

The Effect of Mineral-Based Soil Conditioners on the Improvement of Acidified Soils and Microbial Communities

5 **Jina Ding^{1,2,3}, Yaqi Zhang^{4,5}, Jia Liu⁶, Kailou Liu⁷, Shuang Wang^{2,3}, Sang Yoon Kim⁸, Yakov Kuzyakov⁹, Zhenke Zhu^{2,3}, Tida Ge^{2,3}, Zhaofeng Yuan^{2,3,*}**

1 Ningbo Key Laboratory of Agricultural Germplasm Resources Mining and Environmental Regulation, College of Science and Technology, Ningbo University, Ningbo 315300, China; dingjina@nbu.edu.cn

10 2. State Key Laboratory for Quality and Safety of Agro-Products, Key Laboratory of Biotechnology in Plant Protection of MARA, Zhejiang Key Laboratory of Green Plant Protection, Ningbo University, Ningbo 315211, China; wangshuang1@nbu.edu.cn, zhuzhenke@nbu.edu.cn, getida@nbu.edu.cn

3 International Science and Technology Cooperation Base for the Regulation of Soil Biological Functions and One Health of Zhejiang Province, Ningbo University, Ningbo 315211, China

15 4 College of Environmental & Resource Sciences, Zhejiang University, Hangzhou 310058, China; yaqi.zhang2@uq.net.au

5 ZJU-Hangzhou Global Scientific and Technological Innovation Center, Hangzhou 311200, China

6 Institute of Soil and Fertilizer & Resource and Environment, Jiangxi Academy of Agricultural Sciences, Nanchang 330200, China; liujia@jxaas.cn

7 Jiangxi Institute of Red Soil and Germplasm Resources, Nanchang 330046, China; liukailou@163.com

20 8 Department of Agricultural Chemistry & Interdisciplinary Program in IT-Bio Convergence System, Suncheon National University, Suncheon 57922, Republic of Korea; sykim@snu.ac.kr

9 Department of Soil Science of Temperate Ecosystems, Department of Agricultural Soil Science, University of Göttingen, Göttingen 37077, Germany; ykuzyakov@yandex.com

* Corresponding author: Yuanzhaofeng@nbu.edu.cn

25

The PCR primers of bacterial and fungi

The soil bacterial 16S V4 region was amplified by the bar-coded forward primer 515F (5'-GTGCCAGCMGCCGCGGTAA-3') and reverse primer 806R (5'-GGACTACHVGGGTATCTAAT-3'). The partial was amplified using the primers 30 1737F (5'-GGAAGTAAAAGTCGTAACAAGG-3') and 2043R (5'-GCTGCGTTCTTCATCGATGC-3').

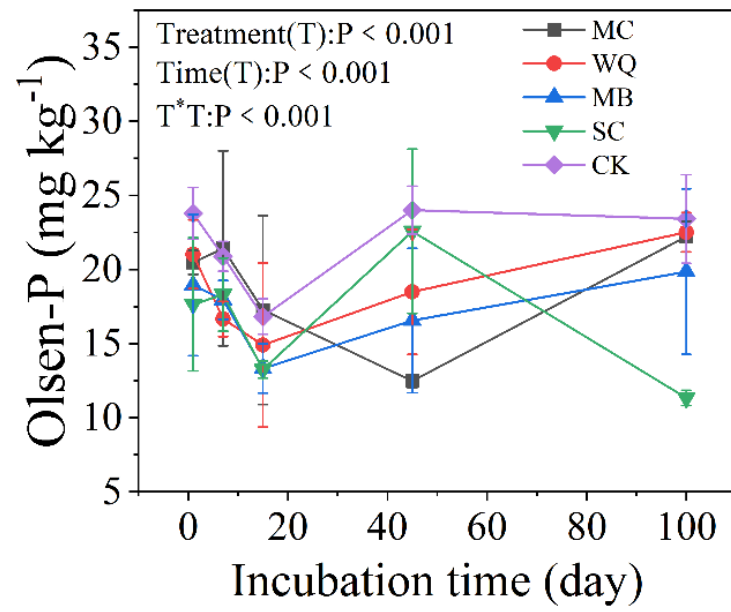


Figure S1. Changes of Olsen-P after the additions of soil conditioners over the 100-d incubation period.

Table S1. Content of different holomorphic chemical elements in soils

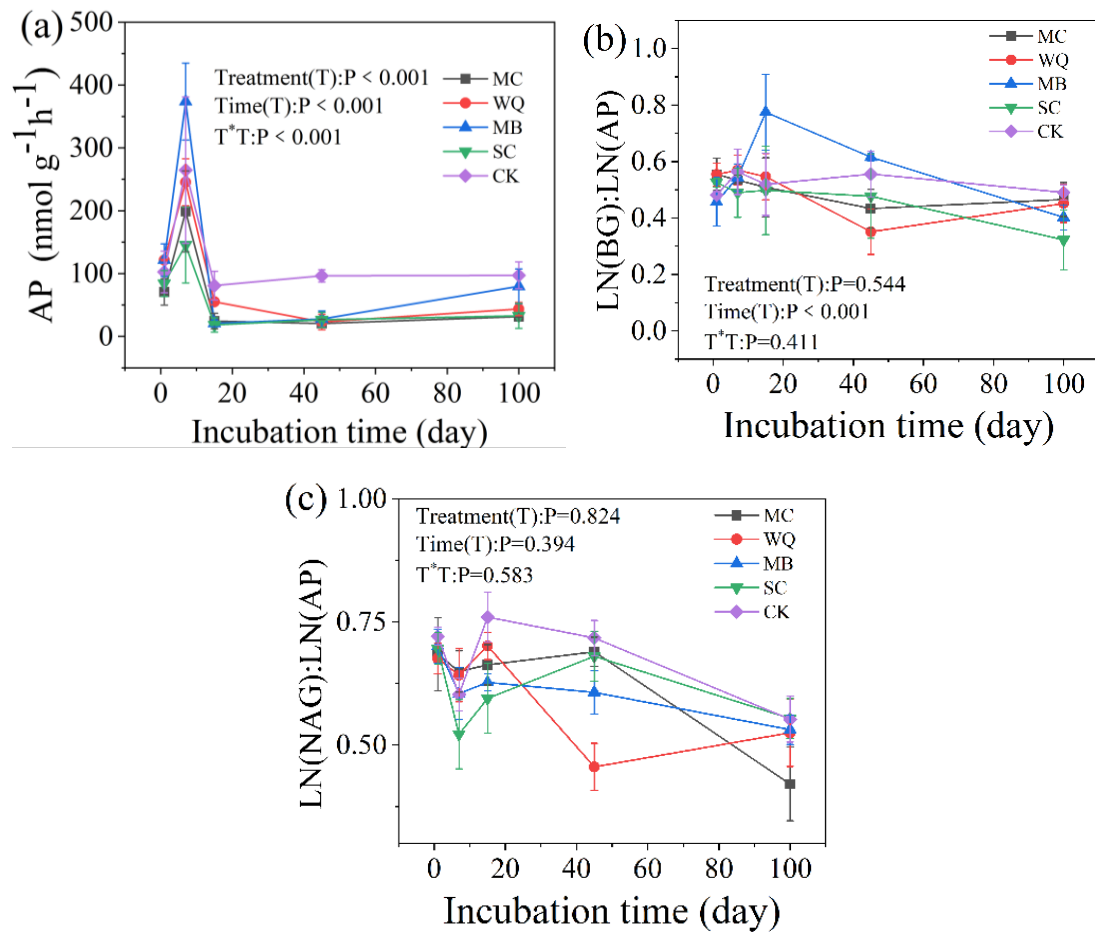
Incubation time	treatment	TC(g kg ⁻¹)	TN(g kg ⁻¹)	AK(mg kg ⁻¹)	ACa(mg kg ⁻¹)	AMg(mg kg ⁻¹)
1D	MC	14.63±0.54b	0.99±0.074a	1.13±0.17a	11.51±1.27a	1.57±0.08a
	WQ	14.65±0.59b	0.99±0.072a	1.10±0.10b	10.72±0.44a	1.50±0.12a
	MB	15.07±0.32ab	0.92±0.057a	1.07±0.07b	11.06±0.33a	1.59±0.04a
	SC	15.68±0.44a	0.95±0.032a	1.38±0.15a	12.08±0.53a	0.97±0.11b
	CK	15.62±0.18a	0.98±0.048a	1.07±0.05b	7.71±0.49b	0.99±0.12b
100D	MC	13.82±0.41b	0.67±0.028b	0.88±0.05c	6.57±1.00ab	1.51±0.26a
	WQ	13.81±0.14b	0.69±0.037ab	1.17±0.24bc	7.11±1.78ab	1.74±0.49a
	MB	13.88±0.32b	0.72±0.048ab	1.32±0.13ab	7.12±2.40ab	1.69±0.22a
	SC	13.96±0.50ab	0.78±0.079a	1.58±0.09a	8.24±1.61a	0.90±0.09b
	CK	14.74±0.40a	0.74±0.036ab	1.22±0.05b	4.41±0.21b	0.84±0.03b

Error bars represent the standard deviation of the mean (n = 3). Letters indicate a significant difference ($p < 0.05$).

The content change of different holomorphic chemical elements in soils

Tab. S1 demonstrates that the content of total potassium (TK), total calcium (TCa), and total magnesium (TMg) increased in the conditioner-treated soils. The TC content in the MC, WQ, and MB-treated soils was significantly lower than that in the CK treated soil ($P < 0.05$). The TK

40 content in both MB and SC-treated soils increased by 8.20% and 29.51%, respectively. TCa content increased by 48.98% to 86.85% across all the four treated soils, while TMg content in the MC, WQ, and MB-treated soils increased by 79.76% to 107.14%.



45 **Figure S2.** Extracellular enzyme activities of soil AP: phosphatase **(a)** and ecological enzymatic characteristics of soil **(b,c)** during incubation.

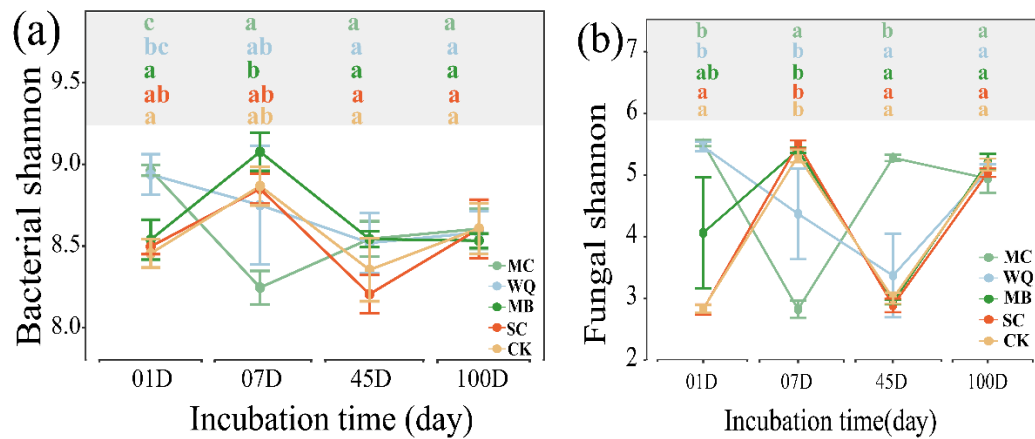


Figure S3. Shannon index of soil bacterial (a) and fungal (b) communities

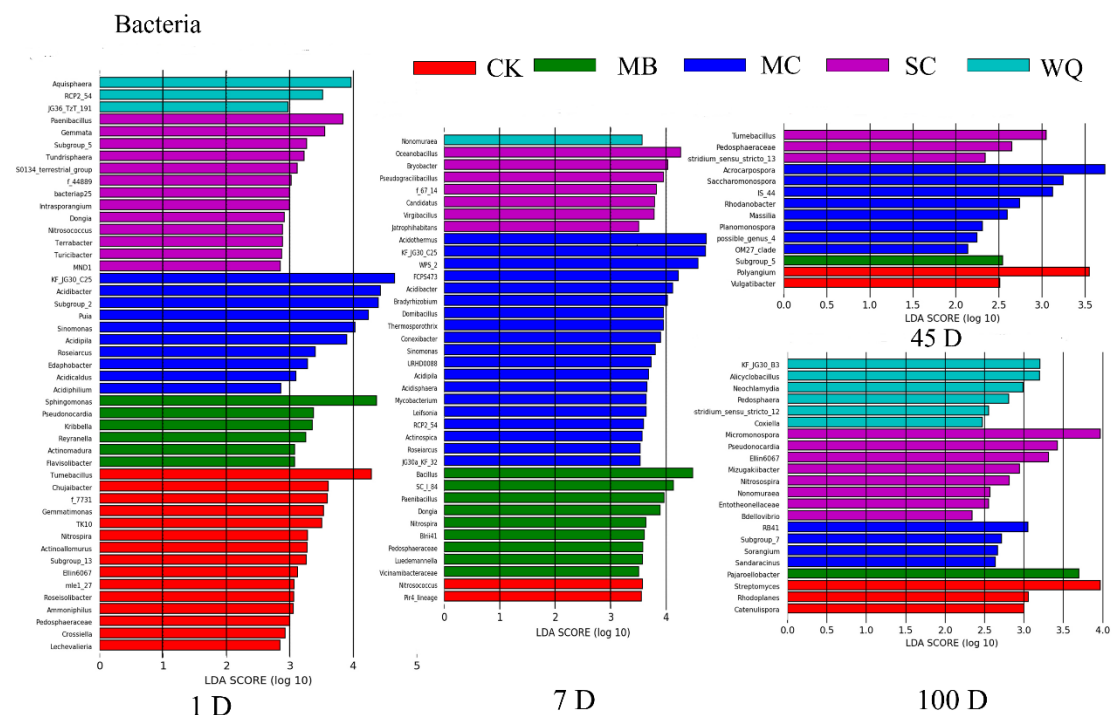


Figure S4. Linear discriminant analysis (LDA) of species differences in soil bacterial communities during incubation

1D

MC: KF_JG30_C25, Acidibacter, Subgroup_2, Puia, Sinomonas, Acidipila, Roseiarcus, Edaphobacter, Acidicaldus, Acidiphilium;

WQ: Aquisphaera, RCP2_54, JG36_TzT_191;

MB: Sphingomonas, Pseudonocardia, Kribbella, Reyranella, Actinomadura, Flavisolibacter;

60 **SC:** Paenibacillus, Gemmata, Subgroup_5, Tundrisphaera, S0134_terrestrial_group, Paenibacillus, r_44889, bacteriap25, IntrasporangiumDongia, Nitrosococcus, Terrabacter, Turicibacter, MNND1;

CK: Tumebacillus, Chujaibacter, f_7731, Gemmatimonas, TK10, Nitrospira, Actinoallomurus, Subgroup_13, Ellin6067, mle1_27, Roseisolibacter, Ammoniphilus, Pedosphaeraceae, Crossiella,

65 Lechevalieria.

7D

MC: Acidothermus, KF_JG30_C25, WPS_2, FCPS473, Acidibacter, Bradyrhizobium, Domibacillus, Thermosporothrix, Conexibacter, Sinomonas, URHD0088, Acidipila, Acidisphaera, Mycobacterium, Leifsonia, RCP2_54, Actinospica, Roseiarcus, JG30a_KF_32;

70 **WQ:** Nonomuraea;

MB: Bacillus, SC_1_84, Paenibacillus, Dongia, Nitrospira, Blrii41, Pedosphaeraceae, Luedemannella, Vicinamibacteraceae;

SC: Oceanobacillus, Bryobacter, Pseudogracilibacillus, f_67_14, Candidatus, Virgibacillus, Jatrophihabitans;

75 **CK:** Nitrosococcus, Pir4_lineage.

45D

MC: Subgroup_5;

SC: Tumebacillus, Pedosphaeraceae, stridium_sensu_stricto_13;

MB: Polyangium, Vulgatibacter; **SC:** Acrocarpospora, Saccharomonospora, IS_44, Rhodanobacter,

80 Massilia, Planomonospora, possible_genus_4, OM27_clade.

100D

MC: RB41, Subgroup_7, Sorangium, Sandaracinus;

WQ: KF_JG30_B3, Alicyclobacillus, Neochlamydia, Pedosphaera, stridium_sensu_stricto_12, Coxiella;

85 **MB:** Pajaroellobacter; **SC:** Micromonospora, Pseudonocardia, Ellin6067, Mizugakiibacter, Nitrospira, Nonomuraea, Enttheonellaceae, Bdellovibrio;

CK: Streptomyces, Rhodoplanes, Catenulispora.

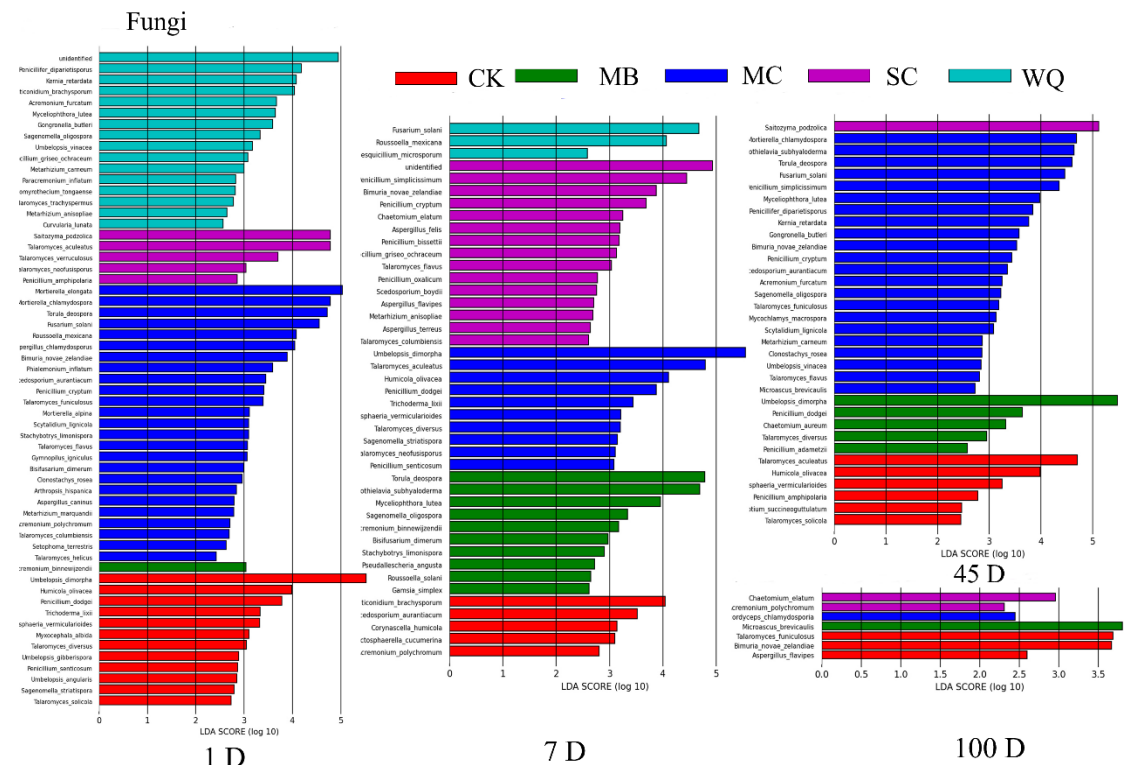


Figure S5. Linear discriminant analysis (LDA) of species differences in soil fungal communities during incubation.

1D

- MC:** *Mortierella_elongata*, *Mortierella_chlamydospora*, *Torula_deospora*, *Fusarium_solani*, *Rousoella_mexicana*, *pergillus_chlamydosporus*, *Bimuria_novae_zelandiae*, *Phialemonium_inflatum*, *cedosporium_aurantiacum*, *Penicillium_cryptum*, *Talaromyces_funiculosus*, *Mortierella_alpina*, *Scytalidium_lignicola*, *Stachybotrys_limonispora*, *Talaromyces_flavus*, *Gymnopilus_igniculus*, *Bisifusarium_dimerum*, *Conostachys_rosea*, *Arthrospis_hispanica*, *Aspergillus_caninus*, *Metarhizium_marquandii*, *cremonium_polychromum*, *Talaromyces_columbiensis*, *Setophoma_terrestris*, *Talaromyces_helicus*;
- WQ:** *unidentified*, *Penicillifer_diparietisporus*, *Kernia_retardata*, *ticonidium_brachysporum*, *Acremonium_furcatum*, *Myceliophthora_lutea*, *Gongronella_butleri*, *Sagenomella_oligospora*,

Umbelopsis_vinacea, cillium_griseo_ochraceum, Metarhizium_carneum, Paracremonium
105 _inflatum, omyrothecium_tongaense, Talaromyces_trachyspermus, Metarhizium_anisopliae,
Curvularia_lunata;

MB: cremonium_binnewijzendii;

SC: Saitozyma_podzolica, Talaromyces_aculeatus, Talaromyces_verruculosus, Talaromyces
_neofusisporus, Penicillium_a_mphipolaria;

110 **CK:** Umbelopsis_dimorpha, Humicola_olivacea, Penicillium_dodgei, Trichoderma_lixii,
Sphaeria_vermicularioides, Myxocephala_albida, Talaromyces_diversus, Umbelopsis_gibberispora,
Penicillium_senticosum, Umbelopsis_angularis, Sagenomella_striatispora, Talaromyces_solicola.

7D

115 **MC:** Umbelopsis_dimorpha, Talaromyces_aculeatus, Humicola_olivacea, Penicillium_dodgei,
Trichoderma_lixii, Sphaeria_vermicularioides, Talaromyces_diversus, Sagenomella_striatispora,
Talaromyces_neofusisporus, Penicillium_senticosum;

SC: Fusarium_solani, Rousoella_mexicana, Esquicillium_microsporum;

MB: Torula_deospora, Othoclavia_subhyalodema, Myceliophthora_lutea, Sagenomella
120 _oligospora, Paracremonium_binnewijzendii, Blaisiifusarium_dimerum, Stachybotrys_limonispara,
Pseudallescheria_angularis, Pousoella_solanii, Gamsia_simplex;

SC: unidentified, Penicillium_simplicissimum, Bimuria_novae_zelandiae, Penicillium_cryptum,
Chaetomium_elatum, Aspergillus_felis, Penicillium_bissettii, cillium_griseo_ochraceum, Talar
omyces_flavus, Penicillium_oxalicum, Scedosporium_boydii, Aspergillus_flavipes, Metarhizium
125 _anisopliae, Aspergillus_terreus, Talaromyces_columbiensis;

CK: Fusicladium_brachysporum, Scedosporium_aurantiacum, Corynascella_humicola,
Cytosphaerella_cucumerina, cremonium_polychromum.

45D

130 **MC:** Mortierella_chlamydospora, Othoclavia_subhyaloderma, Torula_deospora, Fusarium_solani,
Penicillium_simplicissimum, Myceliophthora_lutea, Penicillifer_diparietisporus, Kernia_retardata,

Gongronella_butleri, Bimuria_novae_zelandiae, Penicillium_cryptum, cadosporium_aurantiacum,
 Acremonium_furcatum, Sagenomella_oligospora, Talaromyces_funiculosus,
 Mycochlamys_macrospora, Scytalidium_lignicola, Metarhizium_carneum, Clonostachys_rosea,
 135 Um belopsis_vinacea, Talaromyces_flavus, Microascus_brevicaulis;
MB: Umbelopsis_dimorpha, Penicillium_dodgei, Chaetomium_aureum, Talaromyces_diversus,
 Penicillium_adametzii;
SC: Saitozyma_podzolica;
CK: Talaromyces_aculeatus, Humicola_olivacea, sphaeria_vermicularioides, Penicillium
 140 _amphipolaria, otium_succin eoguttulatum, Talaromyces_solicola.

100D

MC: Microascus_brevicaulis;
WQ: Chaetomium_elatum, cremonium_polychromum;
 145 **SC:** ordyceps_chlamydosporia;
CK: Talaromyces_funiculosus, Bimuria_novae_zelandiae, Aspergillus_flavipes.

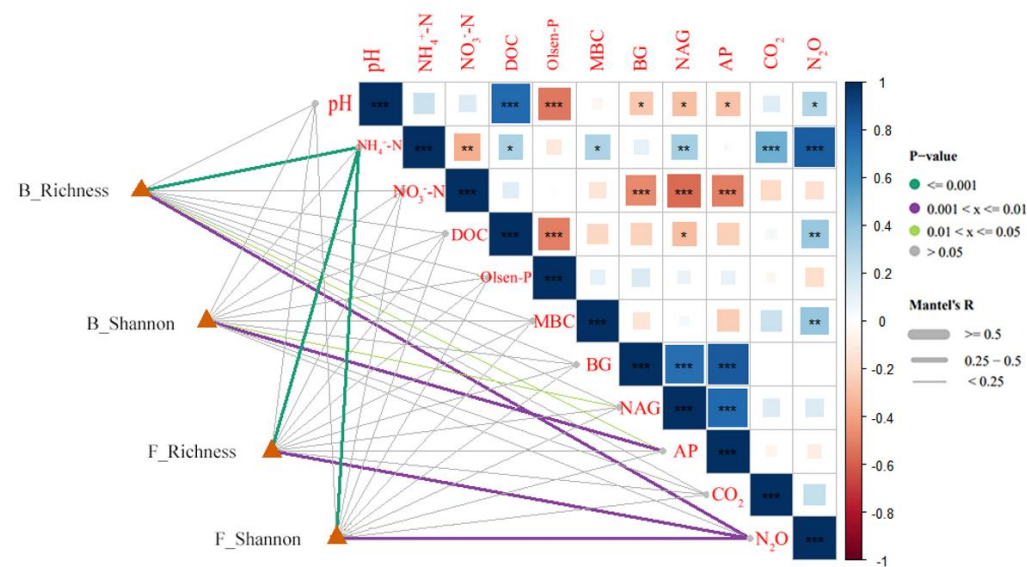


Figure S6. Correlation analysis of environmental factors, greenhouse gases and microbial community structure of soil. NH4+-N: ammonium nitrogen; NO3--N: nitrate nitrogen; DOC: Soluble organic carbon; Olsen-P: available phosphorus; MBC: Microbial biomass carbon; BG: β - glucosidase; NAG: chitinase; AP: phosphatase.
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