

Figure S1. The relative abundance of the first ten rhizosphere bacteria. Different letters on each bar represent significant differences among treatments at a significance level of $p < 0.05$.

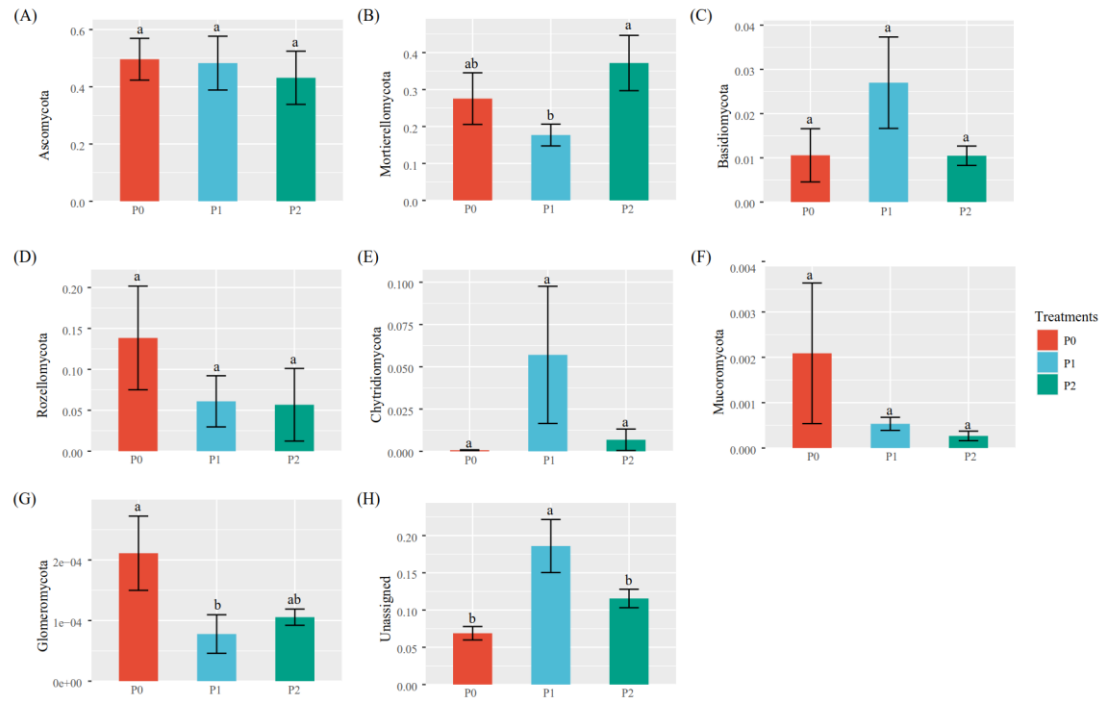


Figure S2. The relative abundance of the first ten rhizosphere fungi. Different letters on each bar represent significant differences among treatments at a significance level of $p < 0.05$.

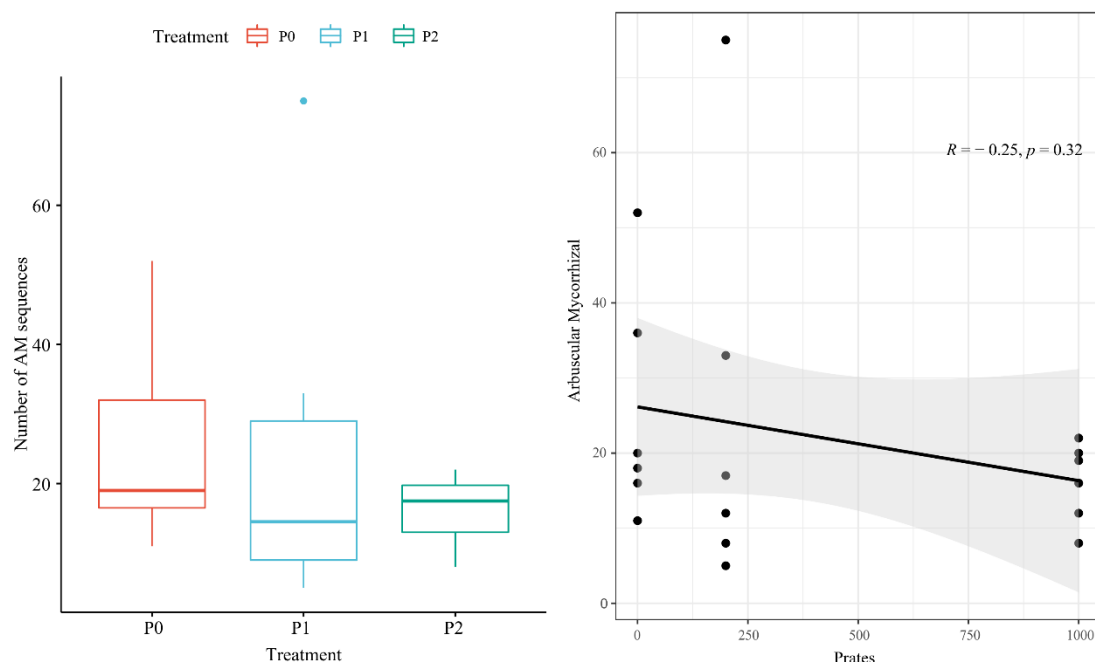


Figure S3. Effect of phosphorus fertilizer addition rates on AMF.

Table S1. Functional gene pathway differences (mean \pm standard error).

Factor	description	TP0	TP1	TP2
ko00010	Glycolysis / Gluconeogenesis	29.4 \pm 0.46b	31.15 \pm 0.23a	31.34 \pm 0.37a
ko00020	Citrate cycle (TCA cycle)	35.57 \pm 0.85b	37.93 \pm 0.31a	37.68 \pm 0.61a
ko00030	Pentose phosphate pathway	35.99 \pm 0.56b	38.05 \pm 0.16a	37.62 \pm 0.35a
ko00051	Fructose and mannose metabolism	16.12 \pm 0.25b	17.11 \pm 0.4ab	17.38 \pm 0.36a
ko00052	Galactose metabolism	18.43 \pm 0.58b	20.46 \pm 0.47a	20.5 \pm 0.46a
ko00072	Synthesis and degradation of ketone bodies	70.49 \pm 0.84b	72.54 \pm 1.01ab	74.68 \pm 0.84a
ko00100	Steroid biosynthesis	1.79 \pm 0.1a	1.56 \pm 0.11ab	1.34 \pm 0.13b
ko00120	Primary bile acid biosynthesis	1.16 \pm 0.09a	0.87 \pm 0.07b	0.84 \pm 0.09b
ko00121	Secondary bile acid biosynthesis	3.17 \pm 0.48a	1.79 \pm 0.16b	2.07 \pm 0.2b
ko00250	Alanine, aspartate and glutamate metabolism	35.94 \pm 0.91b	38.15 \pm 0.4a	36.89 \pm 0.63ab
ko00260	Glycine, serine and threonine metabolism	34.82 \pm 0.43b	36.47 \pm 0.23a	36.5 \pm 0.34a
ko00311	Penicillin and cephalosporin biosynthesis	6.93 \pm 0.31b	7.8 \pm 0.44ab	8.91 \pm 0.5a
ko00364	Fluorobenzoate degradation	14.58 \pm 0.63a	13.13 \pm 0.65ab	12.12 \pm 0.72b
ko00400	Phenylalanine, tyrosine and tryptophan biosynthesis	28.83 \pm 0.71b	30.55 \pm 0.26a	29.68 \pm 0.44ab
ko00430	Taurine and hypotaurine metabolism	27.26 \pm 0.81a	25.45 \pm 0.66ab	24.03 \pm 0.86b
ko00440	Phosphonate and phosphinate metabolism	5.81 \pm 0.23a	5.32 \pm 0.25ab	5.06 \pm 0.25b
ko00460	Cyanoamino acid metabolism	26.58 \pm 0.4b	27.54 \pm 0.08a	27.48 \pm 0.21a
ko00500	Starch and sucrose metabolism	21.29 \pm 0.54b	23.34 \pm 0.52a	23.71 \pm 0.54a
ko00510	N-Glycan biosynthesis	1.41 \pm 0.09b	1.65 \pm 0.04a	1.55 \pm 0.04ab
ko00511	Other glycan degradation	13.53 \pm 0.84b	16.04 \pm 0.82a	15.8 \pm 0.53a
ko00520	Amino sugar and nucleotide sugar metabolism	21.38 \pm 0.53b	23.16 \pm 0.21a	22.55 \pm 0.28a
ko00521	Streptomycin biosynthesis	44.31 \pm 0.75b	47.22 \pm 0.26a	46.13 \pm 0.48a
ko00524	Butirosin and neomycin biosynthesis	7.12 \pm 0.25b	7.99 \pm 0.12a	7.82 \pm 0.14a
ko00531	Glycosaminoglycan degradation	3.93 \pm 0.28b	4.73 \pm 0.21a	4.33 \pm 0.11ab
ko00561	Glycerolipid metabolism	13.04 \pm 0.15b	13.52 \pm 0.04a	13.36 \pm 0.11a
ko00562	Inositol phosphate metabolism	15.4 \pm 0.26b	16.2 \pm 0.37ab	16.87 \pm 0.42a
ko00600	Sphingolipid metabolism	5.66 \pm 0.11ab	5.91 \pm 0.14a	5.53 \pm 0.09b
ko00621	Dioxin degradation	8.58 \pm 0.66a	6.95 \pm 0.48ab	6.25 \pm 0.62b
ko00633	Nitrotoluene degradation	10.42 \pm 0.67a	9.69 \pm 0.67ab	8.06 \pm 0.82b
ko00670	One carbon pool by folate	36.97 \pm 0.85b	39.92 \pm 0.23a	39.61 \pm 0.54a

Factor	description	TP0	TP1	TP2
ko00710	Carbon fixation in photosynthetic organisms	32.97±0.58b	34.41±0.34a	33.46±0.48ab
ko00730	Thiamine metabolism	29.25±0.91b	31.39±0.51a	29.55±0.57ab
ko00760	Nicotinate and nicotinamide metabolism	29.59±0.51b	31.07±0.28a	30.42±0.5ab
ko00785	Lipoic acid metabolism	42.47±0.98b	45.87±0.44a	45.4±0.79a
ko00790	Folate biosynthesis	28.08±0.83b	30.59±0.23a	30.42±0.5a
ko00900	Terpenoid backbone biosynthesis	32.09±0.69b	33.89±0.35a	32.93±0.58ab
ko00941	Flavonoid biosynthesis	1.52±0.08a	1.43±0.1ab	1.15±0.1b
ko00943	Isoflavonoid biosynthesis	0.34±0.08a	0.14±0.02b	0.14±0.02b
ko00965	Betalain biosynthesis	3.01±0.32ab	3.2±0.26a	2.28±0.23b
ko00983	Drug metabolism - other enzymes	21.33±0.66b	23.39±0.15a	23.23±0.37a
ko01053	Biosynthesis of siderophore group nonribosomal peptides	0.95±0.06b	1.09±0.08ab	1.26±0.07a
ko01055	Biosynthesis of vancomycin group antibiotics	54.54±1.4ab	55.73±1.49a	50.21±1.9b
ko02030	Bacterial chemotaxis	49.08±2.45a	45.5±3.19ab	39.14±3.58b
ko02060	Phosphotransferase system (PTS)	3.01±0.05b	3.15±0.04a	3.21±0.03a
ko03030	DNA replication	23.01±0.72b	24.68±0.35a	23.63±0.51ab
ko03050	Proteasome	1.14±0.13b	1.41±0.2ab	1.78±0.21a
ko03060	Protein export	31.97±1.09b	34.54±0.59a	32.94±0.73ab
ko03410	Base excision repair	26.02±0.71b	28.01±0.17a	27.69±0.42a
ko03420	Nucleotide excision repair	17.76±0.43b	18.98±0.15a	18.67±0.23a
ko03450	Non-homologous end-joining	7.26±0.32b	7.91±0.17ab	8.17±0.21a
ko04113	Meiosis - yeast	1±0.03b	1.1±0.02a	1.09±0.02a
ko04142	Lysosome	1.11±0.07b	1.28±0.04a	1.24±0.03ab
ko04962	Vasopressin-regulated water reabsorption	0±0ab	0±0a	0±0b
ko04974	Protein digestion and absorption	0.34±0.04ab	0.37±0.03a	0.27±0.02b
ko05120	Epithelial cell signaling in Helicobacter pylori infection	1.02±0.02ab	1.01±0.02b	1.06±0.01a
ko05143	African trypanosomiasis	1.13±0.06b	1.33±0.04a	1.34±0.05a

Table S2. Highly probable ZOTUs identified by FUNGuild.

OTU_ID	Guild
Zotu_129	Undefined Saprotroph
Zotu_111	Arbuscular Mycorrhizal
Zotu_293	Arbuscular Mycorrhizal
Zotu_264	Arbuscular Mycorrhizal
Zotu_306	Arbuscular Mycorrhizal
Zotu_246	Arbuscular Mycorrhizal
Zotu_298	Arbuscular Mycorrhizal
Zotu_197	Arbuscular Mycorrhizal
Zotu_237	Arbuscular Mycorrhizal
Zotu_320	Plant Pathogen-Wood Saprotroph
Zotu_193	Arbuscular Mycorrhizal
Zotu_252	Arbuscular Mycorrhizal
Zotu_289	Arbuscular Mycorrhizal
Zotu_239	Arbuscular Mycorrhizal
Zotu_260	Arbuscular Mycorrhizal
Zotu_269	Arbuscular Mycorrhizal
Zotu_234	Arbuscular Mycorrhizal
Zotu_302	Arbuscular Mycorrhizal