

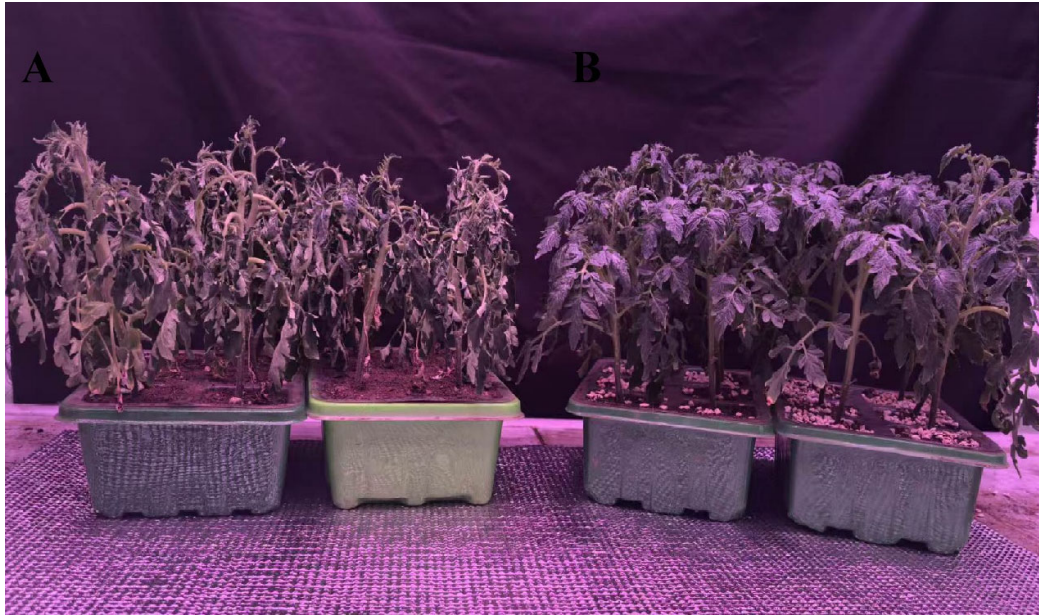


Figure S1. Biocontrol of simplified SynCom on tomato *Ralstonia solanacearum* wilt disease. A, only the pathogen inoculated; B, both SynCom and the pathogen inoculated.

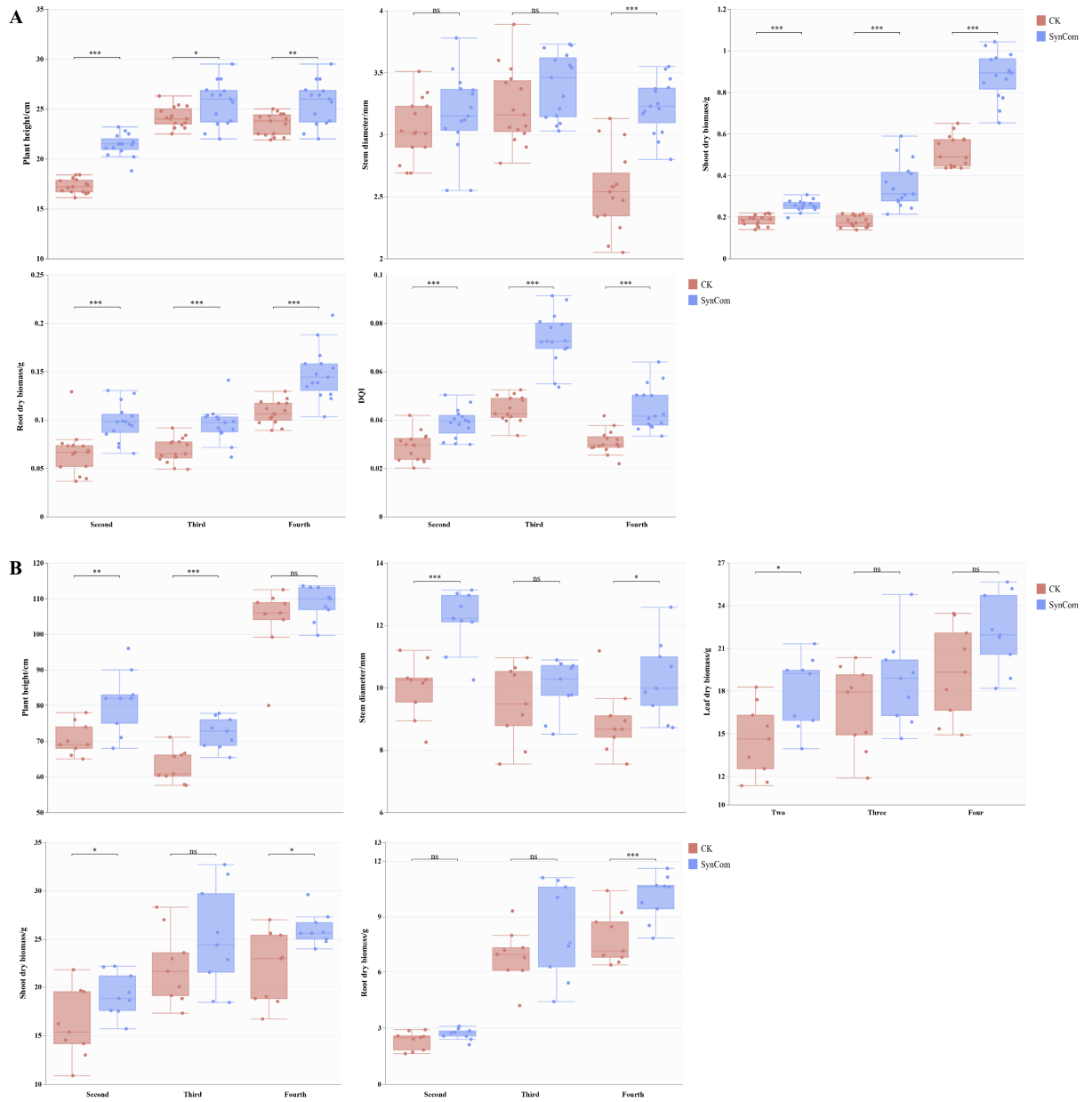


Figure S2. Effects of simplified SynCom on tomato growth indexes. CK and SynCom representing the treatments of non-inoculated and inoculated SynCom, respectively. A and B showing the morphology at the seedling and ripening stages, respectively. In the figure, *, **, *** and ns represents $P < 0.05$, $P < 0.01$, $P < 0.001$ and not significant, respectively.

Table S1. Carbon utilization of candidate strains for SynCom and their overlap with *Ralstonia solanacearum* QL-Rs1115.

Strains	Carbon spectrum	Co-carbon spectrum	NOI (%)	L-glutamic acid utilization
QL-Rs1115	43	—	—	+
Y37	40	29	67.44	+
Bhlm28	23	13	30.23	-
SCGR13	50	29	67.44	+
aHhLer002	55	32	74.42	+
FN0603	58	37	86.05	+
M20	55	35	81.40	+
JN25	47	31	72.09	+
aHhLer0B8	30	19	44.19	-
fHhLee0B1	62	32	74.42	+
BC81	36	24	55.81	+
EPGR011	18	8	18.60	-
aHhLee0J13	53	37	86.05	+
aHhLer0J1	63	38	88.37	+
fHhLee0B2	33	24	55.81	-
aSzStr009	47	28	65.12	+
BP16	48	35	81.40	+

Note: Strains in bold were retained for SynCom construction. Co-carbon spectrum meaning both candidate strain and the pathogen of *R. solanacearum* could utilized carbon species. The symbols of "+" and "-" indicating the positive and negative utilization on L-glutamic acid, respectively.

Table S2-1. The composition of the synthetic community constructed in this study.

SynComs	JN25	M20	FN0603	aHhLer0J1	aHhLer002	fHhLee0B1	BP16	aHhLee0J13	Level
1	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0
4	1	0	0	0	0	0	0	0	1
5	1	0	0	0	0	0	0	0	1
6	0	1	0	0	0	0	0	0	1
7	0	1	0	0	0	0	0	0	1
8	0	0	1	0	0	0	0	0	1
9	0	0	1	0	0	0	0	0	1
10	0	0	0	1	0	0	0	0	1
11	0	0	0	1	0	0	0	0	1
12	0	0	0	0	1	0	0	0	1
13	0	0	0	0	1	0	0	0	1
14	1	1	0	0	0	1	0	0	1
15	0	0	1	1	0	1	0	0	1
16	1	0	1	0	0	0	1	0	1
17	0	1	0	1	0	0	1	0	1
18	0	0	0	0	1	0	0	1	1
19	0	0	0	0	0	1	0	1	1
20	1	1	0	0	0	0	0	0	2
21	0	0	1	1	0	0	0	0	2
22	0	0	0	0	1	1	0	0	2
23	0	0	0	0	0	0	1	1	2
24	1	0	1	0	0	0	0	0	2
25	0	1	0	1	0	0	0	0	2
26	0	0	0	0	1	0	1	0	2
27	0	0	0	0	0	1	0	1	2
28	1	0	0	0	1	0	0	0	2
29	0	1	0	0	0	1	0	0	2
30	0	0	1	0	0	0	1	0	2
31	0	0	0	1	0	0	0	1	2
32	1	1	1	1	0	0	0	0	4
33	0	0	0	0	1	1	1	1	4
34	1	0	1	0	1	0	1	0	4
35	0	1	0	1	0	1	0	1	4
36	1	1	0	0	1	1	0	0	4
37	0	0	1	1	0	0	1	1	4
38	1	0	1	0	0	1	0	1	4
39	0	1	0	1	1	0	1	0	4
40	1	0	1	1	0	1	0	0	4
41	0	1	0	0	1	0	1	1	4
42	1	0	1	0	0	0	1	1	4
43	0	1	0	1	1	1	0	0	4

44	1	1	1	1	1	1	1	1	8
45	1	1	1	1	1	1	1	1	8
46	1	1	1	1	1	1	1	1	8
47	1	1	1	1	1	1	1	1	8
48	1	1	1	1	1	1	1	1	8

Note: 0 and 1 represent the absence and presence of the strain in a given community, respectively.

Table S2-2. SynComs composition used to verify the growth-promoting effect.

SynComs	Strains							
	JN25	M20	FN0603	raJ1	R002	eFB1	BP16	eaJ13
1	0	0	0	0	1	1	0	0
2	0	0	0	0	0	0	1	1
3	1	1	0	0	0	0	0	0
4	0	0	1	1	0	0	0	0
5	1	0	1	0	0	0	0	0
6	0	1	0	1	0	0	0	0
7	0	0	0	0	1	0	1	0
8	0	0	0	0	0	1	0	1
9	1	0	0	0	1	0	0	0
10	0	1	0	0	0	1	0	0
11	0	0	1	0	0	1	0	0
12	0	0	0	1	0	0	0	1
13	0	0	0	0	1	1	1	1
14	1	1	0	0	1	1	0	0
15	0	0	1	1	0	0	1	1
16	0	1	0	0	1	0	1	1
17	1	0	1	0	0	0	1	1
18	0	1	0	1	1	1	0	0
19	1	1	1	1	0	0	0	0
20	1	0	1	0	1	0	1	0
21	0	1	0	1	0	1	0	1
22	1	0	1	0	1	0	1	0
23	0	1	0	1	1	0	1	0
24	1	0	1	1	0	1	0	0
25	1	1	1	1	1	0	1	0
26	1	1	1	1	1	0	0	1
27	1	1	1	1	0	1	0	1
28	1	1	1	1	0	1	1	0
29	1	1	1	1	1	1	1	1

Note: 1. R002, eFB1 and eaJ13 respectively represent aHhLer0J1, aHhLer002, fHLee0B1 and aHhLee0J13.
0 and 1 represent the absence and presence of the strain in a given community, respectively.

Table S3. Growth-promoting effects of SynComs on tomato seedlings.

	Plant height (cm)	<i>p</i> -value	Stem diameter (mm)	<i>p</i> -value
CK	11.98±0.77 ^l		1.79±0.22 ^{kl}	
1	11.78±0.58 ^l	0.3279	1.55±0.07 ^m	0.0747
2	12.88±0.70 ^{kl}	0.0834	1.73±0.14 ^{lm}	0.6228
3	17.84±1.09 ^{bcd^{ef}}	2.1×10 ⁻⁶	2.22±0.12 ^{bcd^{ef}}	0.0076
4	17.02±1.02 ^{efg}	1.8×10 ⁻⁶	2.38±0.15 ^{ab}	0.0015
5	17.14±0.98 ^{efg}	1.5×10 ⁻⁶	2.27±0.12 ^{bcd^e}	0.0047
6	15.40±1.00 ^{hi}	3.2×10 ⁻⁵	2.16±0.12 ^{bcd^{efg}}	0.0149
7	17.18±1.30 ^{efg}	6.8×10 ⁻⁶	2.08±0.16 ^{efghⁱ}	0.0482
8	18.60±1.78 ^{abcd}	1.2×10 ⁻⁶	2.20±0.12 ^{bcd^{efg}}	0.0096
9	17.70±1.22 ^{cdef}	4.9×10 ⁻⁶	2.36±0.18 ^{abc}	0.0021
10	16.74±0.84 ^{efg}	2.7×10 ⁻⁵	2.14±0.16 ^{cdefgh}	0.0214
11	17.32±0.77 ^{defg}	5.3×10 ⁻⁶	2.24±0.15 ^{bcd^{ef}}	0.0063
12	16.06±1.30 ^{gh}	1.9×10 ⁻⁴	2.54±0.21 ^a	0.0006
13	18.94±0.82 ^{abc}	8.7×10 ⁻⁷	1.89±0.14 ^{ijkl}	0.4221
14	13.74±0.94 ^{jk}	0.0213	1.90±0.24 ^{ijkl}	0.4549
15	17.00±1.12 ^{efg}	7.6×10 ⁻⁶	2.32±0.16 ^{abcd}	0.0028
16	12.18±0.69 ^l	0.0615	2.10±0.12 ^{defghi}	0.0283
17	14.58±0.88 ^{ij}	0.0148	1.83±0.19 ^{ijkl}	0.7674
18	15.28±0.70 ^{hi}	0.0092	2.01±0.11 ^{fghijk}	0.0922
19	14.26±0.64 ^{ij}	0.0316	1.92±0.15 ^{hijkl}	0.3108
20	19.64±0.87 ^a	4.3×10 ⁻⁷	2.23±0.19 ^{bcd^{ef}}	0.0100
21	18.88±1.15 ^{abc}	6.1×10 ⁻⁷	2.25±0.14 ^{bcd^e}	0.0057
22	17.32±0.77 ^{defg}	2.9×10 ⁻⁶	2.26±0.12 ^{bcd^e}	0.0049
23	16.54±0.96 ^{fgh}	0.0187	2.36±0.17 ^{abc}	0.0021
24	18.14±0.67 ^{bcd^e}	1.7×10 ⁻⁶	2.04±0.12 ^{efghij}	0.0601
25	17.22±1.24 ^{defg}	0.0124	1.98±0.15 ^{ghijk}	0.1467
26	12.50±0.62 ^{kl}	0.0542	2.06±0.13 ^{efghij}	0.0514
27	18.92±1.00 ^{abc}	5.9×10 ⁻⁷	1.91±0.32 ^{hijkl}	0.4935
28	19.96±1.12 ^a	2.8×10 ⁻⁷	2.05±0.24 ^{efghij}	0.1031
29	19.20±0.62 ^{ab}	3.6×10 ⁻⁷	2.09±0.09 ^{defghi}	0.0315

Table S3. (continued).

	Biomass (g)				DQI	<i>p</i> -value
	Above-ground	<i>p</i> -value	Below-ground	<i>p</i> -value		
CK	0.110±0.010 ^h		0.029±0.010 ⁱ		0.0130±0.0026 ^k	
1	0.110±0.019 ^h	0.9822	0.051±0.012 ^{efghi}	0.0119	0.0164±0.0022 ^{efghijk}	0.0541
2	0.130±0.017 ^{igh}	0.0615	0.054±0.012 ^{cdefg}	0.0085	0.0186±0.0036 ^{cdefghij}	0.0234
3	0.154±0.006 ^{cdefg}	7.54×10 ⁻⁵	0.040±0.014 ^{ghij}	0.2080	0.0161±0.0035 ^{ghijk}	0.1523
4	0.183±0.013 ^{abcd}	1.22×10 ⁻⁵	0.035±0.006 ^{hij}	0.2833	0.0174±0.0018 ^{efghijk}	0.0155
5	0.177±0.027 ^{abcde}	0.0035	0.040±0.015 ^{ghij}	0.2049	0.0177±0.0038 ^{efghijk}	0.0561
6	0.136±0.024 ^{efgh}	0.0766	0.030±0.013 ⁱ	0.9244	0.0136±0.0030 ^{jk}	0.7191
7	0.146±0.028 ^{cdefgh}	0.0412	0.039±0.015 ^{ghij}	0.2454	0.0147±0.0031 ^{hijk}	0.369
8	0.169±0.007 ^{abcdef}	1.07×10 ⁻⁵	0.043±0.018 ^{ghij}	0.1773	0.0166±0.0029 ^{efghijk}	0.0702
9	0.152±0.034 ^{cdefg}	0.0455	0.063±0.021 ^{cde}	0.0207	0.0212±0.0052 ^{abcdefg}	0.0192
10	0.161±0.024 ^{bcdef}	0.0056	0.055±0.019 ^{cdefg}	0.0331	0.0196±0.0035 ^{bcdefghi}	0.0106
11	0.141±0.028 ^{defgh}	0.0681	0.052±0.012 ^{efghi}	0.0100	0.0183±0.0027 ^{defghijk}	0.013
12	0.151±0.034 ^{cdefgh}	0.0543	0.042±0.019 ^{ghij}	0.235	0.0186±0.0062 ^{cdefghij}	0.1139
13	0.171±0.069 ^{abcdef}	0.116	0.072±0.010 ^{bc}	0.0001	0.0193±0.0049 ^{bcdefghi}	0.0412
14	0.142±0.014 ^{defgh}	0.0032	0.055±0.020 ^{cdefg}	0.0420	0.0197±0.0053 ^{bcdefgh}	0.0445
15	0.150±0.005 ^{cdefgh}	2.20×10 ⁻⁴	0.053±0.016 ^{defgh}	0.0244	0.0197±0.0036 ^{bcdefgh}	0.0109
16	0.116±0.020 ^{gh}	0.582	0.033±0.004 ^{ij}	0.3733	0.0161±0.0023 ^{ghijk}	0.074
17	0.137±0.033 ^{efgh}	0.144	0.046±0.010 ^{efghij}	0.0258	0.0164±0.0031 ^{efghijk}	0.0911
18	0.145±0.025 ^{defgh}	0.0335	0.047±0.013 ^{efghij}	0.0428	0.0176±0.0030 ^{efghijk}	0.0306
19	0.135±0.028 ^{efgh}	0.124	0.033±0.007 ^{ij}	0.4441	0.0142±0.0011 ^{ijk}	0.3467
20	0.182±0.058 ^{abcd}	0.0499	0.071±0.010 ^{bcd}	0.0001	0.0220±0.0039 ^{abcde}	0.0037
21	0.158±0.023 ^{cdefg}	0.0061	0.072±0.016 ^{bc}	0.0013	0.0215±0.0022 ^{abcdefg}	5.07×10 ⁻⁴
22	0.144±0.019 ^{defgh}	0.0113	0.061±0.017 ^{cdef}	0.1012	0.0204±0.0044 ^{abcdefg}	0.0152
23	0.165±0.026 ^{abcdef}	0.0061	0.052±0.014 ^{efghi}	0.021	0.0209±0.0041 ^{abcdefg}	0.0087
24	0.166±0.026 ^{abcdef}	0.0062	0.058±0.013 ^{cdefg}	0.0045	0.0188±0.0014 ^{cdefghij}	0.0039
25	0.200±0.014 ^{ab}	4.54×10 ⁻⁶	0.073±0.005 ^{bc}	9.16×10 ⁻⁵	0.0238±0.0014 ^{abc}	1.50×10 ⁻⁴
26	0.118±0.016 ^{gh}	0.372	0.071±0.018 ^{bcd}	0.003	0.0246±0.0053 ^{ab}	0.005
27	0.171±0.038 ^{abcdef}	0.0196	0.088±0.011 ^{ab}	1.79×10 ⁻⁵	0.0218±0.0053 ^{abcdef}	0.0162
28	0.205±0.014 ^a	4.19×10 ⁻⁶	0.096±0.009 ^a	3.45×10 ⁻⁶	0.0255±0.0045 ^a	0.0014
29	0.188±0.015 ^{abc}	2.03×10 ⁻⁵	0.081±0.009 ^{ab}	2.17×10 ⁻⁵	0.0234±0.0019 ^{abcd}	1.28×10 ⁻⁴

Table S4. Molecular identification of SynCom28 strains using 16S rRNA gene sequencing and sequences analysis.

Strains	Fragment Length (bp)	Accession Number	EZ-Biocloud Description	Identity (%)
FN0603	1530	CP017186	<i>Enterobacter hormaechei</i> subsp. hoffmannii EN-114 ^T	99.66
M20	1494	NR_026014	<i>Massilia timonae</i> UR/MT95 ^T	100.00
JN25	1489	AY150046	<i>Azospirillum brasilense</i> ATCC 49958 ^T	100.00
fHhLee0B1	1427	PV569753	<i>Priestia megaterium</i> NBRC 15308 ^T	99.93
aHhLer0J1	1421	NR_114019	<i>Chryseobacterium daecheongense</i> NBRC 102008 ^T	97.91
BP16	1349	MK424302	<i>Pseudomonas brassicacearum</i> subsp. neoaurantiaca ATCC 49054 ^T	99.85

Table S5. The plant-promoting traits of SynCom strains.

	JN25	M20	FN0603	aHhLer0J1	fHhLee0B1	BP16
Nitrogen fixation	++	++	++++	+	-	+++
P-Ca ₃ (PO ₄) ₂ solubilizing	+++	+	++	-	+++	++++
ACC deaminase activity	-	+	++	+	+++	++
Biofilm formation (OD ₅₉₀)	0.23	0.26	0.13	0.34	0.58	0.49
EPS production (μg/mL)	180.52	211.94	236.67	275.60	323.19	253.43
Siderophore production (D/d)	3.20	3.60	4.00	-	1.70	2.50
IAA production (mg/L)	18.28	23.67	19.72	20.51	22.37	8.93

Note: "+" and "-" represents positive and negative, respectively; The more "+" means the stronger their ability.