

Supplementary materials

Table S1 The α -diversity of bacteria and fungi in bulk soil under different farming modes.

Farming	Variety	α -diversity of bulk soil							
		Bacteria				Fungi			
		Richness	Chao1	Shannon	Simpson	Richness	Chao1	Shannon	Simpson
M [‡]	H [‡]	2715.3	2716.7	8.91	0.009	512.7	514.1	8.91	0.095
M [‡]	C [‡]	2734.7	2736.1	9.08	0.006	401.3	403.0	9.08	0.108
R [‡]	H [‡]	2797.3	2798.9	9.02	0.007	424.7	426.5	9.01	0.049
R [‡]	C [‡]	3129.7	3131.0	9.38	0.005	455.7	457.4	9.38	0.052

[‡] The M, R, H, and C represent monoculture mode, rotation mode, rot-conducive variety, and rot-suppressive variety, respectively.

Different letters indicate a significant difference at p<0.05.

Table S2. The keystone taxa of bacteria in rhizosphere of different varieties

		Phylum	Class	Order	Family	Genus	Species
Rot-suppressive variety	OTU_145	Patescibacteria	Saccharimonadia	Saccharimonadales			
	OTU_150	Bacteroidetes	Bacteroidia	Chitinophagales	Saprospiraceae	uncultured	
	OTU_170	Acidobacteria	Thermoanaerobaculia	Thermoanaerobaculales	Thermoanaerobaculaceae	Subgroup_10	
	OTU_334	Chloroflexi	Anaerolineae				
	OTU_405	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Lysobacter	
	OTU_530	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	AKYG587	
Rot-conductive variety	OTU_139	Proteobacteria	Alphaproteobacteria	Tistrellales	Geminicoccaceae	uncultured	uncultured_bacterium
	OTU_1558	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Pedobacter	
	OTU_205	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	uncultured	
	OTU_337	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	uncultured_bacterium
	OTU_35	Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured		
	OTU_3803	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae		
	OTU_551	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Ferruginibacter	uncultured_bacterium
	OTU_665	Proteobacteria	Deltaproteobacteria	Myxococcales			
	OTU_750	Proteobacteria	Deltaproteobacteria	Myxococcales	P3OB-42		
	OTU_81	Bacteroidetes	Bacteroidia	Cytophagales	Hymenobacteraceae	Adhaeribacter	

Table S3. The keystone taxa of fungi in rhizosphere of different varieties

		Kingdom	Phylum	Class	Order	Family	Genus	Species
Rot-suppressive variety	OTU_1076	Fungi						
	OTU_1103	Fungi	Glomeromycota	Glomeromycetes				
	OTU_1349	Fungi	Ascomycota	Eurotiomycetes				
	OTU_1512	Fungi	Ascomycota	Eurotiomycetes		Eurotiales	Aspergillaceae	
	OTU_266	Fungi	unidentified	unidentified				
	OTU_278	Fungi	Basidiomycota	Agaricomycetes	Cantharellales	Ceratobasidiaceae		
	OTU_323	Alveolata	Ciliophora					
	OTU_554	Alveolata	Ciliophora					
	OTU_617	Rhizaria	Cercozoa					
	OTU_674	Fungi	Ascomycota					
	OTU_781	Fungi						
	OTU_807	Fungi						
	OTU_983	Alveolata	Ciliophora	Spirotrichea	Urostylida	Holostichidae	Anteholosticha	Anteholosticha_sp
Rot-conducive variety	OTU_117	Fungi	Ascomycota	Eurotiomycetes				
	OTU_132	Fungi	Ascomycota	Sordariomycetes	Hypocreales	unidentified	unidentified	Hypocreales_sp
	OTU_16	Fungi						
	OTU_162	Fungi	Rozellomycota	unidentified	unidentified	unidentified	unidentified	Rozellomycota_sp
	OTU_172	Fungi	Ascomycota	Sordariomycetes				
	OTU_177	Fungi	Ascomycota	Eurotiomycetes	Eurotiales			
	OTU_383	Fungi	Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	Aspergillus_thesauricus
	OTU_8	Fungi	Ascomycota	Sordariomycetes	Sordariales			
	OTU_91	Fungi	Ascomycota	Sordariomycetes	Microascales	Microascaceae	Kernia	Kernia_sp

Table S4. The keystone taxa of in endophytic bacteria in root of different varieties

		Phylum	Class	Order	Family	Genus	Species
Rot-suppressive variety	OTU_102	Proteobacteria	Gammaproteobacteria	Alteromonadales	Idiomarinaceae	Aliidiomarina	
	OTU_103	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Paracoccus	
	OTU_1314	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae		
	OTU_160	Bacteroidetes	Bacteroidia	Cytophagales	Microscillaceae	uncultured	
	OTU_166	Actinobacteria	Thermoleophilia	Gaiellales	uncultured		
	OTU_182	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	Sphingobacterium_gobiense
	OTU_19	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	
	OTU_37	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardiodaceae	Nocardioides	Nocardioides_sp._RCML-51
	OTU_38	Actinobacteria	Actinobacteria	Pseudonocardiales	Pseudonocardiaceae	Lechevalieria	Saccharothrix_sp._sj68
	OTU_52	Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae		
	OTU_74	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylobacterium	
	OTU_92	Deinococcus-Thermus	Deinococci	Deinococcales	Trueperaceae	Truepera	uncultured_Deinococcales_bacterium
Rot-conducive variety	OTU_96	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylophilaceae		
	OTU_142	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardiodaceae	Aeromicrobium	
	OTU_86	Actinobacteria	Actinobacteria	Propionibacteriales	Nocardiodaceae	Nocardioides	Nocardioides_bigeumensis
	OTU_87	Actinobacteria	Actinobacteria	Glycomycetales	Glycomycetaceae	uncultured	uncultured_bacterium

Table S5. The keystone taxa of in endophytic fungi in root of different varieties

		Phylum	Class	Order	Family	Genus	Species
Rot-suppressive variety	OTU_157	Ascomycota	Saccharomycetes	Saccharomycetales	unidentified	unidentified	Saccharomycetales_sp
	OTU_171	Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	Malassezia_globosa
	OTU_197	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	Dactylonectria_anthuriicola
	OTU_58	Chytridiomycota	Rhizophlyctidomycetes	Rhizophlyctidales	Rhizophlyctidaceae	Rhizophlyctis	Rhizophlyctis_rosea
	OTU_66	Ascomycota	Eurotiomycetes	Eurotiales	Aspergillaceae	Aspergillus	
	OTU_69	Basidiomycota	Malasseziomycetes	Malasseziales	unidentified	unidentified	Malasseziales_sp
	OTU_157	Ascomycota	Saccharomycetes	Saccharomycetales	unidentified	unidentified	Saccharomycetales_sp
	OTU_171	Basidiomycota	Malasseziomycetes	Malasseziales	Malasseziaceae	Malassezia	Malassezia_globosa
	OTU_197	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	Dactylonectria	Dactylonectria_anthuriicola
Rot-conducive variety	OTU_152	Basidiomycota	Microbotryomycetes	Sporidiobolales	Sporidiobolaceae	Sporobolomyces	Sporobolomyces_roseus
	OTU_159	Basidiomycota					
	OTU_177	Basidiomycota	Tremellomycetes	Trichosporonales	Trichosporonaceae	Cutaneotrichosporon	
	OTU_290	Ascomycota	Sordariomycetes	Hypocreales	Cordycipitaceae		
	OTU_313	Ascomycota					
	OTU_42	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		
	OTU_49	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae	Ophiocordyceps	
	OTU_56	Ascomycota	Eurotiomycetes	Chaetothyriales			
	OTU_59	Ascomycota	Sordariomycetes	Hypocreales	Ophiocordycipitaceae		
	OTU_91	Basidiomycota	Agaricomycetes	Agaricales	Tricholomataceae	Tricholoma	Tricholoma_matsutake
	OTU_96	Ascomycota	Leotiomycetes	Helotiales	unidentified	unidentified	Helotiales_sp

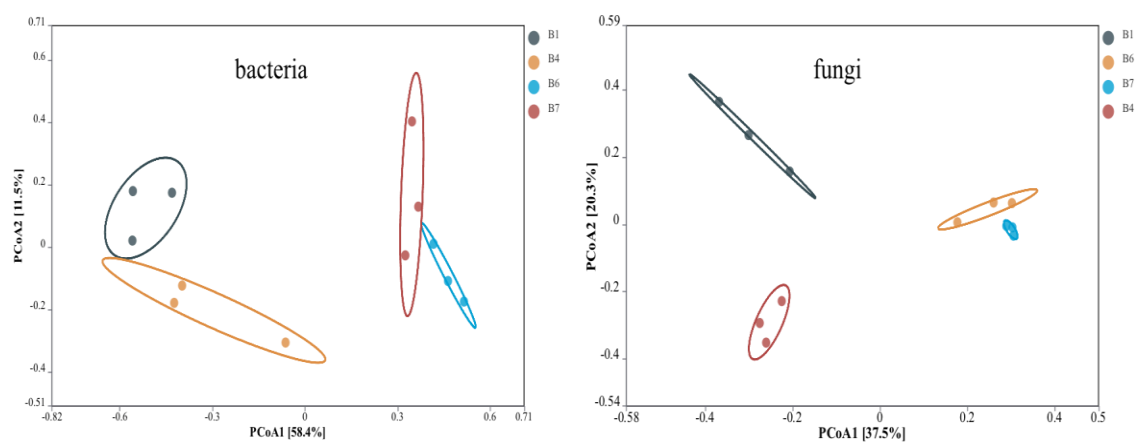


Figure S1. PCoA of the bacterial and fungal communities of bulk soil across the different varieties (1,6 indicate the rot-conductive variety; 4,7 indicate the rot-suppressive variety) and farming modes (1,4 belong to monoculture mode; 6,7 belong to rotation mode).