

Table S1 Site characteristics at our four studied sites.

Site ID	Latitude	Longitude	Altitude (m)	Vegetation type
G1	44.37	85.02	541	Grassland
G2	43.53	81.14	1464	Grassland
G3	43.31	84.16	1526	Grassland
G4	44.61	81.40	1983	Grassland
G5	43.41	81.05	2901	Grassland
F1	46.12	85.65	313	Forest
F2	44.22	86.37	515	Forest
F3	44.20	86.87	521	Forest
F4	44.33	85.21	663	Forest
F5	43.47	81.11	2074	Forest
F6	44.49	81.17	2138	Forest
B1	45.97	85.54	341	Bareland
B2	44.60	84.28	368	Bareland
C1	44.59	84.39	375	Cropland
C2	44.22	86.37	515	Cropland

Table S2 Primers and PCR amplification conditions for nitrogen-cycling functional genes

No.	Functional gene	Primer name	Primer sequence	PCR conditions
1	AOA	AOA-2-F	STAATGGTCTGGCTTAGACG	1. Pre-denaturation: 95 °C for 30 s;
		AOA-2-R	GCGGCCATCCATCTGTATGT	
2	AOB	AOB-1-F	GGGGTTTCTACTGGTGGT	2. Denaturation: 95 °C for 10 s, 40 cycles;
		AOB-1-R	CCTCKGSAAAGCCTTCTTC	
3	nirS	nirS-1-F	GTSAACGTSAAAGGARACSGG	3. Annealing: 52– 65 °C for 30 s, 40 cycles;
		nirS-1-R	GASTTCGGRTGSGTCTTGA	
4	nirK	nirK-1-F	ATCATGGTSC TGCCGCG	4. Extension: 72 °C for 30 s, 40 cycles.
		nirK-1-R	GCCTCGATCAGRTTGTGGTT	
5	nosZ	nosZ-F	AACGCCTAYACSACSCTGTTC	
		nosZ-R	TCCATGTGCAGNGCRTGGCAGAA	

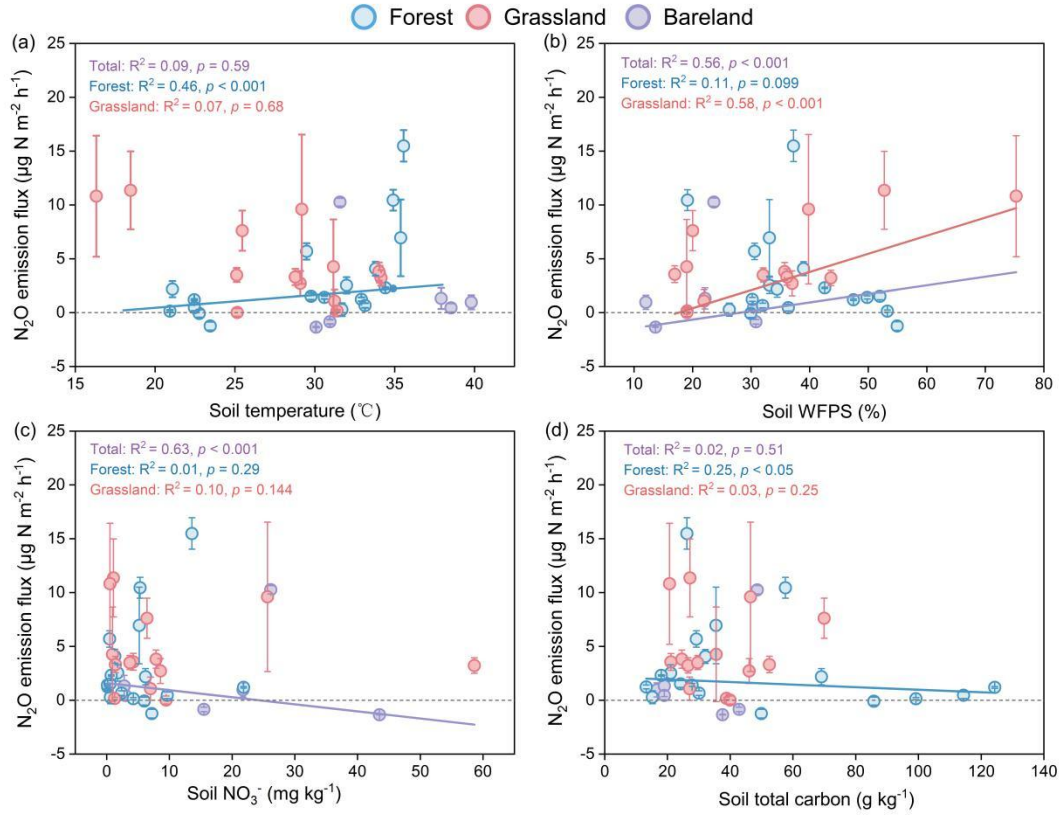


Fig. S1 Relationships between N_2O emission flux and environmental factors including soil temperature (a), water-filled pore space (WFPS) (b), nitrate nitrogen concentration (c), and soil total carbon (d) across forest, grassland, and bareland sites. Coefficients of determination (R^2) and p -values for total, forest, and grassland datasets are provided in each panel. Error bars represent standard errors of the mean.

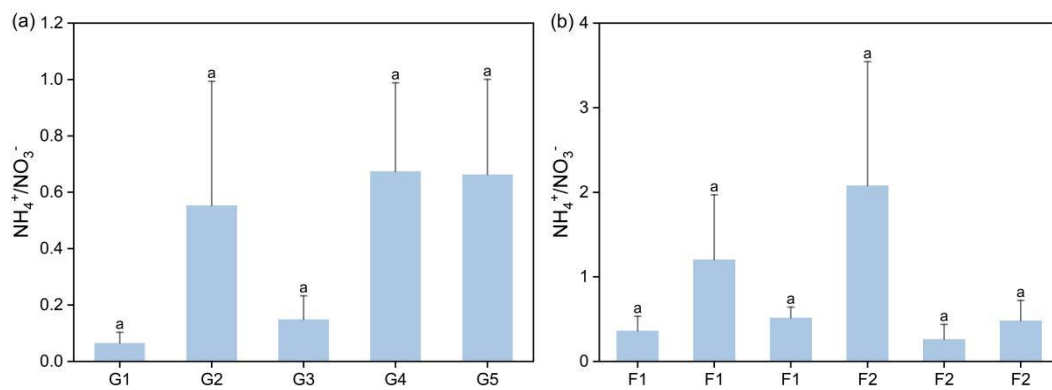


Fig. S2 Soil $\text{NH}_4^+\text{-N}/\text{NO}_3^-\text{-N}$ ratios in grassland (a) and forest (b) sites. Different letters (a, b) above the bars indicate significant differences ($p < 0.05$) among sites within each land-use type. Error bars represent standard errors of the mean.

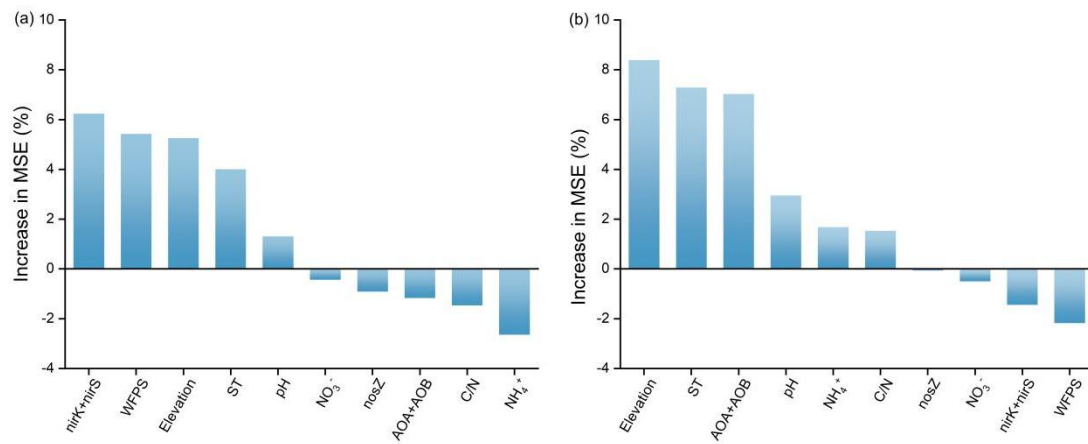


Fig. S3 Variable importance (%IncMSE) of environmental and microbial predictors for N₂O fluxes in grassland and forest soils based on random forest models. (a) Grassland soils; (b) Forest soils. Note: Functional gene abundances (*amoA*, *AOB*, *nirK*, *nirS*, and *nosZ*) were lg-transformed before model fitting.