

Figure S1. The colony morphology of strain WXCDD51

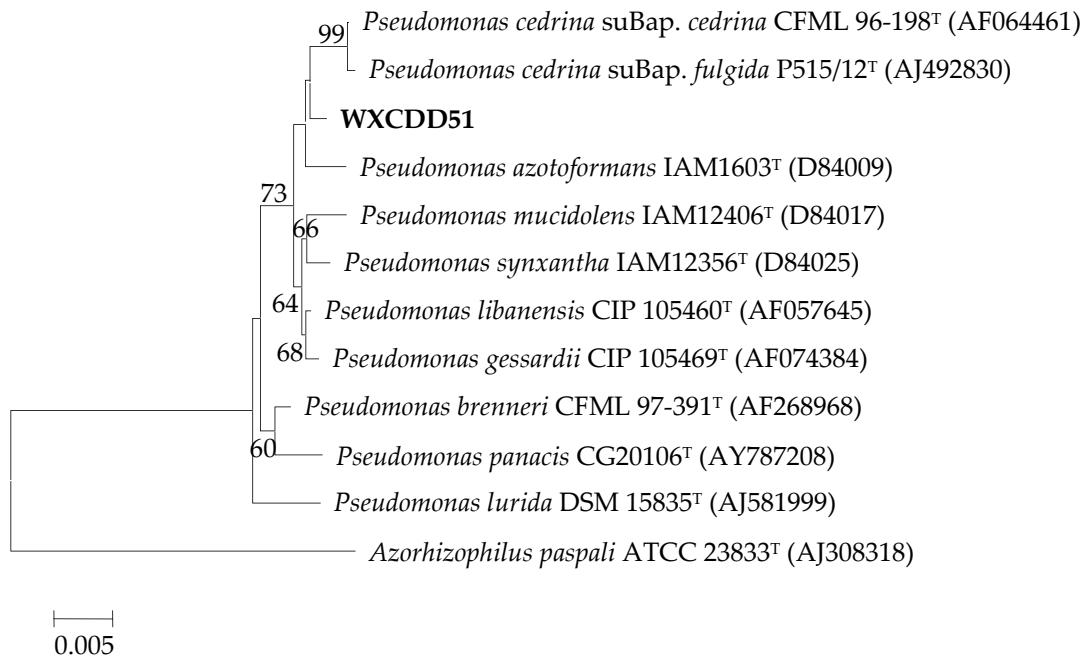


Figure S2. Phylogenetic tree based on 16S rDNA sequence of strain WXCDD51

Note: Only bootstrap values greater than 50% was noted in the graph and the superscript "T" indicates the strain in the model.

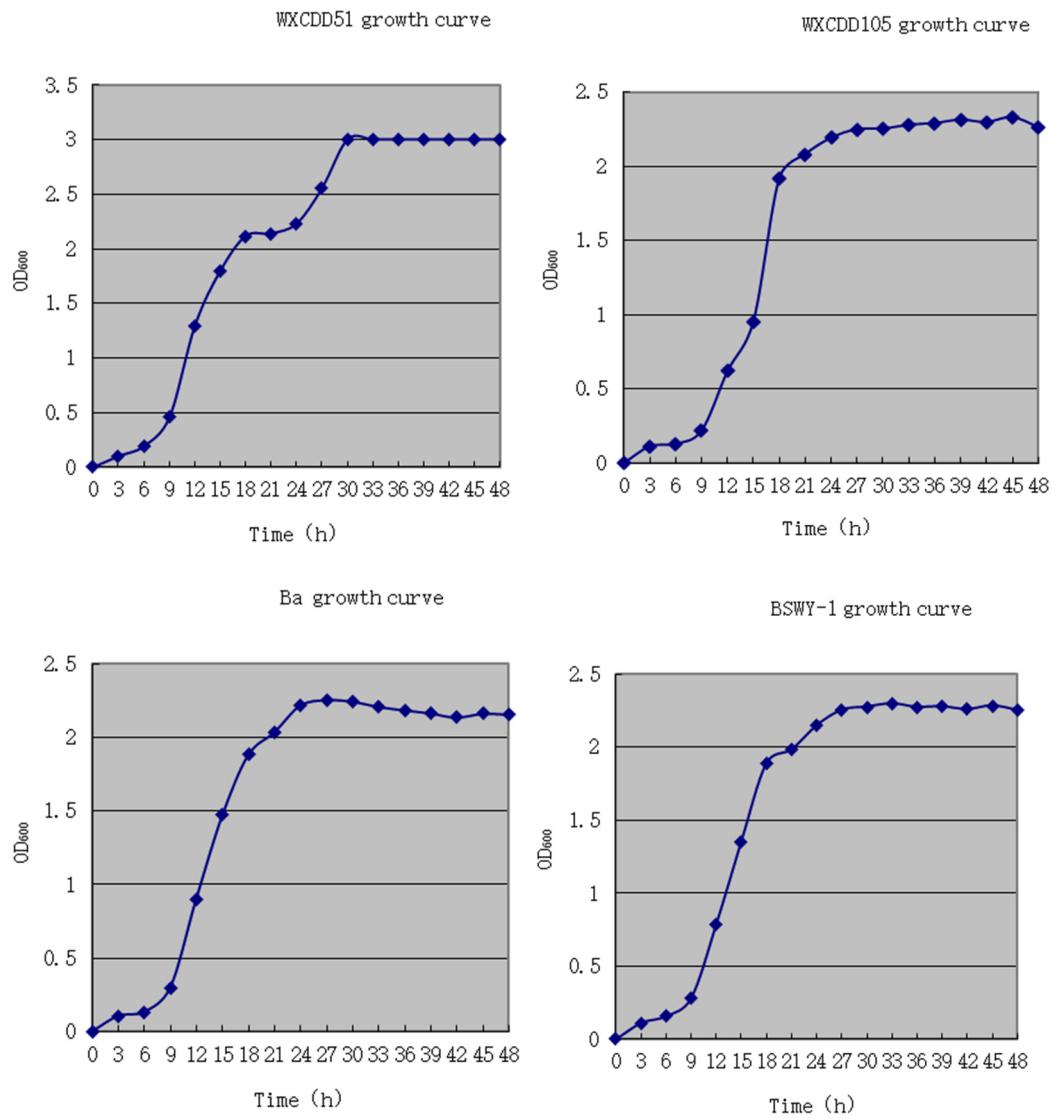


Figure S3 .The growth curve of four biocontrol bacteria

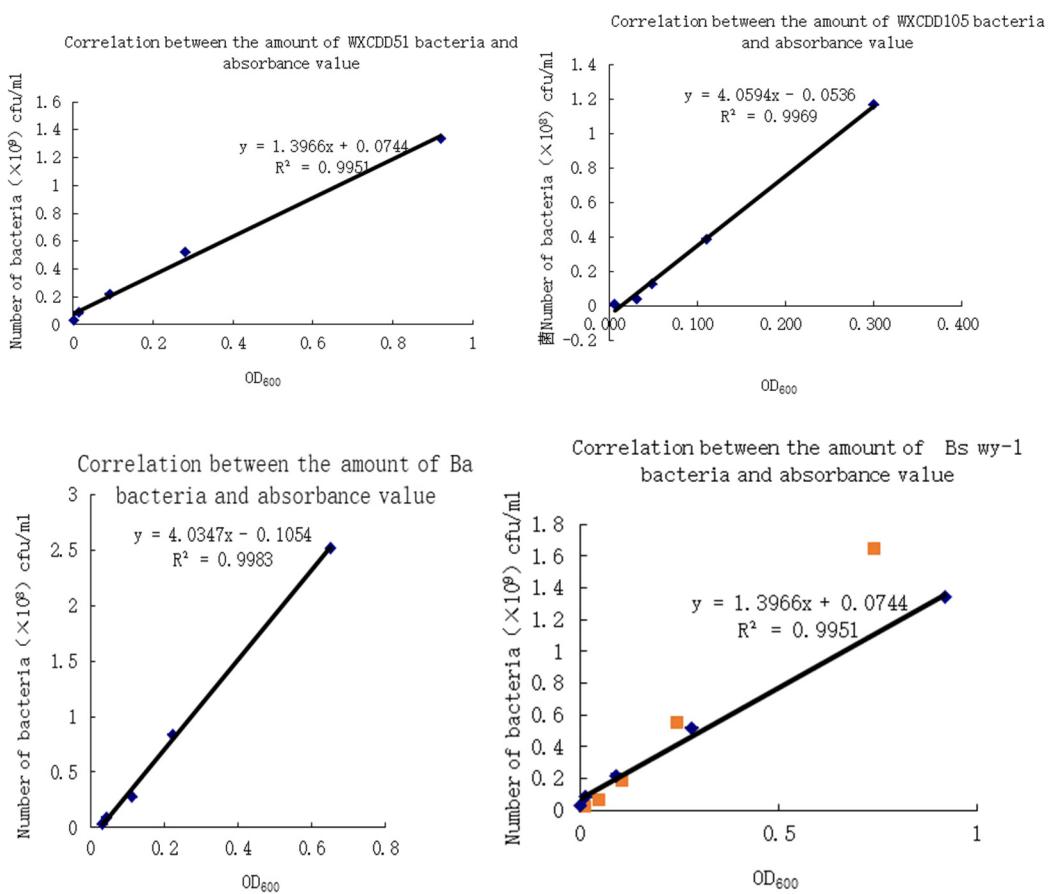


Figure S4 .Linear relationship between bacteria population and absorbance

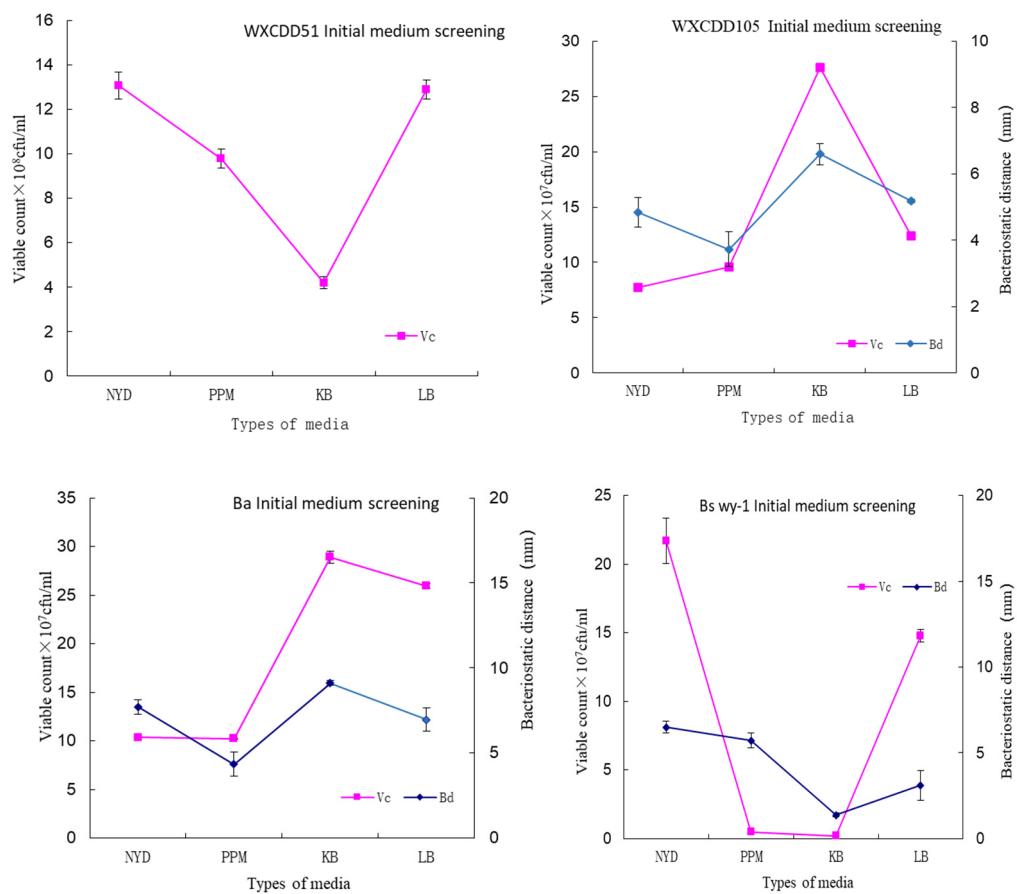


Figure S5 .Effects of different medium on growth of four biocontrol bacteria

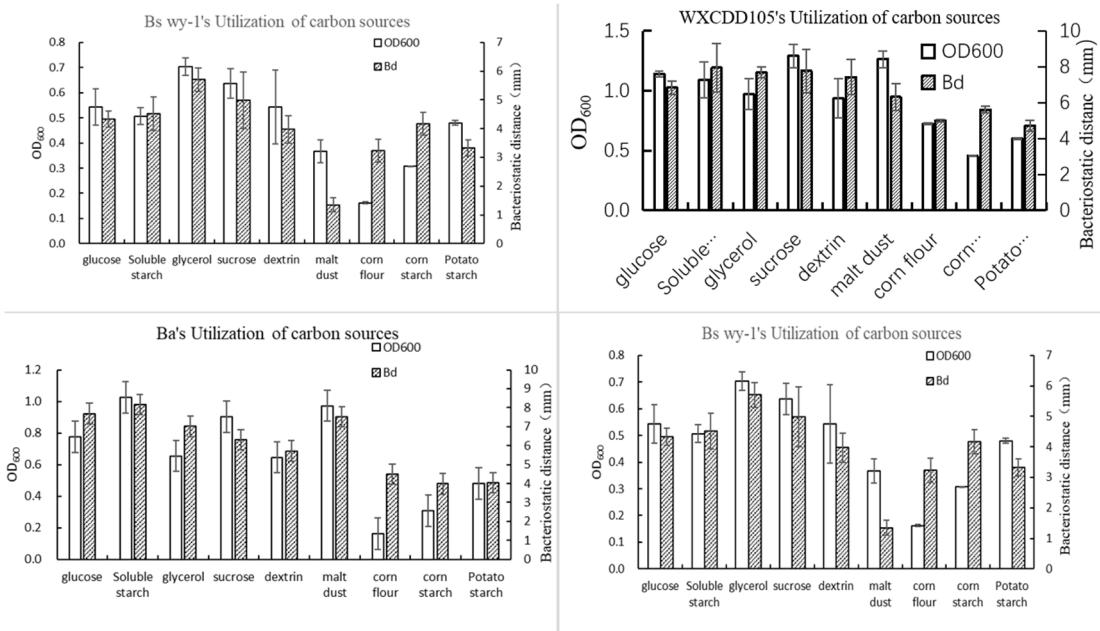


Figure S6. Carbon source utilization map of biocontrol bacteria

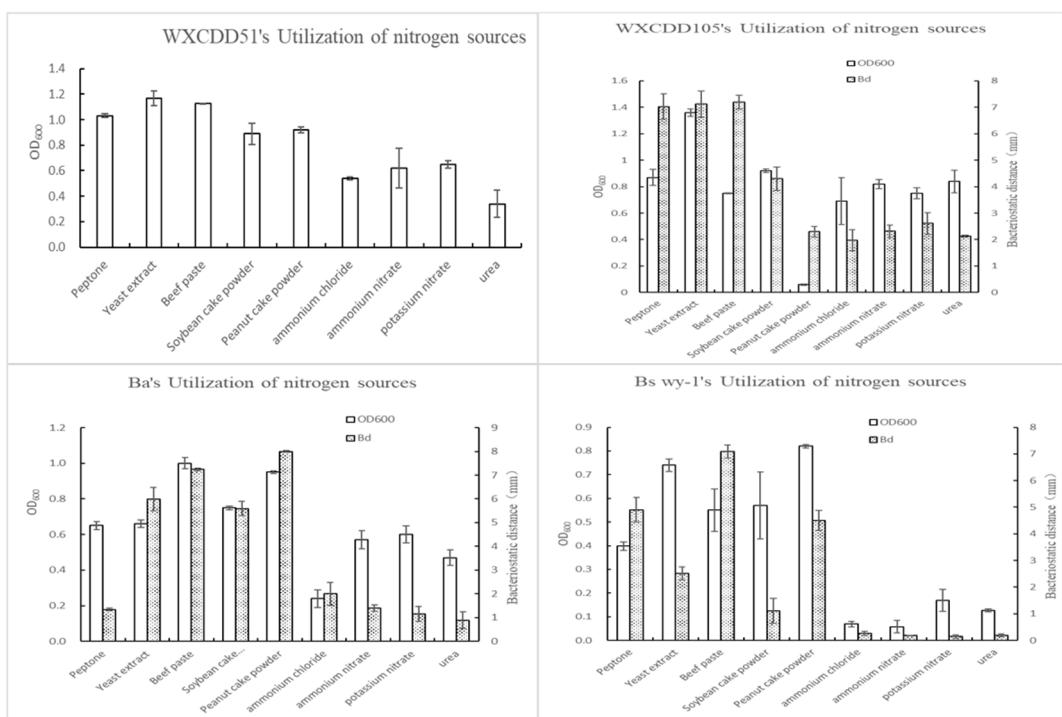


Figure S7. Nitrogen utilization map of biocontrol bacteria

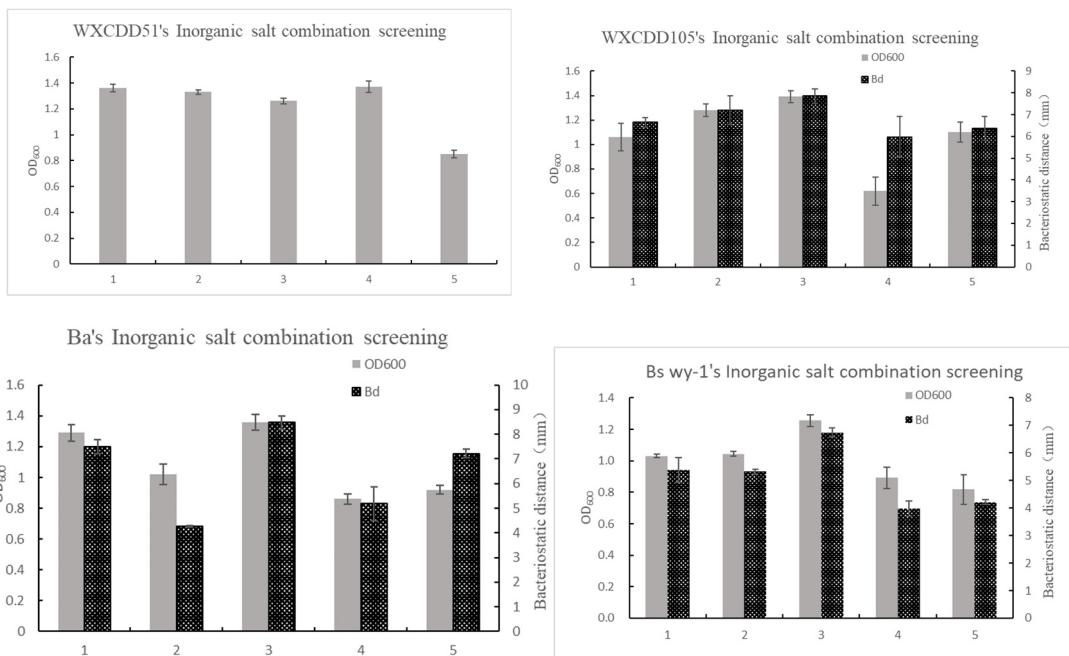


Figure S8. Application of inorganic salt combinations for biocontrol bacteria

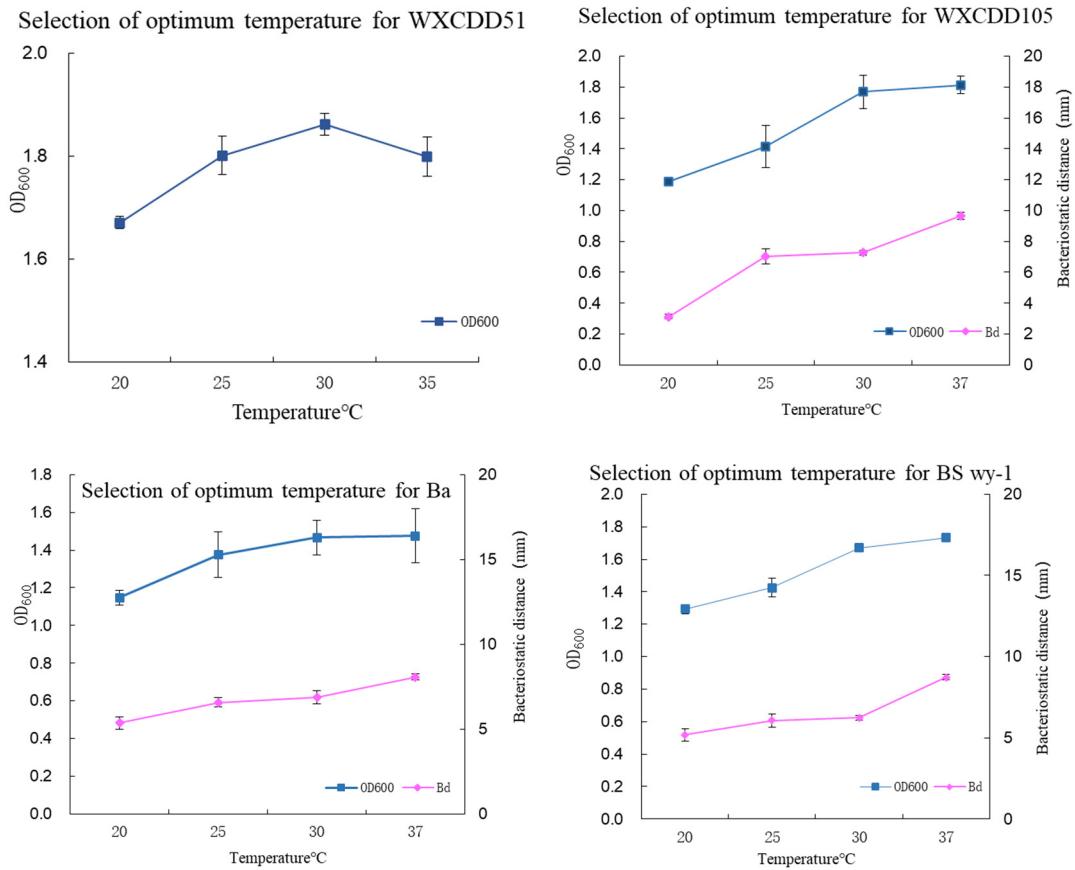


Figure S9 .Effects of culture temperature on fermentation of four biocontrol bacteria

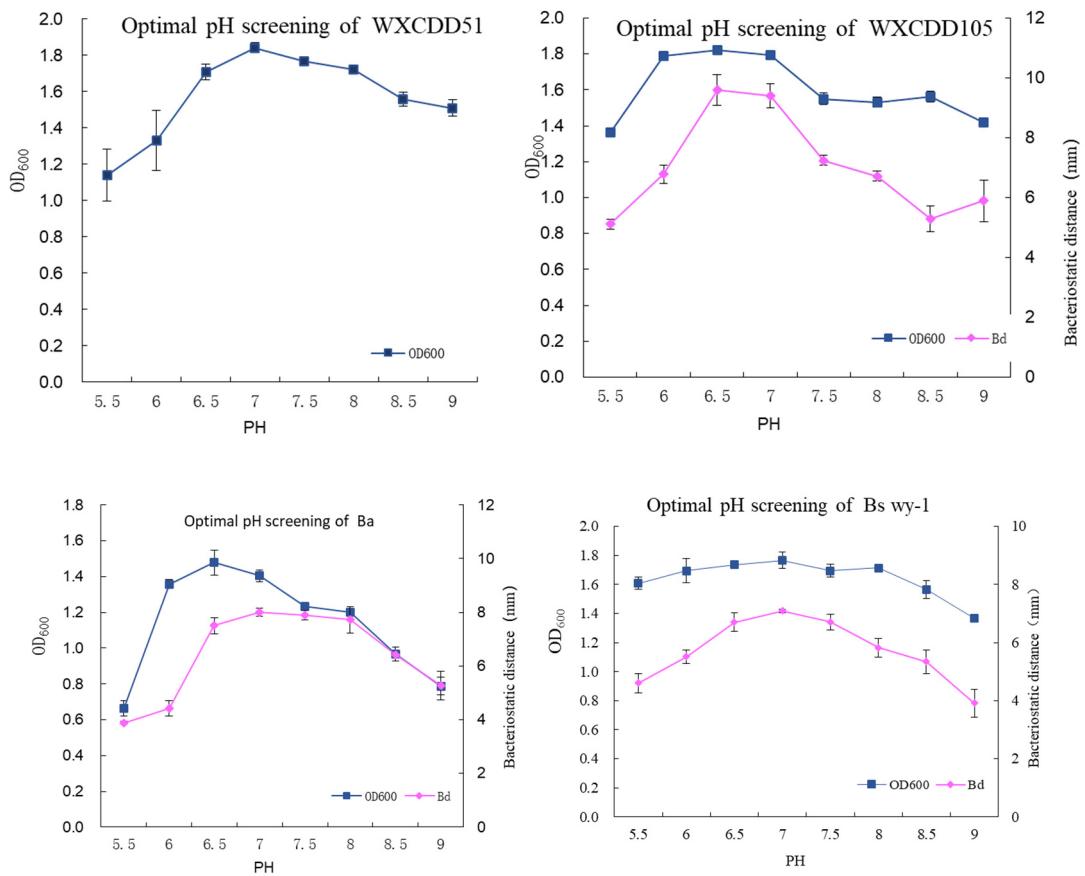


Figure S10 .Effects of pH value on the fermentation of four biocontrol bacteria

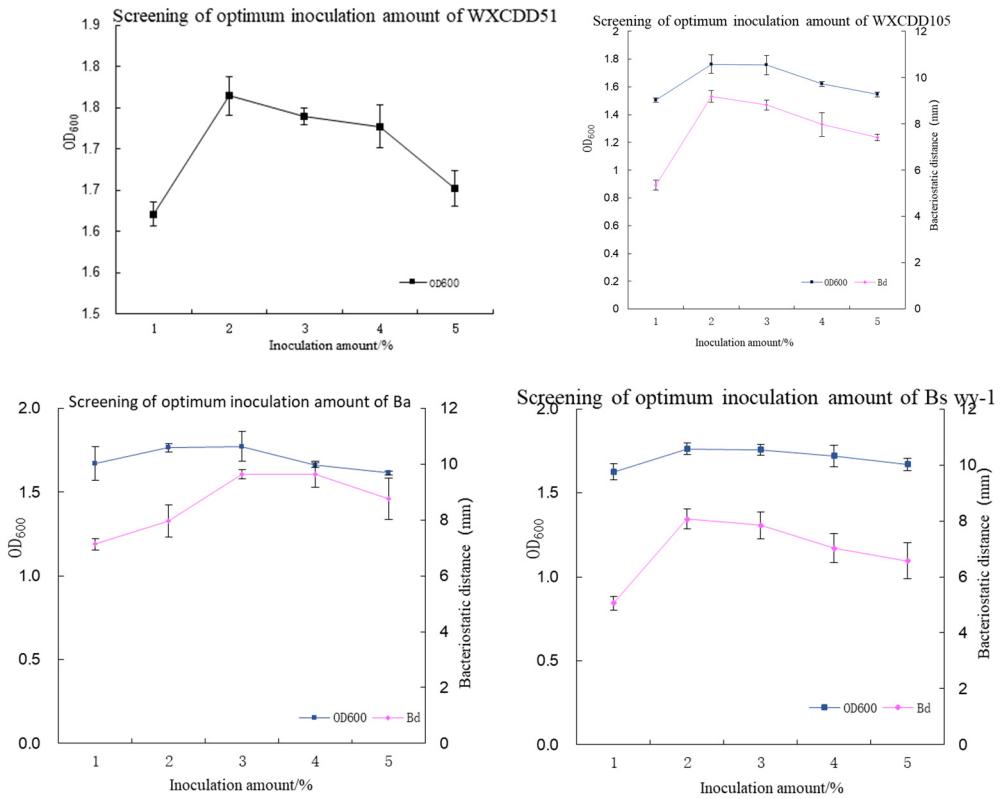


Figure S11 .Effects of inoculation amount on fermentation of four biocontrol bacteria

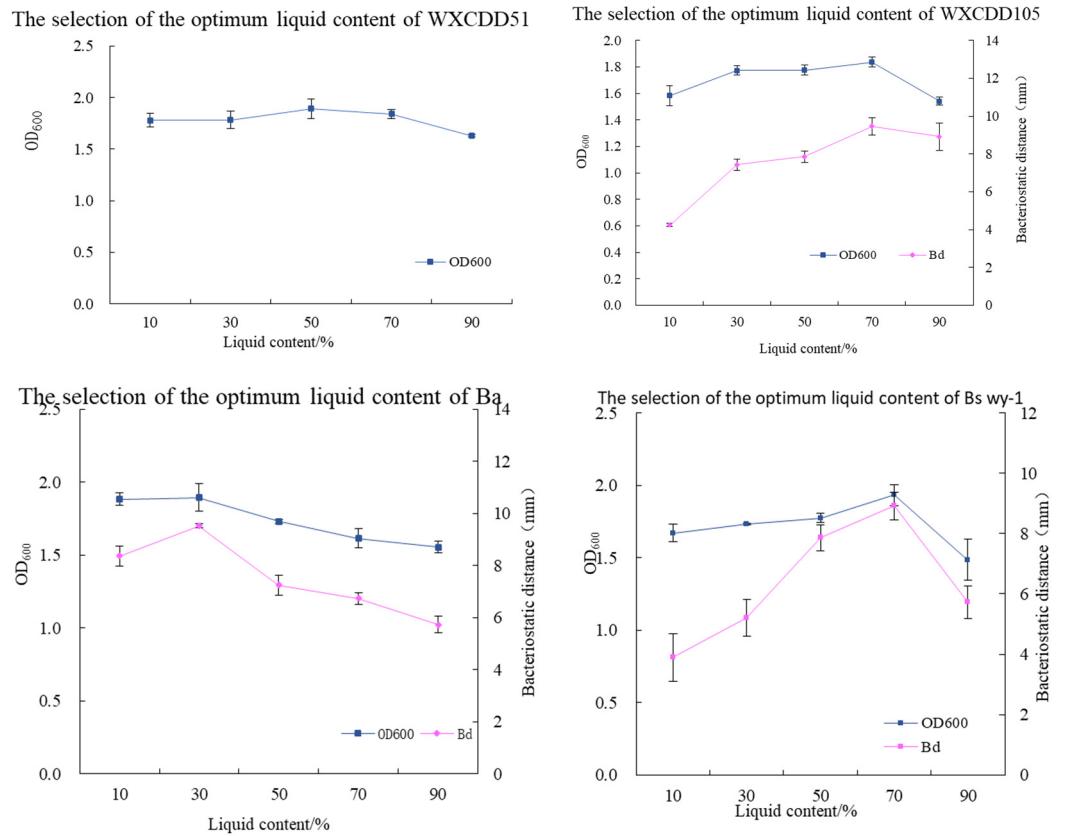


Figure S12 .Effects of liquid loading on fermentation of four biocontrol bacteria

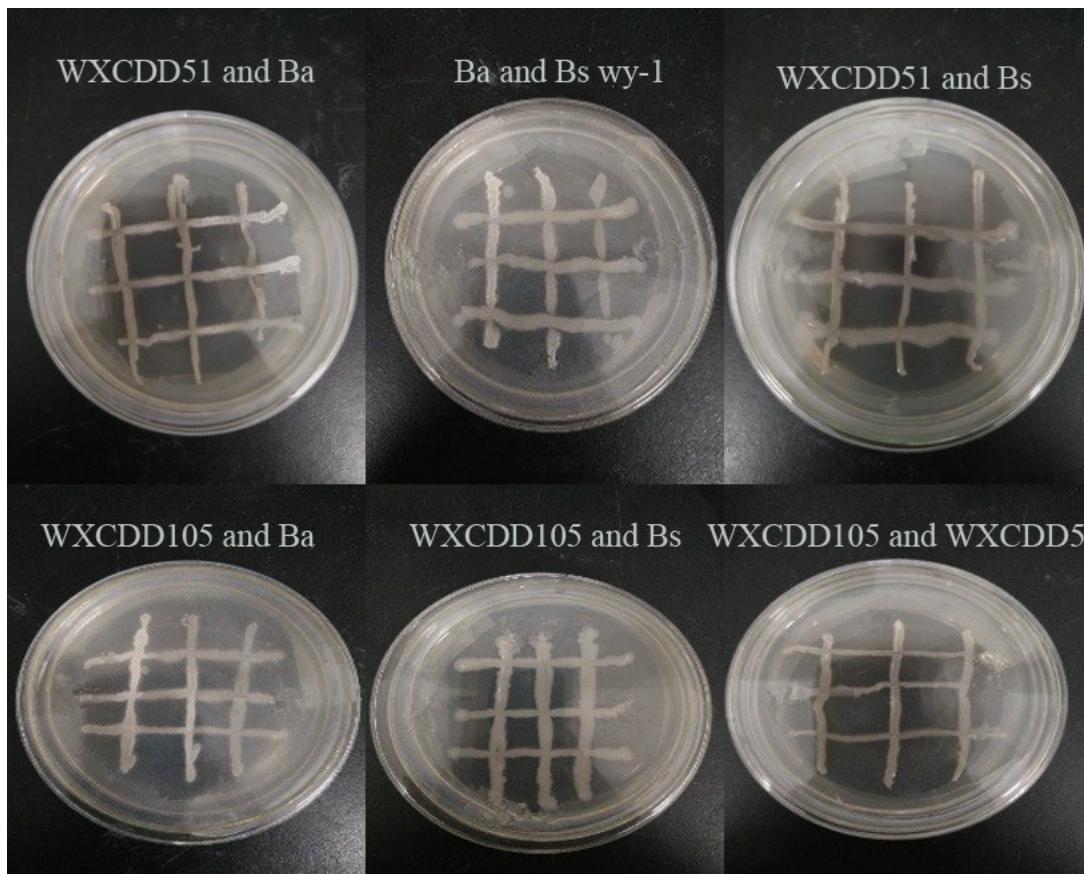


Figure S13. The growth of cross marking of four biocontrol bacteria

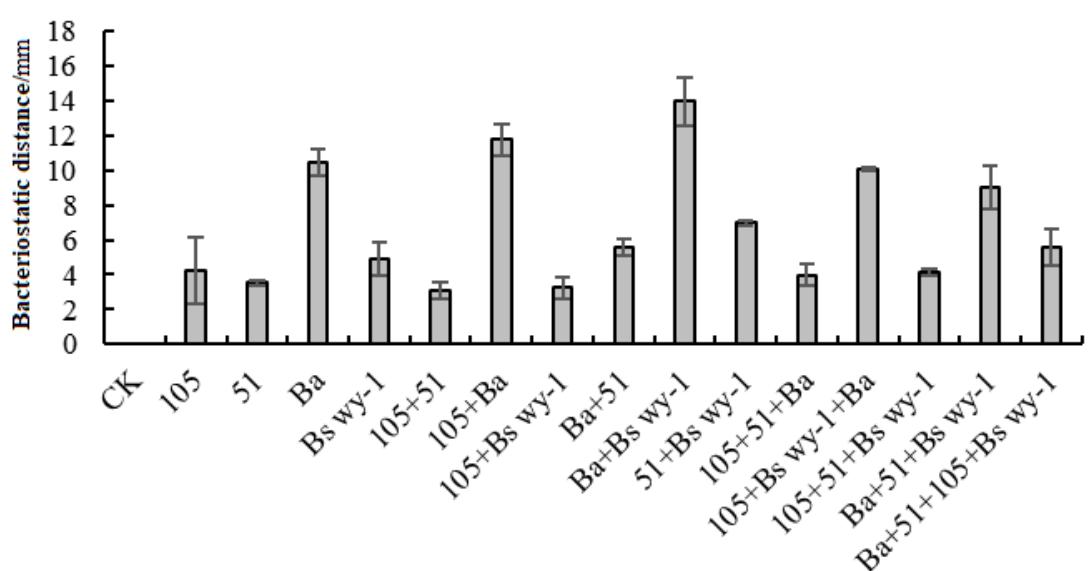


Figure S14. Inhibitory effects of different treatments on tomato gray mold and leaf mold

Table S1. Screening of different mixing proportions of Ba+WXCDD105

Treatment	<i>Botrytis cinerea</i>		Tomato leaf mould	
	Bacteriostatic distance /mm	Bacteriostatic rate /%	Bacteriostatic distance /mm	Bacteriostatic rate /%
1: 1	9.28±0.19	70.69b	7.18±0.01	65.46bc
1: 2	8.58±0.24	68.94c	5.70±0.10	61.74e
2: 1	10.70±0.30	74.26a	7.63±0.20	66.58b
1: 3	9.66±0.23	71.65b	6.69±0.11	64.23cd
3: 1	7.46±0.23	66.15d	6.69±0.09	64.23cd
1: 4	7.59±0.20	66.47d	9.25±0.84	70.63a
4: 1	3.54±0.01	56.34e	6.32±0.01	63.31de
CK	0.00	-	0.00	-

Table S2. Screening of different mixing proportions of Ba+Bs wy-1

Treatment	<i>Botrytis cinerea</i>		Tomato leaf mould	
	Bacteriostatic distance /mm	Bacteriostatic rate /%	Bacteriostatic distance /mm	Bacteriostatic rate /%
1: 1	5.14±0.06	60.36f	7.22±0.38	65.56abc
1: 2	6.66±0.15	64.16e	7.59±0.07	66.47ab
2: 1	8.14±0.20	67.85c	6.66±0.24	64.15c
1: 3	10.89±0.36	74.73a	5.54±0.38	61.34d
3: 1	7.51±0.30	66.28d	7.80±0.18	67.01a
1: 4	10.19±0.18	72.98b	7.08±0.28	65.20bc
4: 1	7.41±0.24	66.02d	6.72±0.26	64.30c
CK	0.00	-	0.00	-