Microbial Biotechnology

Electronic supplementary material

Lime and ammonium carbonate fumigation coupled with bio-organic fertilizer application steered banana rhizosphere to assemble a unique microbiome against Panama disease

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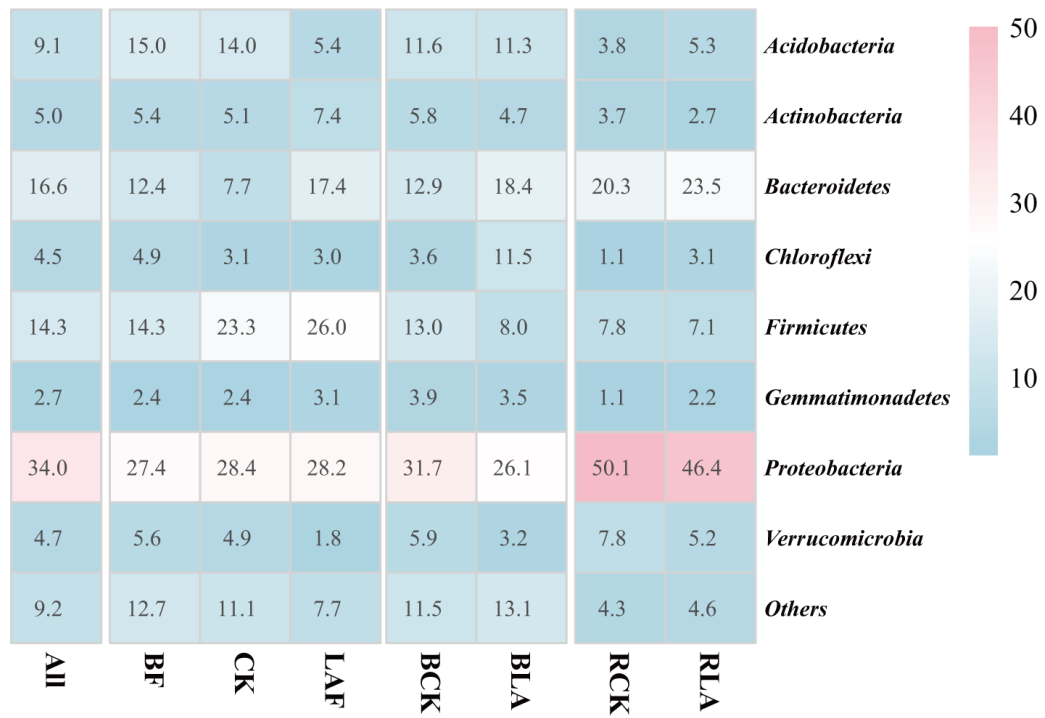
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Fig. S1 Sketch map for each season of the two seasonal greenhouse experiments.
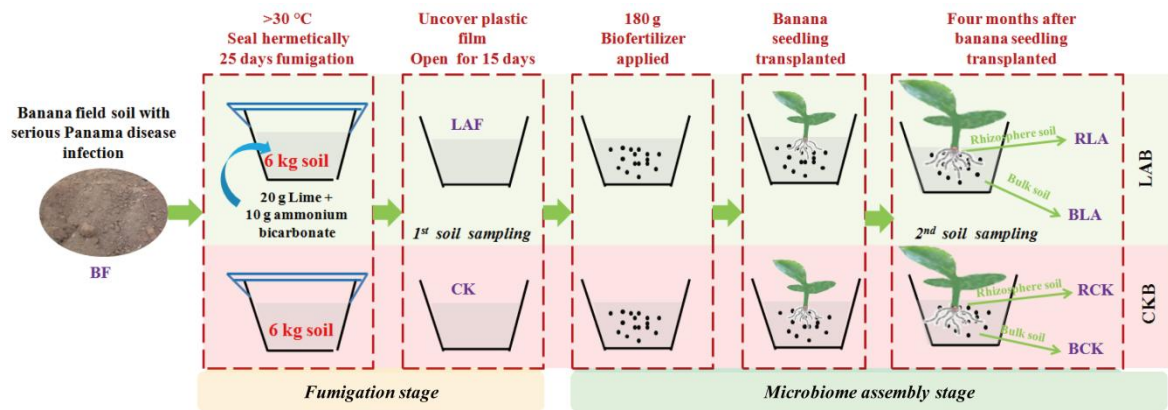
Fig. S2 Heatmap displaying the abundance of dominated bacterial phyla in each soil sample. Numbers in each cell represent the mean relative abundance of each phylum.

All	BF	CK	LAF	BCK	BLA	RCK	RLA	
9.1	15.0	14.0	5.4	11.6	11.3	3.8	5.3	*Acidobacteria*
5.0	5.4	5.1	7.4	5.8	4.7	3.7	2.7	*Actinobacteria*
16.6	12.4	7.7	17.4	12.9	18.4	20.3	23.5	*Bacteroidetes*
4.5	4.9	3.1	3.0	3.6	11.5	1.1	3.1	*Chloroflexi*
14.3	14.3	23.3	26.0	13.0	8.0	7.8	7.1	*Firmicutes*
2.7	2.4	2.4	3.1	3.9	3.5	1.1	2.2	*Gemmatimonadetes*
34.0	27.4	28.4	28.2	31.7	26.1	50.1	46.4	*Proteobacteria*
4.7	5.6	4.9	1.8	5.9	3.2	7.8	5.2	*Verrucomicrobia*
9.2	12.7	11.1	7.7	11.5	13.1	4.3	4.6	*Others*

Fig. S3 Spearman correlations between the abundance of *F. oxysproum* quantified by qPCR with the phylogenetic relatedness of based on nearest net relatedness (NRI) (a) and nearest taxon index (NTI) (b) in bacterial community.
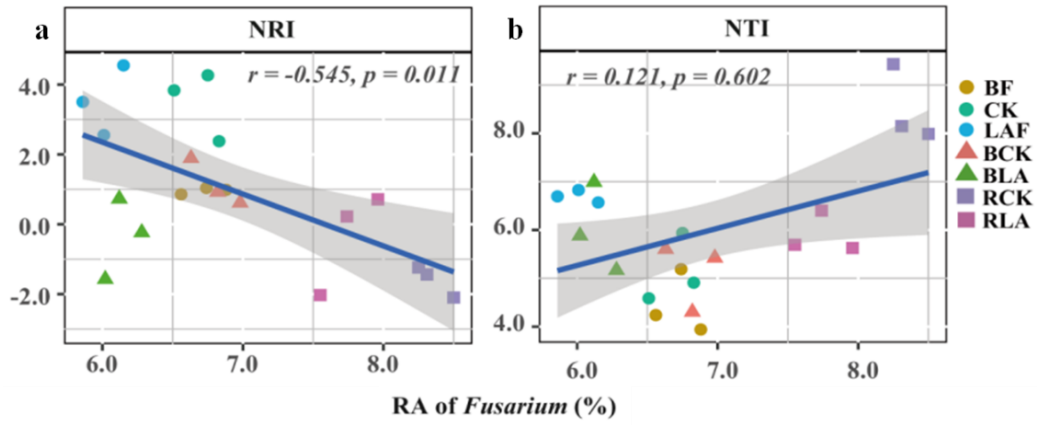
Fig. S4 Boxplot of the relative abundance of OTU10 (*Rhizobium*), OTU120 (*Gemmatimonas*), OTU130 (*Flavobacterium*), OTU14 (*Pseudomonas*), OTU277 (*Lysobacter*), and OTU2915 (*Sphingomonas*) for each soil sample. Different letters indicate a significant difference ($p < 0.05$) according to two independent sample t-test or ANOVA analysis.
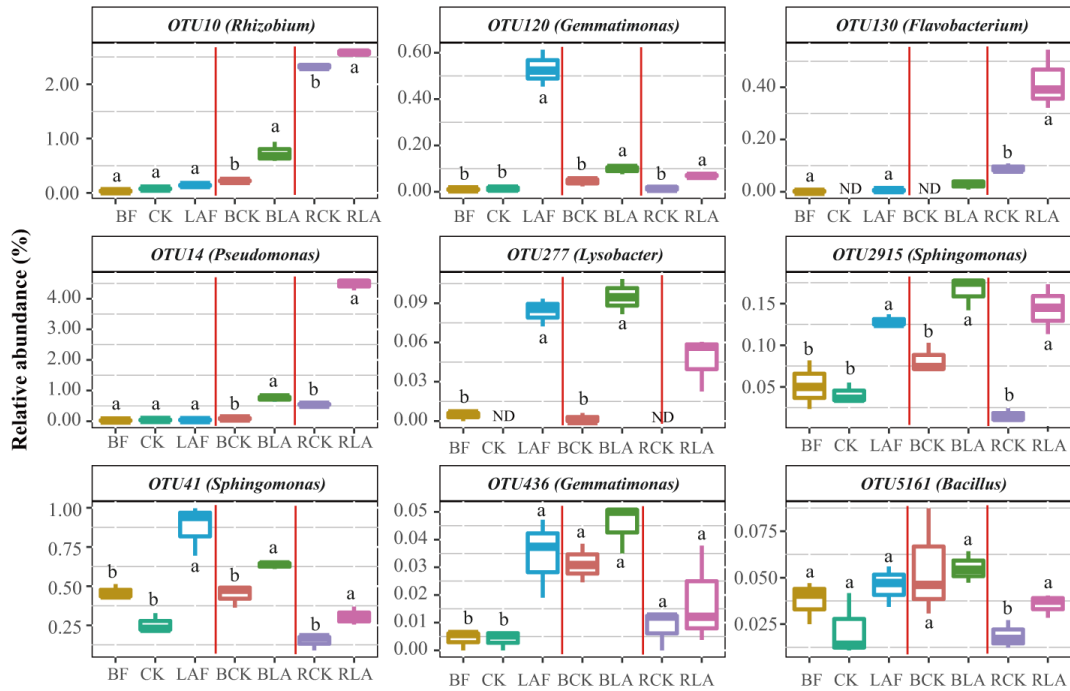
Table S1 Number of sequences and OTUs from rawdata and processed final good quality sequences that were used to further analysis after basic quality control for different treatments.

Sample	Rawdata		Final	
	No. of sequences	No. of OTUs	No. of sequences	No. of OTUs
BF1	19,286	3,179	16,999	2,787
BF2	10,986	2,483	9,788	2,213
BF3	17,668	3,095	16,007	2,725
BCK1	14,543	2,596	13,001	2,330
BCK2	21,679	3,107	19,457	2,620
BCK3	18,210	2,899	16,269	2,551
BLA1	18,852	2,293	17,133	2,034
BLA2	28,063	2,650	25,349	2,213
BLA3	26,859	2,651	23,956	2,218
CK1	15,844	2,814	14,481	2,472
CK2	20,462	3,067	18,451	2,523
CK3	18,481	2,880	16,794	2,531
LAF1	24,574	2,835	23,332	2,411
LAF2	27,449	2,851	26,248	2,460
LAF3	16,807	2,412	16,055	2,147
RCK1	11,298	1,384	11,059	1,275
RCK2	24,103	2,007	23,570	1,793
RCK3	16,704	1,670	16,404	1,521
RLA1	27,281	2,114	26,577	1,860
RLA2	25,449	2,034	24,816	1,783
RLA3	10,809	1,375	10,577	1,259
Total	415,407	7,580	386,323	5,448

Table S2 Spearman correlation coefficients and significant *p* value between the relative abundance of *F. oxysproum* with abundant bacterial and fungal phyla.

Phyla	r	*p* value
Acidobacteria	-0.374	0.095
Actinobacteria	-0.640	0.002
Bacteroidetes	0.370	0.099
Chloroflexi	-0.538	0.012
Firmicutes	-0.596	0.004
Gemmatimonadetes	-0.669	0.001
Proteobacteria	0.782	<0.001
Verrucomicrobia	0.827	<0.001