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Full Length Article

Effects of Land Use Conversion from upland to Paddy Field on Ammonia-oxidizing Archaeal and Ammonia-oxidizing Bacterial Communities in Jianghan Plain, Hubei Province, China

Sumaira Hafeez[1,2], Jin Tao[1,2*], Liu Zhangyong[1,2], Zhu Bo[1,2], Nie Jiangwen[1,2] and Zhu Jie[1,2]
[1]*Hubei Collaborative Innovation Center for Grain Industry,Wuhan, 430070, P.R. China*
[2]*Engnieering Research of Ecology and Agricultural Uses of Wetlands (China Ministry of Education), Yangtze University, Jingzhou, 434025,P.R. China*
[*]For correspondence: jintao@yangtzeu.edu.cn; Cell No: +8618986661197

Abstract

The current study investigated the relationships between genes of two key microorganisms (Arch-*amo*A and Bac-*amo*A,) and soil physicochemical properties for the upland conversion to paddy field in Jianghan plains of China. Randomized complete block design was used for three treatments: Upland, paddy field and upland to paddy field. Our results revealed that ammonia oxidizing archaea (AOA) and soil properties such as ammonium nitrate, pH, and nitrate contents showed a positive correlation with upland and upland to paddy field treatments. While on the other hand, total available nitrogen was negatively correlated with paddy field treatment. Redundancy analysis of ammonia oxidizing bacteria (AOB) and soil properties like pH, ammonium nitrate, and nitrate contents were positively correlated with the upland and upland to paddy field treatments whereas the paddy field treatment was negatively correlated with the total available nitrogen. Total number of Operational taxonomic unit numbers shared by three treatments in the archaeal community was 41, whereas 134 for bacterial community. However, it is concluded that land conversion from upland to paddy field significantly altered the structure of bacterial and archaeal ammonia oxidizing community simultaneously. © 2019 Friends Science Publishers

Keywords: Ammonia oxidizing archaea; Ammonia oxidizing bacteria; Land use change; Soil microbial communities

Introduction

Land use change is one of major driving forces of regional system amendment and affects the environmental balance greatly such as in Jianghan Plain of China. In this region, water logging has forced the farmers to cultivate uplands and such a shift in land use patterns also creates a need of monitoring soil health. The integrative measure of soil health cannot be obtained only by physical/chemical perspective that's why microorganisms are considered as key parameter of soil health. Despite the fact that soil microbial communities perform different functions in the ecosystem, the structure and availability of microorganisms are sensitive to such land use changes (Delgado-Baquerizo *et al*., 2016). Therefore, changes in soil microbial communities are key indicator of soil degradation (Nielsen *et al*., 2002).

The soil microbial communities are affected by agricultural management practices, which have an impact on ecological services such as nutrient cycling and crop protection (Pimental *et al*., 2005). Therefore, it is important to recognize the functional diversity, composition and dynamics of soil microbial communities. Moreover, to stabilize the soil structure and maintain soil ecosystem services contributed by the stable microbial community, it is important to understand ecological consequences of various agricultural practices (Bisset *et al*., 2013). Carbon and nitrogen present in the soil are correlated with the microbial diversity and community composition (Trivedi *et al*., 2016).

Ammonia-oxidizing archaea (AOA) and Ammonia oxidizing bacteria (AOB) play an important role in the biogeochemical cycle of nitrogen. AOA or AOB converts ammonia to nitrite, nitrate by using the nitrite oxidizers. The function of AOA and AOB depends on ammonia and oxygen. They have different metabolic pathways and physiology but are functionally correlated. Tourna *et al*. (2011) investigated that AOA and AOB get energy from ammonia oxidation to support their growth. Moreover, Kowalchuk and Stephen (2001) investigated that ammonia oxidation is the first and rate-limiting step of nitrification that plays a significant role in the global nitrogen cycle. It was believed for many years that only bacteria possessing *amo*A genes are involved in microbial ammonia oxidation process, but recent discoveries have expanded the known ammonia oxidizers from the domain bacteria to archaea (Treusch *et al*., 2005).

Gene quantification is still considered a novel and frequently improving technique. Agricultural soils show a high content of nitrifiers (*amo*A) during the wet season, but

forest soil shows high content of denitrifiers related to an increased nitrous oxide emission (Rocca *et al*., 2014). Peterson *et al*. (2012) investigated the indicators during nitrification and denitrification by quantification of *amo*A, *nir*K, *nir*S and *nos*Z genes in Alaskan soils. However, little attention has been paid to the functions of particular soil bacterial communities.

Arable land use change like upland conversion to a paddy field is a common agricultural practice in low altitude regions in Jianghan Plain in the middle region of the Yangtze River. However, few studies have focused on the effects of land use change on soil microbial communities. So, the current study aimed at measuring the effects of upland conversion to paddy field on soil microbial communities from the field and to explore further mechanisms by revealing the relationships between soil physicochemical parameters and the quantity and structure of two most related soil microorganism genes (A-*amo*A, B-*amo*A).

Material and Methods

Experimental Site

The experimental site is located near the Yangtze University, Jingzhou P.R. China in the middle reach of the Yangtze River. The climate of this region is subtropical, humid with distinctive four seasons, clearly demarcated cloudy and sunny weather in spring, humid and hot weather in summer, fine autumns, and dry cold winter. It has plenty of sunshine and a frost-free period of 220–300 days annually. Soil characteristics and climatic conditions are given in Table 1A and B.

Experimental Design and Treatments

Randomized complete block design with three replications was used for three treatments: upland, paddy field and upland to paddy field. Total 9 experimental units were established with plot size of about 5×10 m² each. All plots were separated from each other by ridges (40 cm wide on the top, 60 cm wide on the bottom and 40 cm high) to prevent water and nutritional loss through runoff. The study was conducted trice in 2015, 2016 and 2017. Every time rice seedlings were planted in paddy field and upland to paddy field treatments during July and harvested in November. However, late maize was planted during the end of June and harvested in the September; watermelon was cultivated in the December and harvested during April in upland treatment. For rest of the time, soil was remained fallow. Field management, with the help of fertilizer, water, and pesticides, was performed as per the local farming practices.

Determination of Soil Characteristics

Soil sampling: Soil samples were collected in every August from all experimental units and average of three years was represented as final result. One soil sample per replication/plot was collected from plough layer about 10 cm deep of each experimental site. At the same time samples were collected at 15 cm depth and stored at -20ºC for determination of soil microbial activity.

Table 1A: Site Characteristics and Soil Properties

	Soil Type	Calcareous Alluvial soil
1	Soil Texture	Loam
2	Ph	7.5

Table 1B: Climate characteristics of site

1	Average sunshine	1744 h
2	Average Annual Precipitation	1090.3 mm
3	Average Annual Temperature	16.6°C

Physicochemical Analysis of Soil

Soil pH was measured with soil to water at a ratio of 1:25 by using pH meter. Soil organic matter was measured by $K_2Cr_2O_7$ oxidation reduction colorimetric method (Schulte, 1995). Ammonium (NH_4^+-N) concentration from soil samples extracted by using 100 mL of 2 M KCL solutions at a ratio of about 1:20 (Kempers and Zweers, 1986). Nitrate (NO_3^--N) concentration from soil samples was extracted by distillation as described by Bremner and Shaw (1955). Total Nitrogen (TN) and Carbon (TC) were measured by Auto elemental analyzer (Vario EL III, Elementer, Germany) (Batjes, 1996). Available nitrogen (AN) was calculated by using Alkali hydrolysis diffusion methods.

Determination of Soil Microbial Activities

Ammonia oxidizing archaea and ammonia oxidizing bacteria were examined in soil samples while focused on Quantification of functional genes and structure (includes diversity, community composition of Genes, operational Taxonomic Units, and changes in community composition). In order to determine all above indexes, the following procedure was adopted.

DNA Extraction

DNA from the soil samples was extracted by using the MoBio-Power soil DNA extraction Kit (MoBio Laboratories, Carlsbad, CA, USA) according to recommended protocol. NanoDrop ND-2000c UV-Vis (NanoDrop Technologies, Wilmington, USA) spectrophotometer was used to examine the quality and quantity of extracted DNA. Quantity PCR (qPCR) was used to examine the abundance of bacterial 16S rRNA gene on an iCycler iQ5 thermocycler (BioRad Laboratories, Hercules, CA, USA).

PCR Amplification and Gene Sequencing

The PCR amplification and gene sequencing was performed according to Khaksar *et al*. (2016) with a slight modifications described as: The 25 μL containing 12.5 μL of Premix Ex Taq (Takara Biotechnology, Dalian, China) 0.25 μL of each primer (10 μM) 0.25 μL of probe (10 μM) and 1 μL of DNA template (1–10 ng) were used. Thermo-cycling conditions were as follows: first Denaturation (3 min) at 94°C, after this Six touchdown cycles for 45 s at 94°C, 60 s 65°C to 58°C, 70 s at 72°C followed by 22 cycles of 45 s at 94°C, 60 s at 58°C, and 60 s at 72°C and finally Elongation at 72°C for 10 min. Before sequencing, the PCR products were fluorometrically quantified by using Qubit dsDNA HS assay kit (Invitrogen, Carlsbad, CA, USA). QIIME 1.7.0 was used to process raw sequences. Gene sequences were trimmed and clustered into Operational taxonomic units (OTUs). Each OTU's sequence was adjusted against Green genes core set using PyNAST. RDP classifier was used for taxonomic assignment. The primer sequences archaeal and bacterial *amo*A genes are mentioned in Table 2.

Statistical Analysis

Statistical analysis was performed by using SPSS version 13.0 for windows (SPSS Inc., Chicago, IL, USA). Statistical significance difference among three treatments was analyzed by using one way analysis of variance (ANOVA) and Least Significant Difference (LSD).

Results

Variation in Soil Characteristics

Variations in soil characteristics are displayed in Table 3. Soil pH varies between 7.47 and 8.31 in all treatments. Available nitrogen ranged from 87 to 136 mg/kg. The NO_3^--N concentration showed a maximum value of 4.42 mg/kg in U while minimum value was observed in UTP and P fields (0.5 and 0.31 mg/kg, respectively). NH_4^+-N content was greater in UTP and P field treatments (13.69 and 13.61 mg/kg respectively) on the other hand, U treatment showed a lower content of 11.65 mg/kg. Total Nitrogen in the U and UTP field showed similar value of 1.27 g/kg while P field showed a maximum value of 1.86 g/kg. Total carbon concentrations were higher in P field treatment (18.16 g/kg) whereas U showed a value of 12.9 g/kg and the minimum value were recorded in UTP (11.70 g/kg). Organic matter accumulation rate in the P field was higher 31.31 g/kg among all. Conversely UTP field showed maximum value of carbon to nitrogen ratio 10:19.

AOA and AOB Richness, Diversity and Abundance

The Archaeal and bacterial richness and diversity of the various treatments are displayed in Table 4. The richness indices of Archaeal community sobs, Chao and Ace showed higher values in U while the P fields have the lowest number without any significant difference. The highest number and diversity was detected in UTP and P fields, those exhibited higher Shannon and Simpson diversity indices than U treatment. For the bacterial community, the highest value of sobs, simpson and Chao indices were recorded in U while P field showed lowest richness indices without any significant difference. The Shannon indices showed the highest values in the P field with a significant difference. All treatments exhibited high Good's query coverage (98%) in the archaeal community and 100% coverage in the bacterial community and no significant difference was observed. AOA and AOB abundance at three treatments level is displayed in Fig. 1A and B respectively. The AOA abundance percentage was higher in UTP > 3.6E + 06, followed by U (> 1.2E + 06) and P. Similarly, in the AOB highest gene, abundance percentage was observed in UTP while P did not show any abundance percentage (Fig. 1B).

Table 2: Sequence and Product size of Archaeal and Bacterial *amo*A genes

	Gene	Sequence (5-3)	Product Size
1	Arch-*amo*A	ATGGTCTGGCTWAGACG	594
		GCCATCCATCTGTATGTCCA	
2.	Bac-*amo*A	GGGTTTCTACTGGTGGT	
		CCCCTCKGSAAAGCCCTTCTTC	

Archaeal and Bacterial Community Composition

The archaeal community composition at species level is shown in Fig. 2A. The sequences were found to be affiliated with seven species of uncultured archaeon and unclassified archaea. The U treatment was dominated by unclassified norank archaea (75%), followed by unclassified ammonia oxidizing archaeon (15%), uncultured ammonia oxidizing crenarchaeota (5%), unclassified environmental samples Thaumarchaeota (3%), and uncultured crenarchaeota (2%). While in the case of UTP, 70% unclassified norank archaea, 15% uncultured ammonia oxidizing archaeon, 10% uncultured ammonia oxidizing crenarchaeota, 3% unclassified environmental samples Thaumarchaeota and 2% uncultured crenarchaeota were recorded. The P comprised of 30% unclassified norank archaea, 55% unclassified norank environmental samples Thaumarchaeota, 5% uncultured ammonia oxidizing crenarchaeota, 5% unclassified environmental samples crenarchaeota, 3% unclassified crenarchaeota, 1% uncultured archaeon, and 1% others.

The bacterial community composition of three treatments on species level is provided in Fig. 2B. U treatment contained 70% unclassified norank archaea, 20% uncultured ammonia oxidizing archaeon, 5% uncultured ammonia oxidizing crenarchaeote, 3% unclassified norank environmental samples Thaumarchaeota, and 2%

Table 3: Soil Characteristics at Three treatments

Treatments	Soil pH	AN (mg/kg)	NO_3-N (mg/kg)	NH_4-N (mg/kg)	TN (g/kg)	TC (g/kg)	OM (g/kg)	C/N
U	8.31±0.33^a	87±2.64^c	4.42±0.22^a	11.65±3.44^a	1.27±0.1^b	11.79±0.04^c	20.32±0.06^c	9.34±0.71^a
UTP	8.03±0.08^a	102.41±6.62^b	0.5±0.08^b	13.69±1.41^a	1.27±0.05^b	12.9±0.16^b	22.25±0.28^b	10.19±0.29^a
P	7.47±0.07^b	136.17±8.19^a	0.31±0.03^b	13.61±3.41^a	1.86±0.01^a	18.16±0.18^a	31.31±0.31^a	9.78±0.12^a

U-Upland, UTP-Upland to Paddy, P-Paddy, NH4-N- Ammonium Nitrogen, NO3-N-Nitrate Nitrogen, AN-Available Nitrogen, TN-Total Nitrogen, TC-Total Carbon, OM- organic matter, C/N-Carbon to nitrogen ratio

Table 4: Comparison of AOA and AOB Richness and Diversity at three treatments Level

	Treatment	Sobs	Shannon	Simpson	Ace	Chao	Coverage
	U	59.33 ±5.03^a	1.95 ± 0.2^a	0.22 ± 0.05^b	64.38 ± 7.05^a	61.96 ± 6.27^a	0.9998 ± 0.0001^a
AOA	UTP	50.67 ± 5.03^b	2.15 ± 0.14^a	0.16 ± 0.02^b	59 ± 7.01^a	56.4 ± 6.16^a	0.9997 ± 0.0001^a
	P	37.67 ± 1.53^c	1.54 ± 0.12^b	0.36 ± 0.02^a	47.04 ± 15.51^a	42.17 ± 6.83^b	0.9999 ± 0.0001^a
	U	28.67 ± 2.89^a	1.09 ± 0.06^a	0.47 ± 0.02^a	29.06 ± 3.57^a	29 ± 3.46^a	1 ± 0^a
AOB	UTP	26 ± 3.61^a	1.29 ± 0.14^a	0.39 ± 0.04^b	31.14 ± 7.32^a	28.5 ± 4.77^a	1 ± 0^a
	P	25 ± 6.08^a	1.32 ± 0.07^a	0.32 ± 0.02^c	25.23 ± 5.92^a	25 ± 6.08^a	1 ± 0^a

AOA-Ammonia oxidizing Archaea, AOB-Ammonia oxidizing bacteria, U-Upland
UTP-Upland to paddy, P-Paddy

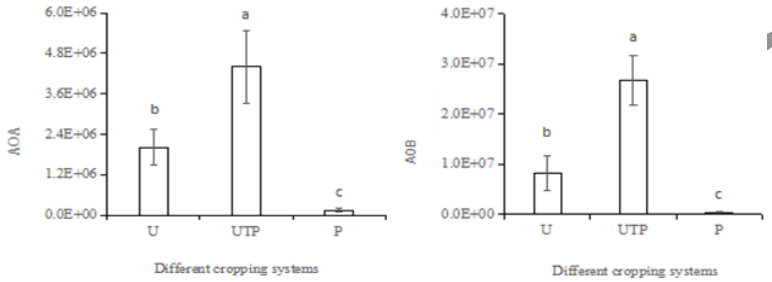

Fig. 1A: AOA Abundance at three Treatments level; B: AOB Abundance at three Treatments level

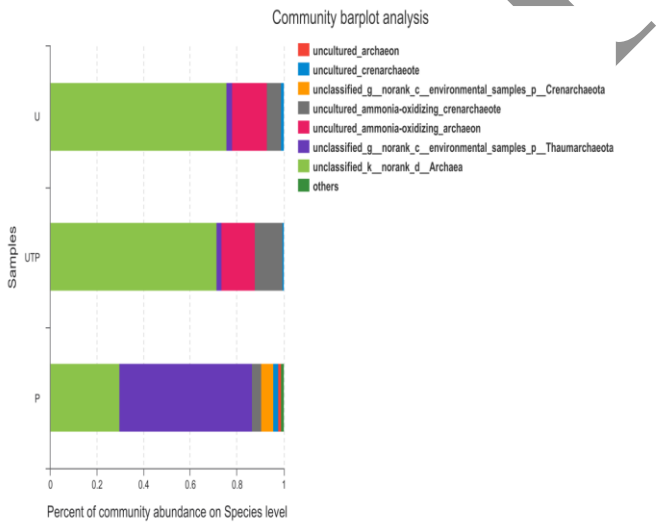

Fig. 2A: Archaeal Community Composition at species level

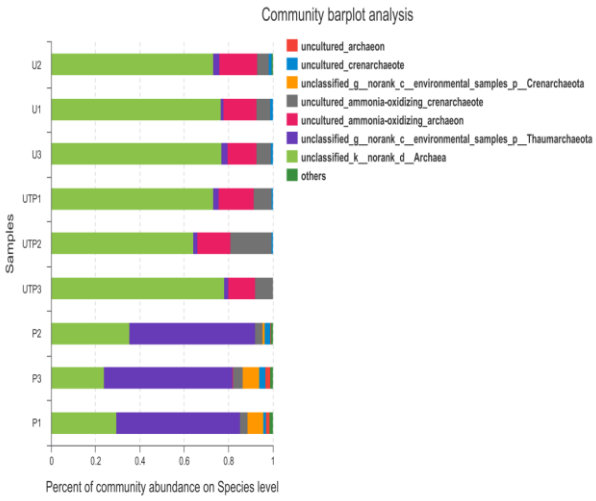

Fig. 2B: Bacterial Community Composition at species level

uncultured crenarchaeote. The most abundant specie in the UTP was unclassified norank archaea about consisted of 75%. While P was composed of unclassified norank archaea 30%, unclassified norank environmental samples Thaumarchaeota (60%), unclassified norank environmental samples crenarchaeota (5%), uncultured crenarchaeota (2%), uncultured archeaon (1%), uncultured crenarchaeota (1%), and 1% others.

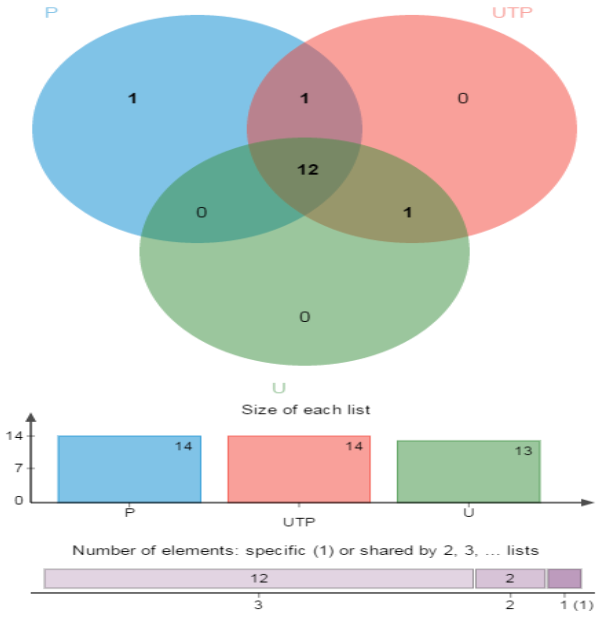

Fig. 3A: Venn diagram of Ammonia Oxidizing Archaea

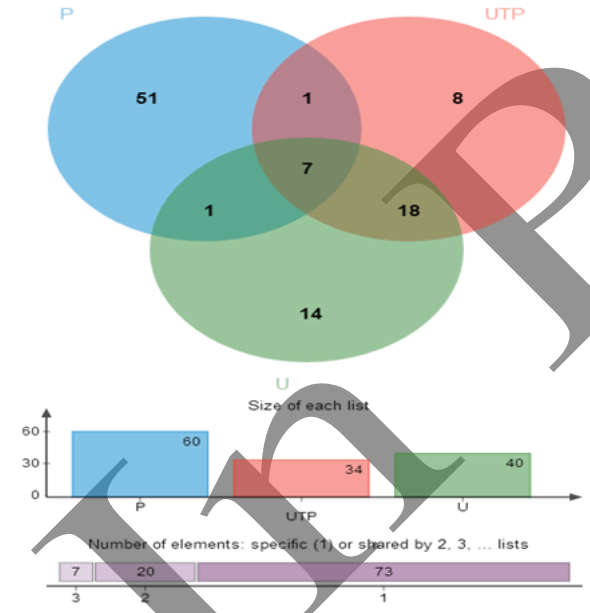

Fig. 3B: Venn diagram of Ammonia Oxidizing Bacteria

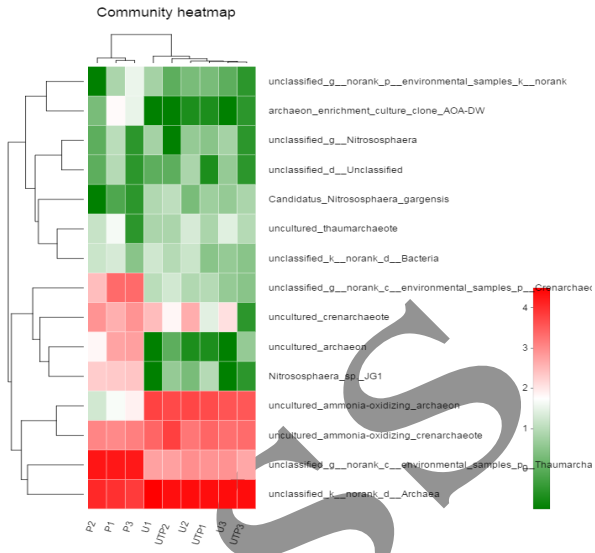

Fig. 4A: Community Heatmap of Ammonia Oxidizing Archaea

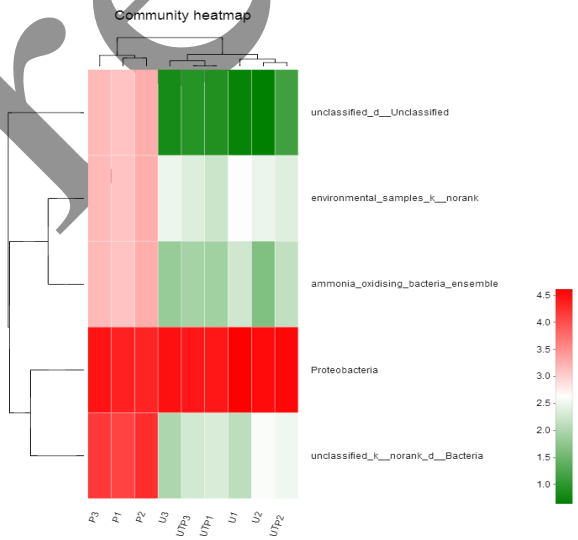

Fig. 4B: Community Heatmap of Ammonia Oxidizing Bacteria

Comparison of OTUs in Archaeal and Bacterial Community

The Venn diagram depicts Operational taxonomic unit numbers (OTUs) in the Archaeal and Bacterial community at three treatment levels (Fig. 3A and B). The total number of OTUs shared by three treatments in archaeal community was 41, whereas bacterial community showed 134 OTUs. In the Archaeal community, P shared 14, UTP shared 14 and U shared 13 OTUs (Fig. 3A). In bacterial community, P shared 60, UTP shared 34, and U shared 40 OTUs numbers (Fig. 3B).

Heat Map

Community heat map of AOA and AOB of three treatments is shown in Fig. 4A and B. The value ranges from 1 to 4.5. As the value moves from 1 to 4.5 the intensity of presence increased. The heat map for AOB has proteobacteria as most dominant community member, represented by the highest wave length among the three treatments.

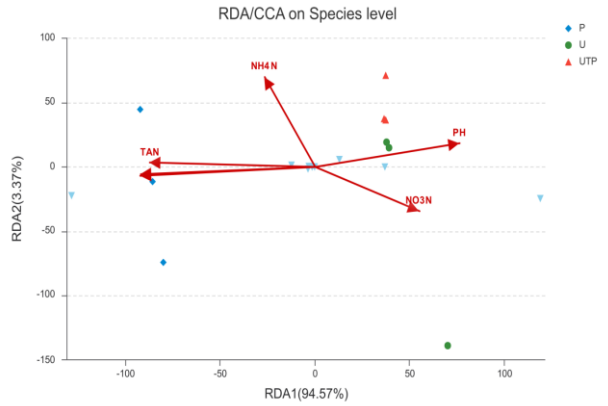

Fig. 5A: Redundancy Analysis of Ammonia oxidizing Archaea with soil properties

P-Paddy, U-Upland, UTP-Upland to paddy, TAN-Total Available Nitrogen, NH4-N- Ammonium Nitrogen, NO3-N-Nitrate Nitrogen

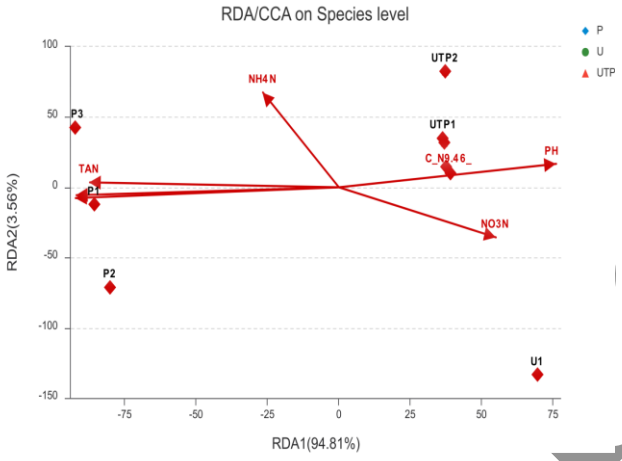

Fig. 5B: Redundancy Analysis of Ammonia Oxidizing Bacteria with soil properties

P-Paddy, U-Upland, UTP-Upland to paddy, TAN-Total Available Nitrogen, NH4-N- Ammonium Nitrogen, NO3-N-Nitrate Nitrogen

Correlation between the Composition of Archaeal and Bacterial Communities and Soil Properties

The redundancy analysis (RDA) of AOA on soil properties showed that first two variables were responsible for 97.94% of the total variation (Fig. 5A). The first component (RDA1) separated U and UTP from the P and accounted for 94.57% variation. The RDA2, which was separated P from other treatments, caused 3.37% variation in data set. The soil properties such as NH_4^+-N, pH and NO_3^--N contents showed a positive correlation with U and UTP. While on the other hand, TN was negatively correlated with paddy field treatment.

The redundancy analysis of AOB on species level is shown in Fig. 5B. The RDA1, 2 accounted for 98.37% of the total variation. The first component RDA1 was comprised of U and UTP while responsible for 94.81% of variation. The RDA2 consisted of only P and accounted for 3.56% variation. It is clear from the above-mentioned interpretations that maximum variation was caused by U and UTP.

Discussion

The diversity of the microbial population is an important indicator of the soil ecological functions including its quality and fertility along with its interaction with plants or animals. The physicochemical characterization of the soil (Table 3) varied significantly between three different treatments, implying that these parameters could be important governing factors of microbial metabolic activity. In this study, the diversity of microbial species in soil was affected by the physicochemical properties of soil that varied between the three different types of land use. The pH decreased from upland to paddy field, which was consistent with results reported by Cao and co-workers, (Cao *et al*., 2017) and similar results were also reported by Cai *et al*. (2016) while conducting a study on uplands. Moreover, different patterns of land also affected the metabolic activities of microbial community inhabited in that soil showed. Conversion of P to U, in the present study significantly altered soil pH from 7.47 to 8.31, indicating that soil pH might play a major role in shaping the community structure of soil microbes. The pH of soil determines the ammonia availability, which influences the structures of ammonia oxidizers community in the soil (Nicol *et al*., 2008; Lu and Jia, 2013).

Besides that, it has been reported that the community structures of soil microorganisms might be affected by the type of plant species cultivated in that land (Chu *et al*., 2009; Mao *et al*., 2011). In this study, rice plants were cultivated in P and UTP. While, in U, water melon and late maize was planted. It appeared to be quite likely that the diversification of the microbial community might be associated with changes in soil properties caused by different crop cultivation systems. Nevertheless, further investigations are required to determine the exact mechanism through which entering of root exudates in soils can affect the structure of the microbial community in the soil. Furthermore, limitation of organic matter induced by root uptake might affect the growth of microorganisms in soil due to greater affinity for nutrient uptake. Vegetation composition and plant diversity clearly varied between the different land use types, which can significantly affect the composition and quantity of the litter, as reported by Liu *et al*. (2014).

In the present study, our results revealed that the Available Nitrogen and Total Carbon contents are showing positive increasing trend responding to different land use, with the highest value for P and the lowest value for U. The total carbon content available in the soil greatly depends on input from above-ground external sources, which may indirectly influence the metabolic characteristics of soil bacteria. Also, a significantly positive correlation was

noticed between soil NO_3^--N and organic matter content in another study. One of the possible explanation of this relation is that the added nitrogen mostly had neutral or negative effects on the litter and decomposition of soil organic matter (Keeler *et al*., 2009), which may have led to organic matter accumulation in soil. The addition of organic matter in soil through organic manure-inorganic fertilizers treatment has improved the microhabitats for aerobes, thus, favors the process of nitrification. Furthermore, the data of soil chemical properties and phyla indicated that the composition of microbial communities and organic matter content are related. Similar results are observed by Helgason *et al*. (2010), Lou and Cui (2011), Guo *et al*., 2015; Zhang *et al*., 2015.

The diversity and richness indices of AOA and AOB vary at three treatments levels (Table 4). It was observed that maximum values of diversity richness and coverage percentage were recorded in AOA as compared to AOB. Our results are in conformation with the studies of Fujii *et al*. (2004), Jifeng *et al.* (2017).

When an aerobic upland soil is converted into a flooded paddy field, it may represent specialized niche with oxygen as a limitation on the divergence of AOA and AOB community into the soil. Long-term flooding of field lead to significant stimulation of AOA community growth in paddy soils, leading to the predominance of the *Thaumarcheota* (55%) that was detected in U soils in low abundance (3%) as cleared from Fig. 2A and B. Additionally, long-term application of nitrogen fertilizers further increased the abundance of both AOA and AOB in UTP and U soils. These results indicate that long-term ammonia exposure and flooding act as two of the most dominant selective forces regulating the divergence of microbial communities in soil.

In the current study, a significant shift of ammonia oxidizing microbial community, archaea and bacteria, has been reported with the conversion of U soil to the P. All field including U, P and UTP were originated from parental material of the same origin. Since flooding and rice cultivation in a field leads to oxygen depletion, its supply can serve as one of the fundamental selective agents to shape the structure of obligate aerobic community (AOA and AOB) in heterogeneous soil medium. However, it seems that the in paddy soil flooded condition favored the development of AOA communities in comparison to upland soils. The results of the current study are consistent with previous findings about the dynamics of ammonia oxidizer in upland (He *et al*., 2007) and paddy soil (Chen *et al*., 2011). The shift in diversification of AOA community might be related to fluctuations in oxygen availability and other ecological factors, consequent of upland conversion to flooded paddy soil (Chen *et al*., 2011). The relative abundance of AOA communities was indeed commonly observed in zones of marine environments with minimum oxygen (Bouskill *et al*., 2012) as well as water of oligotrophic lakes (Auguet *et al*., 2012). By comparing the OTUs of AOA and AOB the maximum OTUs were observed in AOB (Fig. 4A and B). Heat map showed that proteobacteria had highest community composition of 4.5 wavelengths among three treatments (Fig. 4B). The redundancy analysis of ammonia oxidizing communities and soil physicochemical properties represented in this study exhibited significant correlations, thus further supporting the hypothesis that physicochemical properties of soil affect the activity and composition of the microbial functional community (Fig. 5A and B).

The results of numerous batch culture studies suggested that AOA has higher affinity for dissolved oxygen concentration than AOB (Wells *et al*., 2009; Kim *et al*., 2012; Song and Lin, 2014), indicating that AOA could easily be adapted to environments with low oxygen. However, it is difficult to conclusively relate the community shift of AOA to a single environmental factor in association to different land-use, because of the enormous soil heterogeneity in term of variations in oxygen, pH, temperature, and ammonia under field conditions as described previously (Pett-Ridge *et al*., 2013). On the other hand, it seems that AOB communities could readily be reactivated subsequent to severe oxygen starvation, but the relationship of oxygen content with AOB and AOA in natural habitats still needed to be examined as a future prospect of this study (Geets *et al*., 2006).

Conclusion

The results of this study demonstrated that the practice of three different land use pattern, U, P and UTP on top soils of field significantly altered the structure of bacterial and archaea ammonia oxidizing communities simultaneously in Jianghan plain, P.R. China. Ammonia oxidizing archaea and ammonia oxidizing bacteria both participated in the nitrification process during the land use conversion. However, both microbes act differently among the three land use types. Findings of our study present strong evidence for the ecotype divergence possibility of ammonia oxidizers in heterogeneous complex soil systems and furthermore reveal the community diversification and succession of ecologically significant microbial guilds in natural habitats. Moreover, the insights on the structures and functions of soil microbial communities in different land use patterns are also provided complemented with recent analytical technologies such as metagenomics. However, there is a need for further investigation of the upland conversion to paddy field effects on the relationship of microorganisms' genes (Arch- *amo*A, Bac-*amo*A) and soil properties.

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