

Electronic Supplementary Material

Morphological diversity of cultured cold-active lytic bacteriophages isolated from the Napahai plateau wetland in China

Xiuling Ji¹, Chunjing Zhang¹, Anxiu Kuang², Jiankai Li¹, Yinshang Cui¹, Kunhao Qin¹, Lianbing Lin¹, Benxu Cheng³, Qi Zhang¹, Yunlin Wei¹✉

1. Faculty of Life Science and Technology, Kunming University of Science and Technology, Kunming 650500, China

2. Department of Biology, University of Texas Rio Grande Valley, Edinburg, Texas 78539, USA

3. Regional Academic Heath Center, School of Medicine, University of Texas Rio Grande Valley, Edinburg, Texas 78541, USA

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Table S1. Host isolate and phage taxonomy

Phylum	Class	Order	Family	Genus	Gram staining	Morphology	PhageFamily	Host trains
Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	<i>Athrobacter</i>	G ⁺	rod	<i>Siphovirus</i>	LSW-9
Bacteroidetes	Flavobacteria	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	G	rod	<i>Siphovirus</i>	PSW-7, PSW-12
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>	G	rod	<i>Siphovirus</i>	LS-15; LS-4; PS-7; PSW-10
Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Exiguobacterium</i>	G ⁺	rod	<i>Siphovirus</i>	LSW-8
Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Bacillus</i>	G ⁺	rod	<i>Podoviridae</i>	LS-8
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	<i>Acinetobacter</i>	G	rod	<i>Podoviridae</i>	LSW-7
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>	G	rod	<i>Podoviridae</i>	PS-1;
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	<i>Pseudomonas</i>	G	rod	<i>Podoviridae</i>	PSW-5
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Stenotrophomonas</i>	G	rod	<i>Myoviridae</i>	PS-3; PS-4; PS-12;
Proteobacteria	Gammaproteobacteria	Aeromonadales	Aeromonadaceae	<i>Aeromonas</i>	G	rod	<i>Myoviridae</i>	LSW-10
Proteobacteria	Gammaproteobacteria	Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	G	rod	<i>Myoviridae</i>	NPH-1
Bacteroidetes	Flavobacteria						<i>Myoviridae</i>	PSW-8

Table S2. Temperature ranges of plaque formation

Phage	4°C	10°C	15°C	20°C	25°C	30°C	37°C	42°C
LS-4	+	+	+	+	+	+	-	-
LS-8	+	+	+	+	+	+	+	-
LS-15	+	+	+	+	-	-	-	-
PS-1	+	+	+	+	-	-	-	-
PS-3	+	+	+	+	+	-	-	-
PS-4	+	+	+	+	-	-	-	-
PS-7	+	+	+	+	-	-	-	-
PS-12	+	+	+	+	+	-	-	-
NPH-1	+	+	+	+	-	-	-	-
LSW-7	+	+	+	+	+	-	-	-
LSW-8	+	+	+	+	+	+	+	-
LSW-9	+	+	+	+	+	-	-	-
LSW-10	+	+	+	+	-	-	-	-
PSW-5	+	+	+	+	-	-	-	-
PSW-7	+	+	+	+	+	-	-	-
PSW-8	+	+	+	+	+	-	-	-
PSW-10	+	+	+	+	-	-	-	-
PSW-12	+	+	+	+	+	-	-	-

Note: "+" indicates plaque formation, "-" indicates no plaque formation.

Table S3. The host ranges of isolated phages

Phages \ Host cells	Host cells	LS-4	LS-8	LS-15	PS-1	PS-3	PS-4	PS-7	PS-12	NPH-1	LSW-7	LSW-8	LSW-9	LSW-10	PSW-7	PSW-8	PSW-10	PSW-12
Phages	VLS-4	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
VLS-8	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
VLS-15	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
VPS-1	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-
VPS-3	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-
VPS-4	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-
VPS-7	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-
VPS-12	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-
VNPH-1	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-
VLSW-7	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-
VLSW-8	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-
VLSW-9	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-
VLSW-10	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
VPSW-5	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-
VPSW-7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-
VPSW-8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-
VPSW-10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-
VPSW-12	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+

Note: "+" indicates could infect host cell, "-" indicates could not infect host cell.

Table S4. Mean sizes of phages observed by TEM isolated from the Napahai plateau wetland, Yunnan province, China

Number	Family	Head capsid diameter (nm)	Tail length (nm)	Tail diameter (nm)	Host strain
A	Myoviridae	116.0±2.31	296.7±3.01	29.3±0.76	PS-4
B	Myoviridae	108.6±1.86	173.3±2.55	32.4±1.22	LSW-10
C	Myoviridae	134.1±1.56	154±3.02	38.2±1.15	PSW-8
D	Myoviridae	70.9±2.09	106.5±2.63	25.8±0.56	PS-3
E	Myoviridae	121.6±2.47	194.6±2.17	21.6±1.09	NPH-1
F	Myoviridae	70.3±0.98	118.9±1.83	20.5±0.66	PS-12
G	Podoviridae	60.8±1.10	13.5±0.58	10.8±0.87	LSW-7
H	Podoviridae	78.0±1.36	28.2±0.72	11.4±1.20	PS-1
I	Podoviridae	57.0±1.53	23.3±0.68	13.6±1.27	PSW-5
J	Podoviridae	57.7±1.64	15.4±0.71	7.7±0.88	LS-8
K	Siphoviridae	76.9±2.31	192.3±1.93	7.7±0.85	PSW-10
L	Siphoviridae	52.7±2.01	196.2±1.84	8.1±1.10	PS-7
M	Siphoviridae	57.7±1.86	199.6±1.76	11.5±0.78	LSW-8
N	Siphoviridae	53.3±1.42	166.7±1.68	6.7±0.34	LSW-9
O	Siphoviridae	58.7±1.38	204.2±2.04	7.6±0.48	LS-15
P	Siphoviridae	59.1±2.04	190.1±1.57	9.1±0.43	PSW-7
Q	Siphoviridae	42.3±1.67	165.4±1.36	7.7±0.50	PSW-12
R	Siphoviridae	83.3±2.34	190.5±3.05	9.5±0.62	LS-4

Note: Means ± SD ($n = 3$)

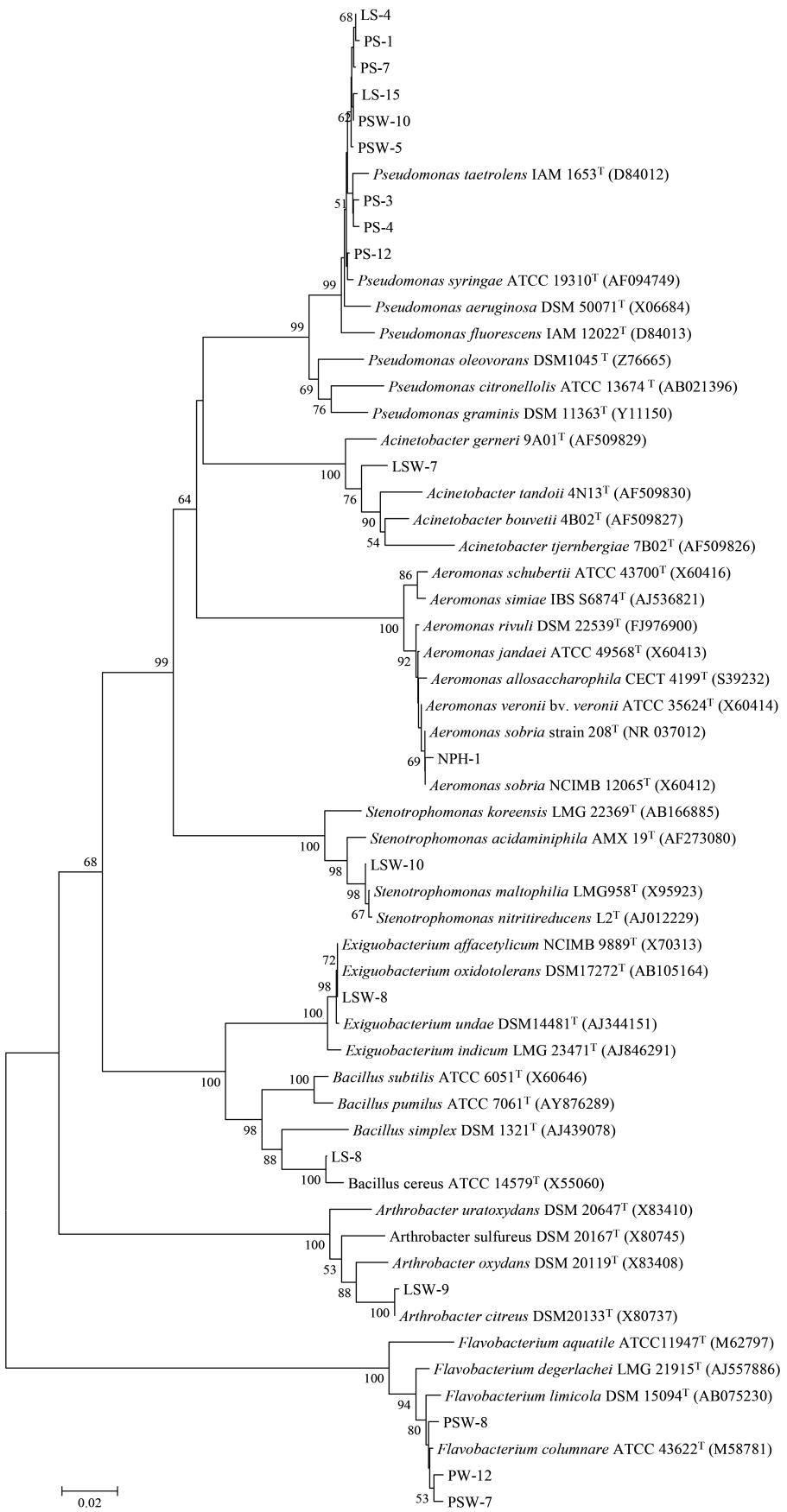


Figure S1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences available from the NCBI GenBank