

Supplementary Materials

Table S1. Primers used for PCR amplification of archaeal and bacterial *amoA*, *nirS* and *nosZ* genes sequences.

Functional genes	Primer name	Sequence (5'-3')	PCR conditions	Reference
<i>AOA-amoA</i>	Arch-amoA26F	GACTACATMTTCTAYACWGAYTGGGC	94°C for 5 min × 1 cycle;	(Park et al., 2008)
	Arch-amoA417R	GGKGTCAATRTATGGWGGYAAAYGTTGG	94°C for 30 s, 53°C for 30 s, 72 °C for 60 s × 35 cycles;	
<i>AOB-amoA</i>	amoA-1F	GGGGTTTCTACTGGTGGT	72 °C for 7 min × 1 cycle	(Rotthauwe et al., 1997)
	amoA-2R	CCCCTCKGSAAAGCCTTCTTC	94°C for 30 s, 50°C for 30 s, 72 °C for 60 s × 35 cycles;	
<i>nirS</i>	Cd3aF	G TSAACG TSAAGGARACSGG	72 °C for 7 min × 1 cycle	(ThrobbÃ Ck et al., 2004)
	R3cd	GASTTCGGRTGSGTCTTGA	94°C for 5 min × 1 cycle;	
<i>nosZ</i>	nosZ-F	CGYTGTTCMTCGACAGCCAG	94°C for 30 s, 57°C for 30 s, 72 °C for 60 s × 30 cycles;	(Kloos et al., 2001)
	nosZ1622R	CGSACCTTSTTGCCSTYGCG	72 °C for 7 min × 1 cycle	
			94°C for 5 min × 1 cycle;	
			94°C for 60 s, 63°C for 30 s, 72 °C for 60 s × 35 cycles;	
			72 °C for 7 min × 1 cycle	

REFERENCES

- Kloos, K., Mergel, A., Rösch, C., Bothe, H. (2001). Denitrification within the genus *Azospirillum* and other associative bacteria. *Australian Journal of Plant Physiology*. 28, 991-998
- Park, S., Park, B., Rhee, S. (2008). Comparative analysis of archaeal 16S rRNA and *amoA* genes to estimate the abundance and diversity of ammonia-oxidizing archaea in marine sediments. *Extremophiles*. 12, 605-615
- 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. Microb.* 63, 4704-4712
- Throback, I.N., Enwall, K., Jarvis, A.S., Hallin, S. (2004). Reassessing PCR primers targeting *nirS*, *nirK* and *nosZ* genes for community surveys of denitrifying bacteria with DGGE. *FEMS Microbiol. Ecol.* 49, 401-417

Table S2. Soil chemical properties among treatments (mean \pm SE, $n = 5$).

	pH	AP mg kg ⁻¹	AK mg kg ⁻¹	AN mg kg ⁻¹	NH ₄ ⁺ -N mg kg ⁻¹	NO ₃ ⁻ -N mg kg ⁻¹	TC g kg ⁻¹	TN g kg ⁻¹	TC/TN
CK	5.11 \pm 0.07	5.3 \pm 1.3	51.3 \pm 7.2	62.9 \pm 5.6	4.70 \pm 0.96	4.91 \pm 0.74	11.2 \pm 0.1	2.10 \pm 0.03	5.31 \pm 0.04
AR	4.71 \pm 0.12	11.3 \pm 3.3	46.6 \pm 5.6	63.8 \pm 1.1	5.52 \pm 0.15	5.35 \pm 0.20	11.6 \pm 0.3	1.99 \pm 0.01	5.81 \pm 0.16
<i>p</i> -values	0.021*	0.128	0.625	0.890	0.447	0.586	0.255	0.004**	0.030*

CK: control, AR: acid rain with pH of 4.0. AP: available phosphorus; AK: available potassium; AN: alkaline nitrogen; NH₄⁺-N: ammonium nitrogen; NO₃⁻-N: nitrate nitrogen; TC: total carbon; TN: total nitrogen. The *p*-values refer to the independent-samples t-test results. ** Different at $p < 0.01$, * Different at $p < 0.05$, ^{ns} Non-different.

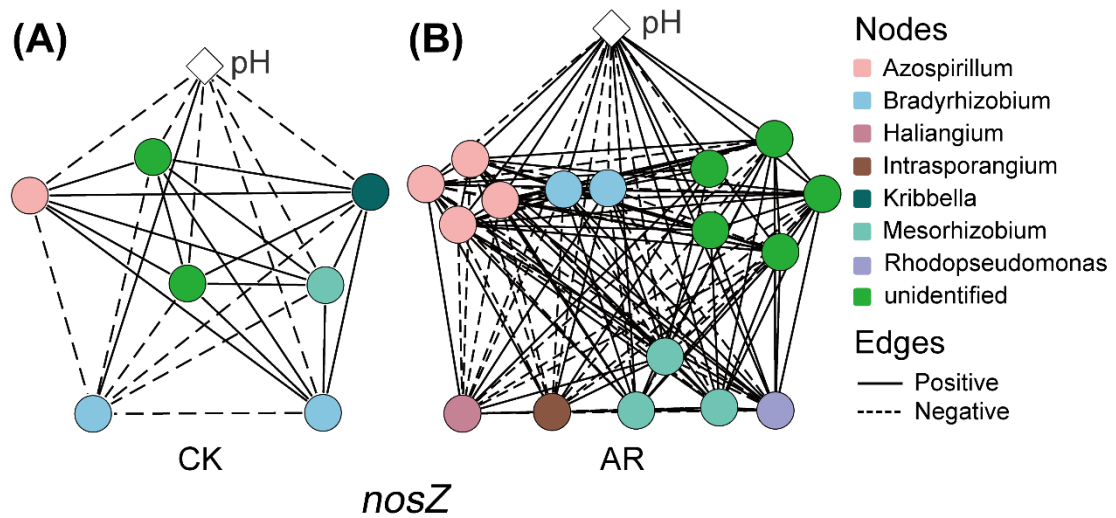


Figure S1. Subnetwork of microbial taxa and soil pH in CK **(A)** and AR **(B)** treatments. Connections stand for Spearman's correlation with $r > 0.7$ and statistically significant at $p < 0.05$. Nodes represent OTUs and soil factors with different shapes, and OTUs are colored by genus-level taxonomy. *nosZ*: denitrifiers harbouring *nosZ* gene.

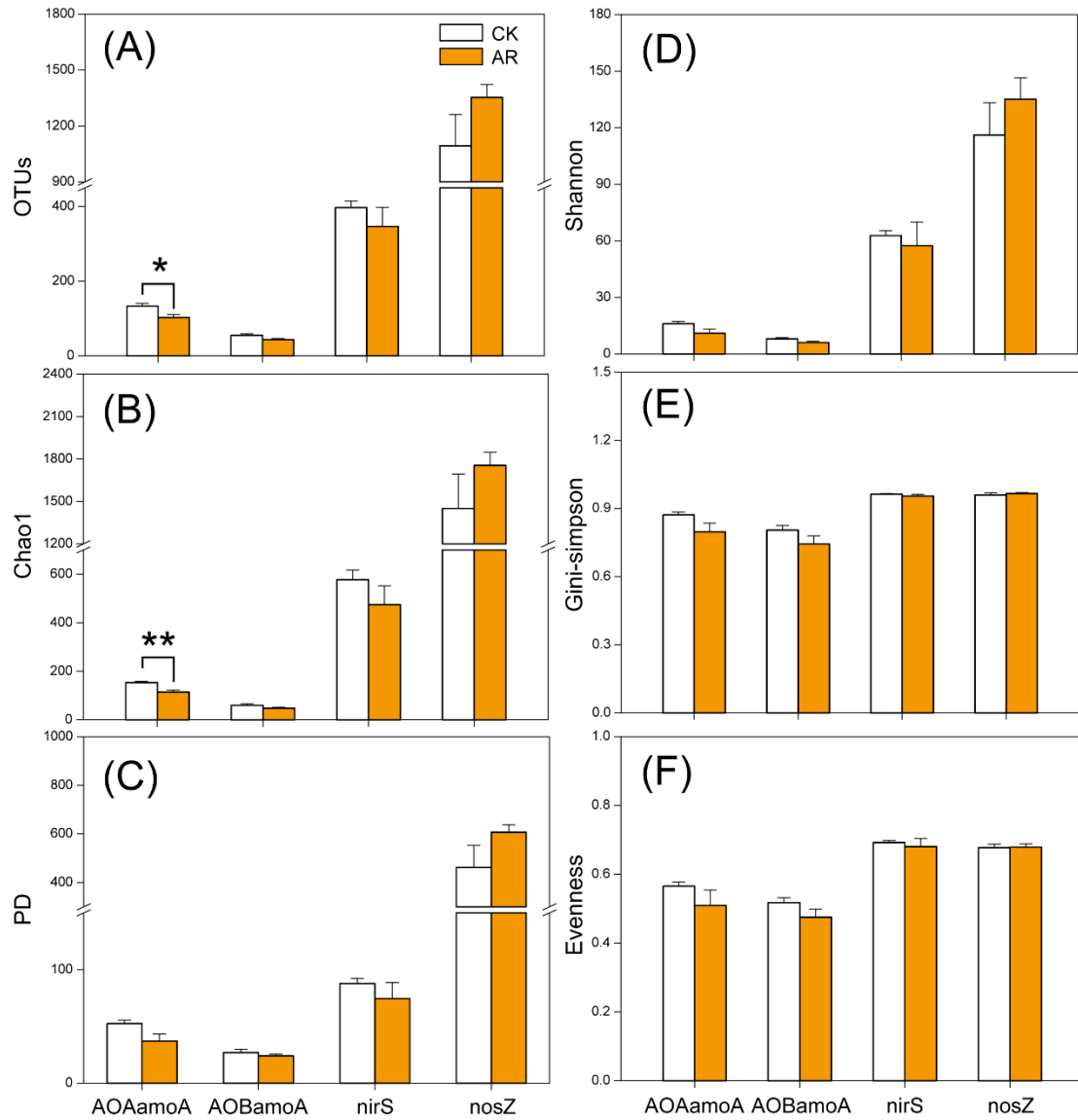


Figure S2. The microbial community richness and diversity indices of functional genes among treatments. OTUs: observed number of OTUs (A); Chao1: Chao1 richness index (B); PD: phylogenetic diversity index (C); Shannon: Shannon diversity index (D); Gini-Simpson: Gini-Simpson index (E); Evenness: Shannon's evenness index (F). CK: non-acid addition, AR: pH 4.0 acid rain. Data were presented as mean ± standard error ($n = 5$). ** $p < 0.01$, * $p < 0.05$.

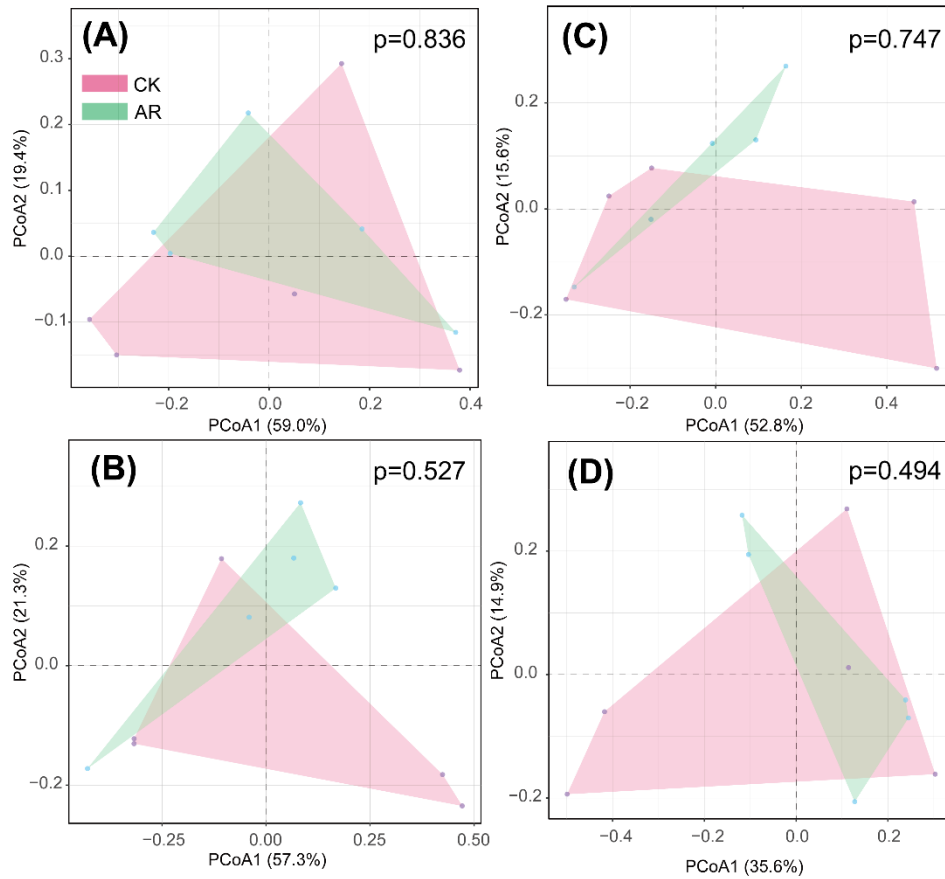


Figure S3. The principle coordinate analysis (PCoA) of the microbial communities structure of AOA (A), AOB (B), *nirS*-harboring denitrifiers (C) and *nosZ*-harboring denitrifiers (D). CK: non-acid addition, AR: acid rain of pH 4.0. Five points in the same color block represent one treatment. The *p*-values refer to PERMANOVA results.

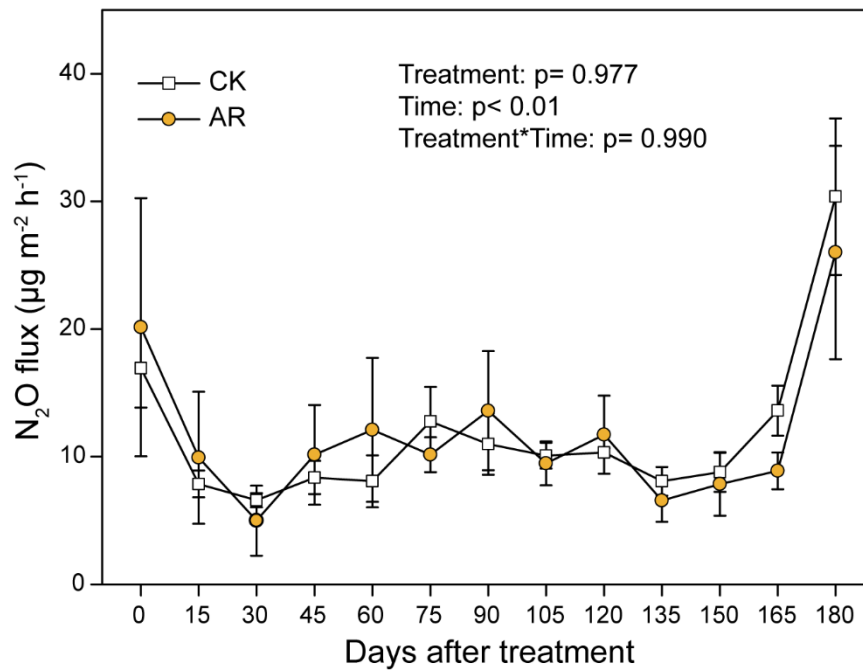


Figure S4. N₂O fluxes over sampling time. CK: non-acid addition, AR: pH 4.0 acid rain. Data were presented as mean \pm standard error ($n = 5$).