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SHAN DONG WEIFANG TOBACCO CO.,LTD

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Changes of soil bacterial community structure and its response to soil physicochemical properties after addition of wheat straw and its biochar

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Background

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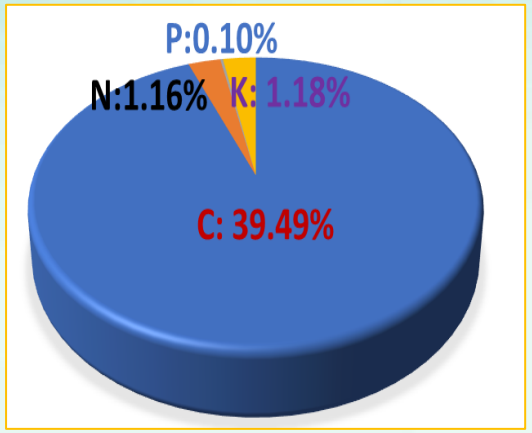
Relief map of Shandong Province

The most important tobacco planting areas in Shandong province

Removal of tobacco straw to avoid soil borne disease

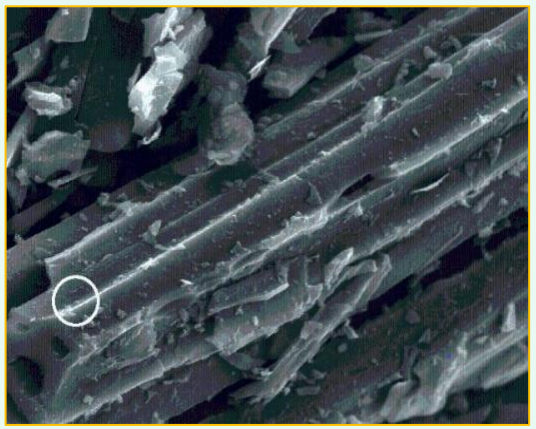
Soil degradation caused by unreasonable cultivation management

➢ Comparative effect of wheat and wheat straw-derived biochar on soil biological quality improvement

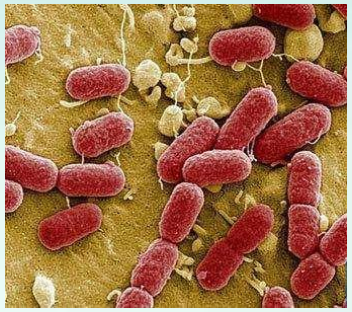


Wheat straw

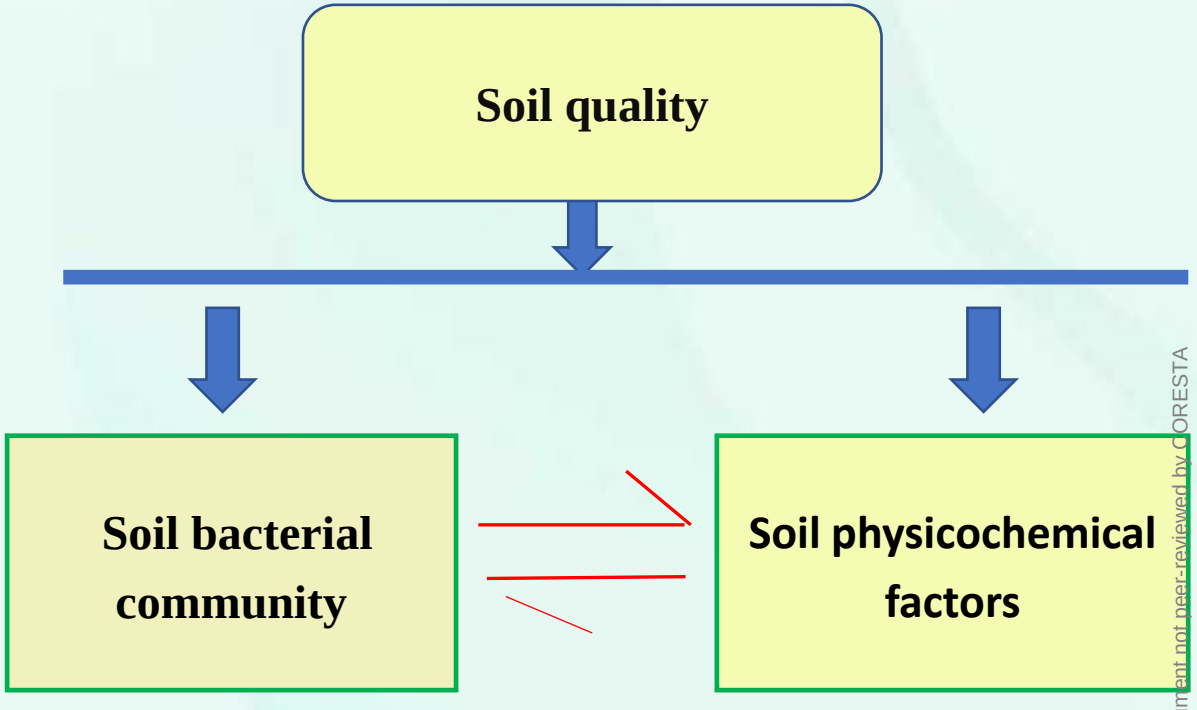
VS



Wheat straw derived biochar



Objective



Experiment design

Four treatments:

CK: chemical fertilizer only (control)

WS: chemical fertilizer plus 6.75 t hm^{-2} wheat straw

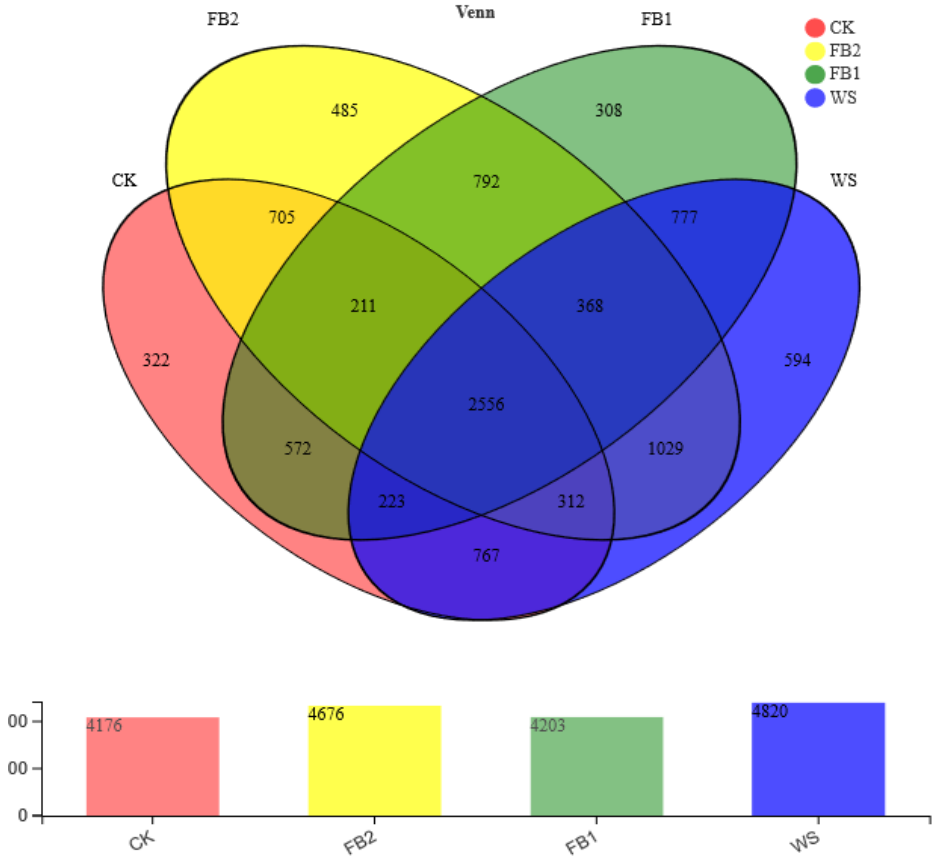
FB1: chemical fertilizer plus 2.25 t hm^{-2} wheat straw-derived biochar

FB2:chemical fertilizer plus 4.5 t hm^{-2} wheat straw-derived biochar




Result

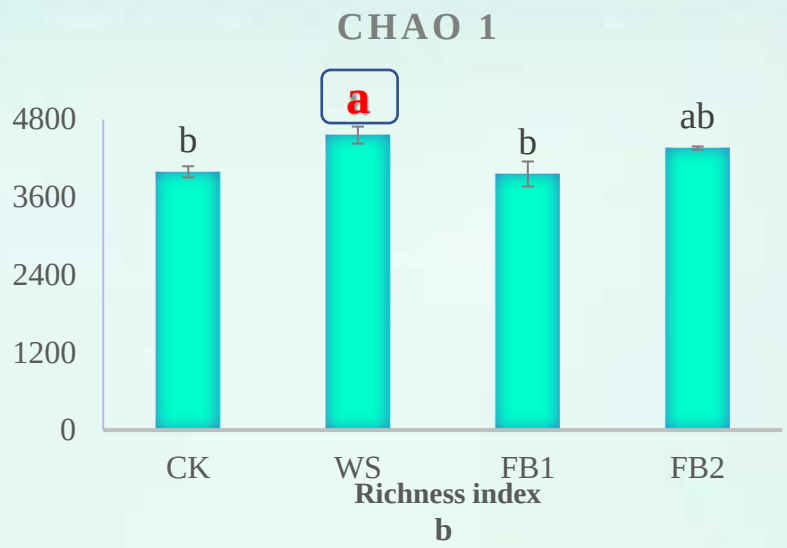
➢ Structure and function analysis of bacteria (16S rRNA) in rhizosphere soil microbial community

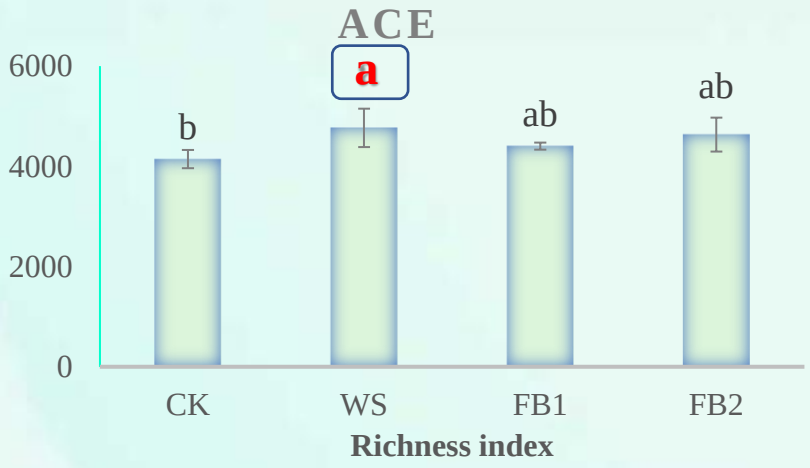


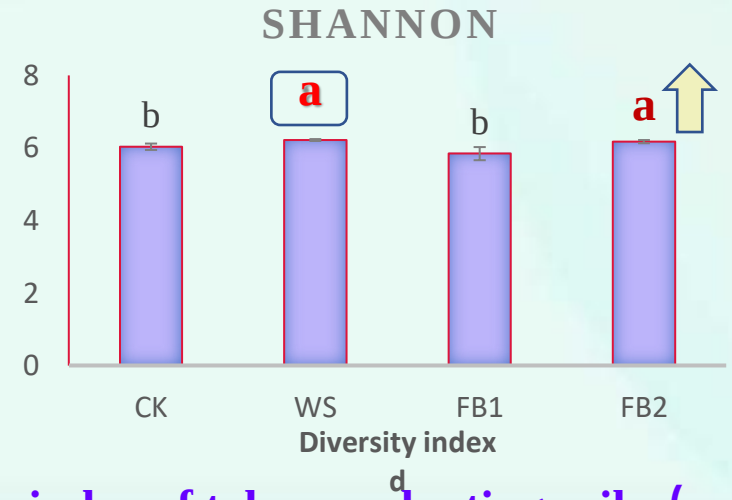
The Species richness of bacteria in the soil samples of different treatments was WS>FB2>FB1>CK; which indicated the WS treatment were more favorable to increase the OTU richness of bacteria in the soil.

Fig. 1 Venn distribution of bacterial community of tobacco planting soil on OUT level (97% similarity)

➢ Bacterial community alpha diversity analysis







Compared with CK, WS treatment significantly increased the values of Sobs, Chao 1, Ace and Shannon; FB2 treatment significantly increased the values of Sobs and Shannon.

Fig. 2 Bacterial community alpha diversity index of tobacco planting soil （a, b, c, d）

➢ Soil organic carbon fractions under different treatments

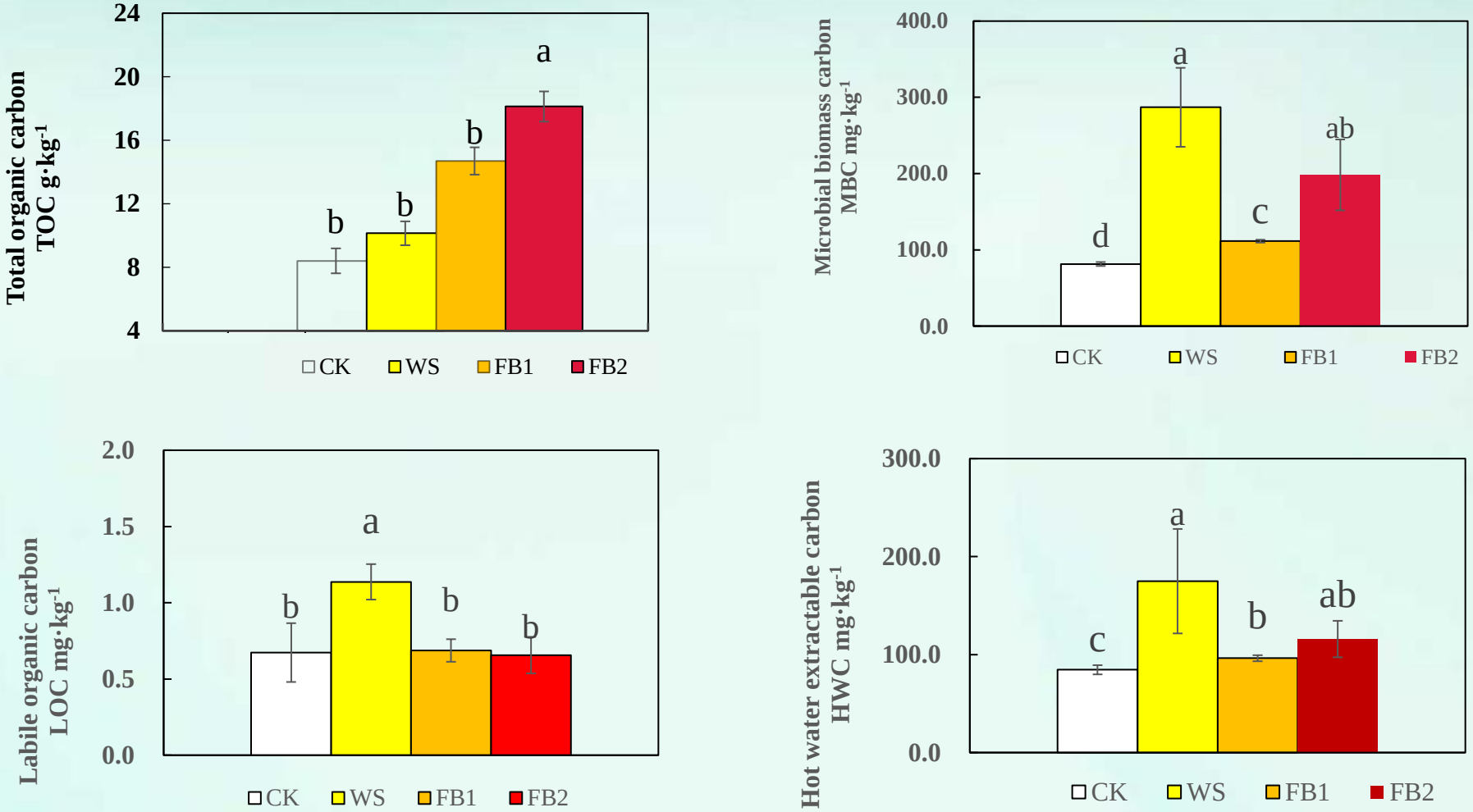


Fig. 3 Effects of wheat straws or biochar addition on soil TOC and SOC fractions

➢ Pearson correlation analysis and stepwise regression analysis

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Table 1 Pearson correlation between diversity of bacterial community and soil labile organic carbon fractions

Index	Soil Total Organic Carbon（TOC）	Hot Water Extractable Carbon（HWC）	Microbial Biomass Carbon（MBC）	Light Fraction Organic Carbon LFOC	Labile Organic Carbon LOC
Ace	0.21	0.373	**0.672***	0.185	0.279
Chao 1	0.108	0.686*	**0.880****	0.07	0.584*
Shannon	0.004	0.541	**0.623***	0.043	0.301
Simpson	0.044	-0.28	-0.184	-0.022	0.074

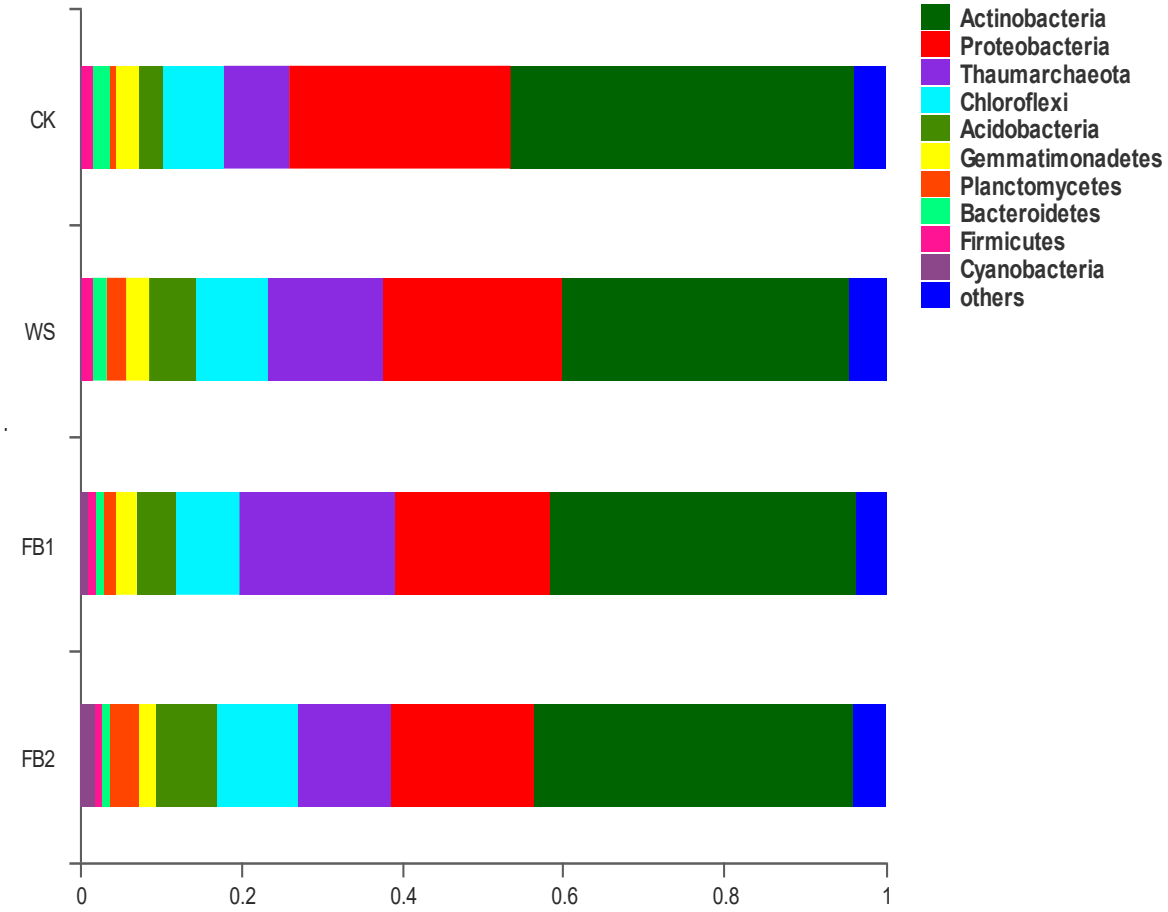
Pearson correlation analysis showed that soil microbial biomass carbon (MBC) correlated positively with indices of Ace, Chao 1 and Shannon.

Table 2 Stepwise regression analysis of bacterial community diversity and labile organic carbon fractions

Dependent variable	Regression equation	independent variable	Dependent variable	Adjustment coefficient of regression equation R^2
Ace	y^=2.569X1+4050.48	X1	MBC	0.397
Chao 1	y^=2.823X1+3736.7	X1	MBC	0.751
Shannon	y^=0.001X1+5.863	X1	MBC	0.320

Stepwise regression analysis showed the MBC explained 39.7% of the bacterial Ace index, 75.1% of the Chao 1 index and 32.0% of the Shannon index, respectively.

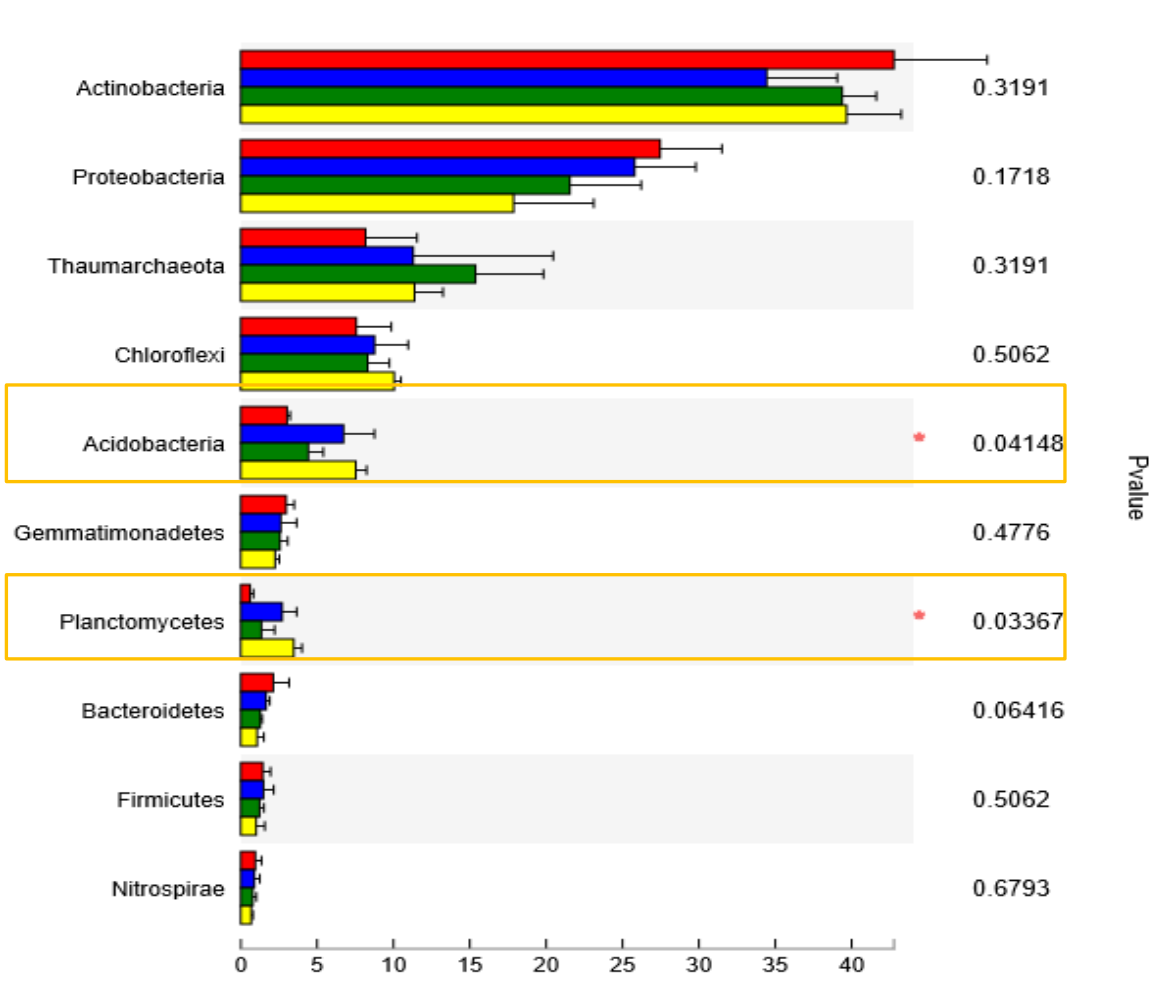
➢ the composition and relative abundance of bacteria on phylum level



Actinobacteria, Proteobacteria, Thaumarchaeota and Chloroflexi were the dominant phyla of each test treatment.

Fig.4 The composition and relative abundance of bacteria on phylum level in different treatments of tobacco planting soil

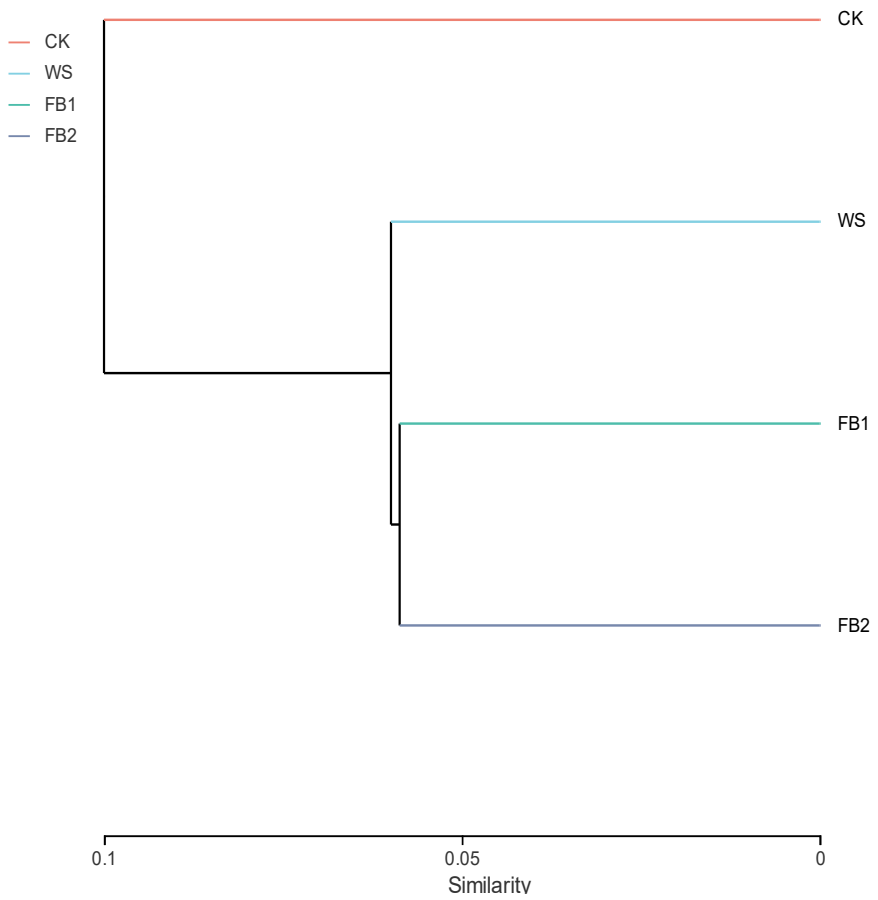
➢ Differences among the relative abundance of dominant bacteria



Among the top ten dominant phyla of each treatment, the relative abundance of Acidobacteria and Planctomycetes treated by WS and FB2 were significantly increased compared with CK. However, no significant difference in other phyla were found among these treatments.

Fig. 5 Significant comparison of the differences among the relative abundance of dominant bacteria in tobacco planting soil

➢ UPGMA cluster analysis



UPGMA clustering analysis based on the phylum level, showed that:

CK could be clustered into a single large class and was clearly different from other treatments;

WS treatment could be clustered into a single large class;

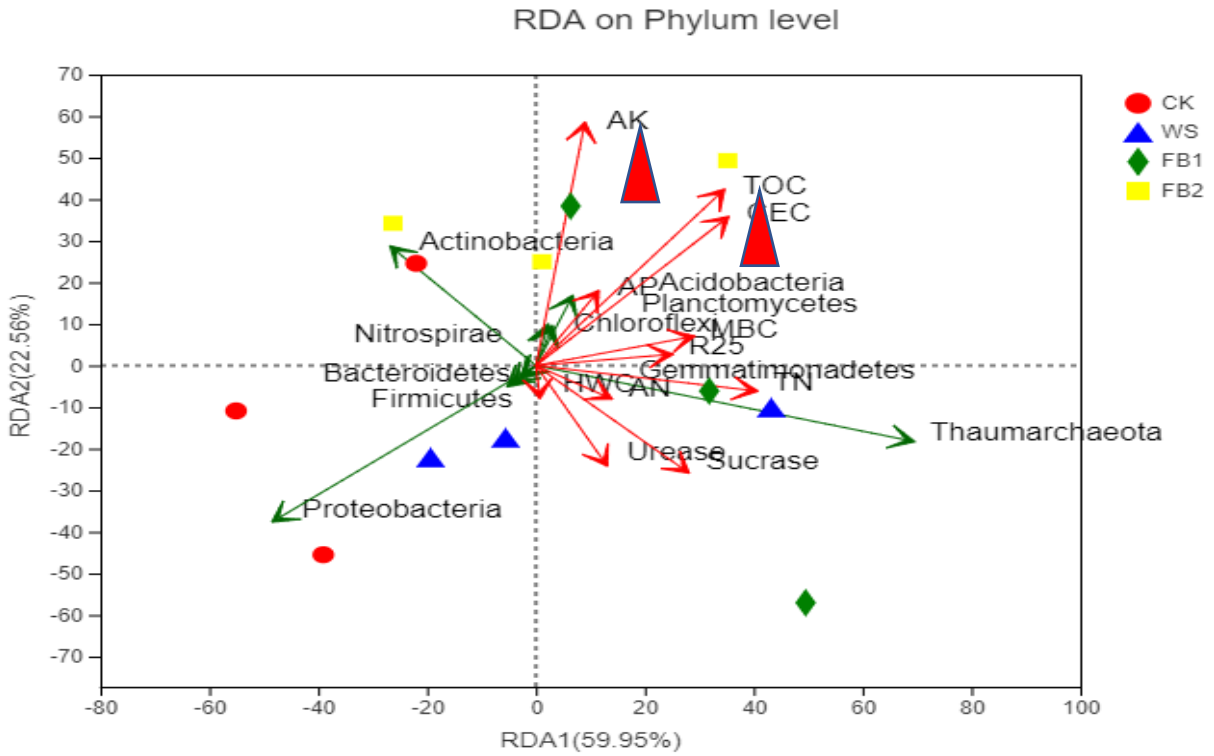
FB1 and FB2 treatments could be clustered into a single large class, which indicated that the soil bacterial communities of FB1 and FB2 treatments were more similar.

Fig. 6 UPGMA cluster analysis of bacterial communities of tobacco planting soil on phylum level

➢ RDA analysis

Table 3 Soil enzyme activities and soil physicochemical indices of different treatments

T	Sucrase mg glucose g^{-1} dry soil·24h^{-1}	Urease μg $NH^{4+}N$ g^{-1}drysoil·24h^{-1}	Phosphatase P nitro-phenol released g^{-1}dry soil· h^{-1}	TN mg·kg^{-1}	AN mg·kg^{-1}	AP mg·kg^{-1}	AK mg·kg^{-1}	CEC
CK	26.51b	1023.01b	0.74b	0.627a	56.03b	22.47b	229.47b	26.56a
WS	56.34a	1102.95a	0.999a	0.8a	99.8a	41.1a	253.8ab	27.93a
FB1	37.95ab	1029.614b	0.74b	0.697a	57.57b	23.2b	246.93ab	27.44a
FB2	32.82ab	929.77b	0.63b	0.693a	60.4b	37.4a	308.00a	28.08a

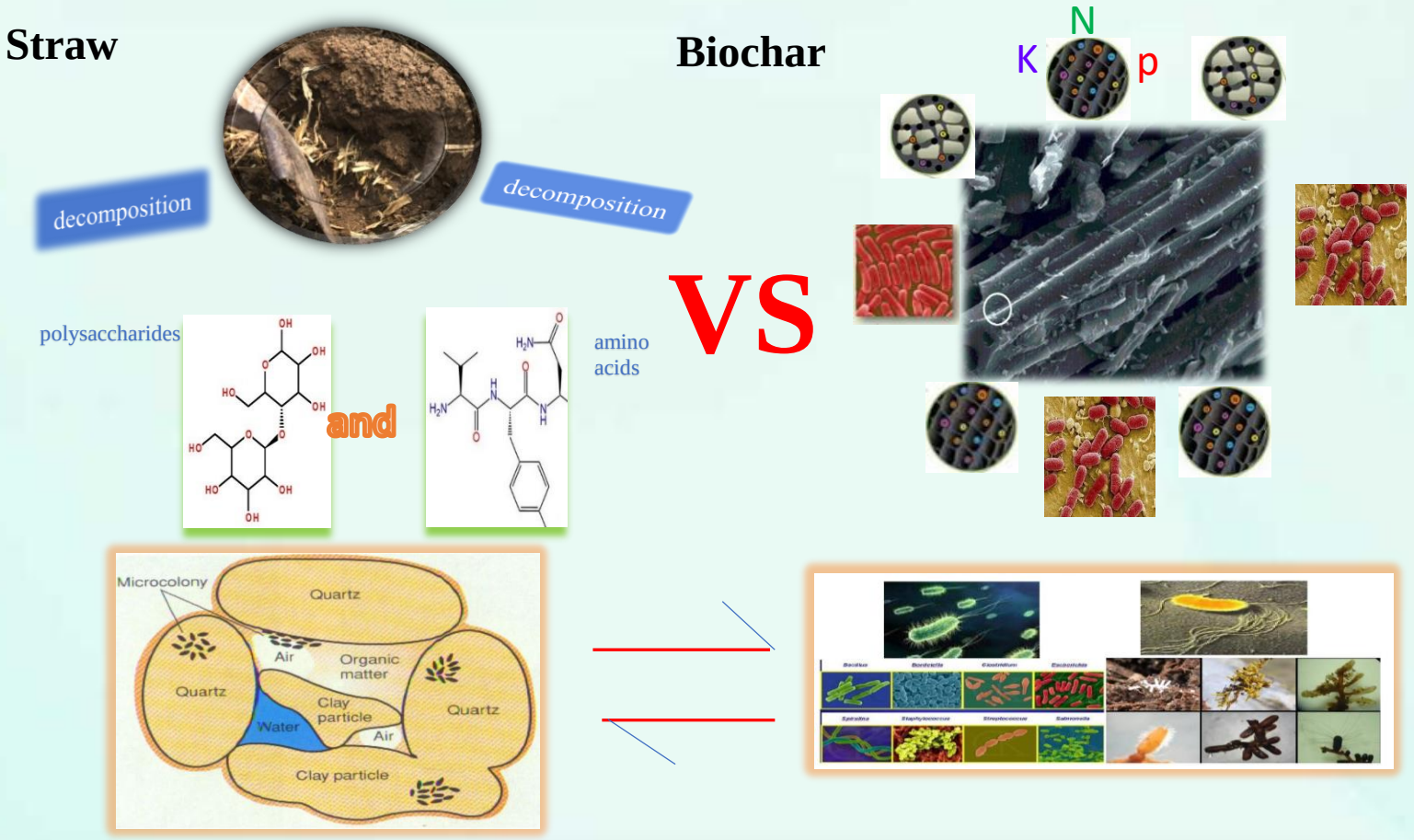


RDA analysis showed the soil total organic carbon (TOC) and soil available potassium (AK) were the dominant factors to the changes of soil bacterial community structure.

Fig. 7 RDA analysis of bacterial compositions of tobacco planting soil on phylum level

Conclusion

- **Differences in the properties of organic materials differed in their effects on soil physicochemical properties and on the diversity and community structure of bacteria.**



- **Microbial biomass carbon (MBC) explained the changes of soil microbial diversity.**

- **TOC and AK were the dominant environmental factors for soil bacterial community change in tobacco-planting soil.**

Thanks expression

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Qinghong Meng


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