

Responses of nitrifying and denitrifying bacteria to flooding-drying cycles in flooded rice soil



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ABSTRACT

The flooding-drying cycle can cause obvious increases of nitrous oxide (N₂O) emissions from paddy soil. However the relationships between N₂O flux and N₂O concentrations in soil and the microbial driving mechanisms during the flooding-drying process are unclear. In this study, a flooding-drying incubation experiment was carried out with a paddy soil. The topsoil (0–6 cm) was divided into 6 micro-sublayers each of 1 cm depth which were sampled independently. Terminal restriction fragment length polymorphism (T-RFLP) and real-time quantitative polymerase chain reaction (qPCR) were employed to determine the community composition and abundance of nitrifiers and denitrifiers, respectively. Results showed that the dynamics of N₂O flux were more closely related to the N₂O concentrations at 2–3 cm in comparison with that at 4–5 cm depth in the soil profile. During the peak period of N₂O flux, the top three micro-sublayers (0–3 cm) simultaneously harbored significantly higher ammonia oxidizing bacteria (AOB) population sizes, and contained higher nitrate and lower ammonia concentrations. Therefore, the top soil (0–3 cm) possesses a strong ability to produce nitrate substrate for denitrification during the flooding-drying process, and the drying surface soil, with O₂ penetration, favoured N₂O generation. In contrast, although the bottom soil (4–6 cm) contained abundant nitrate reductase gene (*narG*) copy numbers, it maintained low levels of AOB abundance, which could suggest that low nitrifying activity would be the major restriction limiting N₂O production in this layer. In conclusion, the flooding-drying process induced significant N₂O emissions from the paddy soil, which were closely related to the increasing nitrifying capability in the topsoil within 0–3 cm and the dynamics of N₂O concentrations at 2–3 cm depth.

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1. Introduction

Nitrous oxide (N₂O) is a potent greenhouse gas contributing to global warming with 298 times higher global warming potential than carbon dioxide (CO₂) on a 100-year time scale (Pachauri and Reisinger, 2007). N₂O is also involved in the destruction of stratosphere ozone (Ravishankara et al., 2009). Agricultural systems are the main emission source of anthropogenic N₂O, and accounted for 58% of the global anthropogenic N₂O emissions in 2005 (Metz et al., 2007). Paddy rice fields comprise about 10% of the world's cultivated land, and the properties of paddy soils are greatly affected by human activities. Among various management practices, flooding-drying is a common manipulation for rice

cultivation, and large amounts of N₂O are emitted during this process (Xu et al., 1997; Peng et al., 2011). However, the microbial driving mechanisms of N₂O emissions during this process are unclear.

Soil N₂O emissions are influenced by various environmental factors, such as temperature, moisture, substrate availability and pH and etc. (Skiba et al., 1998; Hou et al., 2000; Smith et al., 2003). Among them, soil moisture is considered as a key factor (Weitz et al., 2001; Jauhiainen et al., 2012). Soil moisture influences soil redox status (Xing et al., 2002) and also affects the activities of nitrifiers and denitrifiers (Jha et al., 1996; Amha and Bohne, 2011; Ruser et al., 2006; Scheer et al., 2008). It has been shown that substantial N₂O fluxes occur when water filled porosity (WFPS) is between 70–90% (Dobbie et al., 1999; Hou et al., 2012; Xu et al., 2013). In paddy fields, N₂O fluxes mainly occur during the flooding-drying process while they are at minimum levels under flooding (Minami, 1987; Chen et al., 1997; Tsuruta et al., 1997).

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N_2O fluxes from agricultural soils have been intensively studied in recent years (Freney, 1997; Bateman and Baggs, 2005; Lin et al., 2012), but the relationships between the N_2O flux from soil and the N_2O concentration produced in soil profile and the mechanisms involved have rarely been investigated. Previous research has demonstrated that soil N_2O concentrations are largely related to the water table or water level, and N_2O accumulates in the narrow depth just above water table (van Groenigen et al., 2005; Jørgensen et al., 2012; Minamikawa et al., 2013). However, N_2O emissions may not always be directly related to the N_2O concentration in the soil profile (Hosen et al., 2000, 2002; Gao et al., 2014), but are dependent on its location. Generally, N_2O in the subsoil is barely emitted through the topsoil due to the microbial consumption of N_2O during long distance diffusion (Arah et al., 1991; Hopkins et al., 1997). It is predicted that the N_2O produced in surface soil might be the important source for N_2O emissions (Gao et al., 2014; Denmead et al., 1979). Gradients of soil texture, chemical and biochemical properties within topsoil still exist, which could largely influence N_2O production, consumption and emission (Weitz et al., 2001), especially during the flooding-drying process, but the mechanisms involved remain unknown.

To date, the community composition and abundance of nitrifiers and denitrifiers in upper soil layers (0–15 cm or 0–20 cm) in relation to N_2O emissions have been well investigated. It has been demonstrated that the variations in ammonia oxidizing archaea (AOA) are not correlated to N_2O fluxes in cultivated soils (Di et al., 2010a; Andert et al., 2011) except for acidic soils where AOA are the major functional nitrifiers (Lehtovirta-Morley et al., 2011; Yao et al., 2011; Jung et al., 2014). In contrast, ammonia oxidizing bacteria (AOB) are the important nitrifying community in most soils (Di et al., 2009; Xia et al., 2011) and have been linked to N_2O emissions (Di et al., 2010b, 2014; Xia et al., 2013). Among the denitrifiers, the role of the nitrate reductase gene (*narG*), nitrite reductase genes (*nirK*, *nirS*) and nitrous oxide reductase gene (*nosZ*) have commonly been studied. It has been reported that shifts in *narG*-containing communities, including cell numbers and community composition, in the top layer (0–5 cm) of paddy soils were closely related to N_2O emissions during flooding-drying cycles while *nosZ*-containing communities, although sensitive to water content changes, were not linked to N_2O fluxes (Liu et al., 2012). Recently, Uchida et al. (2014) also found that the abundance of denitrifying gene transcripts (*nirK*, *nirS* and *nosZ*) in the top 1 cm layer of soil was more significantly related to N_2O flux than those in the 1–3 cm layer. These results suggest that sublayers within the top soil might differentially produce and emit N_2O . Therefore, it is important to understand the differential microbial driving mechanisms of N_2O production and emission of defined micro-sublayers within the top soil, which would be crucial for efficient nitrogen fertilization and manipulation of N_2O emissions in paddy fields. We hypothesise that the differential responses of nitrifiers and denitrifiers to the flooding-drying process within the upper soil profile could trigger the variations of N_2O production, consumption and emission.

In the present study, micro-sublayers of one centimeter thickness were sequentially sampled from soil cores. The objectives were to investigate the relationships between N_2O concentrations at various soil depths and N_2O emissions during the flooding-drying process, and the microbial driving mechanisms of N_2O production and consumption.

2. Materials and methods

The soil sampling site is located in Changsha, China (28°14'08"N and 113°13'05"E), which had been under double rice cropping for over 100 years. The paddy soil (0–20 cm) was collected after late rice harvest in December 2012. After air-drying the soil was sieved

through a 2 mm sieve while visible plant residues were removed manually. This soil was derived from quaternary red clay and classified as loamy clay (Hydragric Anthrosols) (Soil Survey Staff, 2010), its basic properties were as follows: Soil pH=5.3, total C = 16 g C kg⁻¹, total N = 1.7 g N kg⁻¹, NH₄⁺-N = 36 mg kg⁻¹, NO₃⁻-N = 5.2 mg kg⁻¹, organic matter = 27 g kg⁻¹.

2.1. Soil incubation

The soil incubation experiment consisted of two groups, one for gas collection with 6 pots continuously flooded (CF) and flooding-drying (FD) treatments. The other was for soil sampling at four time points during the flooding-drying process with 12 pots. All the treatments had three replicates. Each pot (19 cm diameter, 20 cm high) contained 5 kg air-dried soil which was well mixed with 1.09 g urea (100 mg N kg⁻¹ dry soil). The pots were filled with distilled water leaving about 2 cm of free water on the soil surface and incubated at 28 °C. After 17 days under flooding, the pots for the flooding-drying treatment were drained (Liu et al., 2012) while the rests remained flooded.

For soil gas collection, twin silicon tubes (total 30 cm long, internal diameter 10 mm, wall thickness 2 mm) connected with a U

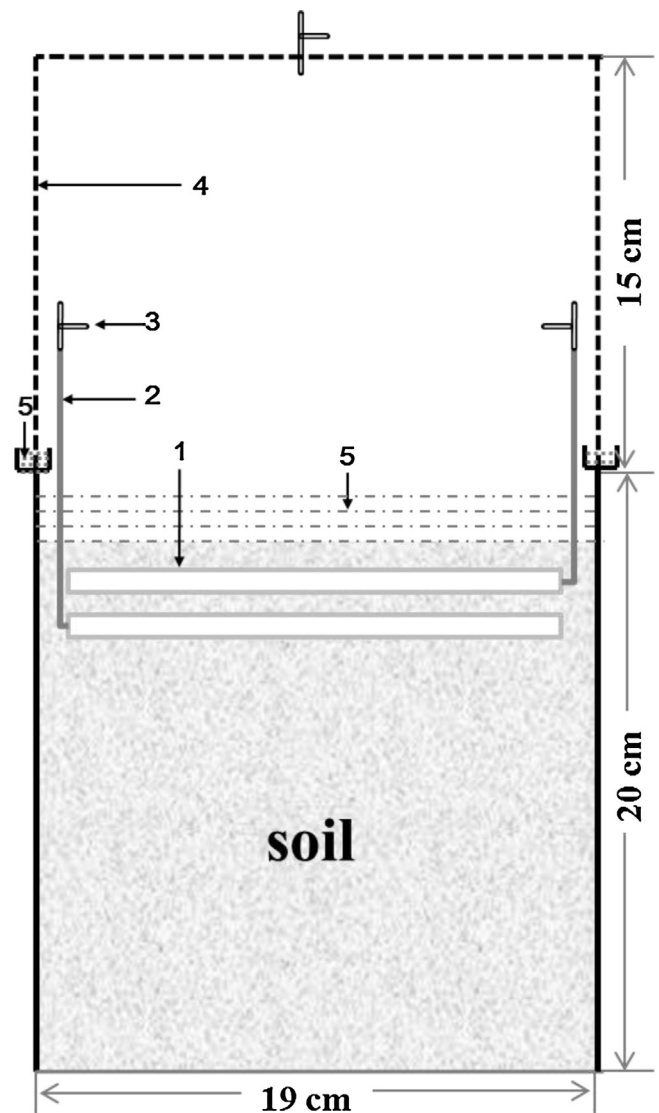


Fig 1. Schematic diagram of the pot for gas sampling. 1: silicon tubes, 2: U type stainless steel tube, 3: three-way stopcock, 4: gas sampling cover, 5: water.

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