 and 19, respectively (Fig. 1a). Soil nitrification activity was determined as the increase of soil nitrate concentrations during incubation of microcosms for 19 days. Soil nitrate content significantly increased from 11.1 μg NO_3^--N /g *d.w.s* in urea-amended microcosms at day 0, to 61.0 and 137.6 μg NO_3^--N /g *d.w.s.* at 5 and 19 days, respectively (Fig. 1b, Fig.S2). The presence of CH_4 in the headspace of urea-amended microcosms significantly inhibited production of soil nitrate at day 19, although statistically significant inhibition was not observed at day 5 (Fig. 1b, 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 (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 was affiliated with bacteria. Relative abundance of bacterial 16S rRNA genes in total microorganism was ranged from 95.3% to 98.8% in these microcosms, which was much higher than that of archaeal 16S rRNA genes (Table S3). Pyrosequencing data provided the information about relative abundance of targeted microbial 16S rRNA gene sequences in the total microbial communities. Methanotrophic 16S rRNA genes comprised only 0.28% of total microbial communities in paddy soil tested (Fig. 1c). However, methane oxidation led to a remarkable increase of MOB-like 16S rRNA genes up to 27.9% of the total microbial communities 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% at day 5 to 7.42% to day 19. Nonetheless, urea addition resulted in higher abundance of methanotroph-like 16S rRNA gene sequences up to 19.8% and 27.9% at day 5 and day 19, respectively, representing 1.3- and 4-fold increase relative to CH_4-amended microcosms (Fig. 1c). The population size of MOB community determined by real-time PCR of *pmoA* genes (Fig. S3a) showed the similar result with 16S rRNA pyrosequencing analysis. The copy number of *pmoA* genes increased significantly from 4.44×10^8 copies g^{-1} *d.w.s.* at 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, respectively. Urea addition led to 1.35 and 3.16 times more *pmoA* genes than that in only CH_4-incubated microcosms at day 5 and day 19, respectively. The family *Methylophilaceae*, using methanol as sole source of carbon and energy (Devries et al., 1990; He et al., 2012), 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%) at day 19.

AOB 16S rRNA gene sequences comprised only a tiny fraction of the total microbial communities during a 19-day incubation period (Fig. 1d). The relative abundance

increased significantly in urea-amended microcosms from 0.21% at day 0 to 0.35% at day 19. The presence of CH_4 significantly suppressed the proportional increase of AOB-like 16S rRNA gene reads leading to a relative frequency down to 0.15% at day 19 (Fig. 1d). The copies of bacterial *amoA* gene detected by real-time PCR increased from 4.08×10^7copies g^{-1} *d.w.s.* at day 0 to 1.06×10^8copies g^{-1} *d.w.s.* at day 19 in the microcosms incubated with urea (Fig. S3b). The increasement also was observed in the urea+CH_4 treatment, however, the presence of CH_4 resulted in 1.33-fold decrease relative to only urea-amended microcosms 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% at day 0 to 1.42% at day 19 in the urea-amended microcosms, while soil microcosms with Urea+CH_4 displayed a relative abundance as low as 0.42% at day 19 (Fig. 1f). As for AOA, there was no significant change in relative abundances upon urea fertilization during SIP microcosm incubation, although the decreasing trend was observed in the presence of CH_4 (Fig. S4). The similar result was also detected by the real-time PCR of archaeal *amoA* gene (Fig. S3c).

High-throughput fingerprinting of functional guilds against the total communities

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 16S rRNA gene (Fig. S5a) and *pmoA* genes (Fig. S5b). Though type II methanotrophs dominate MOB communities in background soil at 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% at day 0 to 14.4% at 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

366 incubation period, whereas significant increase was observed from 0.12% at day 0 to
367 0.55% at day 19. Urea fertilization further stimulated the relative abundance of type Ia
368 methanotrophs reaching 1.3 and 4 times higher in the CH_4+Urea-amended
369 microcosms than that in the microcosms amended only with CH_4 at day 5 and day 19,
370 respectively. However, urea nitrogen appeared to have no effect on the relative
371 abundance of type II methanotrophs. Similar results were obtained by pyrosequencing
372 analysis of *pmoA* genes (Fig. S5b). Phylogenetic analysis of *pmoA* genes indicated
373 that type Ia *pmoA* sequences were stimulated from 7.4% at day 0 to 69.8% of total
374 methanotrophic communities after incubation with CH_4 for 19 days. Urea addition
375 further stimulated the proportion of type Ia methanotroph *pmoA* gene sequences to a
376 greater extent up to85.0%.

377 AOB communities were exclusively dominated by *Nitrosospira*-like 16S rRNA gene
378 sequences at day-0, and none of 16S rRNA gene sequences could be assigned to
379 *Nitrosomonas* (Fig. S6a). However, the relative abundance of *Nitrosomonas*-like 16S
380 rRNA genes rose to 0.04% and 0.06% of the total microbial communities in
381 urea-amended microcosms after incubation for 5 and 19 days, respectively (Fig. 2b).
382 CH_4 addition resulted in lower abundance of *Nitrosomonas*-like 16S rRNA genes in
383 the total microbial communities at day 5 and day 19, representing 2- and 3-fold
384 decrease relative to that in urea-amended microcosms (Fig. 2b). The relative
385 abundance of *Nitrosospira*-like AOB was stimulated by urea fertilization, but
386 suppressed in the presence of CH_4 (Fig. 2b). These results were further verified by
387 phylogenetic analysis of the *amoA* pyrosequencing reads (Fig. S6b). For instance,
388 none of *amoA* gene sequences was affiliated with *Nitrosomonas* in background soil at
389 day 0, whereas 7% of *amoA* gene sequences were affiliated with *Nitrosomonas* at day
390 19 in the urea-amended microcosms.

391 ***Stable isotope probing of active methanotrophs and ammonia oxidizers***

392 The incorporation of ^{13}C-label into nucleic acid of active microbial communities in
393 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 (Table S4), while about 409,000 sequences were affiliated with bacteria. Pyrosequencing the relative abundance 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 methanotrophic communities in soils 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 (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% at day 5 (Fig. 3c). The prolonged incubation for 19 days increased the proportion of methanol-oxidizing bacteria significantly up to 11.0% of the 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 at 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 at day 19 (Fig. 3f). Similar results were obtained for nitrite-oxidizing bacteria (Fig.3g

and Fig.3h). 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 (Fig. S8).

Phylogenetic analysis of the ^{13}C-labeled 16S rRNA genes demonstrated that active MOB were affiliated with 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* clusters and the *Nitrosomonas communis* lineage on the basis of ^{13}C-16S rRNA gene analysis (Fig. 5a). DNA-SIP demonstrated remarkable community 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 at 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 at 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 at 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 21% to 2% of active AOB

communities upon by CH_4 addition (Fig. 5b).

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; Gärdenäs et al., 2011). 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; Oneill 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 as reported previously (Jia and Conrad 2009, Xia et al 2011).

No apparent changes of ammonia oxidizer communities were observed during a 4-week pre-incubation without ammonium fertilization, significant shift of AOB communities occurred in the ammonium-amended soils (Jia and Conrad 2009). The nitrogenous fertilization of paddy field 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 to 15000 μL L^{-1} were generally detected in paddy soil during rice-growing season (Nouchi et al 1990, Nouchi et al 1994). Therefore, the microcosms were incubated with 100 μg urea-N g^{-1}*d.w.s.* and 10000 μL L^{-1} methane to extrapolate the microbial interactions between methane- and ammonia-oxidation under field conditions. It suggests that microcosms might represent largely what is occurring under *in situ* conditions, although it could not reproduce the physiochemical and biological conditions in field. For instance, it also has been reported that the results of microcosm incubations remained largely consistent with population dynamics of methanotrophic communities in 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 nitrogen source for biomass generation of MOB. The decreased NH_4^+-N concentrations corresponded with 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 (Table S1), suggesting that part of consumed ammonia was not oxidized to nitrate via nitrification or 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

511 and Laanbroek, 2004), the amount of N-assimilated can be calculated using a 70:30
512 ratio of respiration of CH_4 vs assimilation. This calculation shows that of the total
513 amount of urea added 69% was assimilated by MOB, while 20% was nitrified (Table
514 S6). However, the fate of unaccounted remaining nitrogen (11%) need further
515 experiment to investigate.

516 Our results even demonstrate the dependency of the MOB on sufficient N-availability.
517 The relative abundance of both 16S rRNA and *pmoA* genes decreased when
518 incubating with methane only, demonstrating loss of activity and growth potential
519 when N is limiting. A similar result was obtained in microcosms planted with rice
520 (Bodelier et al., 2000a), where MOB even lost their potential for oxidizing methane.
521 However, adding ammonium to these inactive communities led to immediate
522 re-activation of oxidation (Bodelier et al., 2000a), indicating that N-limitation is not
523 only inhibiting growth but also regulated methane consumption enzyme machinery.
524 This inactivation and rapid re-activation of methane oxidation has even been
525 demonstrated on field scale in rice paddies (Dan et al., 2001; Kruger and Frenzel,
526 2003). It has been proposed that nitrogen fixation may deplete reducing equivalents
527 leading to lowering and even cessation of methane oxidation (Bodelier and Laanbroek,
528 2004; Dan et al., 2001). The available inorganic nitrogen source was indeed almost
529 depleted after incubation in CH_4-amended microcosms, decreasing from 11.6 µg/g
530 *d.w.s* at day 0, to 1.37 and 1.19 µg/g *d.w.s* at day 5 and day 19, respectively (Table 1).
531 This suggests that under conditions of high methane and low N availability, there is a
532 niche for methanotrophy where they seem to overwhelmingly outcompete nitrifying
533 communities. Nitrifiers can operate in the absence of competition with MOB, which
534 may be inactivated due to energy-depletion as the result of N_2-fixation. Hence, this
535 points to niche differentiation or avoidance strategies of the nitrifiers.

536 It is obvious that only a subset of the MOB profit substantially from the combined
537 addition of methane and urea-N. Although type II MOB increase in relative
538 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 capable of nitrogen fixing (Murrell and Dalton 1983). This suggested that these *Methylocystis parvus*-like type II may respond under 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 either lower growth rates as compared to type I or dependency of type II MOB 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). Labelled 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 are getting 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 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, implying that *Methylosarcina* thrives under

568 low-methane ('oligotrophic') conditions, in contrast to *Methylobacter* which
569 dominates the zone of high methane flux. However, remarkably, in our experiments
570 *Methylosarcina* clearly is dominant at high methane supply but is replaced partly by
571 *Methylobacter* when urea-N is added. This might be attributed to competition for
572 methane, nitrogen, or even oxygen. A similar result was observed in SIP analyses of
573 lake sediment microcosms using a metagenomic approach (Beck et al., 2013)**.** Hence,
574 we speculate that observations by Reim et al (Reim et al., 2012) may also be
575 explained by weak competitive abilities of *Methylosarcina* instead of being restricted
576 to low methane habitats. A comparison of 16S rRNA gene and *pmoA* gene sequences
577 revealed that *Methylobacter* was detected in a higher proportion in the MOB-16S
578 rRNA gene phylogenetic tree than in the *pmoA* gene phylogenetic tree. The
579 incongruence might result from the bias associated with the different coverage of
580 *pmoA* and 16S rRNA gene primers as reported previously (Costello and Lidstrom
581 1999).

582 The significant increase of obligate methanol-oxidizer *Methylophilaceae* was
583 observed in the microcosms incubated with CH_4 plus urea. The occurrence 16S rRNA
584 of these sequences in the 'heavy' DNA fractions indicates that these *Methylophilaceae*
585 assimilated methane derived carbon. Cross feeding of methylotrophs by
586 methanotrophs releasing methanol has been demonstrated before (Antony et al., 2010;
587 Beck et al., 2013; He et al., 2012; Noll et al., 2008). The direct mechanism for this
588 cross feeding and what compound actually is exchanged have not been elucidated yet.
589 We can add another component to this body of unsolved mechanisms which is the
590 strong stimulation of methylotrophs upon urea fertilization, thereby linking the
591 nitrogen and the carbon cycle. It is very likely that the enhanced methane
592 consumption and growth of methanotrophs leads to higher availability of methanol.
593 However, we can not exclude that urea has stimulatory effect on the methylotrophs
594 directly. We also speculate that the active removal of methanol by the methylotrophs
595 is beneficial to methanotrophs given the toxic nature of the compound. However, this
596 would be subject of further study. Interesting is this link between nitrogen and

cross-feeding of methanotrophic metabolites by other microorganism, possibly creating novel niches e.g. more methane-driven carbon substrate, 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, it remains elusive about the toxic effect of intermediates substance during methane oxidation on nitrifying communities. 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 population (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 the 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 the reduced ammonia supply may select for the cluster 4 populations (Kowalchuk and Stephen, 2001). In the presence of methane, the growth of methanotrophs was significantly stimulated and methanotrophic N assimilation could have 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 at day zero. 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 significantly than *Nitrosospira*. This might be explained by the fact that hat *Nitrosomonas* 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 16S rRNA gene (Fig.4a) and *pmoA* gene (Fig.4b) were phylogenetically distinctly different with these known ureolytic methanotrophs. However, the ^{13}C-labeled AOB showed high sequence similarity with 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 batch culture (Pommerening-Roser and Koops 2005). This suggests that

ammonia oxidizers may have to compete for the ammonia released into 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 ureolysis 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 possibly might provide mechanistic mechanisms 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 environment.

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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(μg/g *d.w.s*) [c]	NO_3^--N(μg/g *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.

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.

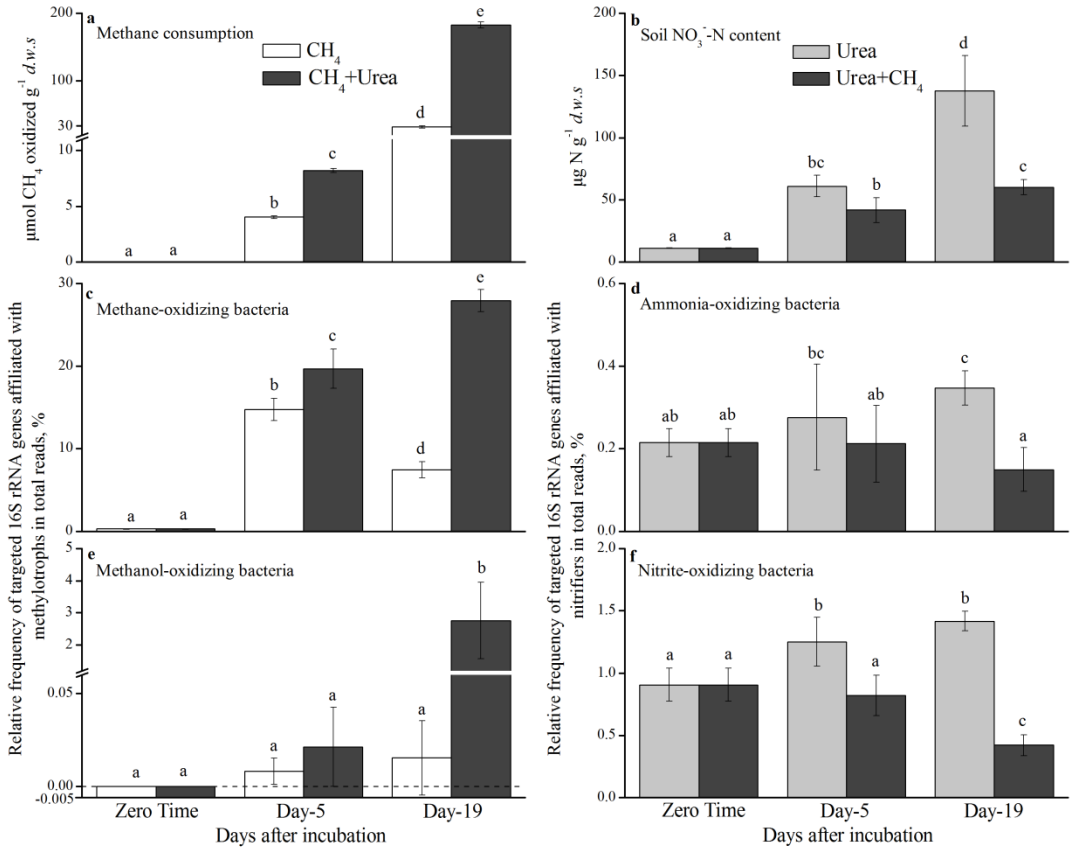

Figure 2. Change in relative abundance of methane-oxidizing bacteria (a) and ammonia-oxidizing bacteria (b) in soil microcosms incubated for 5 and 19 days. The relative abundance of type Ia, type II methanotrophs, *Nitrosospira* and *Nitrosomonas* are expressed as the targeted 16S rRNA gene to total 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.

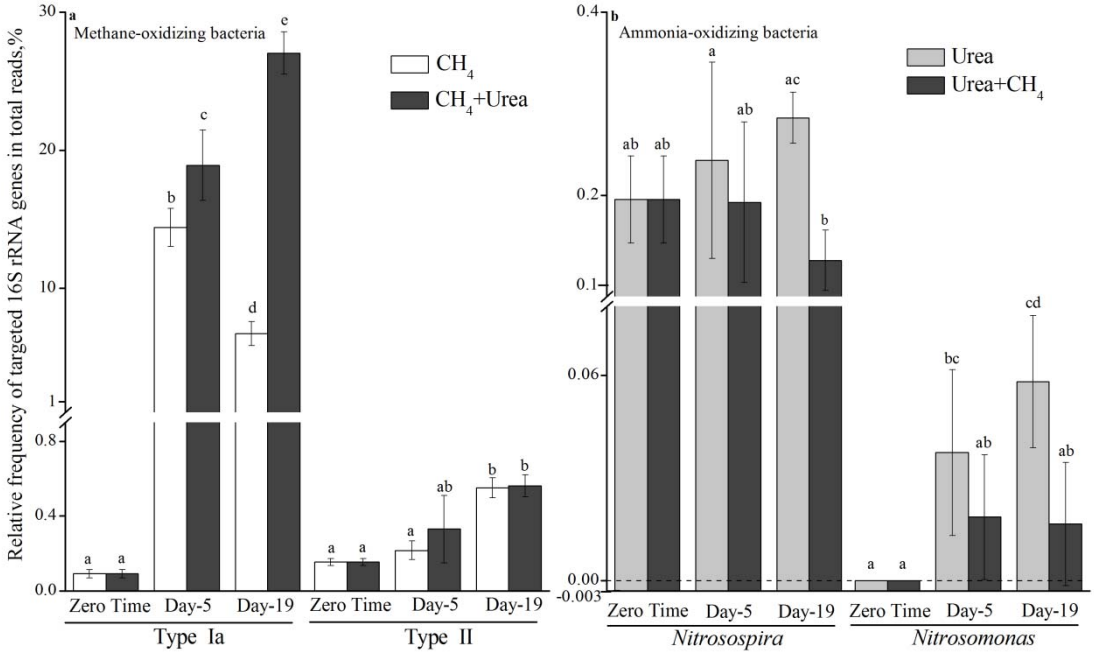

Figure 3. Relative frequency of the 16S rRNA gene sequences affiliated with methane-oxidizing bacteria (a, b), methanol-oxidizing bacteria (c, d), ammonia-oxidizing bacteria (e, f) and nitrite-oxidizing bacteria (g, h) across the buoyant density gradient of DNA fractions from the ^{13}C-labeled and ^{12}C-control 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.

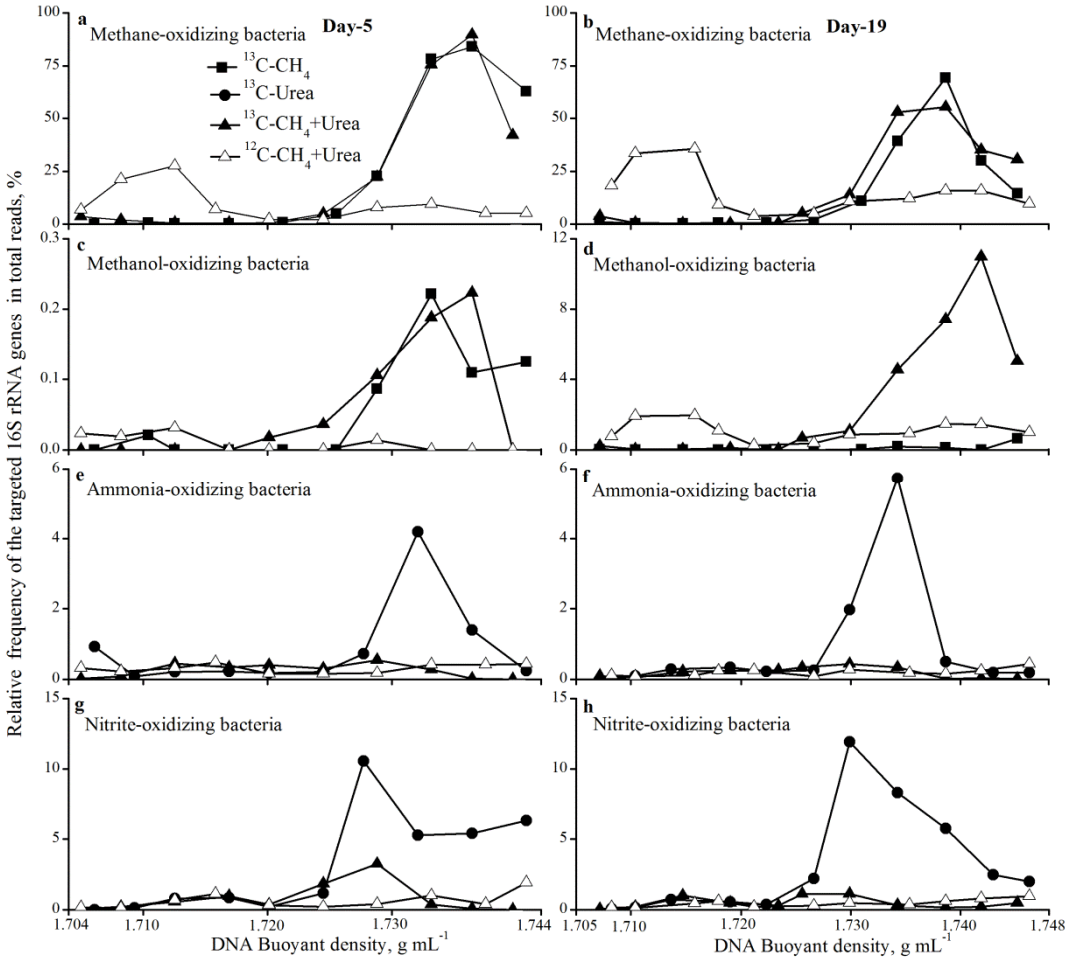

Figure 4. Phylogenetic tree of the ^{13}C-labeled 16S rRNA genes affiliated with methane-oxidizing bacteria (a) and *pmoA* genes (b) from the labeled microcosm after incubation for 19 days. The designations of CH_4 represent soil microcosms incubated with ^{13}C-CH_4, and the designation of CH_4+Urea 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 mothur software package for tree construction. The scale bar represents nucleotide acid substitution percentage.

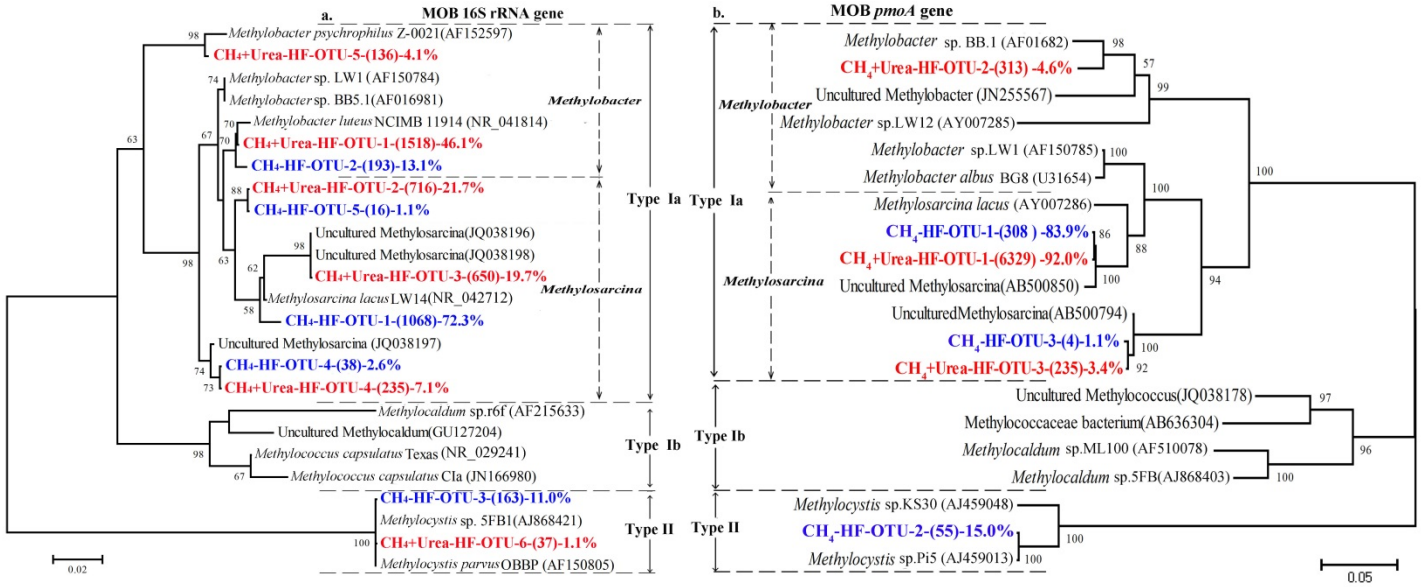

Figure 5. Phylogenetic tree of the ^{13}C-labeled 16S rRNA genes affiliated with ammonia-oxidizing bacteria (a) and bacteria *amoA* genes (b) from the labeled microcosm after incubation for 19 days. The designations of Urea represent soil microcosms incubated with ^{13}C-Urea plus ^{13}C-CO_2, and the 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 mothur software package for tree construction. The scale bar represents nucleotide acid substitution percentage.

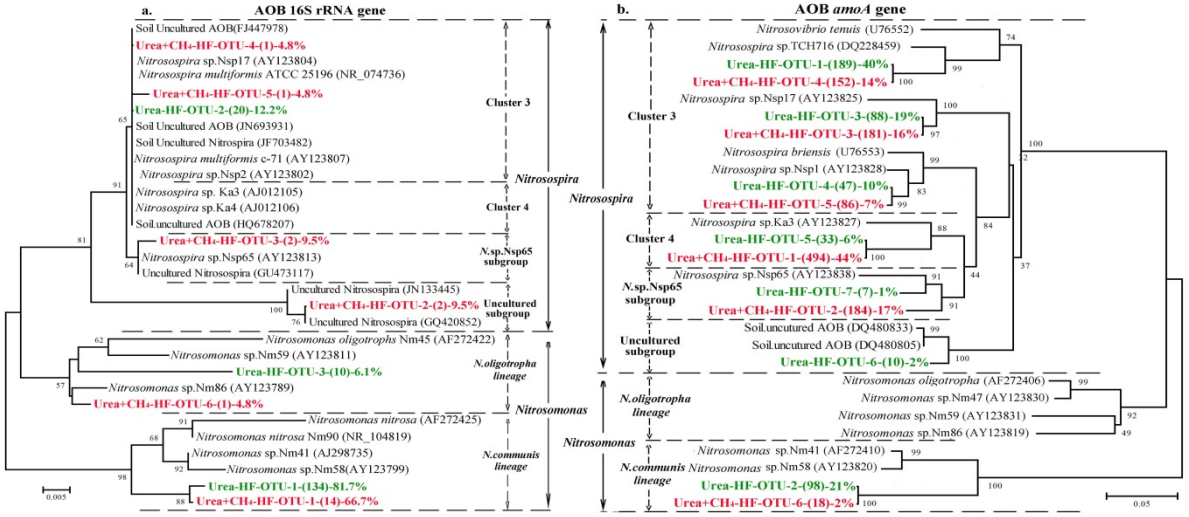

Figure 6. Percent changes of bacterial phylotypes affiliated with methane-oxidizing bacteria (a) and ammonia-oxidizing bacteria (b) in the ^{13}C-DNA fractions from the labeled microcosm after incubation for 5 and 19 days. The designation of CH_4+Urea represents soil microcosms incubated with ^{13}C-CH_4 and ^{13}C-Urea plus ^{13}C-CO_2, and the designation 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.