

Biomass composting combined with dicyandiamide influence greenhouse gas emission and microbial community in rice paddy

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Abstract

Characterizing the rhizosphere microbial community composition associated with enhanced crop yield and (or) greenhouse gases is an important first step towards understanding the role of the microbiota in rice paddies. This research aimed to decipher the influence of straw tea composting product combined with dicyandiamide amendment on greenhouse gas emission and microbial community in rice paddies. The results indicated that amendment of biological nitrification inhibitors can mitigate gas emissions and significantly increase rice yield by 41.70%, and improve the growth and development of the root system. Furthermore, composting product can mitigate greenhouse gas emissions, and bionitrification inhibitor combined with straw compost tea can effectively increase the growth and development of rice, the number of panicles, which are respectively 9.75% and 18.34%. However, the biological nitrification inhibitor impacted the communities of nitrogen-fixing bacteria (Proteobacteria), bacteria capable of eliminating nitrogen (Nitrospirae) as well as Verrucomicrobia known to be one of the most common and diverse phyla in soil habitats. As with bacteria, a distinct community structure and distribution patterns for archaea were observed in soils; however, the abundance, richness, regularity and diversity of archaea communities were significantly less in the different samples. In addition, biological nitrification inhibitors have had an impact in Euryarchaeota, responsible for the elimination of methane.

Introduction

Of the agriculturally important crops, rice is typically cultivated in China with an average annual rice planting area of 35 million ha and contributes about 30% of total world rice production (Bandumula, 2018). Generally, rice is grown in soils deficient in N. As the world's largest consumer of N fertilizer, China currently covers 30% of the world's N consumption while a low nitrogen use efficiency (NUE) of about 30-35% in rice paddies (Peng et al. 2006). However, humanity is facing the dual challenges of both ensuring food productivity while concomitantly minimizing the significant environmental impacts such as greenhouse gas (GHG) emissions of intensive agriculture (Trivedi et al. 2013) due to excessive use of N fertilizer (Ren et al. 2020).

To address these concerns, composting has become an increasingly attractive method for solving excessive use of chemical fertilizer concerns as well as for the long-term improvement of soil fertility and productivity. For instance, Ren et al. (2020) indicated that 15 t ha⁻¹ of straw compost combined with 60 kg ha⁻¹ of dicyandiamide (DCD) application reduced the use of chemical fertilizers dramatically, with a demand of 20% in China. However, as global warming worsens and the greenhouse effect intensifies, emissions of N₂O and CH₄ in rice paddy harbored more concerns (Awasthi et al. 2018). The global warming impact of CH₄ and N₂O would be 30 and 210 times, respectively, compared to carbon dioxide (CO₂) (Alcano et al. 2007). Dicyandiamide (DND) is known to limit speed of the nitrification-denitrification process, thus decreasing the losses of nitrogen (N) and the ubiquitous production of N₂O in soil and other environments.

In agroecosystems, soil microorganisms represent the largest reservoir of biodiversity. The soil microbiome performs various ecological services such as mineralization of organic matter, nutrient cycling, and the promotion of plant growth (Saravanakumar et al. 2017). Remarkably, the microorganisms involved in the nitrification reaction are autotrophic Bacteria which participate in the oxidation of an inorganic substrate as the sole source of energy and mineral carbon (Zhou et al. 2015). Nitrosation and nitrification constitute the fundamental processes of nitrification in farmland soils, during which the intermediate product NH₄⁺ was converted into NO₂⁻ and NH₂OH that mainly completed by Ammonia-Oxidizing Archaea (AOA) and Ammonia-Oxidizing Bacteria (AOB). Accordingly, AOB plays an important role in the transformation of NO₂⁻ into NO₃⁻ (Wu et al. 2020). During the process, the first step is ammonia which is oxidized to nitrite by *Nitrosomonas*, *Nitrococcus*, and *Nitrospira*. When nitrite in turn is oxidized to nitrate by *Nitrobacter*, *Nitrococcus*, and *Nitrospira*, which form the second step. It should be noted that this process only happens with relatively low organic matter. The compositions of AOA and AOB in paddy soils can be influenced by multiple physicochemical properties, such as organic carbon and nitrogen contents, soil type, pH, and flooding-drying cycle. For example, AOB are well adapted to eutrophic environments with high loads of organic carbon and total ammonium (NH₄⁺ and NH₃), such as agricultural soils and wastewaters (Erguder et al. 2009). However, in some paddy soils, AOB is one to three orders of magnitude more abundant than AOA, although paddy soils generally have high nitrogen and organic carbon contents, especially after intense fertilization over long periods of the term (Chen et al. 2011). The net nitrification rate was significantly related to the abundance of AOB (Chen et al. 2015), and DCD exerted more significant inhibition on AOB growth than AOA (Shen et al. 2013). Besides, DCD was mainly studied in croplands and grasslands, where amendment of DCD (10-30 kg ha⁻¹) was indicated to be effective in mitigating N₂O emissions (Belastegui et al. 2003). However, few studies focused on the short-term shifts in the rhizosphere microbial community under the combinatory of straw compost and DCD to better understand the impact on soil quality, improve agroecosystem productivity, and mitigate greenhouse gas emissions.

Therefore, this study aimed to investigate effect of straw composting on the growth and development of rice by substituting organic fertilizer and amendment of biological nitrification inhibitors. The objectives were to: (i) minimize the N₂O emissions in rice paddies; (ii) identify the rhizosphere microbial structure; (iii) decipher the impact of the application of composts as means of restoring soil fertility.

Materials And Methods

Site description and experiment layout

The field experiment was located in the plantation of Anhui Science and Technology University (E117 - 33-39 ", W32 - 52-49 ") from July 2019 to November 2019. Sowing was conducted on June 12th, Transportation in the field was done on July 2nd, rice was harvested on November 1st. The frost-

free period of this region is 230 days, with an average annual temperature and precipitation of 15 °C and 1200 mm, respectively. The soil was characterized as cinnamon soil, with pH 6.02, and contains 20.8 g kg⁻¹ organic matter, 2.14 g kg⁻¹ total N, 3.21 g kg⁻¹ total P, 7.53 g kg⁻¹ total K, and 25.8 mg kg⁻¹ available P, 115 mg kg⁻¹ available K of arable soil layer. The variety of rice was Quan 9 You 063. The rice straw used was obtained after harvesting in our field.

The field experiment was performed in a completely randomized block design with three replicates for each of the following treatments (Table1), and the plots (2 m*2 m) were isolated between any two adjacent plots for preventing water and fertilizer exchange.

Table 1

Treatment setup

Treatment	The concentration
CK	50 kg 15-15-15 compound fertilizer + 30 kg urea per 666.67 m ²
T1	4.05 t/acre compost + nitrification inhibitor DCD (3.5-% of 50 kg)
T2	4.05 t/acre compost + biological nitrification inhibitor spray 6 times (4l/time)
T3	4.05 t/acre compost + straw compost tea spray 15 times (4l/time)
T4	4.05 t/acre compost + straw compost tea 15 times + biological nitrification inhibitor spray 6 times

Gas sampling method

According to the temperature, the gas collection was eight times from July to September. The sampling in the static chamber and back box method was adopted. The gas prefer every five minutes during sampling with a syringe, three times in total for each treatment. The temperature in the static chamber and the soil surface was recorded each time the gas was withdrawn. The main trial greenhouse gas emission flow note (CO₂, NH₄, N₂O) were measured using a gaseous phase chromatograph Agilent 798A (Agilent, USA); the interpolation method was used to calculate unlocked daily emission flows according to Chen et al. (2017). Hence, the relative CO₂, NH₄, and N₂O emissions were obtained by calculating daily values following the given equation below.

$$F = \frac{dc}{dt} \times \frac{M}{V_0} \times \frac{P}{P_0} \times \frac{T_0}{T} \times H$$

Note: F, greenhouse gas emission flux (mg/(m²h⁻¹)), dc/dt, slope of the regression curve of gas volume fraction with time during sampling, M, molar mass of the gas (g mol⁻¹), V₀, molar volume of the gas under the standard gas (22.41 l•mol⁻¹), P and P₀, pressure of sampling point (Pa) and standard state, respectively, T and T₀ are the absolute temperature (K) at the time of sampling and the absolute temperature under standard conditions (273.15 K), H is the height (m) of the sample box.

Soil sampling, properties analysis and DNA extraction

Three rhizosphere sub-samples were collected from each replicate plot and mixed as a soil sample at the harvest time. All soil samples were stored at -70 °C for subsequent DNA extraction. Soil DNA was extracted from 0.25 g soil subsamples using the PowerSoil DNA Isolation Kits (MoBio Laboratories Inc., Carlsbad, USA).

PCR amplification, library preparation and Miseq sequencing

DNA extracted from each soil sample served as a template for 16S rRNA gene Bacteria primers 520F (5'- AYT GGG YDT AAA GNG - 3') and 802R (5'- TAC NVG GGT ATC TAA TCC - 3') (Claesson et al. 2009) were used to amplify the V4 hypervariable regions of the bacterial 16S rRNA gene.

Statistical analysis

As statistical test were considered statistically significant at $P < 0.05$. The sequences retained were analyzed using the UPARSE pipeline to generate an OTU table with representative sequences (Edgar 2013). Subsequent analyses (Alpha and Beta diversities) were based on OTUs by Unifrac distance and map analysis evaluating the similarity of bacterial communities in different samples. Principal coordinates analysis (PCoA) based on Bray-Curtis

distances were conducted to evaluate beta-diversity patterns using the vegan package of R (version 3.5.1, R Core Team. 2015). The classification of the representative sequences for each OTU was performed using the RDP classifier against the RDP Bacterial 16S rRNA database (Cole et al. 2009). The realization of the ternary figure was proceeded using the ggtern package. Co-occurring networks were constructed using ggplot2 packages of R (3.3.1; Duncan Murdoch, 2016) and was derived by defining a boundary between pairs of coexisting OTUs, using as an input matrix with Spearman correlations ($P < 0.4$).

Results

N₂O, CO₂, CH₄ emission characteristics

The N₂O emission in rice paddies sprayed with biological nitrification inhibitors and straw compost. It had two peaks, one occurred on August 11th, and a smaller peak occurred on August 30th. The rank of N₂O emissions was CK>T3>T4>T1>T2 on August 11th. The N₂O emissions from CK processing were 517.75 t C•hm⁻², the N₂O emission of T3 is 481.10 t C•hm⁻², which is 7.08% lower than the N₂O emission of CK. Another smaller peak was on August 21st. The lowest emissions were T1 (55.88 t C•hm⁻²), followed by T4 (61.36 t C•hm⁻²). As a result, T1 with the application of DCD and T2 with the application of biological nitrification inhibitors effectively mitigate the gas emission of rice paddies, T4 with the application of biological nitrification inhibitors and compost tea harbored slight fewer gas emissions.

Figure 1

Note

CK, purified fertilizer; T1, nitrification inhibitor DCD; T2, biological nitrification inhibitor; T3, straw compost tea; T4, straw compost tea + biological nitrification inhibitor. The same as below.

The CO₂ emissions were characterized by two peaks (Fig. 1.B). One occurred on July 21st, which the highest CO₂ emissions were T3 and CK, followed by T4, T2, and T1, the CO₂ emissions of T3 were 1608 t C•hm⁻², which is 129% of T1. Another peak occurred on August 21st, and the lowest emissions were treatment T1 (522.00 t C•hm⁻²).

The lowest value of CH₄ emission occurred on August 11th, rank in gas followed order T2 (-0.10 t C•hm⁻²) > T4 (-0.18 t C•hm⁻²) > T3 (-0.66 t C•hm⁻²) > CK > T1 (-1.16 t C•hm⁻²). The application of DCD (T1) and biological nitrification inhibitor (T2) effectively inhibited gas emissions in rice paddies compared to compost tea and biological nitrification inhibitor combined with compost tea. Overall, T1 with the application of DCD and T2 with the application of biological nitrification inhibitors indicated high efficiency from the perspective of gas emission of rice paddies.

Total greenhouse gas emissions and analysis of rice yield and yield composition

Straw compost combined with nitrification inhibitors throughout the rice growth period significantly migrated CH₄ emissions in rice paddies. T1 significantly reduced CH₄ emissions, followed by T2 with biological nitrification inhibitors compared with CK. The reduction of N₂O emissions in the rice paddies was made by using the combined application of straw compost instead of chemical fertilizers and nitrification inhibitors. N₂O emissions from T1, T2, T3, and T4 decreased by 51.56%, 46.71%, 13.84%, and 30.10%, respectively.

Table 2

Combination of straw compost and nitrification inhibitor treatment on rice field gas emissions and effects of straw compost combined with nitrification inhibitor on rice yield components

Treatment	CO ₂ emission (t C•hm ⁻²)	CH ₄ emission (kgc/hm ²)	N ₂ O emission (kgc/hm ²)	Total emission (t C•hm ⁻²)	Spike number / (ten thousand /hm ²)	Kernels per spike / (per spike)	1000-grain weight (g)	Yield (kg/hm ²)
CK	40.57±1.01a	-5.56±0.14b	2.89±0.07a	40.57±1.01ab	8.20±0.21b	208.20±5.21e	22.09±0.55b	5897.49±10.34e
T1	30.72±0.77c	-9.56±0.24c	1.40±0.03b	30.72±0.77e	9.70±0.24a	240.50±6.01ab	22.36±0.56ab	7288.50±12.51c
T2	34.71±0.87b	-5.36±0.13b	1.54±0.04b	34.71±0.87d	9.00±0.23ab	246.38±6.16a	22.36±0.56ab	7710.25±13.35b
T3	40.81±1.02a	-5.62±0.14b	2.49±0.06a	40.81±1.02a	8.50±0.21b	232.13±5.80c	22.37±0.56ab	6774.72±11.73d
T4	39.74±0.99a	-4.50±0.11a	2.02±0.05b	39.74±0.99b	8.67±0.22b	239.51±5.99ab	22.86±0.57a	8356.78±38.23a

Table 3
Composting straw compost combined with nitrification inhibitors and their potential for comprehensive warming in rice fields

Treatment	CO ₂ GWP (kg/hm ²)	CH ₄ GWP (kg/hm ²)	N ₂ O GWP (kg /hm ²)	Total GWP (kg /hm ²)
CK	40572.15	-139.03	861.37	41294.49
T1	30726.33	-238.88	416.20	30903.65
T2	34710.88	-134.01	460.37	35037.24
T3	40814.00	-140.38	741.64	41415.26
T4	39739.99	-112.43	601.21	40228.78

Rice quality analysis

Table 4
Effects of straw compost combined with nitrification inhibitor on rice quality

Treatment	Albumen (%)	Chalkiness degree (%)	Chalky rice rate (%)	Gel consistency (%)	Indica rice amylose (%)	Brown rice rate (%)	Head rice yield (%)	Luminousness (%)
CK	7.00±0.17a	14.74±0.37c	7.93±0.20b	119.41±2.99b	10.88±0.27b	80.17±2.00ab	72.58±1.81b	0.82±0.02b
T1	6.00±0.15bc	19.77±0.49a	19.53±0.649a	120.30±3.01b	10.44±0.26b	80.73±2.02ab	73.64±1.84a	0.85±0.02ab
T2	5.37 ±0.13c	20.08 ±0.50a	15.34±0.38ab	130.15 ±3.25a	11.73±0.29ab	81.48 ±2.04a	73.64 ±1.84a	0.88 ±0.02a
T4	6.40 ±0.16ab	18.38±0.46ab	18.75±0.547a	120.25±3.01b	12.26±0.31a	81.27±2.03ab	73.43 ±1.84a	0.83 ±0.02b

The protein content of treatments T1, T2, T3, and T4 was significantly lower than that of CK (Table 3). Spraying biological nitrification inhibitors and straw compost tea decreased significantly, but spraying biological nitrification inhibitors and straw compost tea can effectively improve the degree of protein reduction. The chalkiness rate of treatments T1, T2, T3, and T4 increased significantly. Only treatment CK and T3 met the requirements (High-quality premium rice chalky kernel ratio < 10%), and all other treatments had reached second-class high-quality rice requirements. The amylose content of indica rice in each treatment was significantly higher than that of the control group. Except for T1, the amylose content of high-quality indica rice reached the national standard (13.0%-22.0%) and was sprayed with biological nitrification inhibitor and straw. The treatment of composted tea was significantly higher than that of DCD, indicating that biological nitrification inhibitors can effectively replace DCD. Overall, T1, T2, T3, and T4 conformed to the high-quality national rice (brown rice rate>80%, whole rice rate>66%). It comprehensively shows that the quality of rice obtained by using biological nitrification inhibitor instead of DCD and combined with straw compost tea has reached the national high-quality rice standard.

Microbial Diversity Analysis

β-diversity

In order to visualize the differences in the composition of bacterial communities and archaea, the analysis of the principal coordinates (PCoA) was carried out, respectively. The ordination of PCoA revealed a distinct sample grouping based on different treatments (PERMANOVA, pseudo-F = 12.09, P < 0.001; ANOSIM, P < 0.001). Regarding the analysis of the main coordinates, the bacterial communities were separated by the first component (PCoA1) with a total of 48% and the second component (PCoA2) with a total of 23% (Fig. 2A). In archaea, the total of the first component was 59%, and that of the second was 25.5% (Fig. 2B).

Figure 2 Microbial community taxonomic composition of rhizosphere soil bacteria and Archaea communities

The taxonomic sequences of all species were classified into 30 bacterial phyla. The dominant bacteria were: Proteobacteria, Gemmatimonadetes, Acidobacteria, Chloroflexi, Nitrospirae, Verrucomicrobia, accounting for more than 75.0% of the total bacterial 16 rRNA gene sequences. Considering the CK and T3 treatments, most OTUs belonged to Acidobacteria and Proteobacteria (Fig. 3A). It may indicate that Acidobacteria played a key role in the denitrifying activity and used nitrites as a source of nitrogen, suggesting their involvement in the nitrogen cycle. T4 was the highest in OTU-39, followed by T2. OUT-11, belonging to the phylum Chloroflexi, can increase organic carbon and participate in nitrification. After all these analyses, T4 treatment of straw composting tea and biological nitrification inhibitor was the highest, followed by T1 treatment of DCD.

Figure 3B shows an abundance of two phyla Thaumarchaeota and Nanoarchaeota, of CK and T3. The relative abundances of OUT-4, OUT-45, OUT-72, OUT-161, and OTU-1 were high; Nitrososphaeracea usually participates in the soil nitrogen cycle. OUT-105 presents a class of Bathyarchaeia, a class of archaea exhibiting various metabolic modes in the phylum of Crenarchaeota; this can degrade proteins, carbohydrates, fatty acids, and aromatic compounds. Acting as a heterophilic metabolism of organic matter like methyl compounds, this class has the power to perform autotrophic metabolism while using H₂ and CO₂ to produce acetic acid. It also has the ability to conceal the reduction of nitrates and sulfate while participating in the metabolic cycle of methane. OTU-105 was also used in the T4. OTU-161, OTU-188, and OTU-14 were all Archean microorganisms of the phylum Woesearchaeia and Nanoarchaeota; they were affected by pore size and were most abundant in T4 treatment. Besides, the nitrogen and organic carbon content have not influenced the composition of these two communities and have contributed to supporting our rice plant's growth.

Figure 3

The proportions of taxa of Bacteria and Archaea shared due to the high intraspecies variability (Fig. 4). The ternary plot showed that it shared higher proportions of bacterial communities and the higher proportions of Archaea. Proteobacteria have generally been found as essential parts of the rhizosphere community. Besides the compartment type, they were also present at the level of the phylum. The scanty phylum Chloroflexi was significantly increased in the soil of the T2 treatment, whereas in control CK and T1, the bacterial community of the samples sheltered more Acidobacteria, Gemmatimonadetes, Nitrospirae, and Verrucomicrobia (Fig. 4.A). Ternary plots for Archaeal OTUs indicated for the top and subsoil (Fig. 4.B) that the rhizosphere made not house specialized OTUs, which would be located at the respective tip area of the ternary route. For all the treatments, specialized archaea were found when the surface and the subsoil were compared, which were classified as the Euryarchaeota. However, the majority of arched OTUs were located in the middle of the ternary plot, mainly home to Thaumarchaeota including 1, 10, 21, 24, 3, 34, 4, 5, 62, ubiquitous OTUs (all Nitrosphaera), which were present in all samples and contributed to at least 85% of readings analysis.

Figure 4

Discussion

Rice is an exception among cereal crops, as it tolerates a wide range of climatic, soil, and hydrological conditions. Nowadays, with the improvement of the standard of living and the tendency to increase in population and decrease in arable land, increasing rice production is becoming the important subject in China. Over time, the overuse of chemical fertilizers has not only led to deterioration in soil quality but has also led to large-scale degradation of ecosystems and long-term loss of productivity. In order to address these concerns, the substitution of chemical fertilizers with organic amendment is becoming a useful method to increase the efficiency of the use of plant resources as well as to improve the quality of agricultural products. The excessive accumulation of straw resources, the efficient use of straw, and sustainable development have received increasing attention. In the present study, the spraying of organic nitrification inhibitors and compost straw tea instead of DCD and chemical fertilizers were used in the experiment to investigate the effects on rice productivity and greenhouse gas emissions. They were associated with the rhizosphere microbiome.

The effect of the dicyandiamide on greenhouse gases from rice fields showed that nitrification inhibitors significantly reduce N₂O emissions compared with DCD. This finding was consistent with Wang et al. (2017), who investigated the amendment of DCD indicated no significant effect on the CO₂ emissions of rice fields, but significantly reduce CH₄ emissions by 20.7% and N₂O emissions by 31.9%, and significantly increased rice yield by 10.0%. Overall, the biological nitrification inhibitor is the liquid secreted by the roots of sorghum, indicating more suitable for application compared to DCD. In this study, the result revealed that the paddy field's CH₄ emissions under DCD at the late stage of rice growth had the best effect on reducing CO₂ and N₂O. These results are confirmed by Wu et al. (2020), who investigated the use of straw compost to replace chemical fertilizers with DCD partially and found that straw compost can mitigate greenhouse gas emissions while stabilizing wheat yields and improving the wheat quality.

Concerning the effect of the return of straw to the field to replace certain chemical fertilizers on greenhouse gases from paddy fields, in this experiment, the return of straw to the field was mainly used for the composting of tea straw, which can reduce greenhouse gas emissions. The results showed that applying straw compost tea in combination with nitrification inhibitor could significantly increase rice plant height, chlorophyll content, and the number of tillers and nodes. Similar results were found by Yu et al. (2020) when combined application of inhibitors and straw (UIS) relieved the retention of urea-N in soil and decreased urea-N recovery rate by 41.29% compared with US at the tillering stage. As such, straw return stimulates immobilization and as a result changes the way fertilizer N is preserved and supplied (Yu et al 2020; Cui et al. 2021; Isabel et al. 2021). Similarly, with the addition of urease inhibitor and nitrification inhibitor, the forms of inorganic N are structured in soil, and under flooded conditions, the continuity of fertilizer NH₄⁺ influences the retention and distribution pattern of N in soil, in particular combined with the application of straw. Therefore, biological nitrification inhibitors can be used instead of DCD, which can significantly increase rice yield, thousand-grain weight, growth, and development of the root system at the stage of rice seedlings and the height of the plant.

Proteobacteria, Gemmatimonadetes, Acidobacteria, Chloroflexi Nitrospirae and Verrucomicrobia are the main phyla present in all samples (Fig. 3A), for archaea, Thaumarchaeota and Nanoarchaeota are the most abundant (Fig. 3B), in agreement with former studies, the correction organic compost increases bacterial diversity compared to conventional chemical fertilizers (Chaudhry et al. 2012), which could be attributed to the increased input of organic carbon substrates. Still, diversity and wealth weren't much different depending on the payment. Thus, the addition of diseases and natural nitrification impediments didn't completely impact the microbial communities of the rhizosphere in terms of diversity, richness and abundance. The results showed a high abundance of Acidobacteria in our soil with further perfection in the T3 treatment and the CK control. These results are aligned with Eichorst et al. (2018), who confirm that acid bacteria are ubiquitous in colorful agrarian lands, and argue that acid bacteria are veritably well

equipped with genes that beget the metabolism of inorganic and organic sources of nitrogen. Regarding the composting biomass associated with dicyandiamide, our results don't impact the bacterial community of acidobacteria; still, we've plant that this combination plays a vital part in nitrogen obsession. According to Salam et al. (2020), acidic bacteria can effectively reduce nitrates and nitrates, and can also be nitric oxide; this is proven by genomic data which supports their active participation in nitrogenous nutrient circuits.

Numerous other bacterial diversities have been plant in our rice civilization soil, indeed if this bone is scarce because of the influence of the diseases used, it's obviously of the phylum of proteobacteria, of the class of Alphaproteobacteria of the rubric bradyrhizobium known with other rhizobias to take atmospheric nitrogen and fix it in ammonia (NH₃) or ammonium (NH₄), Caetanoanollés (1997); Betaproteobacteriies are known as being a more abundant class that's substantially intended to exclude organic matter and nutrients. While the Acidobacteria and the Proteobacteria are abundant, we plant the Nitrospirae, which develop in nearly all the treatments but in small amounts, these play a function of the elimination of Nitrogen (Rodríguez-Marconi 2015). Also, at the phylum position, we observed a significant reduction in the abundance of Gemmatimonadetes in the soil from T3 treatments. Beseeming to say that these tend to be favored by moisture, the Gemmatimonadetes accumulate the polyphosphate and reduce the vacuity of phosphate to the factory. Verrucomicrobia was another phylum present in our growing soil and lower present; it's the only phylum among numerous others, having a vastly increased soil abundance of the T3 treatment, although little is known about the physiology of these bacteria, studies have shown that Verrucomicrobia can be described as oligotrophic. Their abundance decreases when nitrogen is in excess. These bacteria play a vital part in the declination of organic carbon (Nixon et al. 2019). Chloroflexi was another phylum present in our rice growing soil; this too wasn't detected as an abundant group but was much more represented in the T1 and T4 treatment 6 (Fig. 3B). These results are aligned with other studies that showed these bacteria are acetate Oxidant Syntrophic and belong to bacteria of methanazation (Campanaro and Guivernau 2017).

The soil tested in this study exhibited another of microorganisms called Archaea, comprising the Euryarchaeota and Crenarchaeota, between which is placed the root of the phylogeny Archaea. In addition, the results revealed the presence of four phyla; hence, the most abundant was Thaumarchaeota. Spang et al. (2010) plant that the phylum of Thaumarchaeota revealed by molecular webbing of 16S rRNA genes is an Archaea able of aerobically oxidizing ammonia. The secondary phylum was Nanoarchaeota. Therefore, Nanogearchaeum isolates have only been attained from submarine hydrothermal reflections and terrestrial hot springs. The Euryarchaeota present in our soil from all the treatments were significantly less abundant; still, the phylum contained all the methanogenesis. This can be explained grounded on Garrity et al. (2001), defending that Archaea produces methane CH₄ by methanogenesis. Some of the archaea phylum Euryarchaeota are aerobic and anaerobic hyperthermophiles. The last phylum were Crenarchaeota, Thermoplasmata less abundant than other that if distinguished from other Archaea on the base of their Ribosomal RNA sequence. Cubonova et al. (2005) have shown that some have an absence of Histones in their inheritable material. This cultivated contains numerous obligate anaerobic species which bear sulfur for their development.

Conclusion

In summary, straw composting combined with nitrification inhibitors can mitigate greenhouse gas emissions and improve rice yield. The dominant bacteria were Proteobacteria, Gemmatimonadetes, Acidobacteria, Nitrospirae, and the dominant genus were *Thaumarchaeota* and *Nanoarchaeaeota*. Thus, the overall impact of the combined straw composting and nitrification inhibitor should be taken into consideration when designing a high-efficiency rice field strategy.

Declarations

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Consent for publication

Yes

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Figures

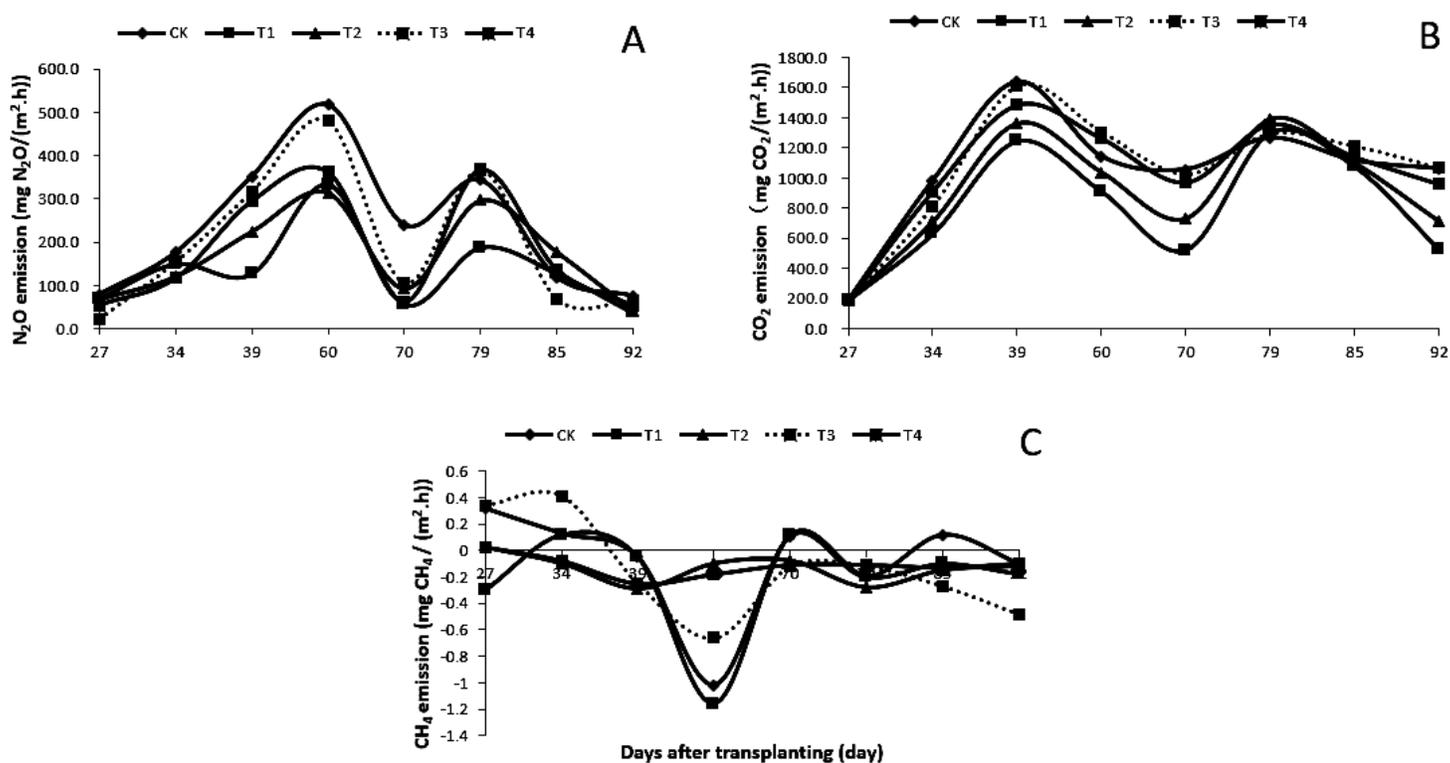


Figure 1

The effects of straw compost combined with nitrification inhibitor treatments on the N₂O (A); CO₂ (B); CH₄ (C) emission rate of rice field soil

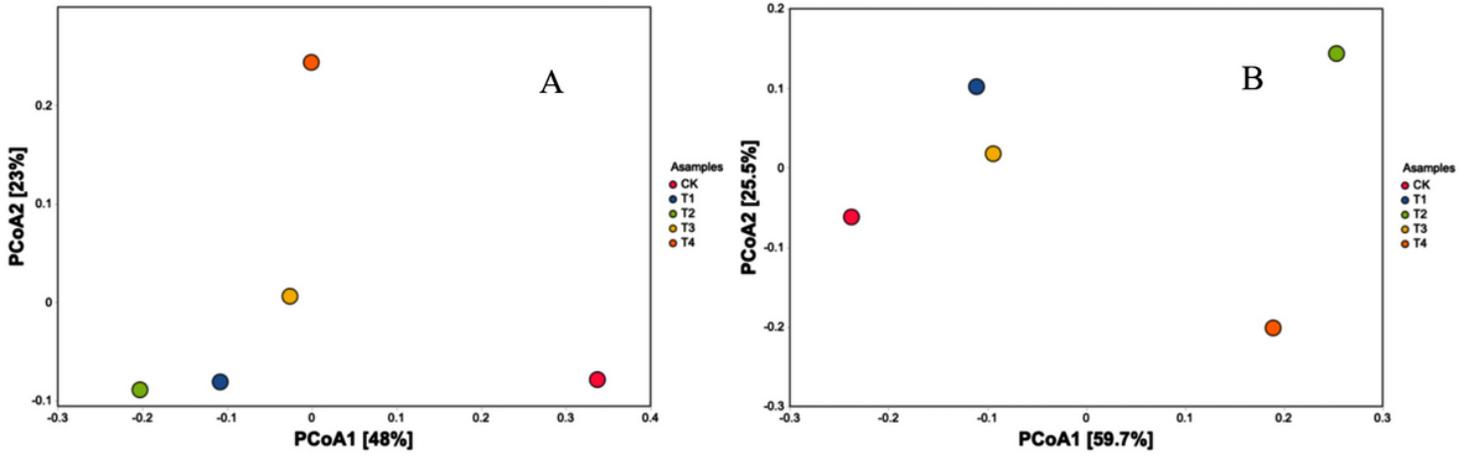


Figure 2

Analysis of the principal coordinates (PCoA) of Bacteria (A) and Archaea (B) over the weighted Unifrac distance

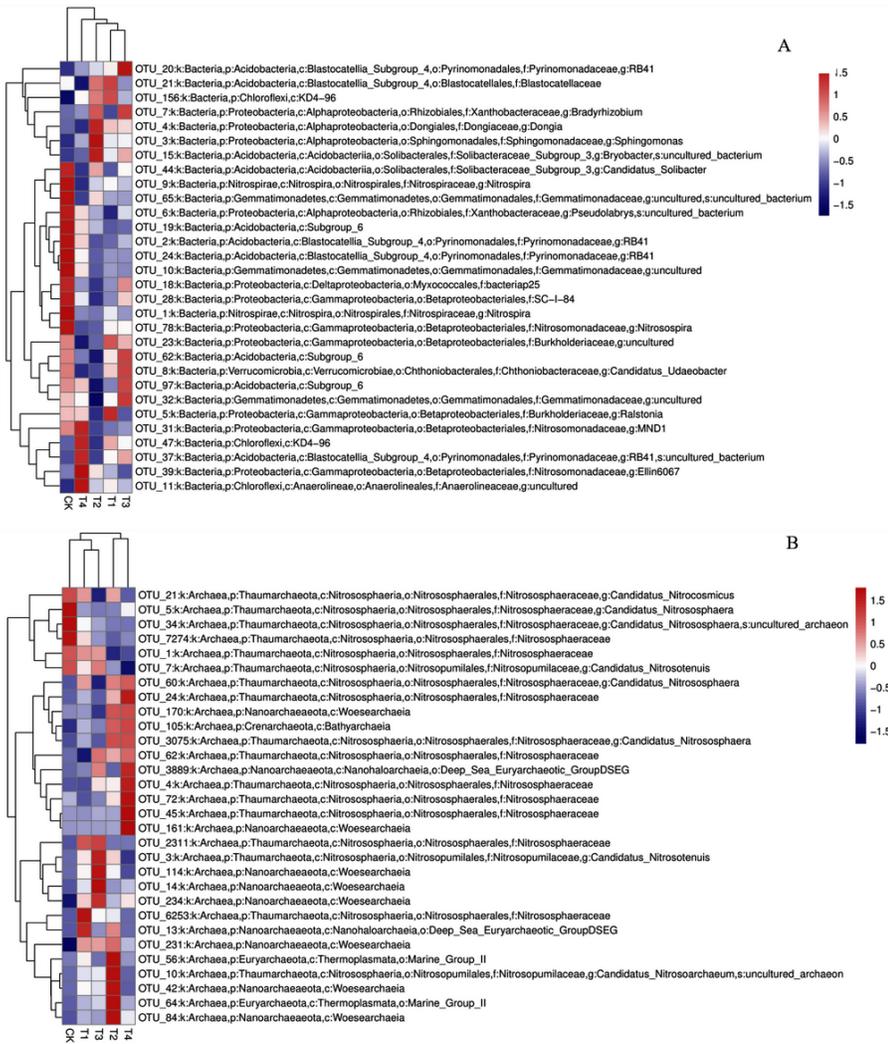
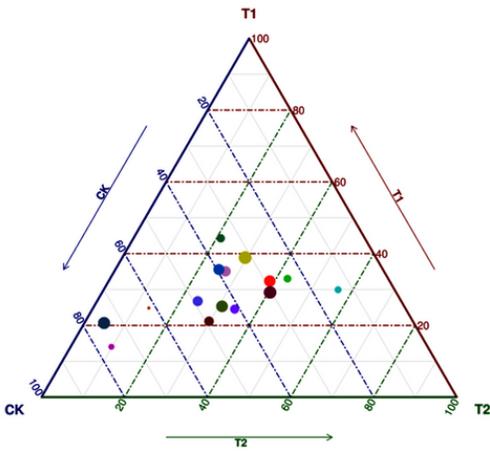


Figure 3

(A) Cluster analysis of the abundance of bacterial species; (B) Cluster analysis of the abundance of archaea species



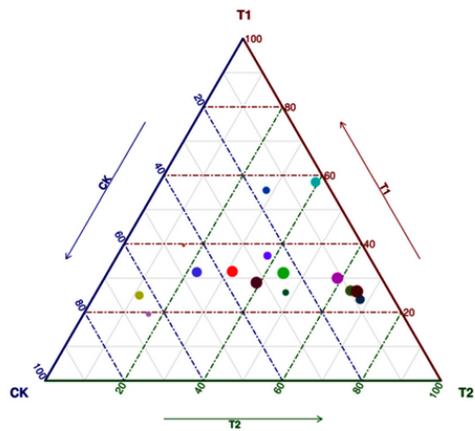
Taxonomy

- OTU_13: Bacteria.p:Nitrospirae.c:Nitrospira.o:Nitrospirales.f:Nitrospiraceae.g:Nitrospira
- OTU_18: Bacteria.p:Proteobacteria.c:Deltaproteobacteria.o:Myxococcales.f:bacteriap25
- OTU_23: Bacteria.p:Acidobacteria.c:Blastocatella_Subgroup_4.o:Pyrinomonadales.f:Pyrinomonadaceae.g:RB41
- OTU_33: Bacteria.p:Proteobacteria.c:Alphaproteobacteria.o:Sphingomonadales.f:Sphingomonadaceae.g:Sphingomonas
- OTU_39: Bacteria.p:Proteobacteria.c:Gammaproteobacteria.o:Betaproteobacteriales.f:Nitrosomonadaceae.g:Ellin6067
- OTU_43: Bacteria.p:Proteobacteria.c:Alphaproteobacteria.o:Dongiales.f:Dongiaceae.g:Dongia
- OTU_44: Bacteria.p:Acidobacteria.c:Acidobacteria.o:Solibacterales.f:Solibacteraceae_Subgroup_3.g:Candidatus_Solibacter
- OTU_47: Bacteria.p:Chloroflexi.c:KD4-96
- OTU_53: Bacteria.p:Proteobacteria.c:Gammaproteobacteria.o:Betaproteobacteriales.f:Burkholderiaceae.g:Ralstonia
- OTU_53: Bacteria.p:Proteobacteria.c:Alphaproteobacteria.o:Rhizobiales.f:Xanthobacteraceae.g:Pseudolabrys.s:uncultured_bacterium
- OTU_52: Bacteria.p:Acidobacteria.c:Subgroup_5
- OTU_55: Bacteria.p:Gemmatimonadetes.c:Gemmatimonadetes.o:Gemmatimonadales.f:Gemmatimonadaceae.g:uncultured_s:uncultured_bacterium
- OTU_73: Bacteria.p:Proteobacteria.c:Alphaproteobacteria.o:Rhizobiales.f:Xanthobacteraceae.g:Bradyrhizobium
- OTU_83: Bacteria.p:Verrucomicrobia.c:Verrucomicrobiales.o:Chthoniobacterales.f:Chthoniobacteraceae.g:Candidatus_Udaebacter
- OTU_93: Bacteria.p:Nitrospirae.c:Nitrospira.o:Nitrospirales.f:Nitrospiraceae.g:Nitrospira

Grade

- 5
- 10
- 15

A



Taxonomy

- OTU_13: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae
- OTU_16: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae.g:Candidatus_Nitrososphaera.s:uncultured_archaeon
- OTU_105: Archaea.p:Crenarchaeota.c:Bathyarchaeia
- OTU_123: Archaea.p:Nanoarchaeota.c:Nanoarchaeota.o:Deep_Sea_Euryarchaeotic_GroupDSEG
- OTU_21: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae.g:Candidatus_Nitrososphaera
- OTU_24: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae
- OTU_33: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae.g:Candidatus_Nitrosotenus
- OTU_34: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae.g:Candidatus_Nitrososphaera.s:uncultured_archaeon
- OTU_43: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae
- OTU_42: Archaea.p:Nanoarchaeota.c:Woesearchaeia
- OTU_53: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae.g:Candidatus_Nitrososphaera
- OTU_56: Archaea.p:Euryarchaeota.c:Thermoplasmata.o:Marine_Group_3
- OTU_62: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae
- OTU_6253: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae
- OTU_73: Archaea.p:Thaumarchaeota.c:Nitrososphaeria.o:Nitrososphaerales.f:Nitrososphaeraceae.g:Candidatus_Nitrosotenus

Grade

- 5
- 10
- 15

B

Figure 4

Ternary phase diagram of Bacteria (A) and Archaea (B)

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