Short communication

Archaea diversity in vegetation gradients from the Brazilian Cerrado

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ABSTRACT
We used 16S rRNA sequencing to assess the archaeal communities across a gradient of Cerrado. The archaeal communities differed across the gradient. Crenarchaeota was the most abundant phyla, with Nitrospphaerales and NRPJ as the predominant classes. Euryarchaeota was also found across the Cerrado gradient, including the classes Methanocellales and Methanomassiliicoccaceae.

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Soil microorganisms constitute a third of the Earth's biomass, playing important ecological and biogeochemical roles in terrestrial ecology. Among the microorganisms that inhabit soils, the domain Archaea is particularly important because it is abundant and plays important roles in C and N cycling. This domain constitutes one of the three major evolutionary lineages of life on Earth, and although it has long been believed that these organisms mainly inhabit extreme environments, previous studies demonstrated that they are widely distributed around the world in different types of soils.

Since the recognition of the archaean domain in the tree of life, studies have been focused to explore their presence and function in a wide range of environments. With the advance of DNA-based molecular tools and genomic analysis, the knowledge of this domain has evolved and the

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current archaeal classification is rapidly moving. Presently, 20 archaeal phyla are recognized by small subunit RNA databases; however, it has been reported that 14 phyla have no cultured representative. Most of culturable members of Archaea belong to the two main phyla Euryarchaeota and Crenarchaeota. Other new phyla have been proposed in the last years, for example Nanoarchaeota, based on the isolation of a hyperthermophilic symbiont Nanoarchaeum equitans and Thaumarchaeota. Most recently, two superphyla have been proposed, namely (i) TACK, which includes the phyla Thaumarchaeota, Aigarchaeota, Crenarchaeota and Korarchaeota, and (ii) Asgard, which consist in a sister group to TACK and are considered more closely related to the original eukaryote. Together with the advance of Archaea classification, their functional role in the ecosystem has also been the focus of recent studies. Members of Archaea carry out many steps in the nitrogen cycle, such as nitrate-based respiration and denitrification. Communities of autotrophic and heterotrophic Archaea catalyze iron and sulfur oxidation, which influence the release rate of metals and sulfur to the environment. Also, regarding the carbon cycle, all known methanogen organisms belong exclusively to Archaea domain and are generally found in oxygen-depleted environments.

In Brazil, studies regarding the diversity of Archaea have been conducted for some important ecosystems, such as Amazonian and Atlantic forests, as well as in mangroves. In the case of the Brazilian Cerrado, previous studies investigated the diversity of archaea in soils from the Central Plateau and found that Crenarchaeota was the most abundant archaeal group in the ecosystem. However, it has been hypothesized that the vegetation and soil conditions in the Cerrado from Northeastern Brazil differs from those of the Central Plateau. Therefore, the pattern of Archaea communities would be different because the vegetation and soil conditions drive soil microorganisms. Previous studies have shown differences between bacterial diversity in the soils obtained from Cerrado in the Northeast when compared to those from the Central Plateau. Therefore, we used next-generation sequencing of the 16S rRNA gene in soil samples from vegetation gradients obtained from Campo graminioide, Cerrado stricto sensu, Cerrado and Floresta decidual to understand the diversity of Archaea in the soils of Cerrado in Northeastern Brazil.

The study was conducted in a preserved Brazilian Cerrado within Sede Cidades National Park (PNSC) (04° 02’-08’S and 41° 40’-45’W), Northeast, Brazil. This region presents two distinct seasons (wet and dry) with an annual average temperature at 25 °C and rainfall of 1558 mm distributed in February through April. We evaluated four different areas (with 1000 m² each one) in a gradient of vegetation (‘Campo graminioide’, ‘Cerrado stricto sensu’, ‘Cerrado’ and ‘Floresta decidual’) (Table 1; Fig. 1).

| Table 1 – Vegetation diversity indices in the Cerrado areas. | |
|--------------------------------|-----------------|-----------------|-----------------|
|                              | Campo graminioide | Cerrado stricto sensu | Cerrado | Floresta decidual |
|--------------------------------|-----------------|-----------------|-----------------|-----------------|
| Plant richness | 4.7 | 11 | 17 | 18 |
| Plant diversity | 0.2 | 0.85 | 1.10 | 1.11 |
| Plant density | 4.7 | 27.1 | 35.0 | 51.8 |
| Vegetation | a | b | c | d |

* Andropogon fastigiatus; Aristida longifolia; Eragrostis mayurensis.  
* Andropogon fastigiatus; Aristida longifolia; Terminalia fagifolia; Magonia pubescens; Hymenaea courbaril; Plathymenia reticulata; Qualea grandiflora; Combretum melliflum; Lippia origanoides; Anacardium occidentale; Simarouba versicolor; Vatairea macrocarpa.  
* Aspidosperma discolor; Parika platycepha; Terminalia fagifolia; Piptadenia moniliformis; Plathymenia reticulata; Qualea parviflora; Anacardium occidentale; Copaífera coriacea; Thiloa glaucocarpa; Casearia grandiflora.  
* Aspidosperma multiflorum; Aspidosperma subincanum; Campomanesia aromatica; Casearia lasiophylla; Casearia ulmifolia; Copaífera coriacea; Ephedrus pisocarpus; Piptadenia moniliformis; Pterocarpus violaceus; Thiloa galucocarpa.  
* Species/100 m².  
* H/100 m².  
* Individual/100 m².  
* Species of plants present.
at 72 °C. In the second step, a unique pair of Illumina Nextera XT indexes (Illumina, San Diego, CA) was added to both ends of the amplified products. Each 50 μL reaction contained the following: 23.5 μL of nuclease-free water (Certified Nuclease-free, Promega, Madison, WI, USA), 5.0 μL of 10× High Fidelity PCR Buffer (Invitrogen, Carlsbad, CA, USA), 4.8 μL of 25 mM MgSO4, 1.5 μL of dNTP (10 mM each), 5.0 μL of each Nextera XT index (Illumina, San Diego, CA, USA), 1.0 unit of Platinum Taq polymerase High Fidelity (Invitrogen, Carlsbad, CA, USA), and 5.0 μL of each product from previous PCR. The conditions for this second round PCR were as follows: 95 °C for 3 min to denature the DNA, with 8 cycles at 95 °C for 30 s, 55 °C for 30 s, and 72 ° C for 30 min, with a final extension of 5 min at 72 °C.

After indexing, the PCR products were cleaned up using Agencourt AMPure XP – PCR purification beads (Beckman Coulter, Brea, CA, USA), according to the manufacturer’s manual, and quantified using the dsDNA BR assay Kit (Invitrogen, Carlsbad, CA, USA) on a Qubit 2.0 fluorometer (Invitrogen, Carlsbad, CA, USA). Once quantified, different volumes of each library were pooled into a single tube in equimolar concentration. After quantification, the molarity of the pool was determined and diluted to 2 nM, denatured, and then diluted to a final concentration of 8.0 pM with a 20% PhiX (Illumina, San Diego, CA, USA) spike for loading into the Illumina MiSeq sequencing machine (Illumina, San Diego, CA, USA).

Sequence data were processed using QIIME following the UPARSE standard pipeline according to Brazilian Microbiome Project22 to produce an OTU table and a set of representative sequences. Briefly, the reads were truncated at 240 bp and quality-filtered using a maximum expected error value of 0.5. Pre-filtered reads were dereplicated and singletons were removed and filtered for additional chimeras using the RDP gold database using USEARCH 7.0. These sequences were clustered into OTUs at a 97% similarity cutoff following the UPARSE pipeline. After clustering, the sequences were aligned and taxonomically classified against the Greengenes database (version 13.8).23 The sequences were submitted to the NCBI Sequence Read Archive under the number SRP091586.

Redundancy Analysis (RDA) was used to determine the correlation between archaeal community structure and soil physicochemical properties. The OTU table was initially analyzed using Detrended Correspondence Analysis (DCA) to evaluate the gradient size of the species distribution, which indicated linearly distributed data (length of gradient <3),
revealing that the best-fit model for the data was RDA. Forward selection (FS) and the Monte Carlo permutation test were applied with 1000 random permutations to verify the significance of soil chemical properties upon a microbial community. We used permutational multivariate analysis of variance (PERMANOVA) to test whether sample categories harbored significantly different archaeal community structure. RDA plots were generated using the software Canoco 4.5 (Biometrics, Wageningen, The Netherlands), and PERMANOVA and alpha diversity index were calculated with the software PAST. To determine the differences in abundance of archaeal groups among soil samples, the Statistical Analysis of Metagenomic Profiles (STAMP) software package was used. The OTU table was used as input, and P-values were calculated using the two-sided Welch’s t-test, while confidence intervals were calculated using DF Welch’s inverted and correction was made using Benjamini–Hochberg false discovery rate.

In this study, we examined the archaeal structure and composition in the soils from vegetation gradients from the Cerrado. We used 16S rRNA sequencing to assess the archaeal communities and correlated them with soil chemical parameters. Our results showed that soil parameters differed between the sampling sites. Areas under Campo graminioide, Cerrado stricto sensu and Cerrado differed from Floresta decidual (Table 2). Soil moisture, pH, and TOC content were similar between Cerrado stricto sensu and Cerrado, and they were the lowest and highest in Campo graminioide and Floresta decidual, respectively.

These markedly different soil conditions, mainly between Campo graminioide and Floresta decidual, exist because of the differences in plant cover and the communities, both of which can influence soil properties. For example, Campo graminioide is covered mostly by grasses, whereas Floresta decidual is covered by trees. RDA showed the differences between the archaeal communities across the gradients (Fig. 2) and indicated that the Floresta decidual was the most distinct compared to the other areas.

Additionally, RDA showed that the composition of archaeal communities was strongly correlated with specific soil properties across the Cerrado gradients. Our results showed that the archaeal community of Floresta decidual correlated with soil moisture, TOC, CEC, P, K, and N. On the other hand, soil temperature and pH correlated with Campo graminioide, Cerrado stricto sensu and Cerrado. These results indicate that the archaeal community differs across the gradients of the Cerrado and is influenced by soil conditions. Because Campo graminioide, Cerrado stricto sensu and Cerrado had similar soil conditions, their archaeal communities were more similar to each other when compared to Floresta decidual. According to Catão et al., the soil conditions drive the differences in the diversity of Archaea in the Brazilian Cerrado. These authors compared and contrasted Cerrado denso and Mata de Galeria from the Brazilian Cerrado and found differences in the community structures of Archaea. The varied soil conditions found across the gradients of vegetation have influenced the bacterial diversity. Interestingly, our results highlight the soil pH as a significant driver of archaeal communities in these soils. According to Gorres, soil pH is the main driver of archaeal community structure in soils. This strong correlation between soil pH and the microbial community structure may be because pH and the other physicochemical soil parameters are so closely related. Most microorganisms have intracellular pH that varies in the range of pH 7 ± 1; therefore, a small variation of the environmental pH could expose microorganisms to stress. Archaea were detected in all analyzed samples and showed very low diversity compared to the bacterial community found in the same samples. Interestingly, Floresta decidual presented the lowest alpha diversity when compared to the other areas (Fig. 3). It has been suggested that an environment in equilibrium, such as forest, the ecosystem functioning is maintained based on lower levels of diversity, but high abundance of microorganisms; in contrast, environments under stress would present an increased diversity, which leads to a higher functional diversity and, consequently,

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**Table 2 – Soil physicochemical properties at different sites across the gradient of Cerrado.**

| Site                  | Moisture (%) | Temperature (°C) | TOC (g kg⁻¹) | pH  | P (mg kg⁻¹) | K (cmol L⁻¹) | CEC (cmol kg⁻¹) |
|-----------------------|--------------|------------------|--------------|-----|-------------|--------------|----------------|
| Campo graminioide     | 7.3a         | 32a              | 4.3c         | 4.5c| 3.9c        | 1.4b         | 2.28b          |
| Cerrado stricto sensu | 10.5b        | 30b              | 8.3b         | 4.3b| 3.9b        | 1.8b         | 2.31b          |
| Cerrado               | 11.9b        | 30b              | 9.1b         | 4.6b| 4.5b        | 1.6b         | 2.35b          |
| Floresta decidual     | 31.8b        | 28b              | 15.2c        | 4.9b| 5.3b        | 3.8b         | 4.91b          |

TOC, total organic C; CEC, cation exchange capacity. Values followed by the same letter within each column are not significantly different at the 5% level, as determined by Student’s t-test.

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**Fig. 2 – Redundancy analysis (RDA) of archaeal community patterns and soil characteristics from samples of Campo graminioide, Cerrado stricto sensu, Cerrado and Floresta decidual.** Arrows indicate correlation between environmental parameters and archaeal profile. The significance of these correlations were evaluated via the Monte Carlo permutation test and is indicated by * (P < 0.05).
The maintenance of essential ecosystem functions. Considering that Cerrado areas are more prone to environmental stress, such as high temperature, low moisture and oligotrophy, the higher archaeal diversity would be expected.

A total of 3,078 reads were clustered in 33 OTUs according to the Greengenes taxonomical classification. We found Crenarchaeota to be the most abundant phyla across the Cerrado gradients, among which Nitrospheerales and NRPJ were the predominant classes (Fig. 4). Organisms belonging to the largely non-thermophilic Crenarchaeota appear to be ubiquitous in soil systems and are dominant over euryarchaeal populations in grassland soils.

These findings agree with previous studies in the Brazilian Cerrado, which have reported Crenarcheota as the most dominant phylum and Nitrospheerales as an important group. The relative abundance of Nitrospheerales and NRPJ differed across the regions. Floresta decidual showed the highest abundance of Nitrospheerales, whereas Campo graminioide, Cerrado stricto sensu and Cerrado showed the highest abundance of NRPJ. Previously, Nicol et al. have indicated that Crenarchaeota from soils may have specific association with plant roots, playing an important role in the rhizosphere. Nitrospheerales are important ammonia-oxidizer organisms, and although ammonia oxidation occurs in both Bacteria and Archaea, the archaeal group dominates in both soil and marine environments. Nitrogen-related microorganisms are commonly found abundantly in forest soils, which may explain the higher abundance of Nitrospheerales in our forest samples. Also, Navarrete et al. showed that the diversity of ammonia-oxidizing archaeal communities tend to be higher in primary forests. On the other hand, the NRPJ group was more abundant in Cerrado sites. This group belongs to the Marine Benthic Group A, an uncultured archaeal cluster initially described from cold continental slope and deep-sea sediments. Members of this group are commonly found in oligotrophic soils, such as boreal forests, which may explain its higher abundance in our Cerrado samples. In summary, our results showed a high abundance of Crenarchaeota groups in our samples, with differential abundance between sites, suggesting that members of this group play distinct and important roles in the soil ecosystem.

The phylum Euryarchaeota is considered the most physiologically diverse and includes methanogens, halophiles and thermophile organisms. Members of this phylum were also found across the Cerrado gradients, including the classes Methanocellales and Methanomassiliicocccaceae. Interestingly, the Methanocellales class was detected only at Campo graminioide, which also had a high abundance of Methanomassiliicocccaceae. Similarly, Cerrado stricto sensu showed high abundance of Methanomassiliicocccaceae. The family Methanomassiliicocccaceae comprises of a methanogenic lineage of the class Thermoplasma, and members of the Methanocellales family are methanogenic organisms, contributing to the global methane cycle. In this sense, our results show that important groups related to carbon cycle are abundant in Campo graminioide and Cerrado stricto sensu.

![Fig. 3 – Diversity measurement based on Shannon’s index of archaeal communities in soils from Campo graminioide, Cerrado stricto sensu, Cerrado and Floresta decidual.](image)

![Fig. 4 – Average relative abundance of the most abundant archaeal groups in soils from Campo graminioide, Cerrado stricto sensu, Cerrado and Floresta decidual as revealed by the 16S rRNA gene ribotyping. For each sample type, the number of replicates is n = 9. Different lower letters indicate significant difference (FDR, P < 0.05) among samples.](image)
As shown in the RDA, pH was the main driver of the archaea communities across the gradients. It has been described that pH dominates the variation of archaeal diversity and community composition in tropical soils. In a large-scale study, the authors showed a niche specialization of terrestrial archaeal ammonia oxidizers based on pH, showing amoA abundance and diversity increased with soil pH. In our samples, the high soil pH found in the Floresta decidual area favored the dominance of Nitrospira, which is sensitive to low pH. On the other hand, a high abundance of Euryarchaeota, specifically Metanocellales, in the Campo graminioide region may be related to the low soil pH found in this area. According to Hu et al., 41 soil pH is a driver of methanogenesis and subsequently may promote shifts in the archaean community composition from Crenarchaeota to methanogenic Euryarchaeota.

In conclusion, our data showed that although the most of detected taxa are shared between all four areas, the archaean structure and abundance differed across these gradients and was strongly driven by soil physicochemical properties. The soil pH was the main driver of archaean communities in the studied soils, and this can be explained by the difference between the sites, where Floresta decidual presented higher values while Campo graminioide was more acidic. Results showed that Crenarchaeota was the most dominant phylum, followed by Euryarchaeota. Additionally, differential soil parameters lead to distinct functional potential of the communities, where Floresta decidual presented high abundance of groups related to the nitrogen metabolism while Campo graminioide and Cerrado stricto sensu presented high abundance of groups related to carbon metabolism. Also, Nitrospira were the most abundant order found across the gradients, and further studies are needed to evaluate their potential in N cycling.

Conflicts of interest

The authors declare no conflicts of interest.

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References

1. Schimel J. Playing scales in the methane cycle: from microbial ecology to the globe. Proc Natl Acad Sci USA. 2004;101:12400–12401.
2. Siles JA, Margesin R. Abundance and diversity of bacterial, archaean, and fungal communities along an altitudinal gradient in Alpine Forest Soils: what are the driving factors? Microb Ecol. 2016;72:207–220.
3. Catao E, Castro AP, Barreto CC, Kruger RH, Kyaw CM. Diversity of archaea in Brazilian savana soils. Arch Microbiol. 2013;195:507–512.
4. Woese CR, Kandler O, Wheelis ML. Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya. Proc Natl Acad Sci USA. 1990;87:4576–4579.
5. Schloss PD, Girard RA, Martin T. Status of the Archaeal and Bacterial census: an update. MBio. 2016;7:e00201–e0216.
6. Huber H, Hohn MJ, Rachel R, Fuchs T, Wimmer VC, Stetter KO. A new phylum of Archaea represented by a nanosized hyperthermophilic symbiont. Nature. 2002;417:63–67.
7. Brenchley-Armanet C, Boussau S, Grimaldi S, Forterre P. Mesophilic Crenarchaeota: proposal for a third archaeal phylum, the Thaumarchaeota. Nat Rev Microbiol. 2008;6:245–252.
8. Guy J, Ettema TJG. The archaeal ‘TACK’ superphylum and the origin of eukaryotes. Trends Microbiol. 2011;19:580–587.
9. Zaremba-Niedzwiedzka K, Caceres EF, Saw JH, et al. Asgard archaea illuminate the origin of eukaryotic cellular complexity. Nature. 2017;541:353–358.
10. Cabello P, Roldán MD, Moreno-Vivián C. Nitrate reduction and the nitrogen cycle in archaea. Microbiology. 2004;150:3527–3546.
11. Baker BJ, Banfield JF. Microbial communities in acid mine drainage. FEMS Microbiol Ecol. 2003;44:139–152.
12. Spang A, Ettema TJG. The methanogenic roots of Archaea. Nat Microbiol. 2017;2:17109.
13. Taketani RG, Tsai SM. Influence of different land uses on the structure of archaean communities in Amazonian anthroposols based on 16S rRNA and amoA genes. Microb Ecol. 2010;59:734–743.
14. Etto RM, Cruz LM, Jesus EC, et al. Prokaryotic communities of acidic peatlands from the Southern Brazilian Atlantic Forest. Braz J Microbiol. 2012;43:661–674.
15. Mendes LW, Taketani RG, Navarrete AA, Tsai SM. Shifts in phylogenic diversity of archaean communities in mangrove sediments at different sites and depths in southeastern Brazil. Res Microbiol. 2012;163:366–377.
16. Castro AP, Silva MRSS, Quirino BF, Bustamante MMC, Krüger RH. Microbial diversity in Cerrado biome (Neotropical Savanna) soils. PLoS One. 2016;11:e0148785.
17. Castro AAJF, Martins FR, Fernandes AG. The woody flora of Cerrado vegetation in the State of Piauí, Northeastern Brazil. Edinb J Bot. 1998;55:455–472.
18. Araujo ASF, Bezerra WM, Santos VM, et al. Distinct bacterial communities across a gradient of vegetation from a preserved Brazilian Cerrado. Anto van Leewu. 2017;110:457–469.
19. Oliveira MEA, Martins FR, Castro AAJF, Santos JR. Classes of cobertura vegetal do parque nacional de sete cidades (transicao campo-floresta) utilizando imagens TM/Landsat, NE do Brasil. Proceedings XIII Simpósio Brasileiro de Sensoriamento Remoto Anais. 2007;13:1775–1783.
20. Tedesco MJ, Gianello C, Bissani CA. Analises de solos plantas e outros materiais. Porto Alegre: UFRGS; 1995.
21. Caporaso JG, Lauber CL, Walters WA, et al. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. Proc Natl Acad Sci USA. 2011;108:4516–4522.
22. Pyro VS, Roesch LFW, Ortega JM, et al. Brazilian Microbiome Project: revealing the unexplored microbial diversity – challenges and prospects. Microb Ecol. 2014;67:237–241.
23. DeSantis TZ, Hugenholtz P, Larsen N, et al. Greengenes, a chimera-checked 16S RNA gene database and workbench compatible with ARB. App Environ Microbiol. 2006;72:5069–5072.
24. Anderson M. A new method for non-parametric multivariate analysis of variance. Aust Ecol. 2001;26:32–46.
25. Hammer Ø, Harper DAT, Ryan PD. Past: Paleontological Statistics Software package for education and data analysis. Paleontol Elect. 2001;4:9.
26. Parks DH, Tyson GW, Hugenholtz P, Beiko RG. STAMP: statistical analysis of taxonomic and functional profiles. Bioinformatics. 2014;30:3123–3124.
27. Welch BL. The generalization of “Student’s” problem when several different population variances are involved. Biometrika. 1947;34:28–35.
28. Benjamini Y, Hochberg Y. Controlling the false discovery rate – a practical and powerful approach to multiple testing. J Royal St Soc. 1995;57:289–300.
29. Gorres C-M, Conrad R, Petersen SO. Effect of soil properties and hydrology on Archaeal community composition in three temperate grasslands on peat. FEMS Microbiol Ecol. 2013;85:227–240.
30. Mendes LW, Tsai SM, Navarrete AA, Hollander M, van Veen JA, Kuramae EE. Soil-borne microbiome: linking diversity to function. Microb Ecol. 2015;70:255–265.
31. Nicol GW, Glover LA, Prosser JI. Molecular analysis of methanogenic archaeal communities in man-aged and natural upland pasture soils. Glob Change Biol. 2003;9:1451–1457.
32. Nicol GW, Tschernko D, Embley TM, Prosser JI. Primary succession of soil Crenarchaeota across a receding glacier foreland. Environ Microbiol. 2005;7:337–347.
33. Stieglmeier M, Mooshammer M, Kitzler B, et al. Aerobic nitrous oxide production through N-nitrosating hybrid formation in ammonia-oxidizing archaea. ISME J. 2014;8:1135–1146.
34. Leininger S, Urich T, Schloter M, et al. Archaea predominate among ammonia-oxidizing prokaryotes in soils. Nature. 2006;442:806–809.
35. Navarrete AA, Taketani RG, Mendes LW, Cannavan FS, Moreira FMS, Tsai SM. Land-use systems affect archaeal community structure and functional diversity in Western Amazon soils. Rev Bras Ci Solo. 2011;35:1527–1540.
36. Vetriani C, Jannasch JW, MacGregor BJ, Stahl DA, Reysenbach A-L. Population structure and phylogenetic characterization of marine benthic archaia in deep-sea sediments. Appl Environ Microbiol. 1999;65:4375–4384.
37. Jurgens G, Lindström K, Saano A. Novel group within the kingdom Crenarchaeota from boreal forest soil. Appl Environ Microbiol. 1997;63:3090–3095.
38. Iino T, Tamaki H, Tamazawa S, et al. Candidatus Methanomassiliicoccaceae fam. nov. and Methanomassiliicoccales ord. nov., for a methanogenic lineage of the class Thermoplasmata. Microb Environ. 2013;28:244–250.
39. Tripathi BM, Kim M, Lai-Hoe A, et al. pH dominates variation in tropical soil archaeal diversity and community structure. FEMS Microbiol Ecol. 2013;86:303–311.
40. Gubry-Rangin C, Hai B, Quince C, et al. Niche specialization of terrestrial archaeal ammonia oxidizers. Proc Natl Acad Sci USA. 2011;108:21206–21211.
41. Hu H-W, Zhang L-M, Yuan C-L, et al. The large-scale distribution of ammonia oxidizers in paddy soils is driven by soil pH, geographic distance, and climatic factors. Front Microbiol. 2015;6:938–946.