

**Table S2** Statistical analysis of top 10 bacterial and fungal phyla or genera in pecan plantations

Phylum		Genus				
	DF	GM		DF	GM	
Bacteria	Acidobacteriota	b	a**	<i>RB41</i>	a	ab
	Proteobacteria	a*	b	<i>Candidatus_Udaeobacter</i>	de	a**
	Chloroflexi	cd	bc	<i>Nitrospira</i>	b**	c
	Verrucomicrobiota	ef	bc***	<i>Bacillus</i>	bc*	c
	Bacteroidota	c	c	<i>ADurbBin063-1</i>	e	bc***
	Planctomycetota	de**	cd	<i>UTCFX1</i>	cd*	c
	Actinobacteriota	f	cd	<i>HSB_OF53-F07</i>	e	bc*
	Patescibacteria	de***	cd	<i>Bryobacter</i>	e	bc**
	Gemmatimonadota	f	cd	<i>Candidatus_Solibacter</i>	e	bc***
	Firmicutes	f*	d	<i>Sphingomonas</i>	de	c
Other	—	—	Other	—	—	
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	DF	GM		DF	GM	
Fungi	Basidiomycota	a	a*	<i>Scleroderma</i>	a*	b
	Ascomycota	b*	b	<i>Clavulina</i>	b	a**
	Mortierellomycota	c**	c	<i>Sphaerosporella</i>	ab	b
	Monoblepharomycota	c*	c	<i>Russula</i>	b	b*
	Rozellomycota	c	c	<i>Astraeus</i>	b	b
	Chytridiomycota	c**	c	<i>Pisolithus</i>	b	b
	Mucoromycota	c	c	<i>Hebeloma</i>	b***	b
	Glomeromycota	c	c	<i>Naucoria</i>	b***	b
	Aphelidiomycota	c	c	<i>Inocybe</i>	b	b*
	Kickxellomycota	c	c	<i>Sebacina</i>	b	b
Other	—	—	Other	—	—	

Statistical analysis was conducted to determine the relative abundance of the top 10 bacterial and fungal phyla or genera in various pecan plantations. The differences in relative abundance of different microorganisms (bacteria and fungi) at the phylum or genus level within the same pecan plantation are represented by different lowercase letters ( $P<0.05$ ). \*, \*\*, \*\*\* indicate that the difference between Dafeng forest farm (DF) and Guomei pecan plantation (GM) under the same phylum or genus is significant at  $P<0.05$ , 0.01 and 0.001 level, respectively.