

Table S1. Antagonistic effect of isolated strains on *A. asolani*

Strain No.	Sampling location	Inhibition rate (%)	16S r DNA Identification	Similarity (%)
YXDHD1-7	Yangjiang	80.00±0.16	<i>Bacillus velezensis</i>	99.86
YXPT1-4-1	Yangjiang	76.22±0.99	<i>Bacillus siamensis</i>	99.86
YXDHD1-4-2	Yangjiang	75.79±0.83	<i>Bacillus velezensis</i>	99.99
YXDHD1-6-2	Yangjiang	74.54±0.01	<i>Bacillus siamensis</i>	99.60
DBBHT1-8-1	Maoming	74.13±0.69	<i>Bacillus siamensis</i>	99.60
YXDHD1-3-1	Yangjiang	73.37±0.17	<i>Bacillus siamensis</i>	99.90
DBBHT2-2	Maoming	72.55±0.09	<i>Bacillus siamensis</i>	99.60
DBBHT2-3-1	Maoming	72.54±0.08	<i>Bacillus siamensis</i>	99.86
YXDHD1-6-1	Yangjiang	70.85±0.94	<i>Bacillus siamensis</i>	99.60
YXDHD1-5	Yangjiang	70.41±0.76	<i>Bacillus siamensis</i>	99.64
YXDHD1-7-1	Yangjiang	70.06±0.33	<i>Bacillus siamensis</i>	99.64
YXXT2-2-2	Yangjiang	69.55±0.97	<i>Bacillus siamensis</i>	99.99
DBSDH3	Maoming	69.03±0.42	<i>Bacillus siamensis</i>	99.90
DBDY-1-5-3	Maoming	68.75±0.32	<i>Bacillus siamensis</i>	99.60
DBSDH5	Maoming	68.02±0.47	<i>Bacillus siamensis</i>	99.60
DBSD2-7-1	Maoming	65.61±0.51	<i>Bacillus tequilensis</i>	99.93
DBBHT1-3-1	Maoming	64.81±0.74	<i>Bacillus velezensis</i>	99.93
DBSDH6-1	Maoming	63.07±0.99	<i>Bacillus velezensis</i>	99.93
			<i>Paenibacillus</i>	
DBBHT1-6	Maoming	62.77±7.41	<i>glycanilyticus</i>	99.60
	Maoming		<i>Streptomyces</i>	
DBGE1-11		62.6±2.38	<i>acidiscabies</i>	99.60
YXDHD1-4-6	Yangjiang	62.57±0.47	<i>Bacillus siamensis</i>	99.93
DBSD2-6	Maoming	62.38±0.16	<i>Bacillus tequilensis</i>	99.90
DBGE1-3	Maoming	61.18±1.44	<i>Bacillus velezensis</i>	99.85
YXPT1-1-1	Yangjiang	60.17±0.99	<i>Bacillus tequilensis</i>	99.93
DBSD2-6-1	Maoming	59.96±0.28	<i>Bacillus tequilensis</i>	99.93
DBGE1-3-1	Maoming	59.47±0.33	<i>Bacillus velezensis</i>	99.93
			<i>Paenibacillus</i>	
DBHHT1-6-1	Maoming	56.32±5.51	<i>glycanilyticus</i>	99.30
DBBHT1-2	Maoming	55.97±1.38	<i>Bacillus siamensis</i>	100
DBBHT1-5	Maoming	55.04±0.24	<i>Bacillus siamensis</i>	99.51

DBKZ2-1-1	Maoming	53.51±0.43	<i>Paenibacillus cineris</i>	99.38
YXXT1-3	Yangjiang	53.27±0.72	<i>Bacillus altitudinis</i>	99.79
YXDHD1-7-2	Yangjiang	52.58±1.68	<i>Bacillus altitudinis</i>	99.79
DBSDH6	Maoming	52.1±0.63	<i>Bacillus velezensis</i>	100
YXXT1-8	Yangjiang	51.19±0.04	<i>Paenibacillus cineris</i>	99.24
DBKZ1-3-1	Maoming	51.13±1.7	<i>Mesobacillus thioparans</i>	99.79
DBBHT2-3	Maoming	51.06±1.53	<i>Metabacillus idriensis</i>	100
DBDY1-7-5	Maoming	50.21±0.01	<i>Bacillus altitudinis</i>	99.79
			<i>Streptomyces</i>	
YXDHD1-1	Yangjiang	48.94±1.28	<i>griseorubiginosus</i>	99.90
YXDHD1-3-2	Yangjiang	48.83±0.41	<i>Bacillus rhizoplanarum</i>	99.56
DBKZ1-5	Maoming	48.53±0.39	<i>Bacillus altitudinis</i>	100
DBKZ1-3-2	Maoming	48.29±0.26	<i>Bacillus rhizoplanarum</i>	99.50
DBBHT1-8-3	Maoming	47.39±1.71	<i>Bacillus altitudinis</i>	99.79
YXXT1-8-2	Maoming	47.39±1.21	<i>Bacillus siamensis</i>	99.86
			<i>Kitasatospora</i>	
DBDY1-4	Maoming	45.94±0.42	<i>aureofaciens</i>	98.85
DBSD2-1-4	Maoming	45.51±1.31	<i>Bacillus subtilis</i>	99.71
DBSDH3-1	Maoming	45.25±0.25	<i>Mesobacillus thioparans</i>	99.43
			<i>Staphylococcus</i>	
DBKZ1-4-1	Maoming	45.1±0.88	<i>haemolyticus</i>	99.79
DBKZ2-2	Maoming	43.61±0.54	<i>Streptomyces fodineus</i>	99.36
DBDY1-4	Maoming	43.44±0.27	<i>Priestia megaterium</i>	99.44
			<i>Staphylococcus</i>	
DBKZ1-3	Maoming	42.42±0.15	<i>haemolyticus</i>	100
DBGE1-2-1	Maoming	38.42±0.5	<i>Bacillus altitudinis</i>	100
			<i>Streptomyces</i>	
DBSD1-11	Maoming	55.17±0.67	<i>albogriseolus</i>	100
DBBHT1-7	Maoming	47.31±0.95	<i>Streptomyces seoulensis</i>	99.49
DBDY1-3	Maoming	36.26±0.36	<i>Streptomyces griseoruber</i>	100

Notice: Inhibition rate values are presented as mean ± SD of three replications. In fact, *Bacillus* strains can only be identified to the genus level using 16S rRNA.

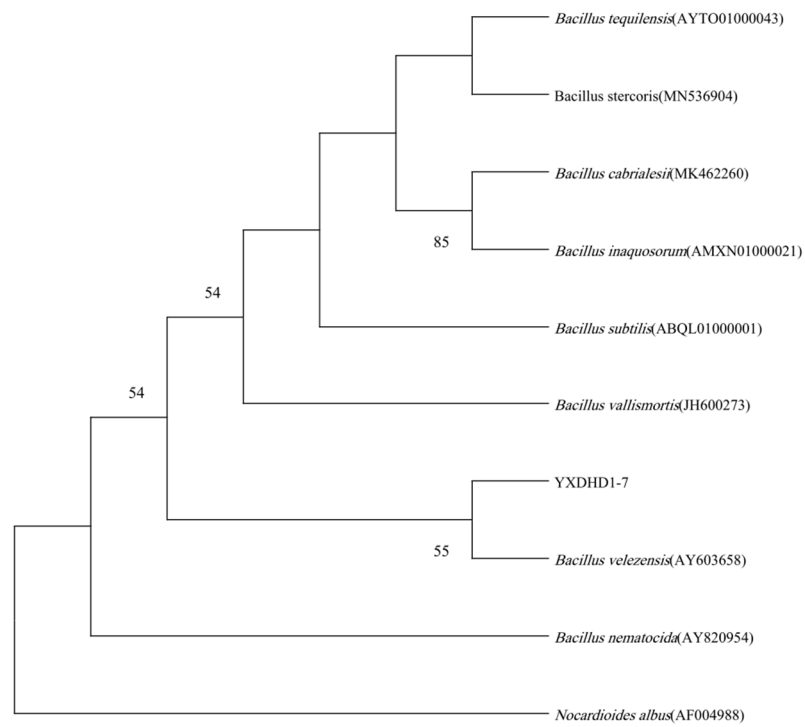


Figure S1. Phylogenetic tree illustrating the relationships between YXDHD1-7 and the examined bacterial strains in EzBioCloud in terms of the evolutionary distances of 16S rRNA gene sequences using the neighbor-joining method.