PSM Microbiology

ISSN(Online): 2518-3834

Review Article | 2019 | Volume 4 | Issue 2 | 20-36

Article Info

Open Access

Citation: Ginawi, A., Yan, Y., 2019. The Function of Ammonia Oxidizers Community in the Environment. PSM Microbiol., 4(2): 20-36.

Received: April 16, 2019

Accepted: June 17, 2019

Online first: June 30, 2019

Published: June 30, 2019

Corresponding Author:
Yunjun Yan

Email:
yanyunjun@hust.edu.cn

Scan QR code to see this publication on your mobile device.

The Function of Ammonia Oxidizers Community in the Environment

Amjed Ginawi[1,2], Yunjun Yan[1*]

[1]Key Lab of Molecular Biophysics of Ministry of Education, College of Life Science and Technology, Huazhong University of Science and Technology, 1037 Luoyu Road, Wuhan, 430074, China.
[2]Faculty of Marine Science and Fisheries, Red Sea University, Port Sudan, Sudan.

Abstract:
This review summarizes the available data regarding the environments of ammonia oxidizers community, the adaptation of ammonia oxidizers communities to shift in the sediment, and denitrifying microbes. The advancements of molecular biology techniques have encouraged the fast recent developments in the sector. Various methods for implementing so are discussed. The function of ammonia oxidizers community and denitrifying microorganism composition was investigated through a high throughput of the 16S rRNA amplicon sequencing procedure. There is a potential need to observe the species-specific appearance of these microorganisms in each environment and determine the relative abundance of several kinds. More effort is required to isolate these microorganisms and determine their functions through biochemical, physiological and molecular techniques. However, the investigation with deoxyribonucleic acid (DNA), antibodies, and the polymerase chain reaction (PCR) was preferred mainly to report the composition of chemolithoautotrophic bacteria.

Keywords: Ammonia oxidizers community, molecular techniques, ammonia oxidizing bacteria, ammonia-oxidizing archaea, chemolithoautotrophic bacteria.

INTRODUCTION

The atmosphere of earth comprises layers of gases involve nitrogen 78%, oxygen 21%, and other gases 1%, which preserves all form of living on the planet. The various degree rates of gases in the atmosphere also involve the glasshouse gases (GHG), CO_2, N_2O, CH_3Cl, CH_4, which are inserted through the natural sources (Thomson *et al.*, 2012), and human activities (Kasting and Siefert, 2002). Several biochemical reactions are included in the various (oxidation–reduction) conversions of the nitrogen cycle, and many of these are novel to prokaryotes. Furthermore, the nitrogen combinations representing transformed through biochemical pathways strained by microbes. The biological conversions are shown in Figure 1. Nitrogen cycling is significantly controllable by the microorganism communities and has been widely focused as a simulated survey in the field of environmental microbiology (Colloff *et al.*, 2008; Kowalchuk and Stephen, 2001). There are unique groups of the ammonia oxidizers community, which can fix N_2 in the atmosphere (Galloway *et al.*, 2004).

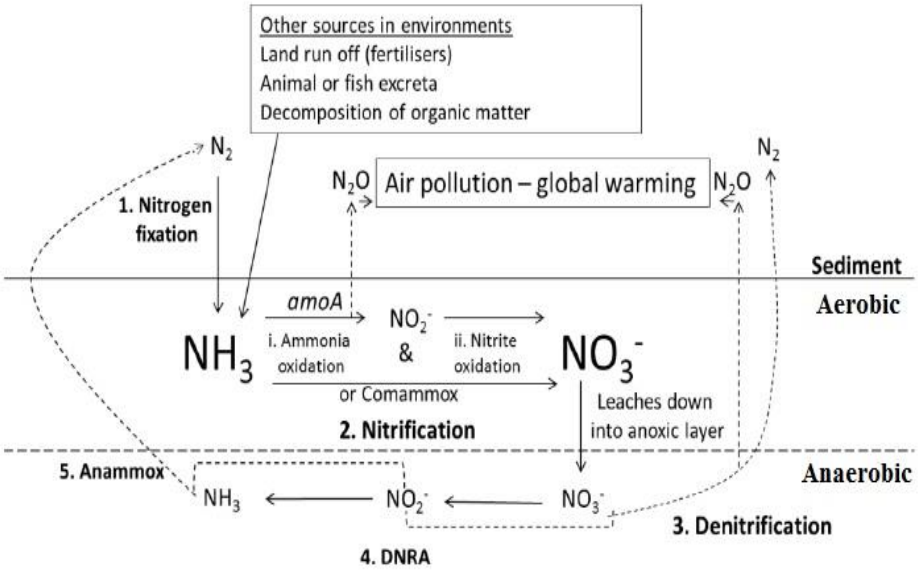

Fig. 1. Schematic representation of the nitrogen process in the ecosystem. Multiple steps in the nitrogen cycle are numbered 1–5, dashed line, the microorganisms processes cycle nitrogen by the biologically possible (NO_3^-, NO_2^-, and NH_4^+) and inaccessible forms (N_2). The oxidation conditions of the various methods are shown (Thomson *et al.*, 2012).

Nitrogen (N) is an indispensable component of the living organisms, involved in the primary organic particles, for example, proteins and nucleic acids (DNA and RNA) couple polymeric compound of life (Canfield *et al.*, 2010), much progress is mediated through a particular community of microbes (Table 1). Nitrogen is one of an essential component in the biosphere but is shown as reaction–less dinitrogen (N_2), which unused is absorbed through each living organisms and except it is at beginning transformed into decreased reactive nitrogen. It is one of the components most commonly limiting in plant nutrition. It levels fourth behind oxygen, carbon, and hydrogen as the most common chemical component in living

cells and requires N of all organisms to grow (Hofstra and Bouwman, 2005). Nitrogen fixation is the just biological achievements for restoring the nitrogen to the atmosphere that is lost by the anammox and denitrification processes, such as nitrogen-fixing microbe involve aquatic microorganisms used the nitrogenase enzyme to catalyze the dinitrogen reduction (Karl *et al.*, 1997).

Table 1. Microbes involved in the nitrogen cycle.

Processes	Example microorganisms
Ammonia Oxidation	*Nitrosomonas, Nitrosopumilus*
Nitrite Oxidation	*Nitrobactor*
Mineralization	*Bacillus, Clostridium, many others*
Denitrification	*Sulfurimonas denitrificans*
Anaerobic Phototrophic Nitrite Oxidation	*Thiocapsa, Rhodopseudomonas*
Ammonium Assimilation	*Rhizobium spp, many others*
N2 Fixation	*Cyanobacteria*
Anammox	*Candidatus Brocadia*
Methane–based Denitrification	*Candidatus Methylomirabilis oxyfera*

Nitrification

Nitrification plays an essential function in the nitrogen cycle. Nitrification is the process where ammonia, the reduced form of nitrogen is oxidized by autotrophic nitrifying bacteria to nitrite and nitrate (Kozlowski *et al.*, 2016). It happens in three bacterial communities: autotrophic ammonia oxidizers (Zhang *et al.*, 2010), autotrophic nitrite oxidizers, and heterotrophic nitrifiers. Autotrophic nitrite and ammonia oxidizers are described as the possibility to oxidize ammonia serially to nitrate. The ammonia oxidizers have essential outcomes for their environment, within the appearances and dynamics of nitrification, and form linkages with other microbes (Ebeling *et al.*, 2006). Heterotrophic nitrification is carried out by certain heterotrophic bacteria and fungi with the potential to oxidize both organic and inorganic N compounds (Stroo *et al.*, 1986). Heterotrophic fungi such as *Aspergillus flavus* and *Alcaligenes spp* were reported to form nitrite in pure culture (Castignetti and Gunner, 1980).

The nitrification is the process where the ammonia is oxidized to nitrite under aerobic condition. This can be performed through two communities of microorganisms ammonia-oxidizing archaea (AOA), and ammonia-oxidizing bacteria (AOB) who are phylogenetically different bacteria, however, execute the same function (Figure 2) (Kozlowski *et al.*, 2016; Suzuki *et al.*, 1974). In this step of nitrification, AOB oxidizes (NH_3) to (NO_2^-) according to formula (1).

$$NH_3 + O_2 \rightarrow NO_2^- + 3H + 2^{e-} \quad (1)$$

Furthermore, the first step is known as the rate–determining step of nitrification; many microbial groups participate in the nitrogen cycle and it has been studied extensively in recent decades (Leininger *et al.*, 2006; Purkhold *et al.*, 2000; Treusch *et al.*, 2005). Communities of Ammonia–oxidizing microorganisms isolated from the various environments have been estimated using ammonia monooxygenase (*amoA*) genes and 16S rRNA genes sequence analysis, which encode a crucial enzyme within this enzyme group (Francis *et al.*, 2003). In the second step nitrite (NO_2^-) is oxidized to nitrate (NO_3^-) which is carried out through nitrite-

oxidizing bacteria (NOB) (Francis *et al.*, 2003). In this step of the process, NOB oxidizes nitrite to nitrate according to formula (2).

$NO_2^- + H_2O \rightarrow NO_3^- + 2H^+ + 2^{e-}$ (2)

This nitrification process transpires achieved through Chemolithoautotrophic microorganisms and in various environments, such as sewage–processing ammonia removal is considered critical (Leininger *et al.*, 2006).

The ammonia removal is crucial for various purposes, such as its toxicity. At an adequately high ratio, ammonia is increased deadly to fish and other aquatic organisms than nitrate (Sayavedra-Soto *et al.*, 2010). Furthermore, it creates the demand for oxygen in obtaining waters that ultimately appear in decreased concentrations of dissolved oxygen. Ammonia encourages eutrophication in freshwater. These environmental consequences exhibit the essential for nitrification as a sewage treatment process and stimulate researchers to investigate methods to design a more clean and flexible system.

Oxidation of ammonia

The primary natural sources of ecological ammonia are a fixation of nitrogen and mineralization (Galloway, 1995; Grennfelt and Hultberg, 1986). Ammonia oxidation is the most critical level in the middle process of nitrogen and consequently the oxidation of ammonia to nitrate (Figure 2) (De Boer *et al.*, 1992; Purkhold *et al.*, 2000), and was considered to be achieved only by particular microorganisms. The detection of AOA corrected this opinion (Zhou *et al.*, 2015). Nitrification of autotrophic had been considered a two-step process: ammonia oxidation to nitrite by ammonia-oxidizing prokaryotes (AOP) and nitrite oxidation to nitrate by nitrite-oxidizing bacteria (NOB), which is implemented using ammonia oxidizers community related to the phylum *Thaumarchaeota / Crenarchaeota* and *Proteobacteria*, respectively.

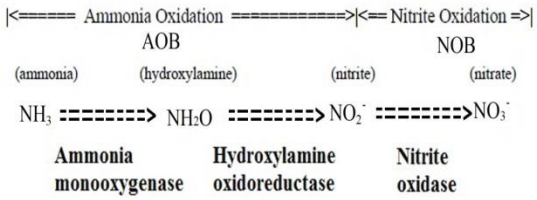

Fig. 2. The Nitrification Process.

Ammonia monooxygenase (AMO)

Understanding the ammonia monooxygenase (AMO) protein is not yet complete now generally due to this protein has still not been obtained in a highly purified active state from autotrophic AOB (Bennett *et al.*, 2016). Several of what is presently understood around the structure and characteristics of AMO appears from indirect evidence recovered from isotope and inhibitor investigation with researches related to the characteristics protein isolated from heterotrophic nitrifying microbes or intact cells (principally with *N. europaea*) (Bothe *et al.*, 2000). AMO protein in *N. europaea* and possibly scarce other autotrophic AOB is a membrane-bound enzyme (Klotz *et al.*, 1997), a copper-containing (Hamaoui *et al.*, 2016). It is allowed that AMO contains at the minimum three subunits, *amoA*, *amoB*, and *amoC*, with various compositions, arrangements, and sizes within the biological membrane periplasmic and membrane space of the cell wall (Figure 3) (Haaijer *et al.*, 2013).

The catalytic oxidation of ammonia is trusted to be found in *amoA*. Predicted from the amino acid sequence, the subunit *amoA* would contain five transmembrane domains and huge periplasmic segments including an unequal number of amino acids, while the subunit *amoB* has two transmembrane segments and two large periplasmic loops (Hooper *et al.*, 1997). The subunit *amoC* might help as a manager that controls *amoA* and *amoB* interactions to conserve AMO usability (Klotz *et al.*, 1997).

Furthermore, AMO could catalyze the oxidation of large range organic substrates, for instance; halocarbons, alcohols, and hydrocarbons (Suzuki *et al.*, 1974).

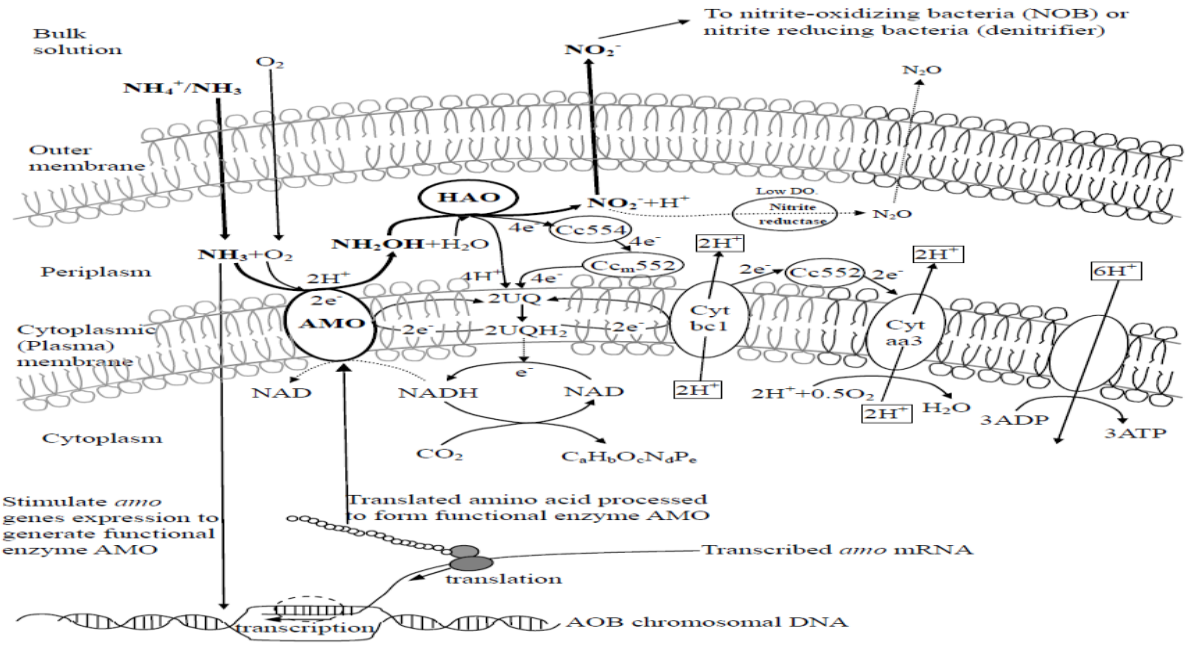

Fig. 2. Diagram of ammonia oxidation pathways and the electron oxidation of ammonia oxidizers community (Whittaker *et al.*, 2000).

Ammonia oxidizing archaea (AOA)

Autotrophic AOB of the gamma– and beta–subgroups of *Proteobacteria* (Kowalchuk and Stephen, 2001; Purkhold *et al.*, 2000) were long thought to represent the particular microbes to oxidize ammonium, it was recently shown that some AOA might also implement this process (Konneke *et al.*, 2005; Treusch *et al.*, 2005; Venter *et al.*, 2004). The AOA is observed after over a century of AOB thought out to be the critical control for ammonia oxidation (Shen *et al.*, 2012). The AOA was uniquely reported since 2005 (Konneke *et al.*, 2005; Treusch *et al.*, 2005). The more reconsideration in our knowledge of the nitrogen process observed the isolation of the first AOA. The capability of AOA converted to nitrite has been determined to a unique phylum *Thaumarchaeota* (Brochier-Armanet *et al.*, 2008; Muller *et al.*, 2010). The *Nitrosopumilus spp* is closely correlated to abundant communities of ammonia-oxidizing archaea identified using a genetic marker of 16S rRNA genes (DeLong, 1992; Fuhrman *et al.*, 1992).

All known AOA are linked with the novel suggested phylum *Thaumarchaeota* (Brochier-Armanet *et al.*, 2008) and are perceptible phylogenetically through their distinct 16S rRNA and *amoA* gene sequences (Stahl and de la Torre, 2012). Early detection of AOA was previously clustered within the phylum *Crenarchaeota*. However, investigation of recently available genomes appeared phylogenetic differences between AOA and

other crenarchaeal microbes, suggesting the cluster *Thaumarchaeota* (Brochier-Armanet *et al.*, 2008; Spang *et al.*, 2010). All modern laboratory AOA cultures carry *amoA* genes, and AOA have appeared a mere possibility to increase power from ammonia and fix inorganic carbon (Stahl and de la Torre, 2012). However, abundance amongst determined AOA extends beyond this summarization, especially regarding optimal growth conditions and metabolism. Such as, some AOA grow optimally in nature habitats distancing from acidic to slightly alkaline situations; *Ca. Nitrosotalea devanaterra* grows at pH 4 (Lehtovirta-Morley *et al.*, 2011), *N. viennensis* and *N. maritimus* were cultured in neutral pH of 7.0–7.5 (Konneke *et al.*, 2005; Tourna *et al.*, 2011), and several AOA of soil grow well at pH 8 (Bengtson *et al.*, 2012). Also, current discovering recommends that some AOA could be capable of heterotrophic or mixotrophic growth. While the natural compositions inhibit ammonia oxidation in *Ca. Nitrosocaldus yellowstonii* (de la Torre *et al.*, 2008) and *N. maritimus* (Tourna *et al.*, 2011). The 16S rRNA genes of these AOA contribute to 98% sequence homology, and 97% sequence homology through *N. maritimus* (Muller *et al.*, 2010), which scales in cell diameter from 0.17–0.22μm (Konneke *et al.*, 2005). This extraordinary discovering, besides a plethora of recent data on AOA since their early detection, indicates that there is much further to learn about these microbes.

Many studies have emphasized the characteristic distribution of AOA and their quantitative dominance higher than AOB in several terrestrial and aquatic environments, e.g. (He *et al.*, 2007). They are observed extensively distributed in several ecological systems (Monteiro *et al.*, 2014) and have the diversity of detectable (Walker *et al.*, 2010). Their physiology, ecology, and genomics in soil and marine ecosystems have been extensively investigated (Hatzenpichler, 2012; Prosser and Nicol, 2012). Furthermore, gaps in our AOA understanding currently exist (Wang *et al.*, 2015; Wang *et al.*, 2013; Wang *et al.*, 2011).

Ammonia oxidizing bacteria (AOB)

Ammonia oxidizing bacteria (AOB) are compelled aerobes and are chemolithoautotrophs. However, several species could be highly tolerant of anoxic or low oxygen environments (Bodelier *et al.*, 1996). AOB isolates of aerobic were confined to two evolutionarily distinct phyla (Head *et al.*, 1993). Moreover, it was presented that whole strains isolated from freshwater and terrestrial habitats related to the same one (monophyletic) evolutionary group, the β-subclass within the class of *Proteobacteria* (Head *et al.*, 1993). Regarding the 16S rDNA sequences, the β-subclass AOB can be divided into two different dominant groups of the family; *Nitrosococcus mobilis* and *Nitrosomonas spp* might be described into one descent, whereas *Nitrosospira*, *Nitrosovibrio*, and *Nitrosolobus* belong to another decent (Figure 4).

The comparative sequence analysis of genes encoding was functioned enzyme catalyzing part of AOB, for instance, *amoA* genes encoding a subunit of a critical protein *amoA*, which catalyzes the beginning stage of ammonia oxidation. The marker relative to phylogenetic investigation using 16S rDNA and *amoA* gene as indicated molecules introduced similar, however not identical, developmental relationships of AOB (Purkhold *et al.*, 2000).

A small number of strains prefer oligotrophic and eutrophic natural habitats, respectively (Bock *et al.*, 1990). In the environment, several strains of AOB have been detected in sub–optimal habitats, for example, marine sediments (extremely low oxygen tensions), hot springs and deserts (temperatures ≥ 60 °C), deep oceans (temperature ≤ 5 °C), building sandstone (low ammonium levels), and acid soils (pH ≤ 4) (Watson *et al.*, 1989). However, the optimum temperature range for growth is 25°C –29°C, and pH value approximately 7.5–8.0 have been determined for whole recently isolated AOB strains (Koops and Pommerening-Roser, 2001). The comparative

relevance of AOA and AOB in ammonia oxidation is their relative contribution to nitrification that could change depending on environmental conditions and yet not completely understood.

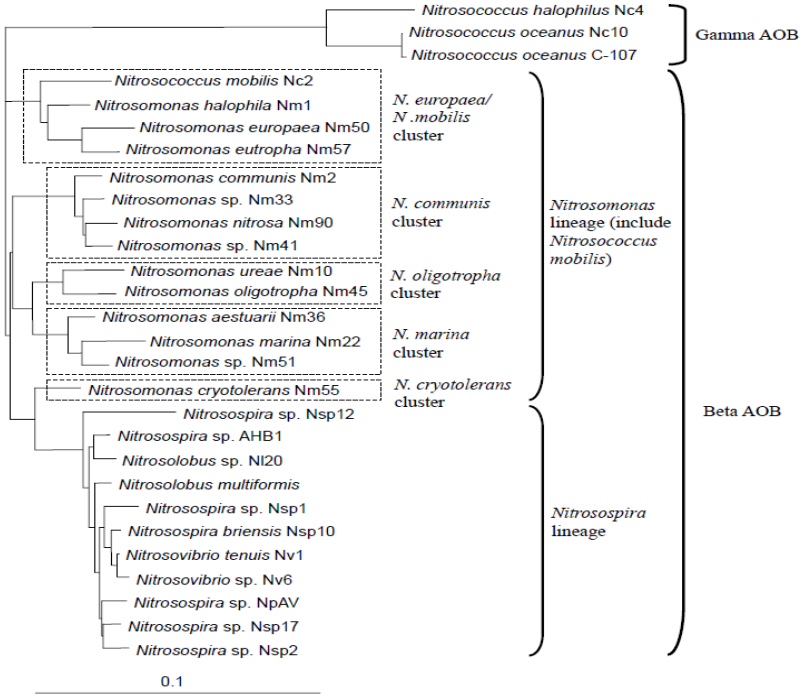

Fig. 3. The phylogenetic correlation of most established AOB based on 16S rRNA gene sequences (~1400 bases) from the GenBank information (Aakra *et al.*, 1999; Head *et al.*, 1993; Pommerening-Röser *et al.*, 1996; Rotthauwe *et al.*, 1997).

Nitrite oxidation bacteria (NOB)

Nitrite oxidizers bacteria (NOB), the second step in nitrification, catalyzing the oxidation of nitrite to nitrate. The unique identification of nitrite-oxidizing bacteria (NOB) is related to the cell shape, the unique appearance of cytoplasm membrane compositions (Watson *et al.*, 1989), and various fatty acid profile (Lipski *et al.*, 2001). NOB was separated into four families. This identification was approved and newly increased to six families, depending on relative to sequence analysis of 16S rRNA. Two electrons are dissipated when nitrite is oxidized to nitrate. The shaping of nitrate is catalyzed through the key enzyme of NOB, nitrite oxidoreductase (Nxr), according to the following formula:

$$\text{Nxr: } NO_2^- + H_2O \leftrightarrow NO_3^- + 2H^+ + 2e^- \quad (3)$$

Chemolithoautotroph NOB fixes carbon dioxide (CO_2), and about 80% of the power produced through nitrite oxidation is utilized for CO_2 fixation (Spieck and Bock, 2005). The nitrite–oxidizing bacteria are very slow–growing microorganisms with the least generation times ranging from 10 hours for *Nitrobacter vulgaris* (Bock *et al.*, 1990), over to 90 hours for

Nitrospira marina (Watson *et al.*, 1986), under Chemolithoautotroph growth conditions.

Complete ammonia oxidizer (comammox) microbes

The complete classification of nitrification into two sequential steps, performed through two various kinds of microbes was a secret for a long time. The present detection of complete ammonia oxidizer (comammox) organisms, which completely oxidize ammonia transforms ammonia into nitrite and then into nitrate (Costa *et al.*, 2006), within the *Nitrospira sp* has importantly transformed our knowledge of the aerobic nitrification process (Daims *et al.*, 2015; van Kessel *et al.*, 2015). The primary comammox microbes were detected within the genus *Ca. Nitrospira inopinata*, *Ca. N. nitrificans* and *Ca. N. nitrosa*. Earlier, this *Nitrospira sp* was famed for characterizing between the highly prevalent NOB, an idea that directed to disregard their responsibility as ammonia oxidizers for numerous years (Daims *et al.*, 2015; van Kessel *et al.*, 2015). Cultivation-independent methods have likewise classified the appearance of comammox in soils, rapid sand filters, wastewater treatment plants (WWTPs), and drinking water systems (Daims *et al.*, 2015; Palomo *et al.*, 2016; Pinto *et al.*, 2016; van Kessel *et al.*, 2015).

Denitrification

Denitrification is the biological mediated process, in which NO, N_2O is produced from NO_3^- and NO_2^-, and N_2 is the final product released into the atmosphere. Denitrification may be an acceptable or unacceptable process based on the habitats. Most denitrifiers use anaerobic respiration. However, several species might continue to denitrify in the presence of oxygen, the phenomenon of aerobic denitrification. The process is achieved through autotrophic denitrifiers (e.g., *Thiobacillus denitrificans*), although heterotrophic bacteria have also been identified (such as *Pseudomonads* and *Paracoccus denitrificans*). The denitrification characteristics are common among archaea, bacteria and may even be detected in a number of the Eukaryotes. Denitrification is generally discussed one of the essential processes managing nitrogen discharges in rivers and streams, due to the responsibility for removing fixed nitrogen (Beaulieu *et al.*, 2011; Pinay *et al.*, 2018).

Dynamic of Ammonia Oxidizers Community in Ecosystems

The dynamics and structure of ammonia oxidation group in environmental ecosystems have presented a comparatively complicated issue given that the computations for natural resources and characteristic environment. Up to now, it is incomprehensible which physiochemical conditions and environmental factors affect AOA than AOB (Jia and Conrad, 2009). Many investigations have recommended that AOA is dominated than β–AOB in ecosystems (Adair and Schwartz, 2008; Bernhard *et al.*, 2010; Kalanetra *et al.*, 2009; Leininger *et al.*, 2006; Santoro *et al.*, 2010). The AOA gene copies were shown several requests for quantity moreover than the beta–*proteobacterial amoA* gene in the North Atlantic (Wuchter *et al.*, 2006). However, the investigation showed functional relationships among the *amoA* genes and abundance described by the qPCR targeting 16S rRNA and using catalyzed reporter deposition CARD–FISH by direct enumeration. Furthermore, it has been confirmed that the number of AOA is higher abundant than AOB in China (Liu *et al.*, 2018), the Gulf of California (Beman *et al.*, 2008), and the Japan Sea (Nakagawa *et al.*, 2007).

Several investigations have shown that the AOA is dominated than β–AOB in ecosystems, some studies have determined the AOB be higher overestimated than the AOA (Dang *et al.*, 2010; Jin *et al.*, 2010; Mosier and Francis, 2008). The qPCR analysis showed that AOA gene copies were lower than β–AOB in the San Francisco Bay, while the AOA was determined at various concentrations than β–AOB in the bay (Mosier and Francis, 2008).

Stream Microbial Community, Function Gene, and Research Methods

Molecular methods are applied as a way of describing and explaining the rational function of these mesophilic aquatic *Crenarchaeota* (Powers *et al.*, 2010). Molecular detection implementing 16S rRNA–based and DNA–based approaches have been the critical method to detect the abundance, diversity, and activity of ammonia oxidation. Identifying the phylotypes and group of nitrifies promoting to the measure and observed nitrify functioning is challenging. Other than artificial environments, most of the scientists have investigated the composition and diversity of ammonia oxidization in aquatic ecosystems using 16S rRNA gene–based techniques. The 16S rRNA method was primarily implemented in phylogenetical taxonomy of AOB (Ahmed *et al.*, 2016; Head *et al.*, 1993; Speksnijder *et al.*, 1998).

Some studies have detected AOA, and AOB found abundances *in situ* as the ammonia oxidization could be a small percentage of the total community. Furthermore, it is complicated to extract the whole mRNA entirely from environmental samples. RNA and DNA amplified can as such be biased due to characteristics polymerase chain reaction (PCR) biases (Smith and Osborn, 2009). Despite these difficulties, it is especially useful to quantify transcripts as it brings us a step closer to identifying the active microorganisms than gene quantification alone. Moreover, they carried out the model on how targeting amplified can be available in correlating nitrification activity to function (Zhang *et al.*, 2015). Several investigations have discussed changes in AOB communities or dynamics under various natural habitats (Li *et al.*, 2012; Wang *et al.*, 2018). They determine that AOB were unaffected by salinity changes, however, they included lower transcriptional activity as salinity raised, and AOA had maximum transcriptional activity at average salinity. Up to now, the publication has provided complementary confirmation on how AOA and AOB respond to salinity, making it more crucial to encouraging field studies with laboratory–based experiments.

Recently, a study has been designed to determine and measure the ammonia oxidizers community in different samples taken from either habitats or engineered methods by combining other molecular approaches, for instance, PCR, fluorescent–labeled oligonucleotides probe hybridization, dot blot hybridization, qPCR, and competitive PCR (Hiorns *et al.*, 1995; Kowalchuk *et al.*, 1998; Liu *et al.*, 1997; Phillips *et al.*, 1999; Wang *et al.*, 2014; Ward, 1996; Ward *et al.*, 1997; Whitby *et al.*, 1999). Terminal-restriction fragment length polymorphism fingerprints (T-RFLP) is an essential microbial environment method, which may be applied to observe abundance and composition and measure communities in a statistical manner (Lueders and Friedrich, 2003). An analysis of T-RFLP profiles will present an insight into the level of abundance and diversity of ammonia oxidizers community within and between sampling locations.

Adaptation of ammonia oxidizers communities in natural habitat

Explaining how various microbes adapt to the ecosystems or how the habitat chooses various microbes remains an essential question in microbial ecology. AOB comprise of eminent genera *Nitrosomonas* and *Nitrosospira*, both of including as a minimum of four subgroups. Besides, *Nitrosococcus* that relates to the *Gammaproteobacteria* is detected mostly in marine environments (Purkhold *et al.*, 2000; Stephen *et al.*, 1998). *Nitrosomonas spp* are dominated in environments of the maximum nitrogen charging, for instance, wastewater treatment plants and eutrophic ponds, while *Nitrosospira spp* are commonly prevalent AOB clusters in sediments (Mintie *et al.*, 2003; Okano *et al.*, 2004). The performance and adaptation of AOB will base on the ecotypes and species but not the genus (Ke and Lu, 2012). Clearing the function and abundance will need an

understanding of the environmental physiology and adaptation of various ammonia-oxidizers communities in habitats (Schleper and Nicol, 2010). The collecting information was recommended that AOA might play more function than AOB under situations, for example, low substrate accessibility and at minimum pH (Martens-Habbena *et al.*, 2009; Roesch *et al.*, 2007; Valentine, 2007).

CONCLUSION

Molecular biology approaches have achieved the investigation of unidentified microorganisms and their function in various natural habitats. Nearly more than one hundred of the diverse genomes per gram occur in soils, and the numbers might be higher in habitats of aquatic likewise. The review describes notes on the various adaptations of AOA and AOB communities to shift in the sediment. Target DNA (functional genes or 16S rRNA sequences encoding) might be amplified by cloned, sequenced and PCR. The technology such as T-RFLP, TGGE, and DGGE might be facilitated to sample sets for the evaluation of regional and seasonal variations. Therefore most obtained sequences for functional genes will be novel. The status did not become dramatic in the 16S rRNA sequences situation. However, the functions of each environment will increase unique sequence data of the 16S rRNA databanks abundances. Recently molecular technology, like microarrays with various copies of all denitrification and nitrification genes, will potentially help to show microorganisms for their specific metabolic facilitate in the nitrogen cycle. The excitement about the molecular biology approaches which allow us to investigate microorganisms directly in their environmental, additional information will demand current observations and an in-depth examination by methodologies such as mRNA transcription investigation and metagenomics under *in situ* environments, and we require extra attempts to develop and characterize molecular methods, for those organisms that are still unidentified.

ACKNOWLEDGMENT

This work is financially supported by the National Natural Science Foundation of China (grant No. 31070089, 31170078, and J1103514), the National High Technology Research and Development Program of China (grant No. 2013AA065805 and 2014AA093510), the National Natural Science Foundation of Hubei Province (grant No. 2015CFA085), and the Fundamental Research Funds for HUST (grant Nos. 2014NY007, 2017KFYXJJ212, 2017KFXKJC010, 2017KFTSZZ001). Many thanks are indebted to the Analytical and Testing Center of Huazhong University of Science and Technology for the measurements of water quality.

CONFLICT OF INTEREST

The author declares no conflict of interest.

REFERENCES

Aakra, A., Utaker, J.B., Nes, I.F., 1999. RFLP of rRNA genes and sequencing of the 16S-23S rDNA intergenic spacer region of ammonia-oxidizing bacteria: a phylogenetic approach. Int. J. System. Bacteriol., 49 Pt 1: 123-30.

Adair, K.L., Schwartz, E., 2008. Evidence that ammonia-oxidizing archaea are more abundant than ammonia-oxidizing bacteria in semiarid soils of northern Arizona, USA. Microbial Ecol., 56(3): 420-6.

Ahmed, W., Hughes, B., Harwood, V.J., 2016. Current Status of Marker Genes of Bacteroides and Related Taxa for Identifying Sewage Pollution in Environmental Waters. Water, 8(6): 231.

Beaulieu, J.J., Tank, J.L., Hamilton, S.K., Wollheim, W.M., Hall, R.O., Jr., Mulholland, P.J., Peterson, B.J., Ashkenas, L.R., Cooper, L.W., Dahm, C.N., Dodds, W.K., Grimm, N.B., Johnson, S.L., McDowell, W.H., Poole, G.C., Valett, H.M., Arango, C.P., Bernot, M.J., Burgin, A.J., Crenshaw, C.L., Helton, A.M., Johnson, L.T., O'Brien, J.M., Potter, J.D., Sheibley, R.W., Sobota, D.J., Thomas, S.M., 2011. Nitrous oxide emission from denitrification in stream and river networks. Proc. Natl. Acad. Sci. U. S. A., 108(1): 214-9.

Beman, J.M., Popp, B.N., Francis, C.A., 2008. Molecular and biogeochemical evidence for ammonia oxidation by marine Crenarchaeota in the Gulf of California. Int. Soc. Microbial Ecol. J., 2(4): 429-41.

Bengtson, P., Sterngren, A.E., Rousk, J., 2012. Archaeal abundance across a pH gradient in an arable soil and its relationship to bacterial and fungal growth rates. Appl. Environ. Microbiol., 78(16): 5906-11.

Bennett, K., Sadler, N.C., Wright, A.T., Yeager, C., Hyman, M.R., 2016. Activity-Based Protein Profiling of Ammonia Monooxygenase in Nitrosomonas europaea. Appl. Environ. Microbiol., 82(8): 2270-2279.

Bernhard, A.E., Landry, Z.C., Blevins, A., de la Torre, J.R., Giblin, A.E., Stahl, D.A., 2010. Abundance of ammonia-oxidizing archaea and bacteria along an estuarine salinity gradient in relation to potential nitrification rates. Appl. Environ. Microbiol., 76(4): 1285-9.

Bock, E., Koops, H.-P., Moller, U.C., Rudert, M., 1990. A new facultatively nitrite oxidizing bacterium, Nitrobacter vulgaris sp. nov. Arch. Microbiol., 153(2): 105-110.

Bodelier, P., Libochant, J.A., Blom, C., Laanbroek, H.J., 1996. Dynamics of nitrification and denitrification in root-oxygenated sediments and adaptation of ammonia-oxidizing bacteria to low-oxygen or anoxic habitats. Appl. Environ. Microbiol., 62(11): 4100-7.

Bothe, H., Jost, G., Schloter, M., Ward, B.B., Witzel, K., 2000. Molecular analysis of ammonia oxidation and denitrification in natural environments. FEMS Microbiol. Rev., 24(5): 673-90.

Brochier-Armanet, C., Boussau, B., Gribaldo, S., Forterre, P., 2008. Mesophilic Crenarchaeota: proposal for a third archaeal phylum, the Thaumarchaeota. Nat. Rev. Microbiol., 6(3): 245-52.

Canfield, D.E., Glazer, A.N., Falkowski, P.G., 2010. The evolution and future of Earth's nitrogen cycle. Sci., 330(6001): 192-6.

Castignetti, D., Gunner, H.B., 1980. Sequential nitrification by an Alcaligenes sp. and Nitrobacter agilis. Can. J. Microbiol., 26(9): 1114-9.

Colloff, M.J., Wakelin, S.A., Gomez, D., Rogers, S.L., 2008. Detection of nitrogen cycle genes in soils for measuring the effects of changes in land use and management. Soil Biol. Biochem., 40(7): 1637-1645.

Costa, E., Pérez, J., Kreft, J.-U., 2006. Why is metabolic labour divided in nitrification? Trends Microbiol., 14(5): 213-219.

Daims, H., Lebedeva, E.V., Pjevac, P., Han, P., Herbold, C., Albertsen, M., Jehmlich, N., Palatinszky, M., Vierheilig, J., Bulaev, A., Kirkegaard, R.H., von Bergen, M., Rattei, T., Bendinger, B., Nielsen, P.H., Wagner, M., 2015. Complete nitrification by Nitrospira bacteria. Nat., 528(7583): 504-9.

Dang, H., Luan, X.W., Chen, R., Zhang, X., Guo, L., Klotz, M.G., 2010. Diversity, abundance and distribution of amoA-encoding archaea in deep-sea methane seep sediments of the Okhotsk Sea. FEMS Microbiol. Ecol., 72(3): 370-85.

De Boer, W., Tietema, A., Gunnewiek, P.J.A.K., Laanbroek, H.J., 1992. The chemolithotrophic ammonium-oxidizing community in a nitrogen-saturated acid forest soil in relation to ph-dependent

nitrifying activity. Soil Biol. Biochem., 24(3): 229-234.

de la Torre, J.R., Walker, C.B., Ingalls, A.E., Konneke, M., Stahl, D.A., 2008. Cultivation of a thermophilic ammonia oxidizing archaeon synthesizing crenarchaeol. Environ. Microbiol., 10(3): 810-8.

DeLong, E.F., 1992. Archaea in coastal marine environments. Proc. Natl. Acad. Sci. U. S. A., 89(12): 5685-9.

Ebeling, J.M., Timmons, M.B., Bisogni, J.J., 2006. Engineering analysis of the stoichiometry of photoautotrophic, autotrophic, and heterotrophic removal of ammonia–nitrogen in aquaculture systems. Aquac., 257(1-4): 346-358.

Francis, C.A., O'Mullan, G.D., Ward, B.B., 2003. Diversity of ammonia monooxygenase (amoA) genes across environmental gradients in Chesapeake Bay sediments. Geobiol., 1(2): 129-140.

Fuhrman, J.A., McCallum, K., Davis, A.A., 1992. Novel major archaebacterial group from marine plankton. Nat., 356(6365): 148-9.

Galloway, J.N., 1995. Acid deposition: Perspectives in time and space. Water Air Soil Pollut., 85(1): 15-24.

Galloway, J.N., Dentener, F.J., Capone, D.G., Boyer, E.W., Howarth, R.W., Seitzinger, S.P., Asner, G.P., Cleveland, C.C., Green, P.A., Holland, E.A., Karl, D.M., Michaels, A.F., Porter, J.H., Townsend, A.R., V�osmarty, C.J., 2004. Nitrogen Cycles: Past, Present, and Future. Biogeochem., 70(2): 153-226.

Grennfelt, P., Hultberg, H., 1986. Effects of nitrogen deposition on the acidification of terrestrial and aquatic ecosystems. Water Air Soil Pollut., 30(3-4): 945-963.

Haaijer, S.C., Ji, K., van Niftrik, L., Hoischen, A., Speth, D., Jetten, M.S., Damste, J.S., Op den Camp, H.J., 2013. A novel marine nitrite-oxidizing Nitrospira species from Dutch coastal North Sea water. Front. Microbiol., 4: 60.

Hamaoui, G.S., Rodrigues, J.L.M., Bohannan, B.J.M., Tiedje, J.M., Nüsslein, K., 2016. Land-use change drives abundance and community structure alterations of thaumarchaeal ammonia oxidizers in tropical rainforest soils in Rondônia, Brazil. Appl. Soil Ecol., 107: 48-56.

Hatzenpichler, R., 2012. Diversity, physiology, and niche differentiation of ammonia-oxidizing archaea. Appl. Environ. Microbiol., 78(21): 7501-10.

He, J.Z., Shen, J.P., Zhang, L.M., Zhu, Y.G., Zheng, Y.M., Xu, M.G., Di, H., 2007. Quantitative analyses of the abundance and composition of ammonia-oxidizing bacteria and ammonia-oxidizing archaea of a Chinese upland red soil under long-term fertilization practices. Environ. Microbiol., 9(9): 2364-74.

Head, I.M., Hiorns, W.D., Embley, T.M., McCarthy, A.J., Saunders, J.R., 1993. The phylogeny of autotrophic ammonia-oxidizing bacteria as determined by analysis of 16S ribosomal RNA gene sequences. J. General Microbiol., 139 Pt 6(6): 1147-53.

Hiorns, W.D., Hastings, R.C., Head, I.M., McCarthy, A.J., Saunders, J.R., Pickup, R.W., Hall, G.H., 1995. Amplification of 16S ribosomal RNA genes of autotrophic ammonia-oxidizing bacteria demonstrates the ubiquity of nitrosospiras in the environment. Microbiol., 141 (Pt 11): 2793-800.

Hofstra, N., Bouwman, A.F., 2005. Denitrification in Agricultural Soils: Summarizing Published Data and Estimating Global Annual Rates. Nutr. Cycl. Agroecosys., 72(3): 267-278.

Hooper, A.B., Vannelli, T., Bergmann, D.J., Arciero, D.M., 1997. Enzymology of the oxidation of ammonia to nitrite by bacteria. Antonie Van Leeuwenhoek, 71(1-2): 59-67.

Jia, Z., Conrad, R., 2009. Bacteria rather than Archaea dominate microbial ammonia oxidation in an agricultural soil. Environ. Microbiol., 11(7): 1658-71.

Jin, T., Zhang, T., Yan, Q., 2010. Characterization and quantification of

ammonia-oxidizing archaea (AOA) and bacteria (AOB) in a nitrogen-removing reactor using T-RFLP and qPCR. Appl. Microbiol. Biotechnol., 87(3): 1167-76.

Kalanetra, K.M., Bano, N., Hollibaugh, J.T., 2009. Ammonia-oxidizing Archaea in the Arctic Ocean and Antarctic coastal waters. Environ. Microbiol., 11(9): 2434-45.

Karl, D., Letelier, R., Tupas, L., Dore, J., Christian, J., Hebel, D., 1997. The role of nitrogen fixation in biogeochemical cycling in the subtropical North Pacific Ocean. Nature, 388(6642): 533-538.

Kasting, J.F., Siefert, J.L., 2002. Life and the evolution of Earth's atmosphere. Sci., 296(5570): 1066-8.

Ke, X., Lu, Y., 2012. Adaptation of ammonia-oxidizing microorganisms to environment shift of paddy field soil. FEMS Microbiol Ecol., 80(1): 87-97.

Klotz, M.G., Alzerreca, J., Norton, J.M., 1997. A gene encoding a membrane protein exists upstream of the amoA/amoB genes in ammonia oxidizing bacteria: a third member of the amo operon? FEMS Microbiol. Lett., 150(1): 65-73.

Konneke, M., Bernhard, A.E., de la Torre, J.R., Walker, C.B., Waterbury, J.B., Stahl, D.A., 2005. Isolation of an autotrophic ammonia-oxidizing marine archaeon. Nature, 437(7058): 543-6.

Koops, H.-P., Pommerening-Roser, A., 2001. Distribution and ecophysiology of the nitrifying bacteria emphasizing cultured species. FEMS Microbiol Ecol., 37(1): 1-9.

Kowalchuk, G.A., Bodelier, P.L.E., Heilig, G.H.J., Stephen, J.R., Laanbroek, H.J., 1998. Community analysis of ammonia-oxidising bacteria, in relation to oxygen availability in soils and root-oxygenated sediments, using PCR, DGGE and oligonucleotide probe hybridisation. FEMS Microbiol. Ecol., 27(4): 339-350.

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

Kozlowski, J.A., Stieglmeier, M., Schleper, C., Klotz, M.G., Stein, L.Y., 2016. Pathways and key intermediates required for obligate aerobic ammonia-dependent chemolithotrophy in bacteria and Thaumarchaeota. In. Soc. Microbial Ecol. J., 10(8): 1836-45.

Lehtovirta-Morley, L.E., Stoecker, K., Vilcinskas, A., Prosser, J.I., Nicol, G.W., 2011. Cultivation of an obligate acidophilic ammonia oxidizer from a nitrifying acid soil. Proc. Natl. Acad. Sci. U. S. A., 108(38): 15892-7.

Leininger, S., Urich, T., Schloter, M., Schwark, L., Qi, J., Nicol, G.W., Prosser, J.I., Schuster, S.C., Schleper, C., 2006. Archaea predominate among ammonia-oxidizing prokaryotes in soils. Nat., 442(7104): 806-9.

Li, X.R., Xiao, Y.P., Ren, W.W., Liu, Z.F., Shi, J.H., Quan, Z.X., 2012. Abundance and composition of ammonia-oxidizing bacteria and archaea in different types of soil in the Yangtze River estuary. J. Zheijang Uni. Sci. B., 13(10): 769-82.

Lipski, A., Spieck, E., Makolla, A., Altendorf, K., 2001. Fatty acid profiles of nitrite-oxidizing bacteria reflect their phylogenetic heterogeneity. System. Appl. Microbiol., 24(3): 377-84.

Liu, J., Yu, Z., Yao, Q., Sui, Y., Shi, Y., Chu, H., Tang, C., Franks, A.E., Jin, J., Liu, X., Wang, G., 2018. Ammonia-Oxidizing Archaea Show More Distinct Biogeographic Distribution Patterns than Ammonia-Oxidizing Bacteria across the Black Soil Zone of Northeast China. Front. Microbiol., 9: 171.

Liu, W.T., Marsh, T.L., Cheng, H., Forney, L.J., 1997. Characterization of microbial diversity by determining terminal restriction fragment length polymorphisms of genes encoding 16S rRNA. Appl. Environ. Microbiol., 63(11): 4516-22.

Lueders, T., Friedrich, M.W., 2003. Evaluation of PCR Amplification Bias by Terminal Restriction Fragment Length Polymorphism Analysis of Small-Subunit rRNA and mcrA Genes by Using Defined Template Mixtures of Methanogenic Pure Cultures and Soil DNA Extracts. Appl. Environ. Microbiol., 69(1): 320-326.

Martens-Habbena, W., Berube, P.M., Urakawa, H., de la Torre, J.R., Stahl, D.A., 2009. Ammonia oxidation kinetics determine niche separation of nitrifying Archaea and Bacteria. Nat., 461(7266): 976-9.

Mintie, A.T., Heichen, R.S., Cromack, J., K., Myrold, D.D., Bottomley, P.J., 2003. Ammonia-Oxidizing Bacteria along Meadow-to-Forest Transects in the Oregon Cascade Mountains. Appl. Environ. Microbiol., 69(6): 3129-3136.

Monteiro, M., Seneca, J., Magalhaes, C., 2014. The history of aerobic ammonia oxidizers: from the first discoveries to today. J. Microbiol., 52(7): 537-47.

Mosier, A.C., Francis, C.A., 2008. Relative abundance and diversity of ammonia-oxidizing archaea and bacteria in the San Francisco Bay estuary. Environ. Microbiol., 10(11): 3002-16.

Muller, F., Brissac, T., Le Bris, N., Felbeck, H., Gros, O., 2010. First description of giant Archaea (Thaumarchaeota) associated with putative bacterial ectosymbionts in a sulfidic marine habitat. Environ. Microbiol., 12(8): 2371-83.

Nakagawa, T., Mori, K., Kato, C., Takahashi, R., Tokuyama, T., 2007. Distribution of Cold-Adapted Ammonia-Oxidizing Microorganisms in the Deep-Ocean of the Northeastern Japan Sea. Microbes and Environ., 22(4): 365-372.

Okano, Y., Hristova, K.R., Leutenegger, C.M., Jackson, L.E., Denison, R.F., Gebreyesus, B., Lebauer, D., Scow, K.M., 2004. Application of Real-Time PCR To Study Effects of Ammonium on Population Size of Ammonia-Oxidizing Bacteria in Soil. Appl. Environ. Microbiol., 70(2): 1008-1016.

Palomo, A., Jane Fowler, S., Gulay, A., Rasmussen, S., Sicheritz-Ponten, T., Smets, B.F., 2016. Metagenomic analysis of rapid gravity sand filter microbial communities suggests novel physiology of Nitrospira spp. Int. Soc. Microbial Ecol. J., 10(11): 2569-2581.

Phillips, C.J., Smith, Z., Embley, T.M., Prosser, J.I., 1999. Phylogenetic differences between particle-associated and planktonic ammonia-oxidizing bacteria of the beta subdivision of the class Proteobacteria in the Northwestern Mediterranean Sea. Appl. Environ. Microbiol., 65(2): 779-786.

Pinay, G., Bernal, S., Abbott, B.W., Lupon, A., Marti, E., Sabater, F., Krause, S., 2018. Riparian Corridors: A New Conceptual Framework for Assessing Nitrogen Buffering Across Biomes. Front. Environ. Sci., 6(47).

Pinto, A.J., Marcus, D.N., Ijaz, U.Z., Bautista-de Lose Santos, Q.M., Dick, G.J., Raskin, L., 2016. Metagenomic Evidence for the Presence of Comammox Nitrospira-Like Bacteria in a Drinking Water System. mSphere, 1(1): pii: e00054-15. doi: 10.1128/mSphere.00054-15.

Pommerening-Röser, A., Rath, G., Koops, H.-P., 1996. Phylogenetic Diversity within the Genus Nitrosomonas. System. Appl. Microbiol. 19(3): 344-351.

Powers, L., Werne, J.P., Vanderwoude, A.J., Sinninghe Damsté, J.S., Hopmans, E.C., Schouten, S., 2010. Applicability and calibration of the TEX86 paleothermometer in lakes. Org. Geochem., 41(4): 404-413.

Prosser, J.I., Nicol, G.W., 2012. Archaeal and bacterial ammonia-oxidisers in soil: the quest for niche specialisation and differentiation. Trends Microbiol., 20(11): 523-31.

Purkhold, U., Pommerening-Roser, A., Juretschko, S., Schmid, M.C., Koops, H.P., Wagner, M., 2000. Phylogeny of

All Recognized Species of Ammonia Oxidizers Based on Comparative 16S rRNA and amoA Sequence Analysis: Implications for Molecular Diversity Surveys. Appl. Environ. Microbiol., 66(12): 5368-5382.

Roesch, L.F., Fulthorpe, R.R., Riva, A., Casella, G., Hadwin, A.K., Kent, A.D., Daroub, S.H., Camargo, F.A., Farmerie, W.G., Triplett, E.W., 2007. Pyrosequencing enumerates and contrasts soil microbial diversity. Int. Soc. Microbial Ecol. J., 1(4): 283-90.

Rotthauwe, J.H., Witzel, K.P., Liesack, W., 1997. The ammonia monooxygenase structural gene amoA as a functional marker: Molecular fine-scale analysis of natural ammonia-oxidizing populations. Appl. Environ. Microbiol., 63(12): 4704-4712.

Santoro, A.E., Casciotti, K.L., Francis, C.A., 2010. Activity, abundance and diversity of nitrifying archaea and bacteria in the central California Current. Environ. Microbiol., 12(7): 1989-2006.

Sayavedra-Soto, L.A., Gvakharia, B., Bottomley, P.J., Arp, D.J., Dolan, M.E., 2010. Nitrification and degradation of halogenated hydrocarbons--a tenuous balance for ammonia-oxidizing bacteria. Appl. Microbiol. Biotechnol., 86(2): 435-44.

Schleper, C., Nicol, G.W., 2010. Ammonia-oxidising archaea--physiology, ecology and evolution. Adv. Appl. Microbiol., 57: 1-41.

Shen, J.P., Zhang, L.M., Di, H.J., He, J.Z., 2012. A review of ammonia-oxidizing bacteria and archaea in Chinese soils. Front. Microbiol., 3: 296.

Smith, C.J., Osborn, A.M., 2009. Advantages and limitations of quantitative PCR (Q-PCR)-based approaches in microbial ecology. FEMS Microbiol Ecol., 67(1): 6-20.

Spang, A., Hatzenpichler, R., Brochier-Armanet, C., Rattei, T., Tischler, P., Spieck, E., Streit, W., Stahl, D.A., Wagner, M., Schleper, C., 2010. Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. Trends Microbiol., 18(8): 331-40.

Speksnijder, A.G., Kowalchuk, G.A., Roest, K., Laanbroek, H.J., 1998. Recovery of a Nitrosomonas-like 16S rDNA sequence group from freshwater habitats. System. Appl. Microbiol., 21(2): 321-30.

Spieck, E., Bock, E., 2005. The Lithoautotrophic Nitrite-Oxidizing Bacteria. Bergey´s manual of systematic bacteriology, 2. Springer Science+Business Media., New York.

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

Stephen, J.R., Kowalchuk, G.A., Bruns, M.A.V., McCaig, A.E., Phillips, C.J., Embley, T.M., Prosser, J.I., 1998. Analysis of beta-subgroup proteobacterial ammonia oxidizer populations in soil by denaturing gradient gel electrophoresis analysis and hierarchical phylogenetic probing. Appl. Environ. Microbiol., 64(8): 2958-65.

Stroo, H.F., Klein, T.M., Alexander, M., 1986. Heterotrophic nitrification in an Acid forest soil and by an Acid-tolerant fungus. Appl. Environ. Microbiol., 52(5): 1107-11.

Suzuki, I., Dular, U., Kwok, S.C., 1974. Ammonia or Ammonium Ion as Substrate for Oxidation by Nitrosomonas europaea Cells and Extracts. J. Bacteriol., 120(1): 556-558.

Thomson, A.J., Giannopoulos, G., Pretty, J., Baggs, E.M., Richardson, D.J., 2012. Biological sources and sinks of nitrous oxide and strategies to mitigate emissions. Philos. Trans. R. Soc. Lond. B. Biol. Sci., 367(1593): 1157-68.

Tourna, M., Stieglmeier, M., Spang, A., Konneke, M., Schintlmeister, A., Urich, T., Engel, M., Schloter, M., Wagner, M., Richter, A., Schleper, C., 2011.

Nitrososphaera viennensis, an ammonia oxidizing archaeon from soil. Proc. Natl. Acad. Sci. U. S. A., 108(20): 8420-5.

Treusch, A.H., Leininger, S., Kletzin, A., Schuster, S.C., Klenk, H.P., Schleper, C., 2005. Novel genes for nitrite reductase and Amo-related proteins indicate a role of uncultivated mesophilic crenarchaeota in nitrogen cycling. Environ. Microbiol., 7(12): 1985-95.

Valentine, D.L., 2007. Adaptations to energy stress dictate the ecology and evolution of the Archaea. Nat. Rev. Microbiol., 5: 316.

van Kessel, M.A., Speth, D.R., Albertsen, M., Nielsen, P.H., Op den Camp, H.J., Kartal, B., Jetten, M.S., Lucker, S., 2015. Complete nitrification by a single microorganism. Nat., 528(7583): 555-9.

Venter, J.C., Remington, K., Heidelberg, J.F., Halpern, A.L., Rusch, D., Eisen, J.A., Wu, D., Paulsen, I., Nelson, K.E., Nelson, W., Fouts, D.E., Levy, S., Knap, A.H., Lomas, M.W., Nealson, K., White, O., Peterson, J., Hoffman, J., Parsons, R., Baden-Tillson, H., Pfannkoch, C., Rogers, Y.H., Smith, H.O., 2004. Environmental genome shotgun sequencing of the Sargasso Sea. Sci., 304(5667): 66-74.

Walker, C.B., de la Torre, J.R., Klotz, M.G., Urakawa, H., Pinel, N., Arp, D.J., Brochier-Armanet, C., Chain, P.S., Chan, P.P., Gollabgir, A., Hemp, J., Hugler, M., Karr, E.A., Konneke, M., Shin, M., Lawton, T.J., Lowe, T., Martens-Habbena, W., Sayavedra-Soto, L.A., Lang, D., Sievert, S.M., Rosenzweig, A.C., Manning, G., Stahl, D.A., 2010. Nitrosopumilus maritimus genome reveals unique mechanisms for nitrification and autotrophy in globally distributed marine crenarchaea. Proc. Natl. Acad. Sci. U. S. A., 107(19): 8818-23.

Wang, B., Zhao, J., Guo, Z., Ma, J., Xu, H., Jia, Z., 2015. Differential contributions of ammonia oxidizers and nitrite oxidizers to nitrification in four paddy soils. Int. Soc. Microbial Ecol. J., 9(5): 1062-75.

Wang, B., Zheng, Y., Huang, R., Zhou, X., Wang, D., He, Y., Jia, Z., 2014. Active ammonia oxidizers in an acidic soil are phylogenetically closely related to neutrophilic archaeon. Appl. Environ. Microbiol., 80(5): 1684-91.

Wang, C., Zhu, G., Wang, W., Yin, C., 2013. Preliminary study on the distribution of ammonia oxidizers and their contribution to potential ammonia oxidation in the plant-bed/ditch system of a constructed wetland. J. Soils and Sedim., 13(9): 1626-1635.

Wang, L., Li, Y., Niu, L., Zhang, W., Zhang, H., Wang, L., Wang, P., 2018. Response of ammonia oxidizing archaea and bacteria to decabromodiphenyl ether and copper contamination in river sediments. Chemosphere, 191: 858-867.

Wang, S., Wang, Y., Feng, X., Zhai, L., Zhu, G., 2011. Quantitative analyses of ammonia-oxidizing Archaea and bacteria in the sediments of four nitrogen-rich wetlands in China. Appl. Microbiol. Biotechnol., 90(2): 779-87.

Ward, B.B., 1996. Nitrification and Denitrification: Probing the Nitrogen Cycle in Aquatic Environments. Microbial Ecol., 32(3): 247-61.

Ward, B.B., Voytek, M.A., Witzel, K., 1997. Phylogenetic Diversity of Natural Populations of Ammonia Oxidizers Investigated by Specific PCR Amplification. Microbial Ecol., 33(2): 87-96.

Watson, S.W., Bock, E., Harms, H., Koops, H.-P., Hooper, A.B., 1989. Nitrifying bacteria. Bergey's manual of systematic bacteriology, 3. Baltimore, Md: The Williams and Wilkins Co.

Watson, S.W., Bock, E., Valois, F.W., Waterbury, J.B., Schlosser, U., 1986. Nitrospira marina gen. nov. sp. nov.: a chemolithotrophic nitrite-oxidizing bacterium. Arch. Microbiol., 144(1): 1-7.

Whitby, C.B., Saunders, J.R., Rodriguez, J., Pickup, R.W., McCarthy, A., 1999. Phylogenetic differentiation of two closely related Nitrosomonas spp. That inhabit different sediment environments in an oligotrophic freshwater lake. Applied and Environ. Microbiol., 65(11): 4855-62.

Whittaker, M., Bergmann, D., Arciero, D., Hooper, A.B., 2000. Electron transfer during the oxidation of ammonia by the chemolithotrophic bacterium Nitrosomonas europaea. Biochimica et Biophysica Acta, 1459(2-3): 346-355.

Wuchter, C., Abbas, B., Coolen, M.J., Herfort, L., van Bleijswijk, J., Timmers, P., Strous, M., Teira, E., Herndl, G.J., Middelburg, J.J., Schouten, S., Sinninghe Damste, J.S., 2006. Archaeal nitrification in the ocean. Proc. Natl. Acad. Sci. U. S. A., 103(33): 12317-22.

Zhang, L.M., Offre, P.R., He, J.Z., Verhamme, D.T., Nicol, G.W., Prosser, J.I., 2010. Autotrophic ammonia oxidation by soil thaumarchaea. Proc. Natl. Acad. Sci. U. S. A., 107(40): 17240-5.

Zhang, Y., Chen, L., Dai, T., Tian, J., Wen, D., 2015. The influence of salinity on the abundance, transcriptional activity, and diversity of AOA and AOB in an estuarine sediment: a microcosm study. Appl. Microbiol. Biotechnol., 99(22): 9825-33.

Zhou, L., Wang, S., Zou, Y., Xia, C., Zhu, G., 2015. Species, Abundance and Function of Ammonia-oxidizing Archaea in Inland Waters across China. Sci. Rep., 5: 15969.