



Figure S1 Growth of sunflower with different treatments (mature stage).

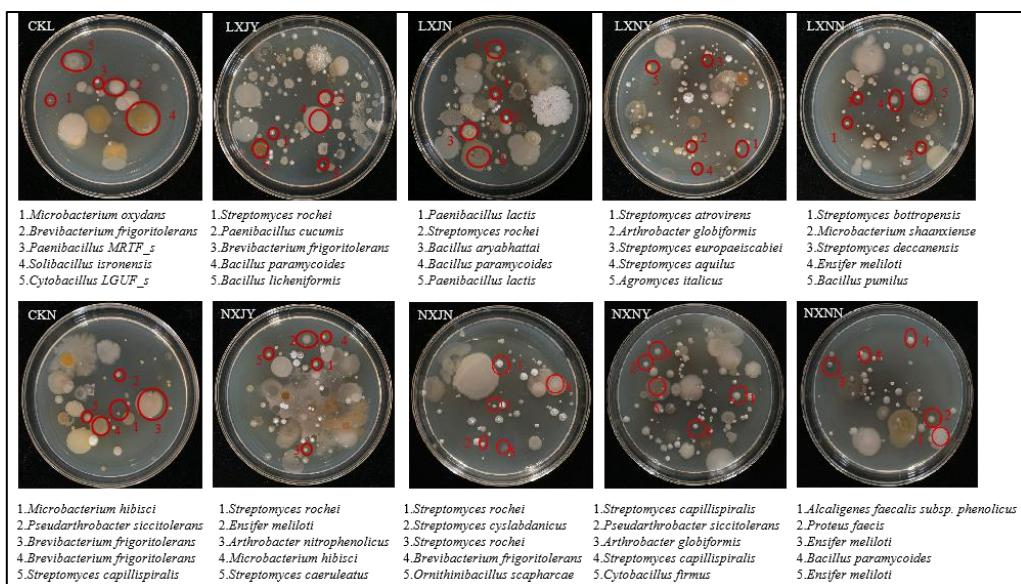


Figure S2 Effects of different treatments in TSB medium on sunflower rhizosphere soil cultivated bacteria.

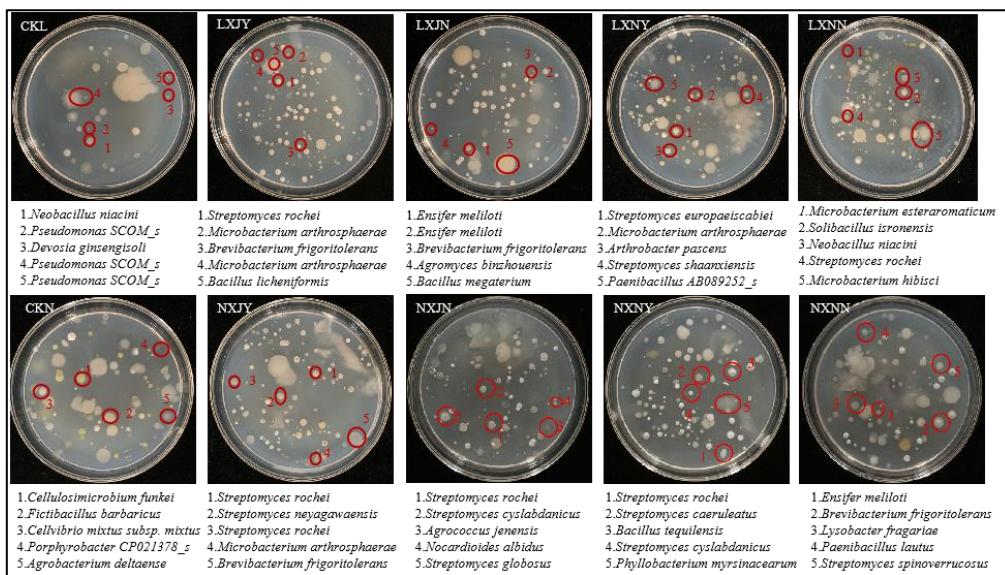


Figure S3 Effects of different treatments in R2A medium on sunflower rhizosphere soil cultivated bacteria.

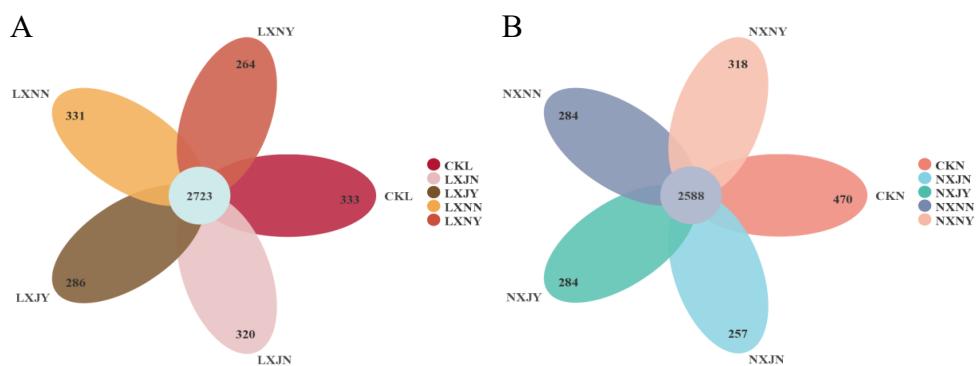


Figure S4 Comparison of differences in OTUs of sunflower rhizosphere bacterial communities with (A) and without (B) *O. cumana*.

Table S1. Effects of different treatments in TSB medium on the number of dominant strains in sunflower rhizosphere soil ($\times 10^5$ CFU/g).

Phylum	Genus	CKL	CKN	LXJY	LXJN	LXNY	LXNN	NXJY	NXJN	NXNY	NXNN	Total
Actinobacteria	<i>Microbacterium</i>	47.62	26.13	—	—	—	20.88	6.99	—	—	—	101.62
	<i>Pseudarthrobacter</i>	—	14.25	—	—	—	—	—	—	7.13	—	21.38
	<i>Streptomyces</i>	—	7.13	70.94	27.21	104.9	30.16	55.94	46.51	14.25	—	357.04
	<i>Arthrobacter</i>	—	—	—	—	11.66	—	11.66	—	7.13	—	30.45
	<i>Agromyces</i>	—	—	—	—	11.66	—	—	—	—	—	11.66
	<i>Brevibacterium</i>	19.05	19	11.44	—	—	—	—	6.98	—	7.03	56.47
Firmicutes	<i>Paenibacillus</i>	19.05	—	57.21	36.28	—	—	—	—	—	—	112.54
	<i>Solibacillus</i>	7.14	—	—	—	—	—	—	—	—	—	7.14
	<i>Cytobacillus</i>	7.14	—	—	—	—	—	—	—	7.13	—	14.27
	<i>Bacillus</i>	—	—	6.86	13.61	—	6.96	—	—	—	—	34.46
	<i>Ornithinibacillus</i>	—	—	—	—	—	—	—	4.65	—	—	4.65
	<i>Ensifer</i>	—	—	—	—	—	11.6	13.99	—	—	9.37	34.96
Proteobacteria	<i>Alcaligenes faecalis</i>	—	—	—	—	—	—	—	—	—	9.37	9.37
	<i>Proteus</i>	—	—	—	—	—	—	—	—	—	7.01	7.01
Total of strains		100	66.51	146.45	77.1	128.22	69.6	88.58	58.14	35.64	32.78	
Total of genus		14	5	4	4	3	3	4	4	3	4	4

Table S2. Effects of different treatments in R2A medium on the number of dominant strains in sunflower rhizosphere soil ($\times 10^5$ CFU/g).

Phylum	Genus	CKL	CKN	LXJY	LXJN	LXNY	LXNN	NXJY	NXJN	NXNY	NXNN	合计
Actinobacteria	<i>Pseudomonas</i>	30.95	—	—	—	—	—	—	—	—	—	30.95
	<i>Cellulosimicrobium</i>	—	45.13	—	—	—	—	—	—	—	—	45.13
	<i>Streptomyces</i>	—	—	162.47	20.41	44.29	11.6	125.87	53.49	95.01	4.68	517.82
	<i>Microbacterium</i>	—	—	25.17	—	27.97	44.08	16.32	—	—	—	113.54
	<i>Agromyces</i>	—	—	—	9.07	—	—	—	—	—	—	9.07
	<i>Arthrobacter</i>	—	—	—	—	13.99	—	—	—	—	—	13.99
	<i>Nonomuraea</i>	—	—	—	—	—	—	—	11.63	—	—	11.63
Firmicutes	<i>Agrococcus</i>	—	—	—	—	—	—	—	13.95	—	—	13.95
	<i>Neobacillus</i>	16.67	—	—	—	—	13.92	—	—	—	—	30.59
	<i>Fictibacillus</i>	—	14.25	—	—	—	—	—	—	—	—	14.25
	<i>Bacillus</i>	—	—	4.58	4.54	—	—	—	—	19.0	—	28.12
	<i>Brevibacterium</i>	—	—	13.73	—	—	—	11.66	—	—	9.37	34.76
	<i>Paenibacillus</i>	—	—	—	—	11.66	—	—	—	—	4.68	16.34
	<i>Solibacillus</i>	—	—	—	—	—	25.52	—	—	—	—	25.52
Proteobacteria	<i>Devosia</i>	14.29	—	—	—	—	5	—	—	—	—	19.29
	<i>Cellvibrio mixtus</i>	—	7.13	—	—	—	—	—	—	—	—	7.13
	<i>Porphyrobacter</i>	—	9.5	—	—	—	—	—	—	—	—	9.5
	<i>Rhizobium</i>	—	18	—	—	—	—	—	—	—	—	18
	<i>Lysobacter</i>	—	—	—	—	—	—	—	—	—	7.03	7.03
	<i>Ensifer</i>	—	—	—	72.56	—	—	—	—	—	21.08	93.64
	<i>Phyllobacterium</i>	—	—	—	—	—	—	—	—	7.13	—	7.13
Total of strains		61.91	94.01	205.95	106.58	97.91	100.12	153.85	79.07	121.14	46.84	
Total of genus	21	3	5	4	4	4	4	3	3	3	5	

Table S3. α - diversity index analysis of sunflower rhizosphere bacterial community.

Group	ACE	observed OTUs	chao1	shannon
CKL	4378.67±97.35ab	3264±60ab	4291±86ab	9.678±0.039a
LXJY	4051.80±148.31ab	3140±38abc	4002±170ab	9.740±0.006a
LXJN	4264.82±153.48ab	3200±66ab	4223±179ab	9.687±0.051a
LXNY	3827.16±324.34ab	2984±114bc	3771±340ab	9.596±0.028a
LXNN	3936.75±338.24ab	3079±144abc	3842±340ab	9.673±0.084a
CKN	4412.44±53.51a	3333±41a	4372±67a	9.752±0.045a
NXJY	4020.15±102.56ab	3034±34abc	3993±95ab	9.656±0.020a
NXJN	3900.41±148.14ab	2963±103bc	3804±157ab	9.320±0.359a
NXNY	4092.56±393.06ab	3121±159abc	4021±400ab	9.639±0.055a
NXNN	3655.16±152.39b	2835±130c	3538±173b	9.253±0.269a