

# Impact of Combined Exposure to Glyphosate and Diquat on Microbial Community Structure and Diversity in Lateritic Paddy Soil

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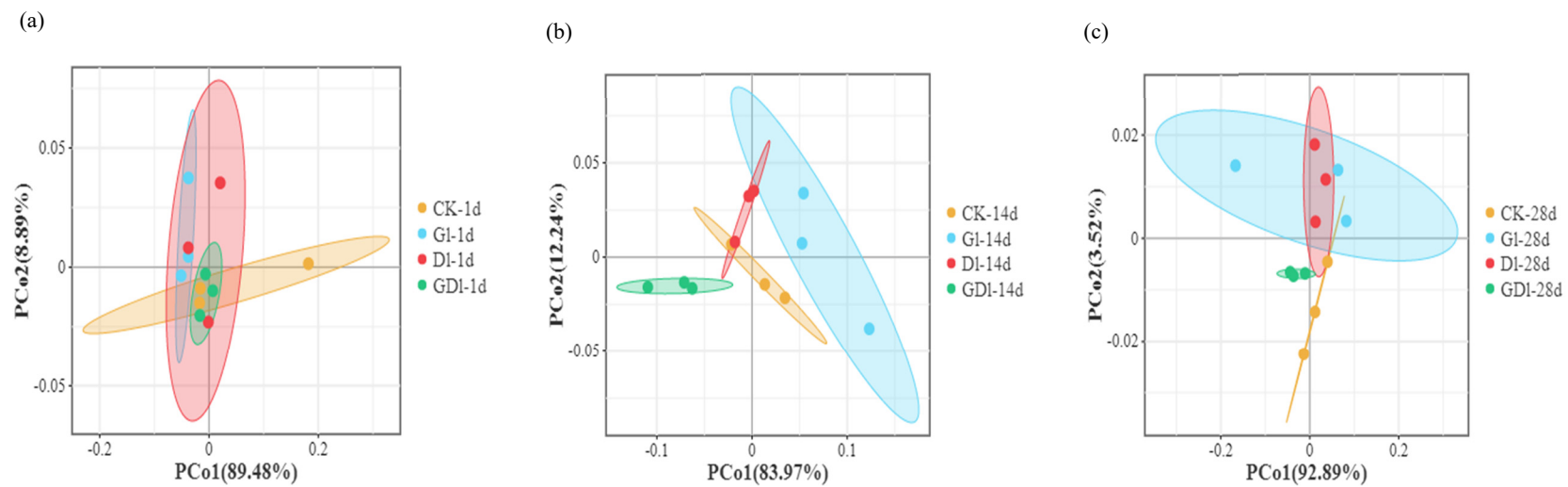
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**Table S1** Primer information

Type	Region	Primer name	Primer sequence	Product length	Reference
16S	V1-V9	27F	AGRGTTTGATYNTGGCTCAG	~1465	[1]
		1492R	TASGGHTACCTTGTTASGACTT		
	V4	515F	GTGYCAGCMGCCGCGGTAA	~292	[1-2]
		806R	GGACTACNVGGGTWTCTAAT		
	V3-V4	341F	CCTACGGGNGGCWGCAG	~466	[3]
		806R	GGACTACHVGGGTATCTAAT		
	V4-V5	515F	GTGCCAGCMGCCGCGGTAA	~412	[4]
		907R	CCGTCAATTCCTTTGAGTTT		
	V5-V7	799F	AACMGGATTAGATACCKG	~414	[5]
		1193R	ACGTCATCCCCACCTTCC		
	V4-V5	Arch519F	CAGCMGCCGCGGTAA	~416	[6]
		Arch915R	GTGCTCCCCGCCAATTCCT		
18S	V4	528F	GCGGTAATTCAGCTCCAA	~260	[7]
		706R	AATCCRAGAATTCACCTCT		
ITS	ITS1	ITS1_F_KYO2	TAGAGGAAGTAAAAGTCGTAA	~366	[8]
		ITS86R	TTCAAAGATTCGATGATTCAC		
		ITS1-F	CTTGGTCATTTAGAGGAAGTAA		
	ITS2	ITS2	GCTGCGTTCTTCATCGATGC	~321	[9]
		ITS3_KYO2	GATGAAGAACGYAGYRAA		
		ITS4	TCCTCCGCTTATTGATATGC		

## Reference

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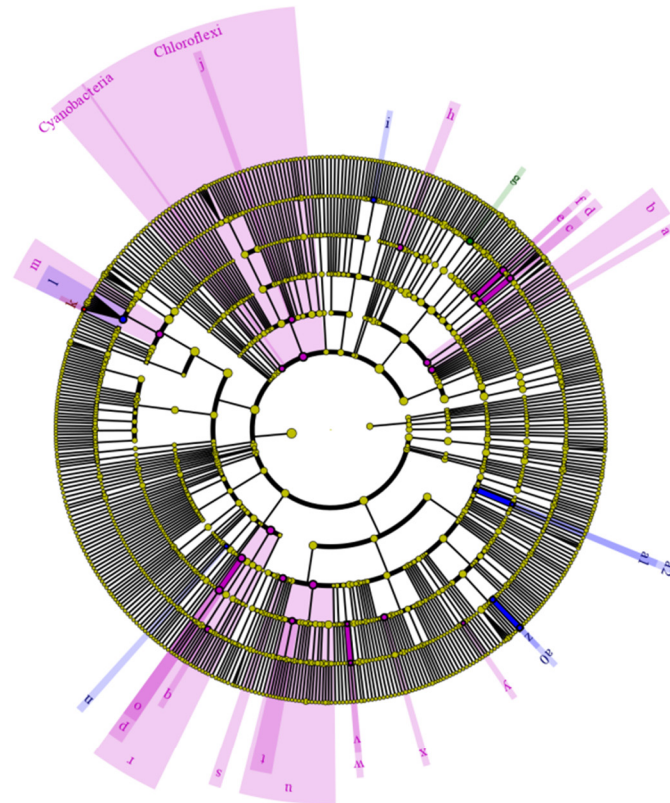


**Figure S1.** Principal coordinate analysis for the bacterial communities at the phylum level. .

(a)

## Cladogram

CK-1d  
DI-1d  
GDI-1d  
GI-1d

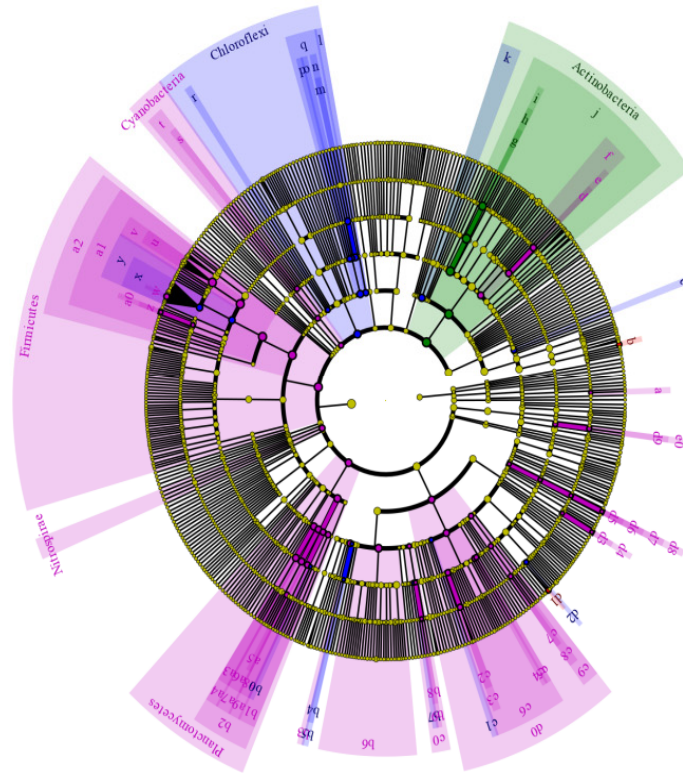


a: Subgroup\_6  
b: Acidimicrobiia  
c: Mycobacterium  
d: Mycobacteriaceae  
e: Acidothermus  
f: Acidothermaceae  
g: Dactylosporangium  
h: Solirubrobacteraceae  
i: Niasella  
j: KID\_96  
k: Streptomyces\_sp\_KP17  
l: Paenibacillus  
m: Paenibacillaceae  
n: S\_70  
o: Gemmataceae  
p: Gemmatales  
q: Singulisphaera  
r: Planctomycetacia  
s: Elsterales  
t: Beijerinckiacae  
u: Rhizobiales  
v: Rickettsia  
w: Rickettsiaceae  
x: Archangiaceae  
y: Desulfovira  
z: Ralstonia\_pickettii  
a0: Ralstonia  
a1: Steroidobacteraceae  
a2: Steroidobacterales

(b)

Cladogram

CK-1d  
Dm-1d  
GDm-1d  
Gm-1d

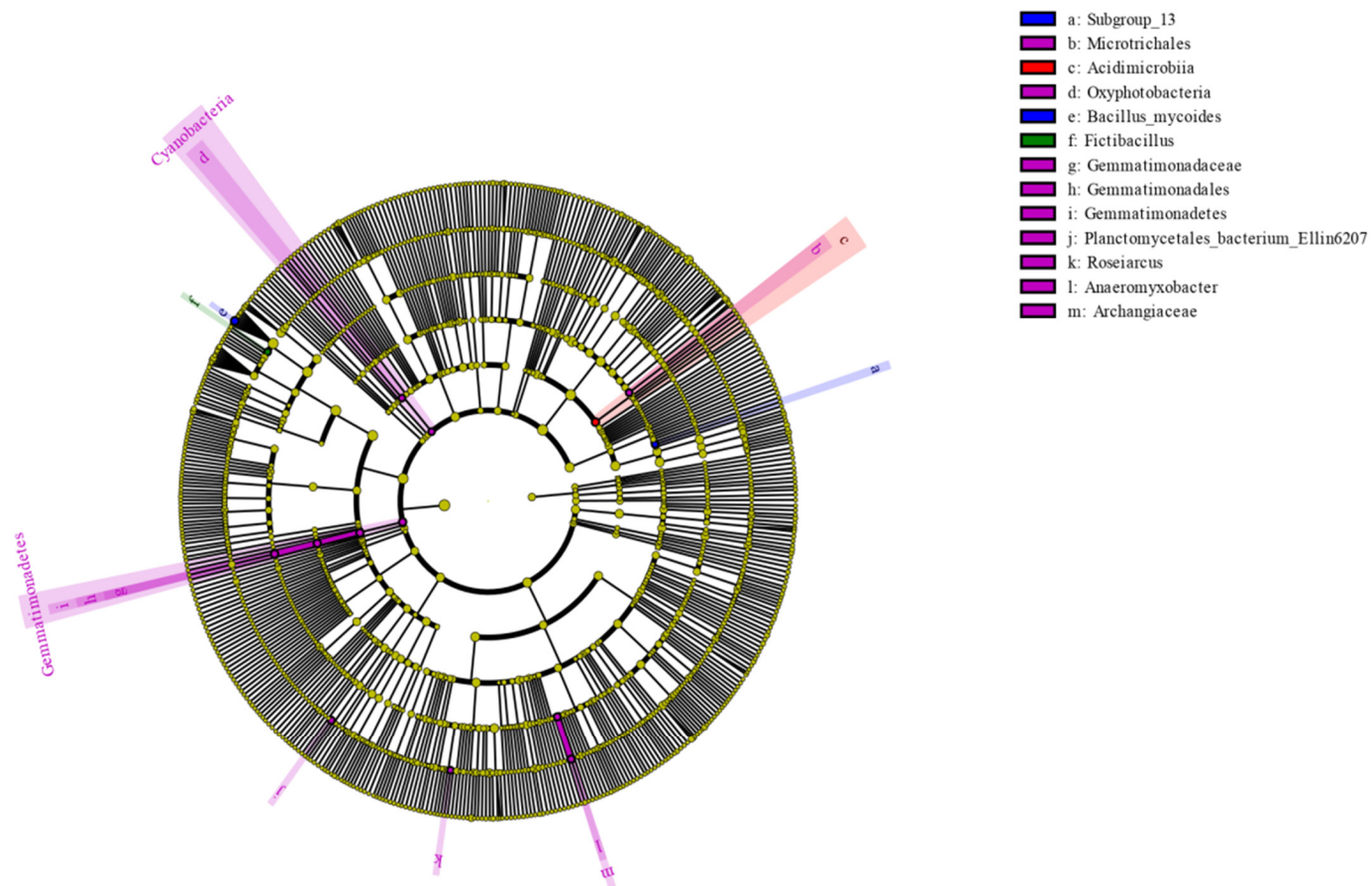


a: Methanocella	x: Paenibacillus	b9: Rickettsiaceae
b: Terracidiphilus_gabretensis	y: Paenibacillaceae	c0: Rickettsiales
c: Subgroup_2	z: Rummeliibacillus_stabekisi	c1: MBNT15
d: Acidothermus	a0: Rummeliibacillus	c2: Anaeromyxobacter
e: Acidothermaceae	a1: Bacillales	c3: Archangiaceae
f: Frankiales	a2: Bacilli	c4: bacteriap25
g: Streptomyces	a3: Gemmataceae	c5: mle1_27
h: Streptomycetaceae	a4: Gemmatales	c6: Myxococcales
i: Streptomycetales	a5: Singulisphaera	c7: Desulfobacca
j: Actinobacteria	a6: Isosphaeraceae	c8: Syntrophaceae
k: Thermoleophilia	a7: Isosphaerales	c9: Syntrophobacterales
l: AD3	a8: Pirellulaceae	d0: Deltaproteobacteria
m: Anaerolineaceae	a9: Pirellulales	d1: Paraburkholderia_kuruiensis_subsp_kuruiensis
n: Anaerolineales	b0: Gimesiaceae	d2: Cupriavidus
o: RBG_13_54_9	b1: Planctomycetales	d3: Pantoea_dispersa
p: SBR1031	b2: Planctomycetacia	d4: Pantoea
q: Anaerolineae	b3: Elsterales	d5: Candidatus_Portiera_aleyrodarum
r: P2_11E	b4: Holosporaceae	d6: Candidatus_Portiera
s: Chloroplast	b5: Holosporales	d7: Halomonadaceae
t: Oxyphotobacteria	b6: Rhizobiales	d8: Oceanospirillales
u: Bacillus	b7: Mitochondria	d9: Candidatus_Xiphinematobacter
v: Bacillaceae	b8: Rickettsia	e0: Xiphinematobacteraceae
w: Paenibacillus_sp_VKM_B_2647		

(c)

## Cladogram

- █ CK-1d
- █ Dh-1d
- █ GDh-1d
- █ Gh-1d

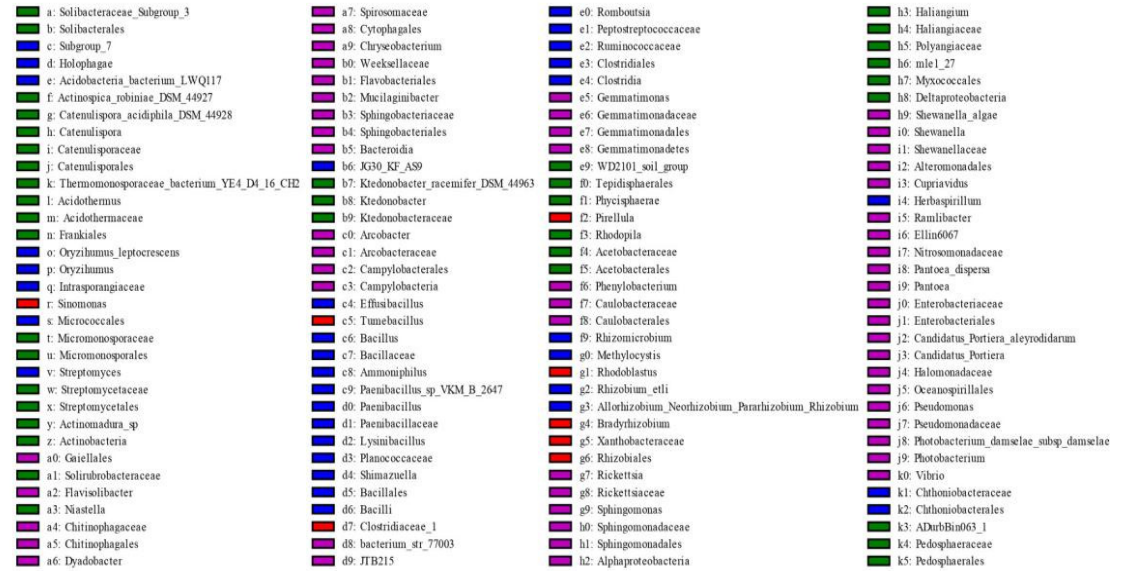
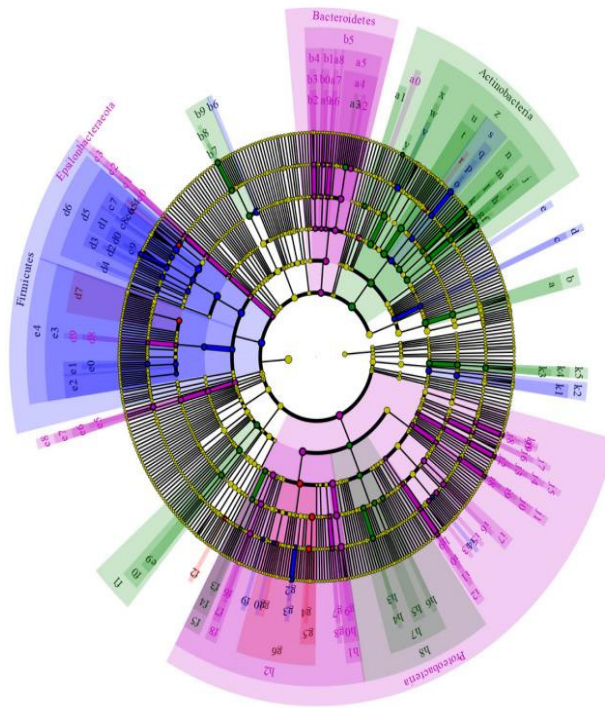




(d)

Cladogram

CK-14d  
Dm-14d  
GDm-14d  
Gm-14d

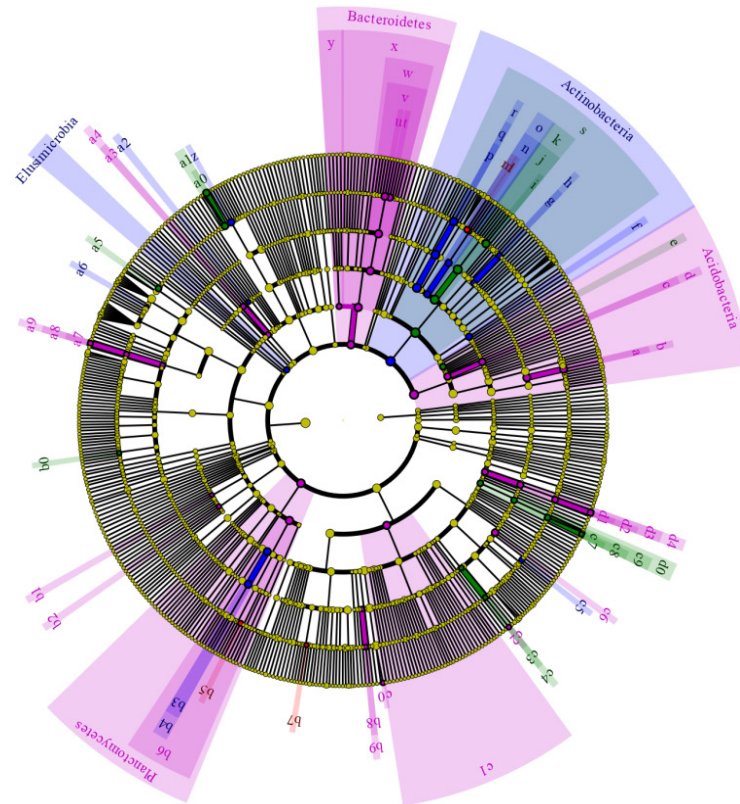




(e)

### Cladogram

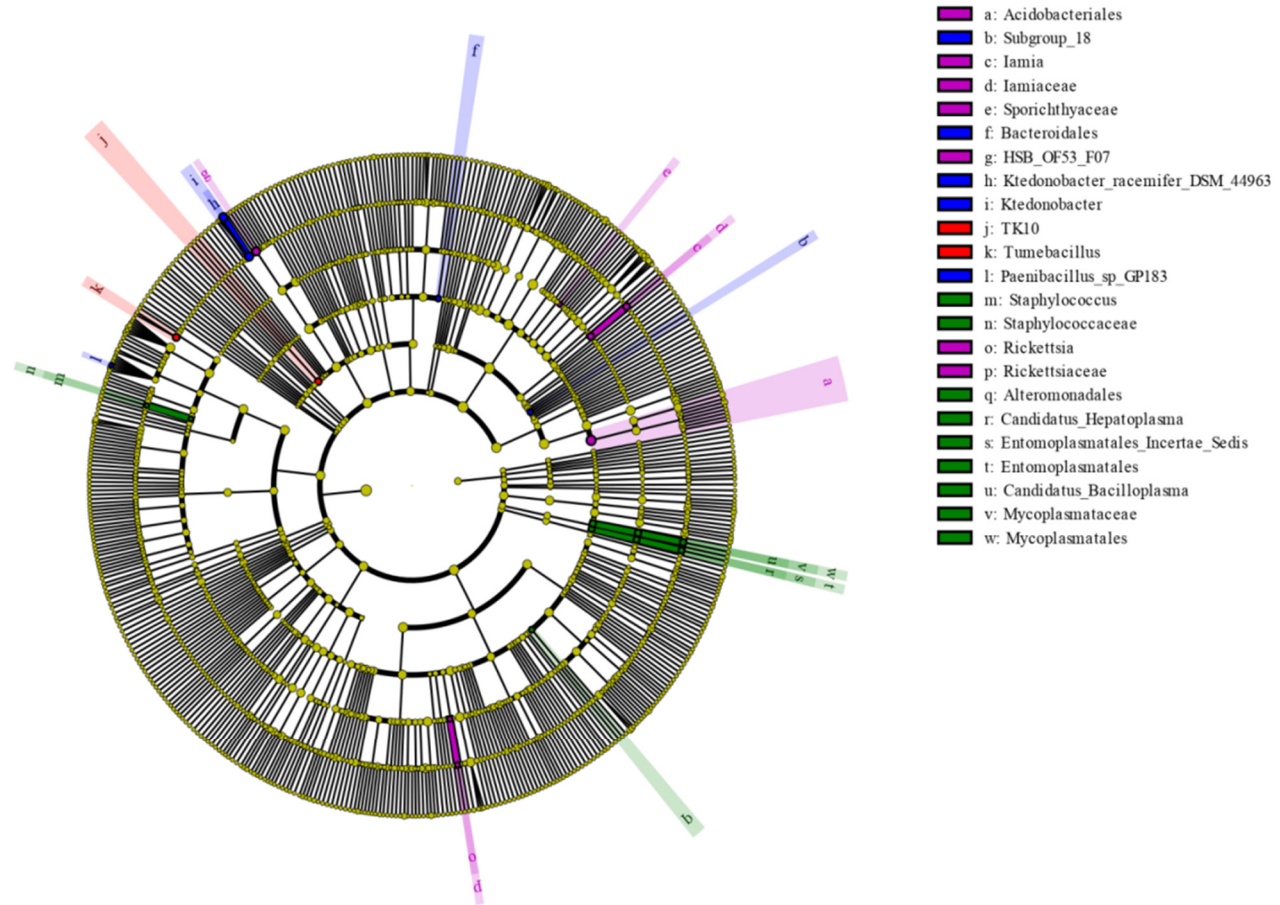
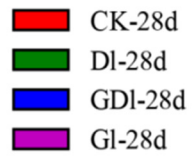
CK-14d  
Dh-14d  
GDh-14d  
Gh-14d



a: Candidatus\_Koribacter  
b: Koribacteraceae  
c: Subgroup\_7  
d: Holophagae  
e: Subgroup\_5  
f: IMCC26256  
g: Cellulomonas  
h: Cellulomonadaceae  
i: Dactylosporangium  
j: Micromonosporaceae  
k: Micromonosporales  
l: Marmoricola  
m: Nocardioidea  
n: Nocardioideae  
o: Propionibacteriales  
p: Streptomyces  
q: Streptomycetaceae  
r: Streptomycetales  
s: Actinobacteria  
t: Flavisolibacter  
u: Niasella  
v: Chitinophagaceae  
w: Chitinophagales  
x: Bacteroidia  
y: Ignavibacteria  
z: HSB\_OF53\_F07  
a0: Ktedonobacter\_racemifer\_DSM\_44963  
a1: Ktedonobacter  
a2: Gastranaerophilales  
a3: Chloroplast  
a4: Oxyphotobacteria  
a5: Effusibacillus  
a6: Oceanobacillus  
a7: Lactococcus\_garvieae\_subsp\_garvieae  
a8: Lactococcus  
a9: Streptococcaceae  
b0: Pseudobacteroides  
b1: Candidatus\_Roizmanbacteria  
b2: Candidatus\_Kaiserbacteria  
b3: Isosphaeraceae  
b4: Isosphaerales  
b5: Prellula  
b6: Planctomycetacia  
b7: Rhodoblastus  
b8: Rickettsia  
b9: Rickettsiaceae  
c0: Sphingomonas\_sediminicola  
c1: Deltaproteobacteria  
c2: Shewanella\_algae  
c3: Shewanella  
c4: Shewanellaceae  
c5: mle1\_7  
c6: SC\_I\_84  
c7: Acinetobacter\_calcoaceticus  
c8: Acinetobacter  
c9: Moraxellaceae  
d0: Pseudomonadales  
d1: Photobacterium\_damselae\_subsp\_damselae  
d2: Photobacterium  
d3: Vibrionaceae  
d4: Vibrionales

(f)

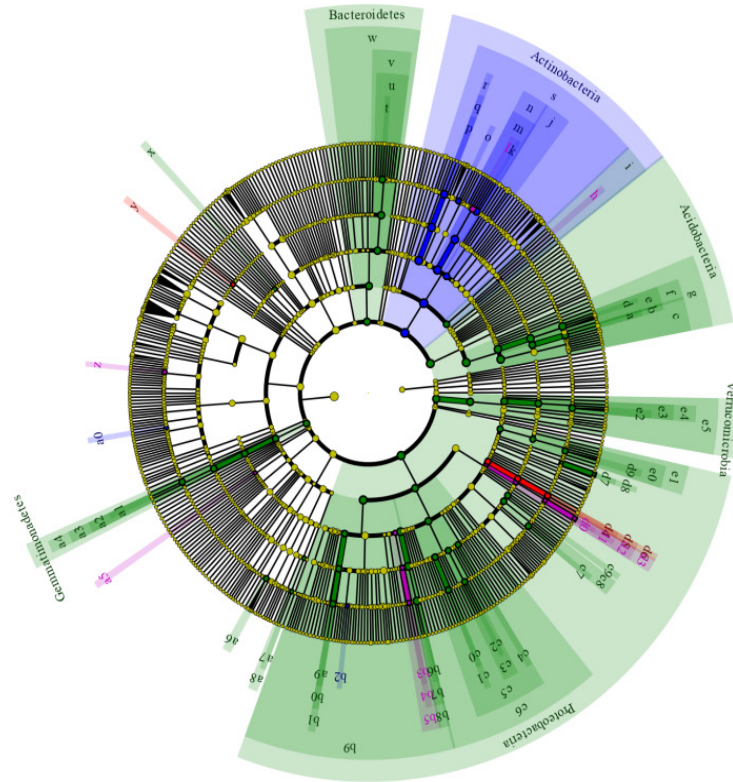
## Cladogram



(g)

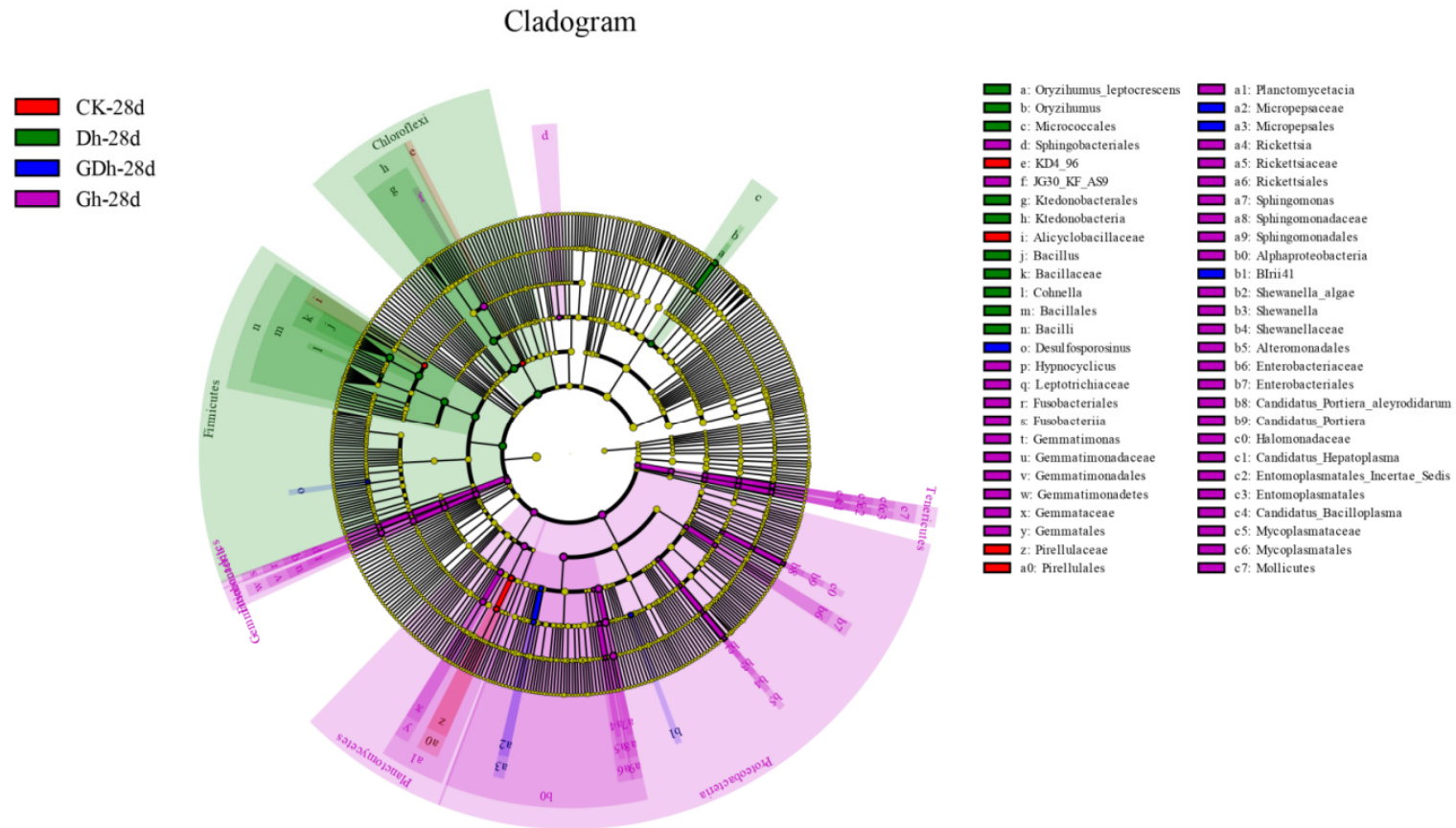
Cladogram

CK-28d  
Dm-28d  
GDm-28d  
Gm-28d

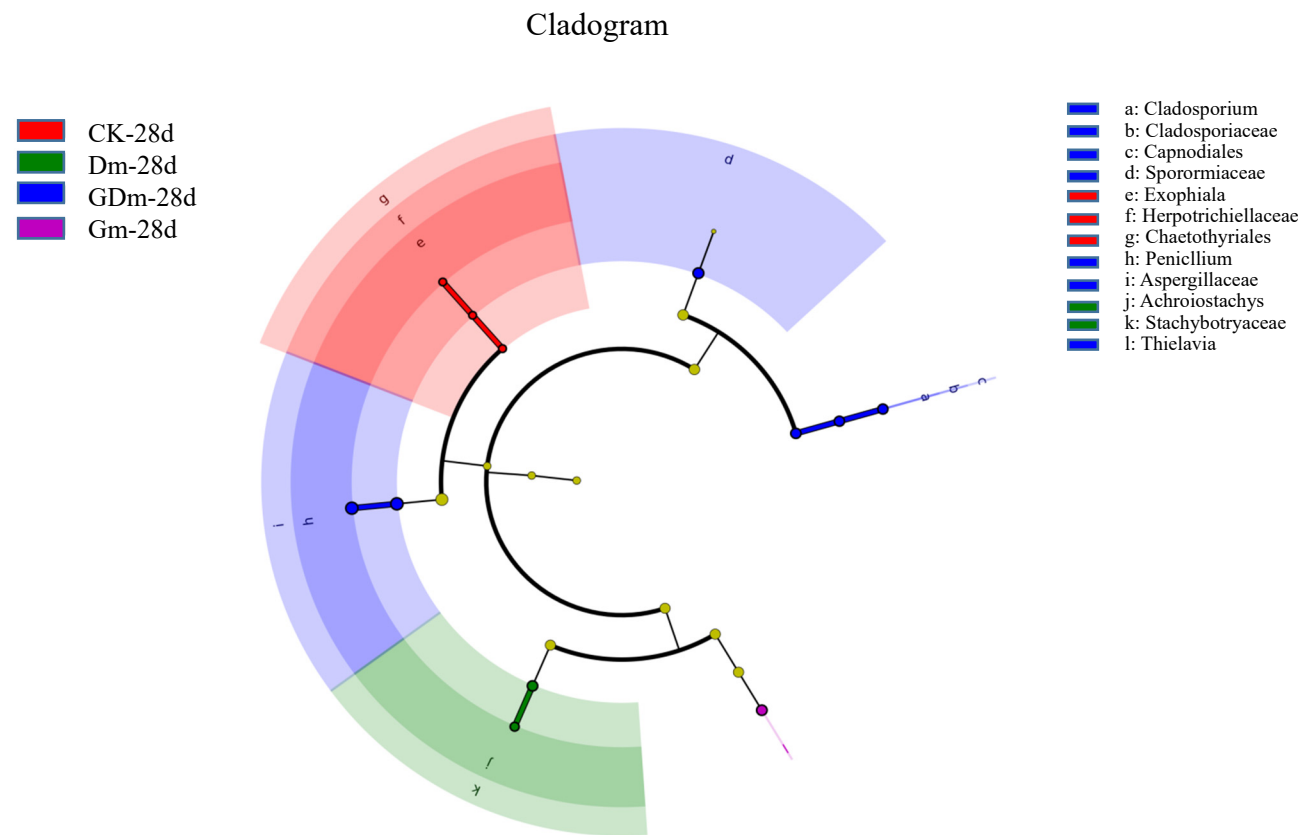


a: Candidatus_Koribacter	y: Vermiphilaceae	c2: Pajaroellobacter
b: Koribacteraceae	z: Clostridium_sensu_stricto_3	c3: Polyangiaceae
c: Acidobacteriales	a0: Paeniciostriidium	c4: mle1_27
d: Candidatus_Solibacter	a1: Gemmatimonas	c5: Myxococcales
e: Solibacteraceae_Subgroup_3	a2: Gemmatimonadaceae	c6: Deltaproteobacteria
f: Solibacterales	a3: Gemmatimonadales	c7: Ellin6067
g: Acidobacteriia	a4: Gemmatimonadetes	c8: Nitrosomonadaceae
h: actinobacterium_YJF2_33	a5: Candidatus_Woesebacteria	c9: SC_I_84
i: Acidimicrobiia	a6: Gemmata	d0: Pantoea_dispersa
j: Micrococcales	a7: Schleseria	d1: Pantoea
k: Dactylosporangium	a8: Schleseriaceae	d2: Enterobacteriaceae
l: Luedemannella	a9: Reyranela	d3: Enterobacteriales
m: Micromonosporaceae	b0: Reyraneliaceae	d4: Acidibacter
n: Micromonosporales	b1: Reyraneliales	d5: Unknown_Family
o: Nocardioides	b2: Rhodoblastus	d6: Gammaproteobacteria_Incertae_Sedis
p: Streptomyces	b3: Rickettsia	d7: Photobacterium_damselae_subsp_damselae
q: Streptomycetaceae	b4: Rickettsiaceae	d8: Photobacterium
r: Streptomycetales	b5: Rickettsiales	d9: Dyella
s: Actinobacteria	b6: Sphingomonas	e0: Rhodanobacteraceae
t: Nostella	b7: Sphingomonadaceae	e1: Xanthomonadales
u: Chitinophagaceae	b8: Sphingomonadales	e2: ADurbBin063_1
v: Chitinophagales	b9: Alphaproteobacteria	e3: Pedosphaeraceae
w: Bacteroidia	c0: Haliangium	e4: Pedosphaerales
x: bacterium_Ellin6543	c1: Haliangiaceae	e5: Verrucomicrobiae

(h)



**Figure S2.** Cladograms of line discriminant analysis effect size (LEfSe) analyses of bacteria.



**Figure S3.** Cladograms of line discriminant analysis effect size (LEfSe) analyses of fungus.