



*Supplement of*

**The role of long-term mineral and manure fertilization on P species accumulation and phosphate-solubilizing microorganisms in paddy red soils**

**Shuiqing Chen et al.**

*Correspondence to:* Xiaoqian Jiang ([jiangxq7@mail.sysu.edu.cn](mailto:jiangxq7@mail.sysu.edu.cn))

The copyright of individual parts of the supplement might differ from the article licence.

**Table S1.** The list of phosphorus-solubilizing microbes.

Bacteria		Fungi	
Genus	Phylum	Genus	Phylum
<i>Acinetobacter</i>	Proteobacteria	<i>Alternaria</i>	Ascomycota
<i>Agrobacterium</i>	Proteobacteria	<i>Aspergillus</i>	Ascomycota
<i>Arthrobacter</i>	Actinobacteria	<i>Chaetomium</i>	Ascomycota
<i>Azospirillum</i>	Proteobacteria	<i>Cladosporium</i>	Ascomycota
<i>Bacillus</i>	Firmicutes	<i>Curvularia</i>	Ascomycota
<i>Bradyrhizobium</i>	Proteobacteria	<i>Fusarium</i>	Ascomycota
<i>Burkholderia</i>	Proteobacteria	<i>Mortierella</i>	Mucoromycota
<i>Enterobacter</i>	Proteobacteria	<i>Oidiodendron</i>	Ascomycota
<i>Erwinia</i>	Proteobacteria	<i>Penicillium</i>	Ascomycota
<i>Flavobacterium</i>	Bacteroidetes	<i>Trichoderma</i>	Ascomycota
<i>Paenibacillus</i>	Firmicutes		
<i>Pseudomonas</i>	Proteobacteria		
<i>Ralstonia</i>	Proteobacteria		
<i>Rhizobium</i>	Proteobacteria		
<i>Rhodococcus</i>	Actinobacteria		
<i>Serratia</i>	Proteobacteria		
<i>Thiobacillus</i>	Proteobacteria		

**Table S2.** The difference between groups based on Bray Curtis distance of NMDS in five treatments (CK, NPK, M, NPKM, NKM) was analyzed by ANOSIM.

Group 1	Group 2	Bulk soil				Rhizosphere			
		Bacteria		Fungi		Bacteria		Fungi	
		R	p-value	R	p-value	R	p-value	R	p-value
CK	M	0.33	0.004 **	0.19	0.035 *	0.79	0.003 **	0.33	0.002 **
CK	NKM	0.34	0.007 **	0.34	0.005 **	0.69	0.005 **	0.32	0.002 **
CK	NPK	0.09	0.200 ns	0.08	0.196 ns	0.36	0.005 **	0.28	0.029 *
CK	NPKM	0.58	0.004 **	0.36	0.013 *	0.92	0.002 **	0.33	0.012 *
M	NKM	0.12	0.100 ns	0	0.465 ns	0.20	0.094 ns	0.19	0.028 *
M	NPK	0.15	0.059 ns	0.01	0.434 ns	0.39	0.015 *	0.12	0.140 ns
M	NPKM	0.28	0.003 **	0.12	0.063 ns	0.26	0.011 *	-0.03	0.577 ns
NKM	NPK	0.28	0.042 *	0.06	0.236 ns	0.44	0.001 **	0.18	0.056 ns
NKM	NPKM	0.23	0.029 *	0.20	0.059 ns	0.35	0.021 *	0.17	0.053 ns
NPK	NPKM	0.35	0.004 **	0.05	0.300 ns	0.57	0.004 **	0.20	0.029 *

\* represents the significant difference between the two treatments, where ns  $p > 0.05$ , \*  $p < 0.05$ , \*\*  $p < 0.01$ .

**Table S3.** Network parameters of all bacteria and fungi in five treatments (CK, NPK, M, NPKM, NKM) were calculated using R and Gephi.

Network parameters	Bacteria					Fungi				
	CK	NPK	M	NPKM	NKM	CK	NPK	M	NPKM	NKM
Total nodes	82	83	89	91	83	62	53	62	63	69
Total edges	501	453	546	713	463	194	138	206	202	250
Positive edges	398	319	326	469	319	157	107	164	154	202
Negative edges	103	134	220	217	144	37	31	42	48	48
P/N ratio	3.9	2.4	1.5	2.2	2.2	4.2	3.5	3.9	3.2	4.2
Average degree	12.22	10.92	12.27	15.67	11.16	6.26	5.21	6.65	6.41	7.25
Average clustering coefficient	0.58	0.58	0.57	0.64	0.59	0.64	0.61	0.59	0.56	0.61
Average path length	2.54	2.75	2.54	2.62	2.61	3.57	3.77	3.29	3.48	3.04
modularity	0.32	0.32	0.29	0.23	0.30	0.32	0.31	0.27	0.37	0.30

**Table S4.** Redundancy analysis of microbes and soil properties was conducted using the CANOCO 5.0. Simple effect of a factor contributing to communities change of microbes was presented.

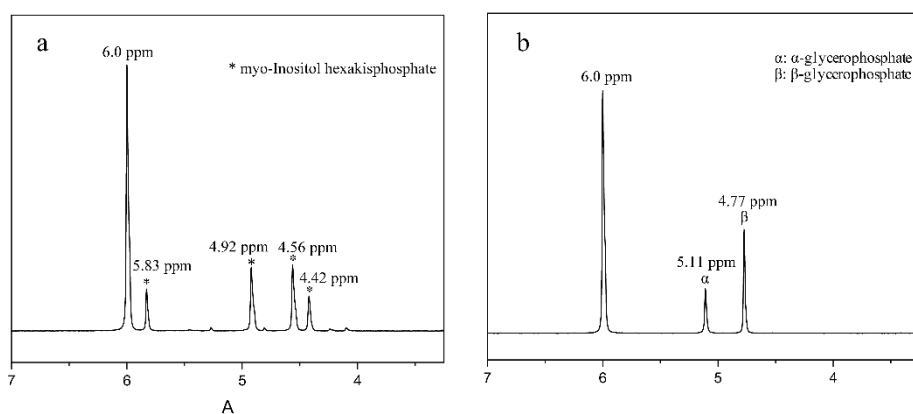
Soil properties	Bacteria			Fungus		
	Explains %	pseudo-F	P	Explains %	pseudo-F	P
pH	10.3	4.4	0.03	3.3	1.3	n.s
moisture	3.1	1.2	n.s	3.6	1.4	n.s
TC	10	4.2	0.03	3.9	1.5	n.s
TN	10.2	4.3	0.03	3.7	1.5	n.s
OC	8.7	3.6	0.03	4.3	1.7	n.s
MBP	6.3	2.6	n.s	2.6	1	n.s
TP	5.8	2.3	n.s	3.2	1.3	n.s
IP	6	2.4	n.s	3.6	1.4	n.s
AP	4.9	1.9	n.s	3.2	1.3	n.s
Orth-mono	7.7	3.2	n.s	4.2	1.7	n.s
Orth-di	7.1	2.9	n.s	3.9	1.5	n.s
Myo-IHP	7.8	3.2	n.s	4.2	1.7	n.s
$\alpha+\beta$ +mono	8.3	3.4	n.s	3.9	1.6	n.s
ACP	4.4	1.7	n.s	4.4	1.8	n.s
ALP	4.8	1.9	n.s	3.8	1.5	n.s

MBP, microbial biomass phosphorus; TP, total phosphorus; IP, inorganic phosphorus; AP, available phosphorus; Orth-mono, orthophosphate monoester; Orth-di, orthophosphate diesters; Myo-IHP, myo-Inositol hexakisphosphate;  $\alpha+\beta$ +mono,  $\alpha$ - and  $\beta$ -glycerophosphates and mononucleotides; ACP, activity of acidic phosphatase; ALP, activity of alkaline phosphatase

**Table S5.** Redundancy analysis of phosphorus-solubilizing microbes and soil properties was conducted using the CANOCO 5.0. Simple effect of a factor contributing to communities change of microbes was presented.

Soil properties	Bacteria			Fungus		
	Explains %	pseudo-F	P	Explains %	pseudo-F	P
pH	10.3	4.4	0.03	5.1	2.1	n.s
moisture	2.8	1.1	n.s	2.8	1.1	n.s
TC	10.4	4.4	0.03	5.2	2.1	n.s
TN	10.1	4.3	0.03	5.1	2	n.s
OC	9.2	3.9	0.03	4	1.6	n.s
MBP	4.7	1.9	n.s	2.5	1	n.s
TP	4.8	1.9	n.s	0.7	0.3	n.s
IP	5	2	n.s	0.6	0.2	n.s
AP	4	1.6	n.s	0.1	<0.1	n.s
Orth_mono	8.3	3.5	0.03	9	3.7	n.s
Orth_di	7.6	3.1	0.03	3.8	1.5	n.s
myo_IHP	6.8	2.8	n.s	2.2	0.8	n.s
$\alpha$ + $\beta$ +mono	8.9	3.7	0.03	1.9	0.8	n.s
ACP	6.2	2.5	n.s	3.7	1.4	n.s
ALP	6.6	2.7	n.s	2.3	0.9	n.s

MBP, microbial biomass phosphorus; TP, total phosphorus; IP, inorganic phosphorus; AP, available phosphorus; Orth\_mono, orthophosphate monoester; Orth\_di, orthophosphate diesters; myo\_IHP, myo-Inositol hexakisphosphate;  $\alpha$ + $\beta$ +mono,  $\alpha$ - and  $\beta$ -glycerophosphates and mononucleotides; ACP, activity of acidic phosphatase; ALP, activity of alkaline phosphatase



**Fig. S1** The solution  $^{31}\text{P}$ -NMR spectrum of NaOH-EDTA extract of sample CK spiked with (a) myo-inositol hexakisphosphate (myo-IHP) and (b)  $\alpha$ - and  $\beta$ - glycerophosphate.

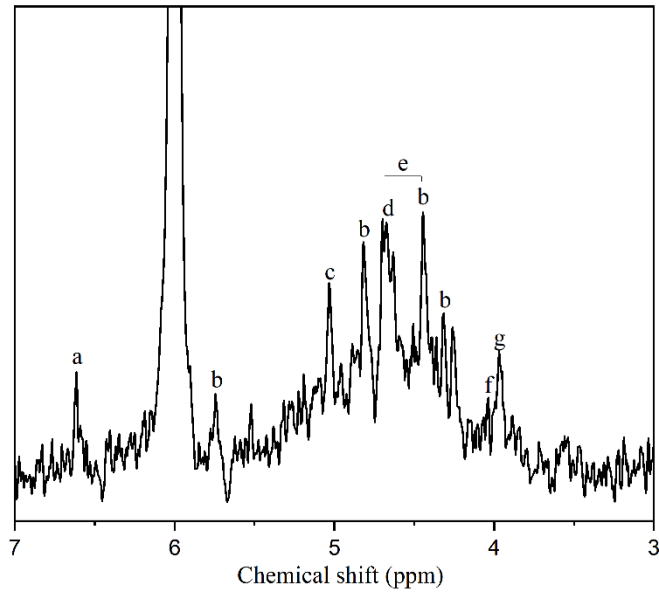


Fig. S2 The solution  $^{31}\text{P}$  NMR spectrum of solution NaOH- $\text{Na}_2\text{EDTA}$  extract of Sample M. Only the phosphate monoester region was shown. The signals were assigned as follows: a, chiro-inositol hexakisphosphate 4e/2a (chiro1); b, myo-Inositol hexakisphosphate (Myo-IHP); c,  $\alpha$  glycerophosphate ( $\alpha$ -glyc); d,  $\beta$  glycerophosphate ( $\beta$ -glyc); e, mononucleotide; f, choline phosphate (Pchol); g, scyllo-inositol hexakisphosphate (Scyllo-IHP).

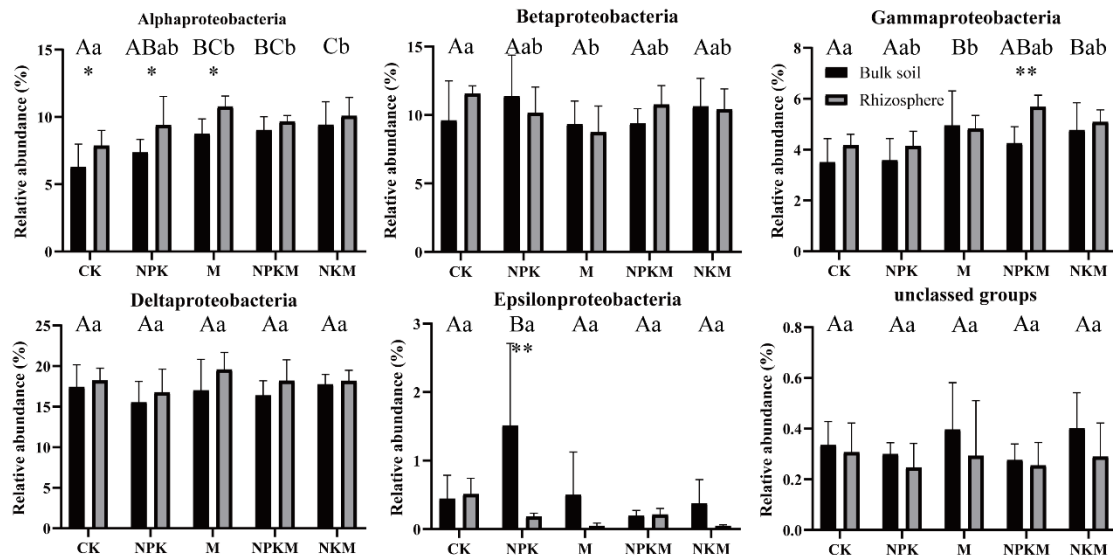


Fig. S3 Changes in the relative abundance of sub-groups of Phylum *Proteobacteria* across the five treatments (CK, NPK, M, NPKM, NKM) and two soil types (rhizosphere and bulk soil). Significant differences between treatments in bulk soil are indicated by capital letters ( $p < 0.05$ ,  $n = 6$ ). Significant differences between treatments in rhizosphere are indicated by lowercase letters ( $p < 0.05$ ,  $n = 6$ ). Significant

differences between rhizosphere and bulk soils are indicated by asterisks, where \*  $p < 0.05$ , \*\*  $p < 0.01$  (Duncan's test,  $n=6$ )