

Supplementary Materials

Table S1. Characteristic of *Exiguobacterium* genomes used for phylogenetic analysis

Strain	Assembly	Size (Mb)	GC%	Gene	Protein	rRNA	tRNA	Other RNA	Pseudogene
<i>Exiguobacterium sibiricum</i> 255-15	GCA_000019905.1	3.03	47.7	3,146	3,015	24	69	4	31
<i>Exiguobacterium sibiricum</i> 7-3	GCA_000620865.1	3.08	46.9	3,181	3,103	10	48	4	16
<i>Exiguobacterium antarcticum</i> DSM 14480	GCA_000685865.1	3.22	47.1	3,350	3,207	29	69	4	41
<i>Exiguobacterium antarcticum</i> B7	GCA_000299435.1	2.82	47.5	2,958	2,784	27	67	4	76
<i>Exiguobacterium undae</i> 190-11	GCA_000620825.1	3.21	47.8	3,272	3,179	14	61	4	14
<i>Exiguobacterium undae</i> KCTC 3810	GCA_001650325.1	3.26	47.7	3,354	3,280	5	42	4	23
<i>Exiguobacterium undae</i> DSM 14481	GCA_000620805.1	3.25	47.8	3,320	3,235	11	56	4	14
<i>Exiguobacterium oxidotolerans</i> JCM 12280	GCA_000702625.1	3.09	47.0	3,142	3,008	27	69	4	34
<i>Exiguobacterium acetylicum</i> SI17	GCA_018604565.1	3.4	47.3	3,541	3,416	27	70	4	24
<i>Exiguobacterium acetylicum</i> DSM 20416	GCA_000702605.1	3.28	47.0	3,432	3,261	27	27	4	71
<i>Exiguobacterium indicum</i> HHS 31	GCA_001939065.1	3.24	46.6	3,354	3,260	5	59	4	26
<i>Exiguobacterium indicum</i> RSA11	GCA_001475665.1	3.08	47.3	3,246	3,154	10	57	4	21
<i>Exiguobacterium enclense</i> NIO-1109	GCA_900096925.1	3.25	46.8	3,365	3,270	18	48	4	25
<i>Exiguobacterium flavidum</i>	GCA_003344535.1	2.7	55.0	2,728	2,662	14	31	4	17
<i>Exiguobacterium profundum</i> PHM 11	GCA_001909285.1	2.92	48.0	3,030	2,940	9	24	4	53
<i>Exiguobacterium marinum</i> DSM 16307	GCA_000620845.1	2.81	47.4	2,877	2,778	18	60	4	17
<i>Exiguobacterium aurantiacum</i> NCTC13163	GCA_900450545.1	3.13	52.6	3,231	3,072	28	67	4	60
<i>Exiguobacterium aurantiacum</i> DSM 6208	GCA_000702585.1	3.04	52.8	3,139	2,997	28	67	4	43
<i>Exiguobacterium alkaliphilum</i> 12/1	GCA_000714435.1	3.1	52.8	3,213	3,113	8	62	5	25
<i>Exiguobacterium aurantiacum</i> PN47	GCA_001766415.1	3.04	52.8	3,139	2,997	28	68	4	43
<i>Exiguobacterium mexicanum</i> HUD	GCA_000763125.1	3.36	51.1	3,771	3,648	9	69	4	41
<i>Exiguobacterium mexicanum</i> A-EM	GCA_005960665.1	2.69	52.3	2,775	2,695	12	40	3	25
<i>Exiguobacterium chiriqhucha</i> GIC31	GCA_000702565.1	2.97	52.1	3,088	2,959	28	67	4	30
<i>Exiguobacterium chiriqhucha</i> N139	GCA_001482445.1	2.95	52.0	3,130	3,000	34	67	4	25
<i>Exiguobacterium chiriqhucha</i> SB27	GCA_008933465.1	2.75	52.4	3,246	3,166	7	28	4	41
<i>Exiguobacterium chiriqhucha</i> RW-2	GCA_000416965.1	3.02	52.0	3,111	3,038	10	47	4	12

Table S2. Secondary metabolism gene clusters in *Exiguobacterium acetylicum* SI17

Cluster	Cluster_number	Gene_number
Non-ribosomal peptide synthetases (NRPS)	1	38
Siderophore	1	12
Terpene	2	44

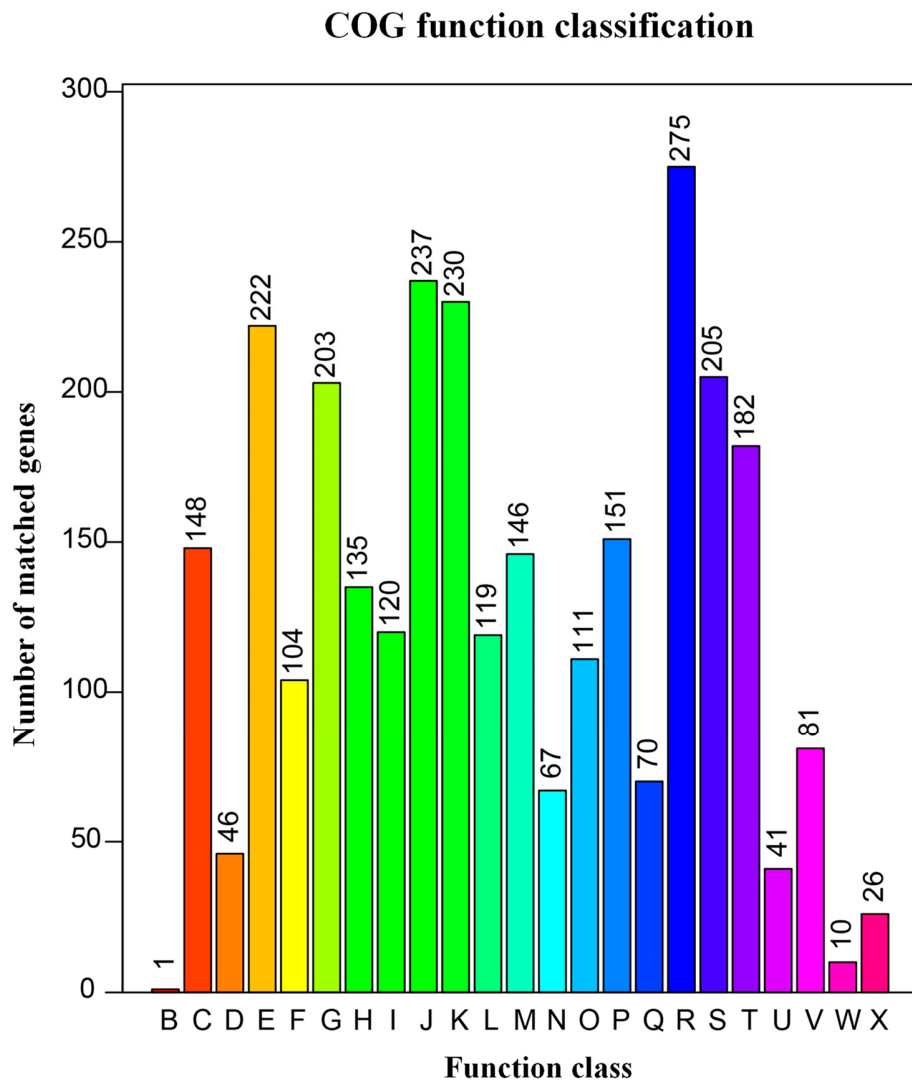


Figure S1. COG function classifications. B: Chromatin structure and dynamics; C: Energy production and conversion; D: Cell cycle control, cell division, chromosome partitioning; E: Amino acid transport and metabolism; F: Nucleotide transport and metabolism; G: Carbohydrate transport and metabolism; H: Coenzyme transport and metabolism; I: Lipid transport and metabolism; J: Translation, ribosomal structure and biogenesis; K: Transcription; L: Replication, recombination and repair; M: Cell wall/membrane/envelope biogenesis; N: Cell motility; O: Posttranslational modification, protein turnover, chaperones; P: Inorganic ion transport and metabolism; Q: Secondary metabolites biosynthesis, transport and catabolism; R: General function prediction only; S: Function unknown; T: Signal transduction mechanisms; U: Intracellular trafficking, secretion, and vesicular transport; V: Defense mechanisms; W: Extracellular structures; X: Mobilome, prophages, transposons.

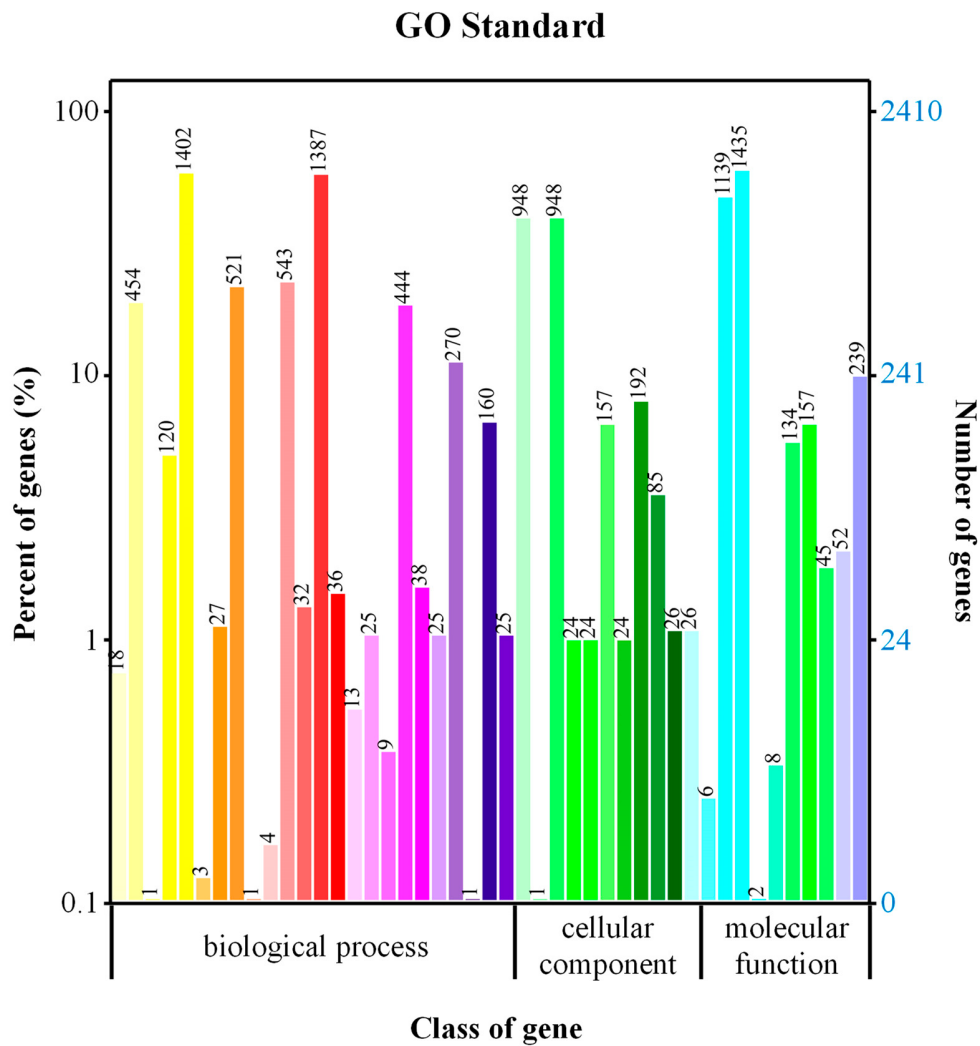


Figure S2. Gene Ontology (GO) analysis. Biological process (from left to right): biological adhesion, biological regulation, cell proliferation, cellular component organization or biogenesis, cellular process, death, developmental process, establishment of localization, growth, immune system process, localization, locomotion, metabolic process, multi-organism process, multicellular organismal process; negative regulation of biological process, positive regulation of biological process, regulation of biological process, reproduction, reproductive process, response to stimulus; rhythmic process, signaling; viral reproduction; cellular component (from left to right): cell, cell junction, cell part, extracellular region, extracellular region part, macromolecular complex, membrane-enclosed lumen, organelle, organelle part, virion, virion part; molecular function (from left to right): Antioxidant activity, binding, catalytic activity, channel regulator activity, enzyme regulator activity, molecular transducer activity, nucleic acid binding transcription factor activity, protein binding transcription factor activity, structural molecule activity, transporter activity.

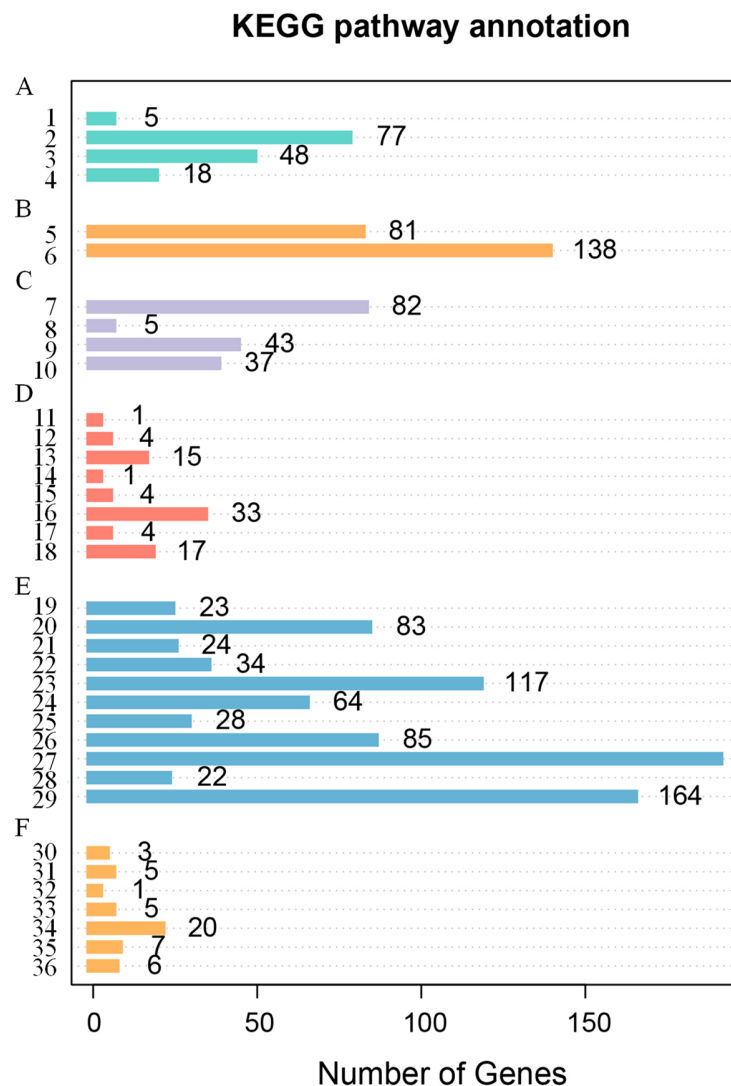


Figure S3. KEGG pathway annotation. Cellular Processes (A): Transport and catabolism (1), Cellular community-prokaryotes (2), cell motility (3), cell growth and death (4); Environmental Information Processing (B): Signal transduction (5), Membrane transport (6); Genetic Information Processing (C): Translation (7), Transcription (8), Replication and repair (9), Folding, sorting and degradation (10); Human Diseases (D): Substance dependence (11), Neurodegenerative diseases (12), Infectious diseases (13), Immune diseases (14), Endocrine and metabolic diseases (15), Drug resistance (16), Cardiovascular diseases (17), Cancers (18); Metabolism (E): Xenobiotics biodegradation and metabolism (19), Nucleotide metabolism (20), Metabolism of terpenoids and polyketides (21), Metabolism of other amino acids (22), Metabolism of cofactors and vitamins (23), Lipid metabolism (24), Glycan biosynthesis and metabolism (25), Energy metabolism (26), Carbohydrate metabolism (27), Biosynthesis of other secondary metabolites (28), Amino acid metabolism (29); Organismal Systems (F): Nervous system (30), Immune system (31), Excretory system (32), Environmental adaptation (33), Endocrine system (34), Digestive system (35), Aging (36).

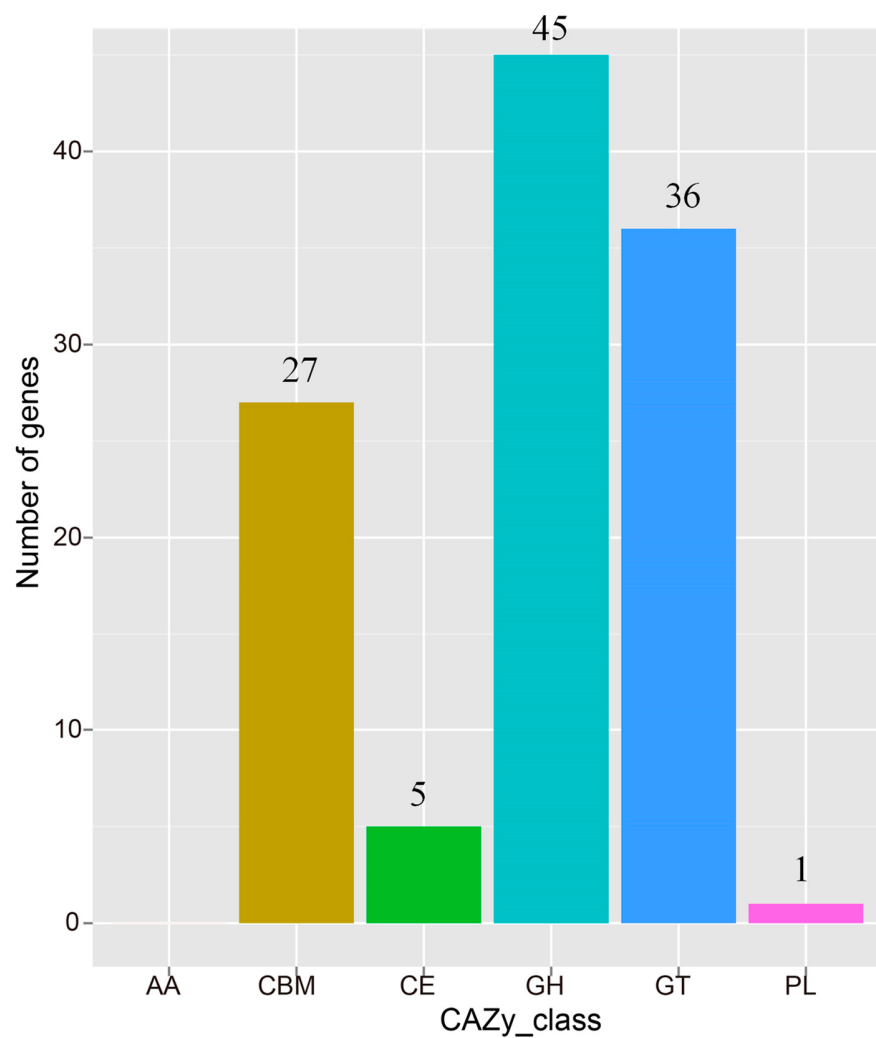


Figure S4. CAZy (Carbohydrate-Active enZYMes Database) annotation. AA: auxiliary activity; CBM: carbohydrate-binding module; CE: carbohydrate esterase; GH: glycoside hydrolase; GT: glycosyl transferase; PL: polysaccharide lyase.

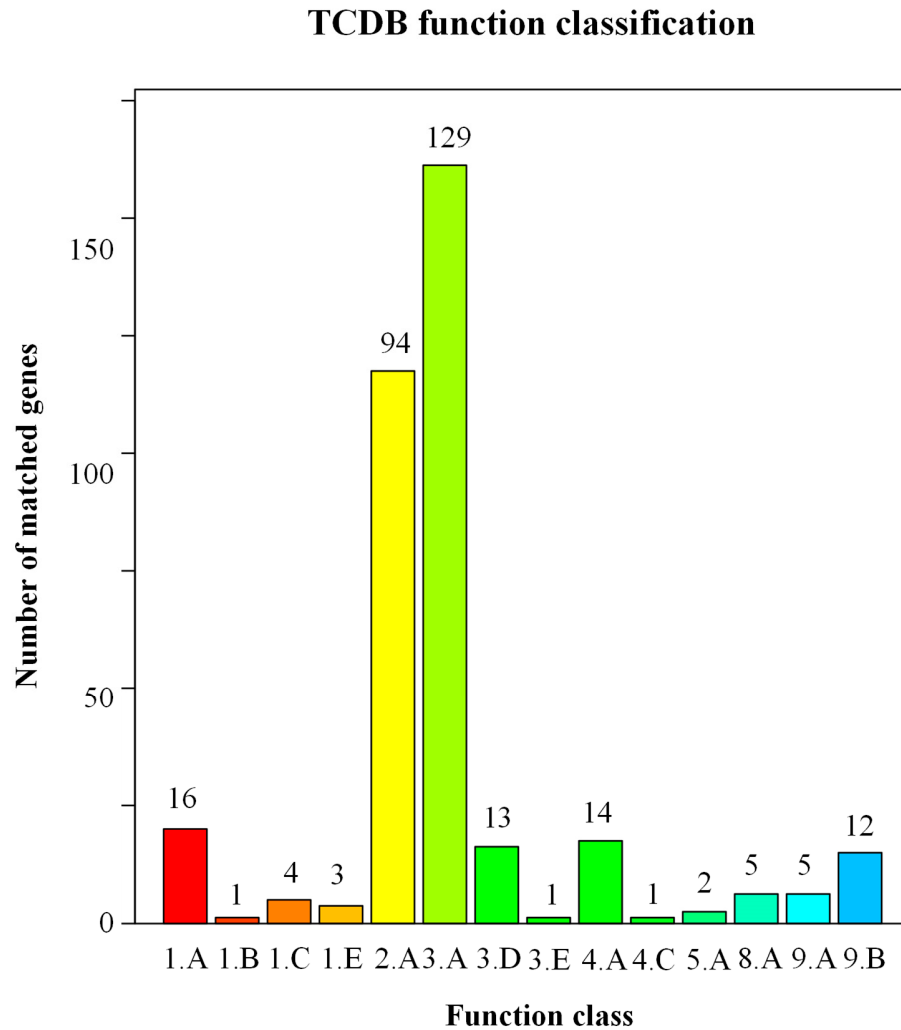


Figure S5. TCDB (Transporter Classification Database) annotation. 1.A: alpha-Type Channels; 1.B: beta-Barrel Porins; 1.C: Pore-Forming Toxins (Proteins and Peptides) ; 1.E: Holins; 2.A: Porters (uniporters, symporters, antiporters); 3.A: P-P-bond-hydrolysis-driven transporters; 3.D: Oxidoreduction-driven transporters; 3.E: Light absorption- driven transporters; 4.A: Phosphotransfer-driven Group Translocators; 4.C: Acyl CoA ligase-coupled transporters; 5.A: Transmembrane 2-electron transfer carriers; 8.A: Auxiliary transport proteins; 9.A: Recognized transporters of unknown biochemical mechanism; 9.B: Putative transport proteins.

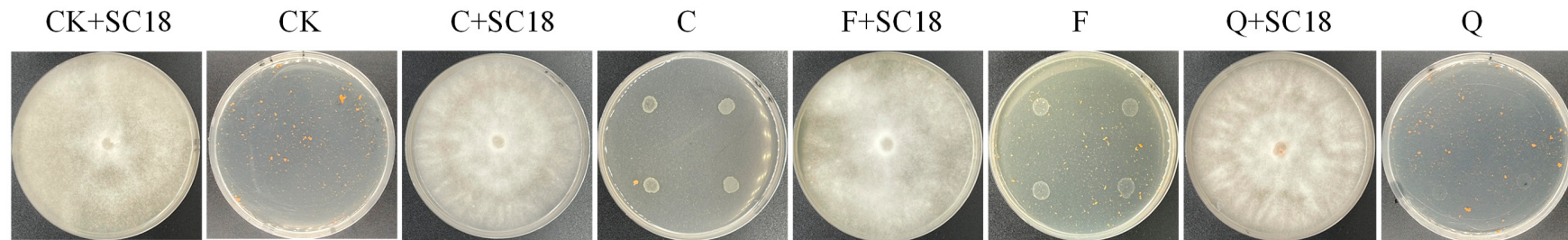


Figure S6. Plate antagonism against *Peronophythora litchii* SC18 of fermentation (C), suspension (F) and supernatant (Q) of SI17.

Fermentation (C): The fermentation broth (bacterial solution after shaking culture in LB broth) was diluted with sterilized water to achieve concentrations of 10^8 CFU/mL and 10^7 CFU/mL. It was then centrifuged at 4 °C and 12000 rpm for 5 mins. The resulting bacteria were resuspended in 0.85% sterilized NaCl to their original volume before centrifugation, while the supernatant was filtered through a 0.45- μ m microporous membrane. The resuspended bacteria were further diluted to concentrations of 10^8 CFU/mL and 10^7 CFU/mL (suspension (F)), and the supernatant was diluted with an equal volume of water to achieve concentrations of 10^8 CFU/mL and 10^7 CFU/mL (supernatant (Q)). For the plate antagonism experiment, control plates included blank plates and those inoculated with *P. litchii* SC18. The experimental variables included C/F/Q with or without SC18.