Supplementary Information

Enhancement of Beneficial Microbiomes in Plant-Soil Continuums through Organic Fertilization: Insights into the Composition and Multifunctionality

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Number of figures: 9

Number of tables: 3

Table S1 Beneficial bacteria chosen in this study.

Beneficial Bacteria	Phylum	Functions	Reference
Rhizobium	Proteobacteria	Nitrogen cycle	(Lugtenberg and Kamilova, 2009)
Pseudomonas	Proteobacteria	Phosphate Solubilization; Pathogen suppression; Salinity resistance	(Lugtenberg and Kamilova, 2009; Richardson and Simpson, 2011; Schmitz et al., 2022)
Bacillus	Firmicutes	Phosphate Solubilization; Nitrogen cycle; Pathogen suppression; Salinity resistance	(Kang et al., 2022; Lugtenberg and Kamilova, 2009; Schmitz et al., 2022; Shao et al., 2021)
Nocardioides	Actinobacteria	Nitrogen cycle	(Kuang et al., 2022)
Devosia	Proteobacteria	Nitrogen cycle	(Rivas et al., 2002)
Micromonospora	Actinobacteria	Nitrogen cycle	(Trujillo et al., 2015)
Cellulomonas	Actinobacteria	Nitrogen cycle	(Sonkurt and ÇIĞ, 2019)
Phenylobacterium	Proteobacteria	Nitrogen cycle	(Mehmood et al., 2022)
Streptomyces	Actinobacteria	Nitrogen cycle; Pathogen suppression; Salinity resistance	(Chen et al., 2020; Dahal et al., 2017; Schmitz et al., 2022)
Conexibacter	Actinobacteria	Nitrogen cycle	(Pedrinho et al., 2020)
Asticcacaulis	Proteobacteria	Carbon cycle	(Wilhelm et al., 2019)
Acidovorax	Proteobacteria	ACC deaminase secretion	(Cavite et al., 2020)
Flavobacterium	Bacteroidetes	Pathogen suppression	(Carrion et al., 2019; Kwak et al., 2018)
Sphingomonas	Proteobacteria	Pathogen suppression	(Deng et al., 2022)
Luteimonas	Proteobacteria	Pathogen suppression	(Deng et al., 2022)
Lysobacter	Proteobacteria	Pathogen suppression	(Deng et al., 2022)
Pseudoxanthomonas	Proteobacteria	Pathogen suppression	(Deng et al., 2022)
Stenotrophomonas	Proteobacteria	Pathogen suppression	(Berendsen et al., 2018; Deng et al., 2022; Liu et al., 2021)
Microbacterium	Actinobacteria	Pathogen suppression	(Berendsen et al., 2018)
Paenibacillus	Firmicutes	Pathogen suppression; Hormone secretion	(Bziuk et al., 2021; Mendes et al., 2018)
Erwinia	Proteobacteria	Phosphate Solubilization; Pathogen suppression; Hormone secretion; Siderophore production	(Bziuk et al., 2021; Lugtenberg and Kamilova, 2009; Rodríguez et al., 2006)
Curtobacterium	Actinobacteria	Hormone secretion; Siderophore production	(Bziuk et al., 2021)
Massilia	Proteobacteria	Salinity resistance	(Schmitz et al., 2022)
Enterobacter	Proteobacteria	Salinity resistance	(Schmitz et al., 2022)
Ensifer	Proteobacteria	Salinity resistance	(Schmitz et al., 2022)
Variovorax	Proteobacteria	Hormone manipulation	(Qi et al., 2022)

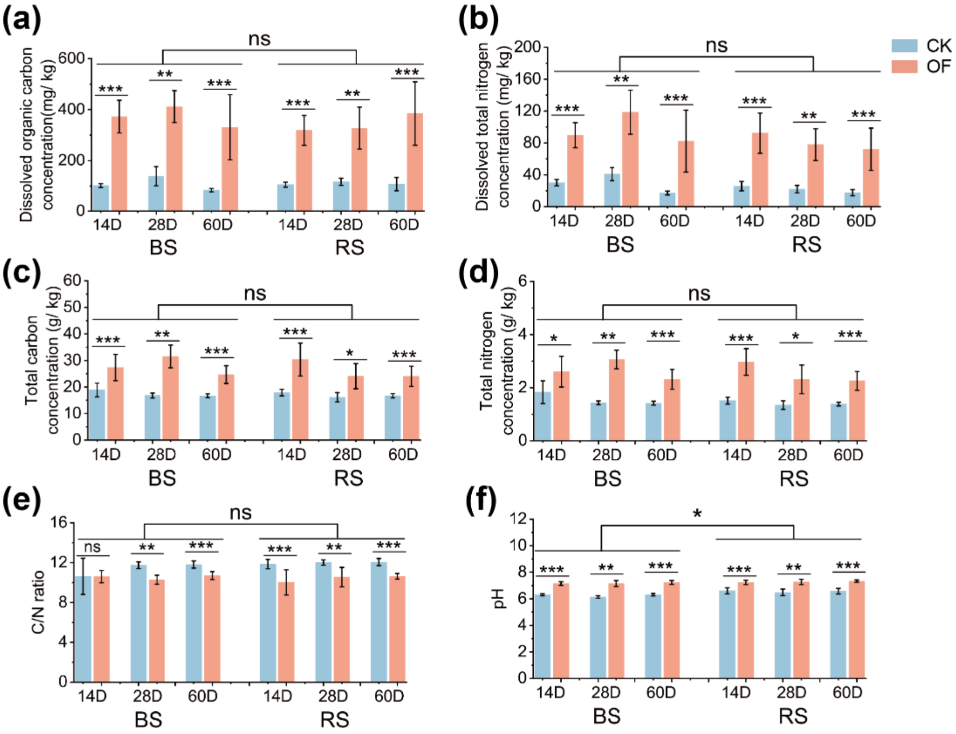

Fig. S1 Changes of dissolved organic carbon (a), dissolved total nitrogen (b), total carbon (c), total nitrogen (d), C/N ratio (e), pH (f) in bulk soil (BS) and rhizosphere soil (RS) across different fertilization treatments and growth time. *P* values are indicated by *, e.g., * represents $P < 0.05$, ** represents $P < 0.01$, and *** represents $P < 0.001$.

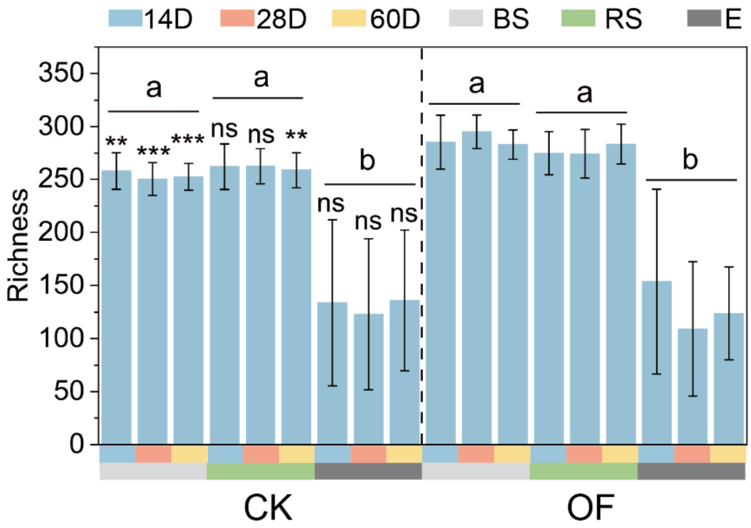

Fig. S2 The richness of bacterial communities in bulk soil (BS), rhizosphere soil (RS) and endosphere (E) with different fertilization treatments and growth time. The richness differences between CK groups and OF groups are tested by t-test. ** represents $P < 0.01$ and *** represents $P < 0.001$. The richness differences across the three compartments are tested by one-way ANOVA. Different letters above the bars indicate significant differences at $P < 0.05$.

Table S2 The effects of plant growth time on bacterial richness in bulk soil (BS), rhizosphere soil (RS) and endosphere (E) based on one-way ANOVA.

		Time	
CK	BS	14D	ns
		28D	
		60D	
	RS	14D	ns
		28D	
		60D	
	E	14D	ns
		28D	
		60D	
OF	BS	14D	ns
		28D	
		60D	
	RS	14D	ns
		28D	
		60D	
	E	14D	ns
		28D	
		60D	

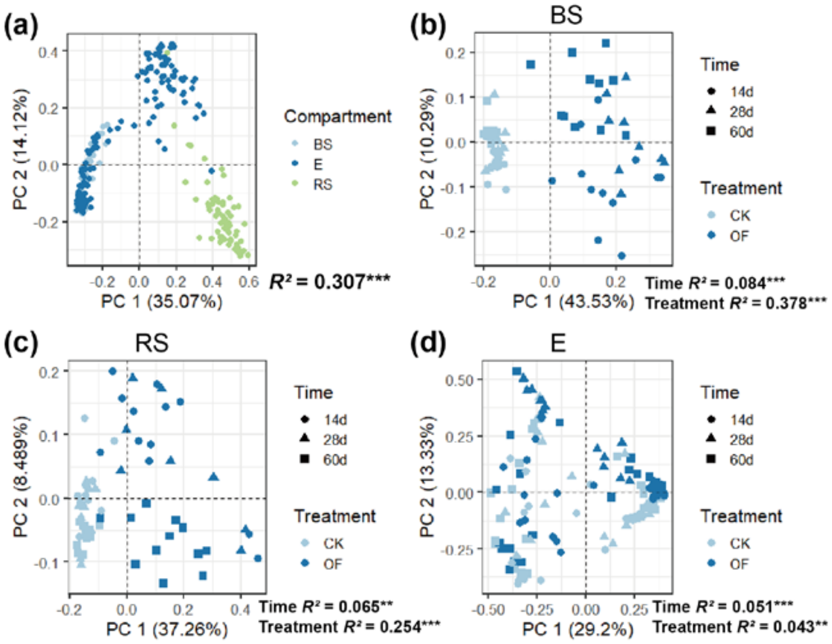

Fig. S3 Principal component analysis (PCA) indicating the dissimilarity of bacterial communities in different compartments (a) and the effects of growth time and fertilization treatments on the dissimilarity of bacterial communities in bulk soil (BS) (b), rhizosphere soil (RS) (c) and endosphere (E) (d). *P* values are indicated by *, e.g., ** represents $P < 0.01$ and *** represents $P < 0.001$.

Table S3 The effects of fertilization treatments and growth time on bacterial communities in different compartments based on Adonis.

	Fertilization		Time		Fertilization × Time	
	R^2	P	R^2	P	R^2	P
Bulk soil	0.378	0.001	0.084	0.001	0.041	0.014
Rhizosphere soil	0.254	0.001	0.065	0.004	0.038	0.050
Endosphere	0.043	0.002	0.051	0.001	0.031	0.009

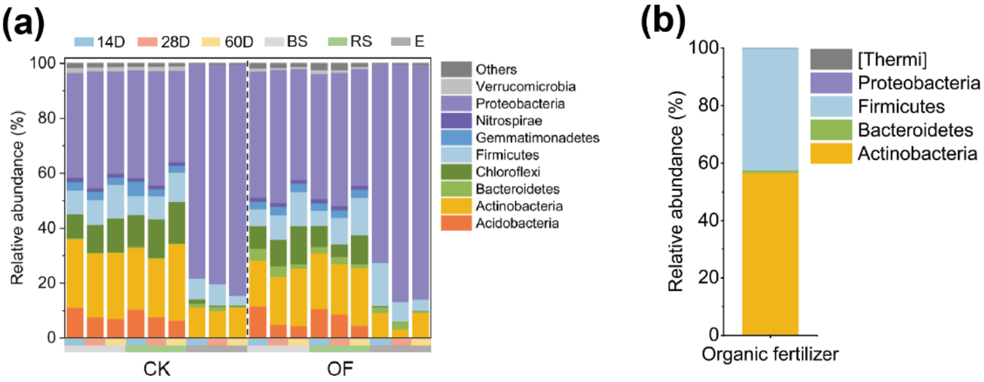

Fig. S4 Changes of bacterial community composition in bulk soil (BS), rhizosphere soil (RS) and endosphere (E) across different fertilization treatments and growth time at phylum level (a). The composition of bacterial communities in the organic fertilizer at a phylum level (b).

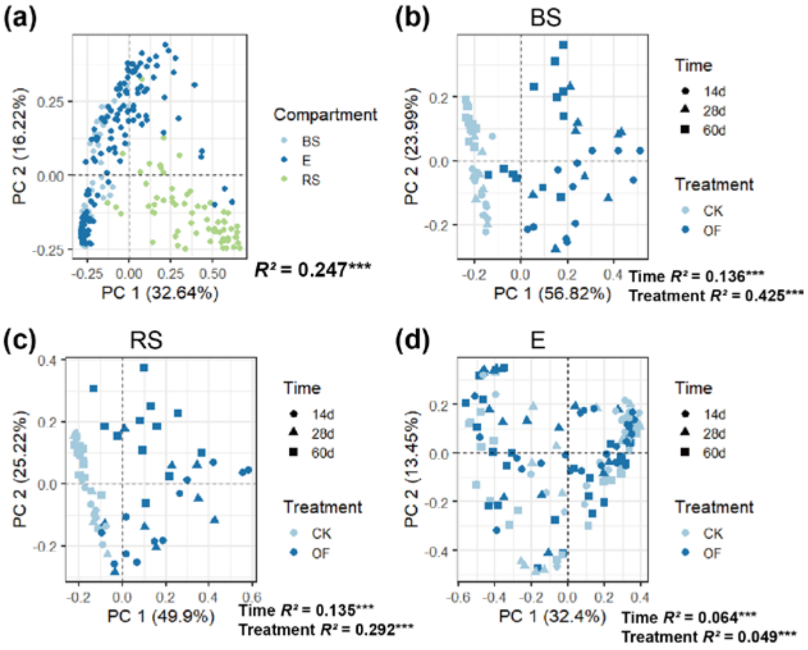

Fig. S5 Principal component analysis (PCA) indicating the dissimilarity of beneficial bacterial communities in different compartments (a) and the effects of growth time and fertilization treatments on the dissimilarity of beneficial bacterial communities in bulk soil (BS) (b), rhizosphere soil (RS) (c) and endosphere (E) (d). *** represents $P < 0.001$.

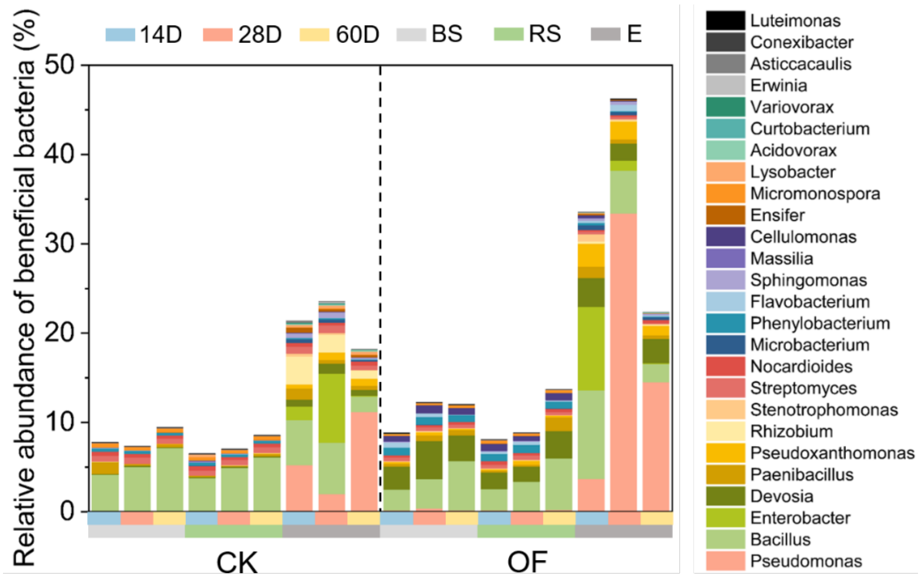

Fig. S6 The composition of beneficial bacteria in bulk soil (BS), rhizosphere soil (RS) and endosphere (E) with different fertilization treatments and growth time.

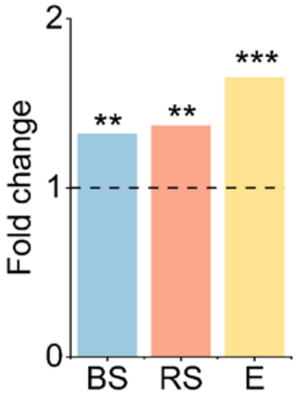

Fig. S7 The fold changes in the relative abundance of beneficial bacteria in the three compartments treated with organic fertilizers compared to that treated without organic fertilizers. Samples of different growth time are included. t-test is used to test differences. ** represents *P* < 0.01 and *** represents *P* < 0.001.

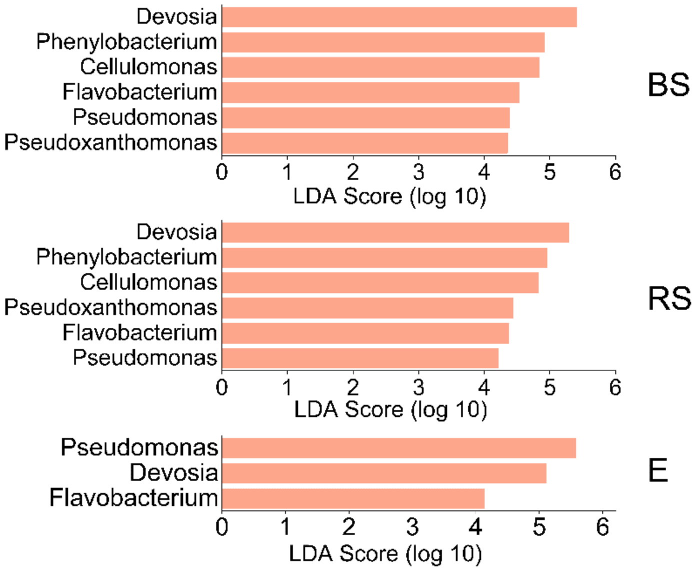

Fig. S8 LEfSe (Linear discriminant analysis Effect Size) showing beneficial bacteria with significant differences between CK groups and OF groups. Samples of different growth time are included.

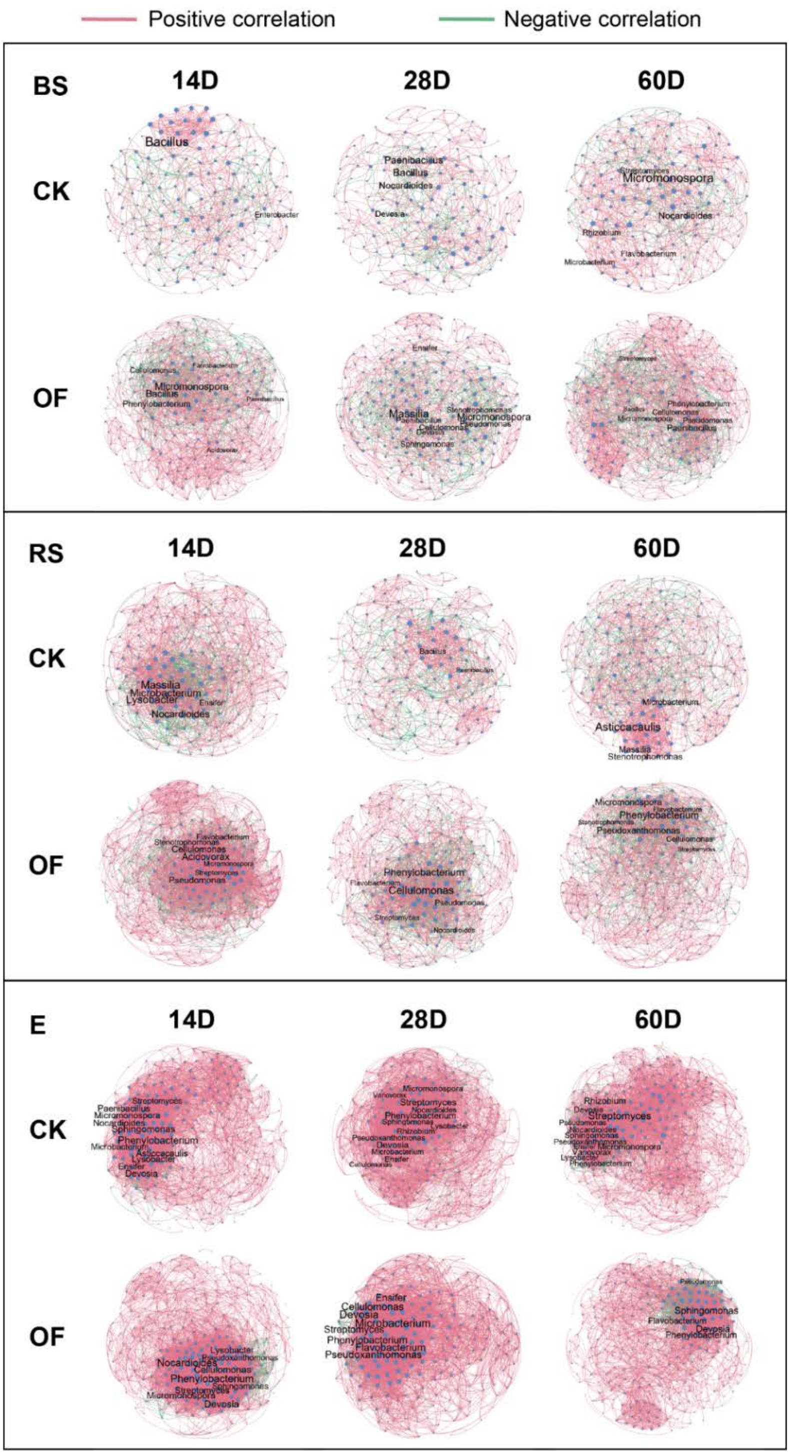

Fig. S9 The networks showing effects of organic fertilizations and growth time on co-occurrence patterns of bacteria taxa in bulk soil (BS), rhizosphere soil (RS) and endosphere (E) at a genus level. Beneficial bacteria with high degree are marked in networks.

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