

Supplementary materials

Cumulative CO₂ emission and microbial diversity depend on the wetting intensity in drying-rewetting cycles from agriculture soil on the Loess Plateau

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Table S1 Topological properties of bacterial and fungal co-occurrence network.

Network metrics	Bacteria		Fungi	
	1-cycle	4-cycle	1-cycle	4-cycle
No. of nodes	198	199	197	193
No. of edges	1386	4284	1161	728
No. of positive edges	893	2300	814	481
No. of negative edges	493	1984	347	247
Average degree	14	43.06	11.79	7.54
Diameter	7	5	9	7
Average Cluster coefficient	0.41	0.59	0.35	0.30
Average path length	2.87	2.08	3.06	3.31
Modularity(M)	0.45	0.26	0.41	0.52

Table S2 The Pearson correlation coefficient between the cumulative CO₂ emission and bacterial and fungal diversity and community properties after four cycles

Microbial Properties	Cumulative CO ₂ emission
Fungal OTUs richness	-0.594*
Fungal Shannon diversity index	-0.341
Fungal Chao 1 index	-0.643**
<i>p__Ascomycota</i>	-0.800**
<i>p__Basidiomycota</i>	0.772**
<i>p__Mortierellomycota</i>	0.275
<i>p__Olpidiomycota</i>	0.180
<i>p__Chytridiomycota</i>	0.198
Bacterial OTUs richness	-0.103
Bacterial Shannon diversity index	-0.068
Bacterial Chao 1 index	-0.080
<i>p__Actinobacteriota</i>	0.034
<i>p__Proteobacteria</i>	0.297
<i>p__Acidobacteriota</i>	-0.198
<i>p__Chloroflexi</i>	-0.490
<i>p__Firmicutes</i>	0.307
<i>p__Bacteroidota</i>	-0.066
<i>p__Gemmatimonadota</i>	0.423
<i>p__Myxococcota</i>	0.230
<i>p__Planctomycetota</i>	-0.069
<i>p__Methylomirabilota</i>	0.516*

* $p < 0.05$; ** $p < 0.01$

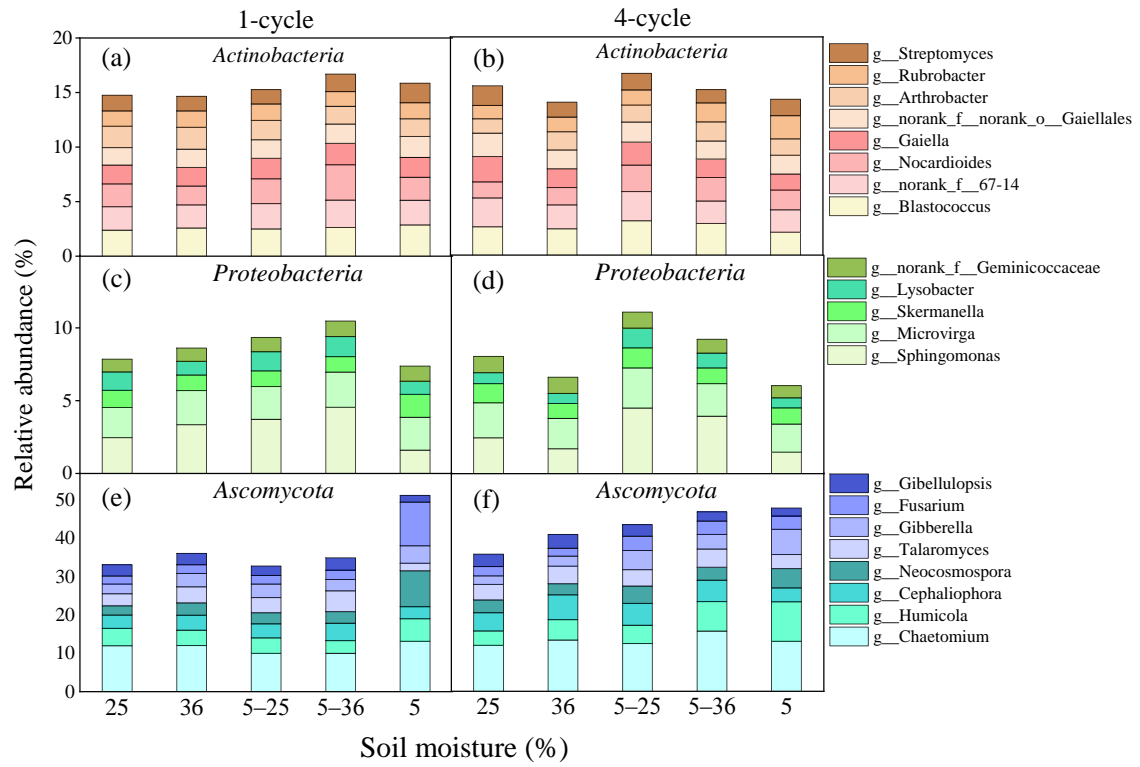


Fig. S1 Relative abundance of dominant bacterial *Proteobacteria* (a, b) and *Actinobacteriota* (c, d) and fungal *Ascomycota* (e, f) at the genera level after 1-cycle and 4-cycle under different moisture condition.

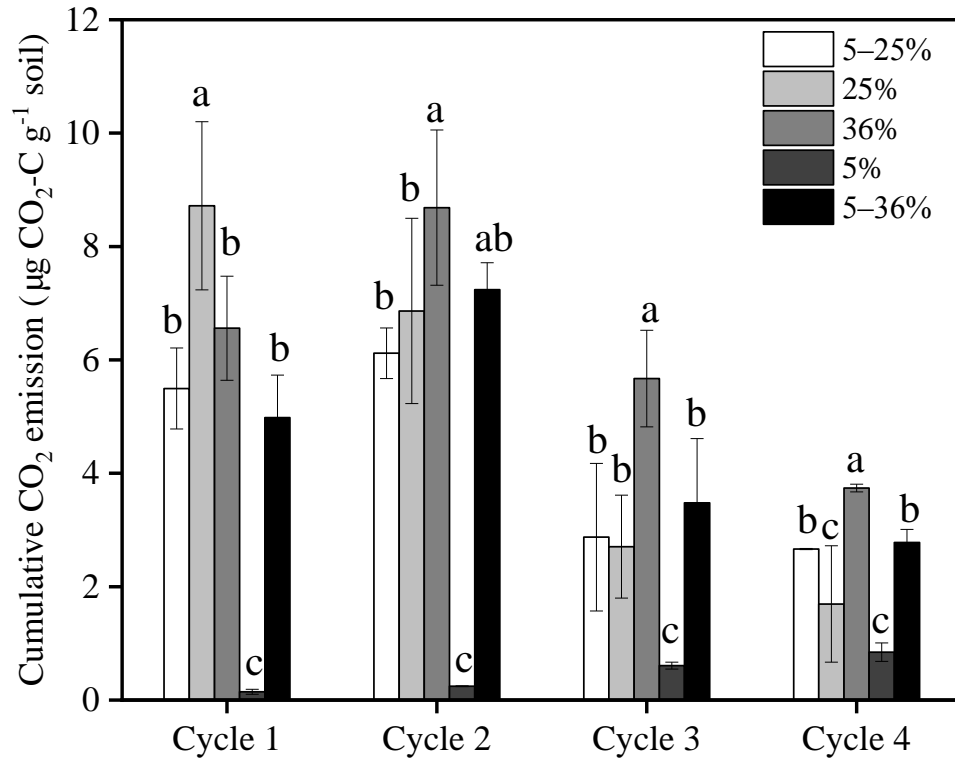


Fig. S2 Dynamic of cumulative CO₂ emission in each cycle under different moisture conditions.