

Supplementary materials to the Article

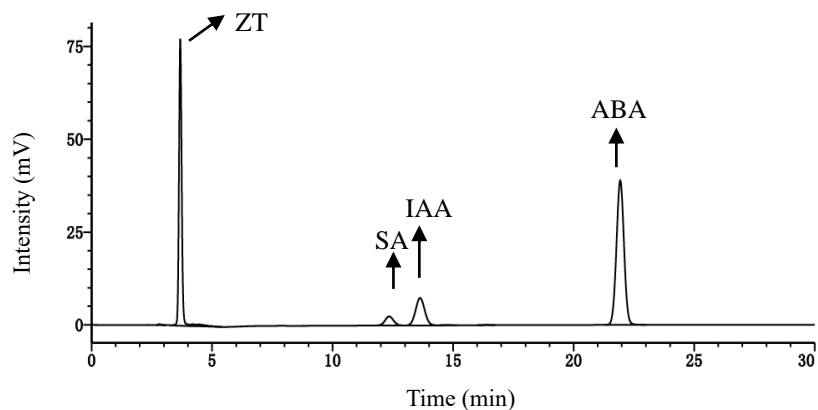
Combination of *Bacillus* and Low Fertigation Input Promoted the Growth and Productivity of Chinese Cabbage and Enriched Beneficial Rhizosphere Bacteria *Lechevalieria*

Shi-Chang Zhang ^{1,2}, Yu-Lu Zhang ¹, Xiao-Jing Guo ¹, Ming Luo ², Shi-Dong Li ¹ and Rong-Jun Guo ^{2,*}

¹ State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, P. R. China;

² College of Agriculture, Xinjiang Agricultural University, Wulumuqi 830052, P. R. China;

* Correspondence: guorongjun@caas.cn



Hormone	Concentration ($\mu\text{g mL}^{-1}$)	Linear equation	Correlation coefficient	Detection limit (ng mL^{-1})
ABA	0.05–1.0	$y = 49115x - 288.82$	1.0000	20.0
IAA	0.2–10.0	$y = 7325.1x - 139.57$	1.0000	100.0
SA	1.0–40.0	$y = 2596.2x - 1230.1$	0.9991	400.0
ZT	1.0–40.0	$y = 28662x - 23967$	0.9983	10.0

Figure S1 Chromatograms and standard curves of plant hormones detected by HPLC at 254 nm.

ABA, abscisic acid; IAA, indole-3-acetic acid; SA, salicylic acid, and ZT, zeatin. Linear equation, x and y represent the concentration and relative peak area of each plant hormone respectively.

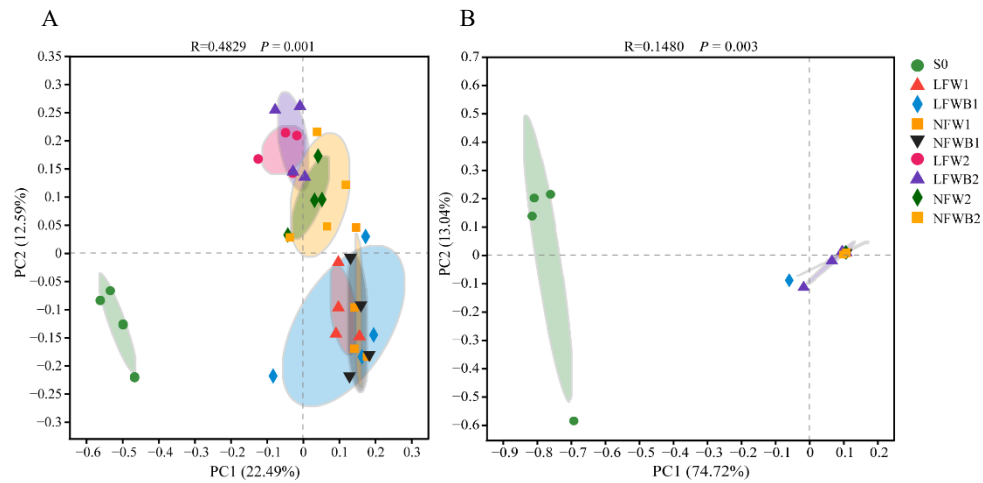


Figure S2 PCoA analysis of the communities of bacteria (A) and fungi (B) in the bulk soil and cabbage rhizosphere soil.

S0, bulk soil samples collected at time 0; LFW, low input fertigation; NFW, normal input fertigation; B, with B006 application; 1 and 2, rhizosphere soil collected at stages T1 and T2, **respectively**.

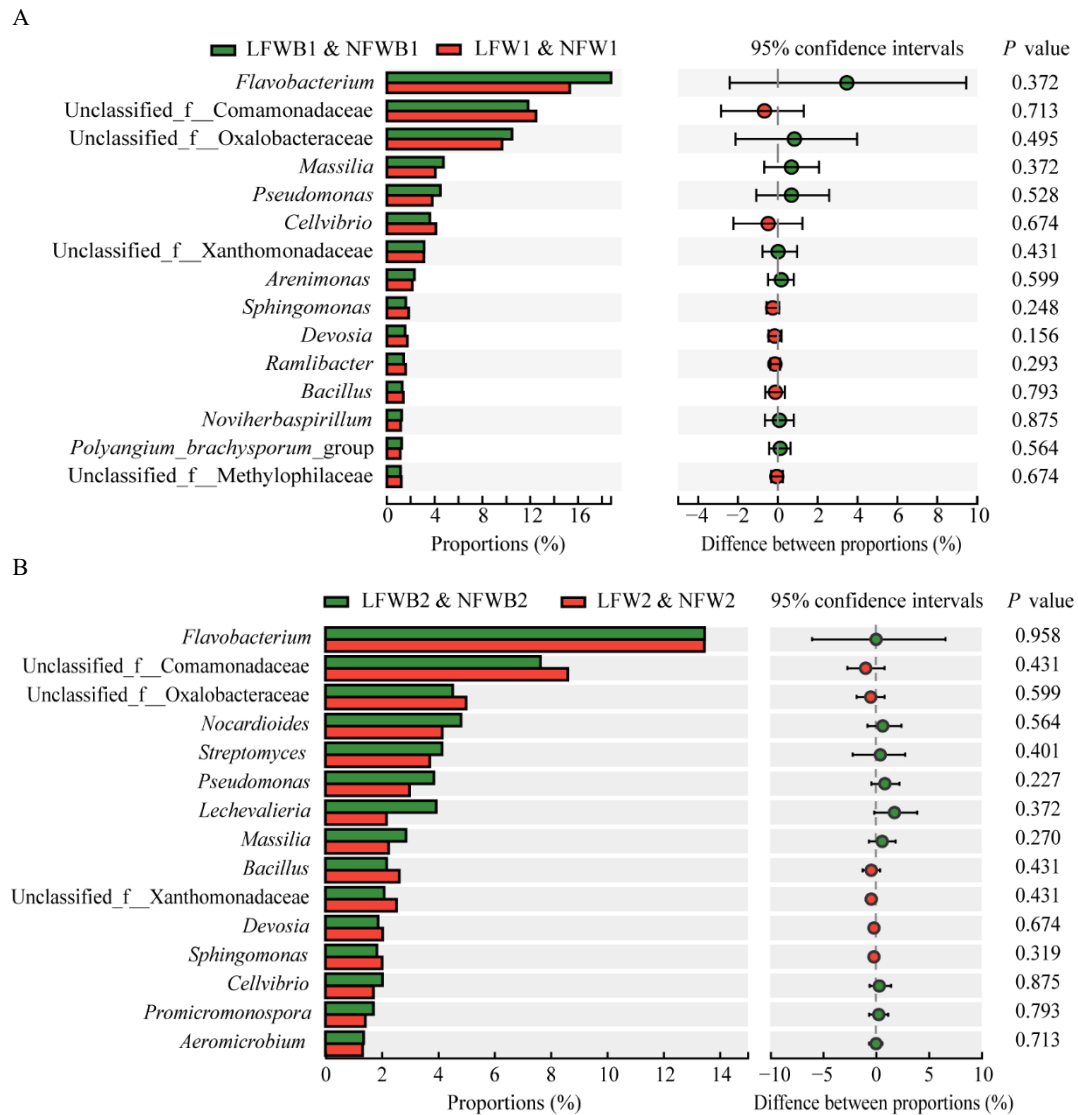


Figure S3 Differential bacterial genera generated from the pair-group comparison of groups LFWB1 & NFWB1 vs. LFW1 & NFW1 (A) and LFWB2 & NFWB2 vs. LFW2 & NFW2 (B).

LFW, low input fertigation; NFW, normal input fertigation; B, application with B006; 1 and 2, rhizosphere soil collected at stages T1 and T2, **respectively**.

Table S1 Experimental design of different fertigation treatments combined with *Bacillus* application.^a

Treatment ^b	S0	T1			T2			T3		
		Soil water potential (kPa)	Practical irrigation (m ³ hm ⁻²)	Amount of water soluble fertilizer (Kg hm ⁻²)	Soil water potential (kPa)	Practical irrigation (m ³ hm ⁻²)	Amount of water soluble fertilizer (Kg hm ⁻²)	Soil water potential (kPa)	Practical irrigation (m ³ hm ⁻²)	Amount of water soluble fertilizer (Kg hm ⁻²)
LFW	Before planting	-30	199.1	- ^c	-50	26.7	62.50	-45	257.8	-
LFWB										
NFW		-30	199.1	-	-30	53.3	165.25	-25	373.3	-
NFWB										

^a S0, bulk soil samples collected at time 0; T1, T2, and T3, rhizosphere soil collected at stages T1,T2, and T3, **respectively**.

^b LFW, low fertigation input; NFW, normal fertigation input; B, application with B006.

^c -, non application.

Table S2 Amounts of reads and ASVs of the microbial communities in each soil sample.

Group name ^a	Sample name	Bacteria		Fungi	
		Reads	ASVs	Reads	ASVs
S0	S01	54070	850	67073	296
	S02	61119	579	70907	369
	S03	67832	1012	67963	123
	S04	65163	798	61486	246
LFW1	LFW11	50847	483	75253	29
	LFW12	73934	590	80822	11
	LFW13	59860	551	123508	14
	LFW14	54764	488	127314	12
LFWB1	LFWB11	51749	477	104343	97
	LFWB12	58491	463	117311	8
	LFWB13	40613	339	106083	22
	LFWB14	51265	387	88739	8
NFW1	NFW11	50644	425	106180	19
	NFW12	46292	328	109460	28
	NFW13	63263	545	118606	13
	NFW14	47175	401	102315	24
NFWB1	NFWB11	50454	453	101350	10
	NFWB12	43308	345	102499	7
	NFWB13	73368	538	108119	17
	NFWB14	58887	439	103881	18
LFW2	LFW21	62799	511	119588	8
	LFW22	61566	520	102902	23
	LFW23	73168	806	91147	26
	LFW24	67553	629	90658	19
LFWB2	LFWB21	66485	797	119972	218
	LFWB22	63583	532	126924	132
	LFWB23	69762	771	98820	41
	LFWB24	73745	716	101622	9
NFW2	NFW21	68692	642	104026	7
	NFW22	70827	718	90111	3
	NFW23	73539	722	140323	10
	NFW24	71075	661	159750	14
NFWB2	NFWB21	70630	523	122690	5
	NFWB22	71494	697	111405	59
	NFWB23	70307	565	120908	8
	NFWB24	72015	664	111322	3
Total		2230338	3755380	20965	1956

^a S0, bulk soil samples collected at time 0; LFW, low input fertigation; NFW, normal input fertigation;

B, application with B006; 1 and 2, rhizosphere soil collected at stages T1 and T2, **respectively**.

Table S3 PERMANOVA analysis on the rhizosphere bacterial communities of cabbage collected at stage T2

Name ^a	Df	Sums of Sqs	Mean Sqs	F. Models	R ²	Pr (>F)
NB vs. B	1	0.100789	0.100789	0.79477	0.049184	0.781
LFW vs. NFW	1	0.299825	0.299825	2.364264	0.146312	0.001
Residuals	13	1.648602	0.126816	-	0.804504	-
Total	15	2.049217	-	-	1	-

^a LFW, low fertigation input; NFW, normal fertigation input; NB, no B006 application; B, application with B006.

Table S4 *Lechevalieria* ASVs identified in the cabbage rhizosphere of different treatment combinations ^a.

ASV	No. of sequences	Proportion (%)	T1				T2			
			LFW1	LFWB1	NFW1	NFWB1	LFW2	LFWB2	NFW2	NFWB2
ASV1	5621	58.45	181	155	331	263	917	2298	584	892
ASV14	3296	34.28	166	141	141	112	910	1269	266	291
ASV13	355	3.69	0	0	29	0	0	204	122	0
ASV268	101	1.05	0	0	0	0	41	60	0	0
ASV108	75	0.78	0	0	0	0	0	75	0	0
ASV2331	48	0.50	0	13	0	0	24	11	0	0
ASV3710	26	0.27	0	0	0	0	0	26	0	0
ASV315	19	0.20	0	0	0	0	0	19	0	0
ASV3701	18	0.19	0	0	0	0	0	18	0	0
ASV4118	16	0.17	0	0	0	0	0	16	0	0
ASV364	14	0.15	0	0	0	0	0	14	0	0
ASV284	13	0.14	0	0	0	0	0	13	0	0
ASV4722	8	0.08	0	0	0	0	8	0	0	0
ASV4173	3	0.03	0	0	0	0	0	3	0	0
ASV2049	3	0.03	0	0	0	0	0	0	0	3

^a LFW, low fertigation input; NFW, normal fertigation input; B, application with B006; 1 and 2, rhizosphere soil collected at stages T1 and T2, **respectively**.