

[Supplementary S2](#). *Eganvirus* phages and other P2-like phages in NCBI used in phylogenetic analysis.

No.	Name	Known Genus	Host strain/source	Country	GC (%)	Sequence Size (bp)	Accession No.	Genes Existence				Ref.
								int	c/cl	cox/ alp	cII	
Bacteriophages 1: genus <i>Eganvirus</i>												
1	186	Eganvirus	<i>Escherichia coli</i>	USA	53.1	30624	NC_001317	√	√	√	√	1
2	EtG	Eganvirus	<i>Erwinia tracheiphila</i> Et-B, <i>Cucumis sativus</i>	Pakistan	54.1	30413	NC_047833	√	√	√	√	8,18
3	PsP3	Eganvirus	<i>Salmonella enterica</i> subsp. <i>enterica</i>	Potsdam	52.8	30636	NC_005340	√	√	√	√	1,13
4	SEN1	Eganvirus	<i>Salmonella enterica</i> subsp. <i>salamae</i> 10/99 II	Czech Republic	53.0	29733	KT630644.2	√	√	√*	√	9
5	SW9	Eganvirus	<i>Salmonella</i> sp.	Canada	53.0	31123	MK972711	√	√	√*	√	14
6	BIS20	Eganvirus	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i> SE-BS17	NA	53.2	29512	NC_070911	√	√	√	√	15
7	SI22	Eganvirus	<i>Salmonella</i> sp.	Canada	53.0	30920	MK972710	√	√	√*	√	—
8	vB_EcoM-613 R3	NA	<i>Escherichia coli</i>	United Kingdom	51.2	44992	ON470592	√	√	√*	√	—
9	vB_Sal_PHB48	NA	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Enteritidis</i> CICC 21482	China	52.4	29575	ON782130	√	√	√	√	16
Bacteriophages 2: 186-type phages or P2-like phages												
1	ENT90	Entnonagintavirus	<i>Erwinia amylovora</i>	China	55.8	29564	NC_019932	√	√	√	√	17,18
2	Fels-2	Felsduovirus	<i>Salmonella typhimurium</i> LT2	NA	52.5	33693	NC_010463	√	√	√	√	1
3	SopE ϕ	Felsduovirus	<i>Salmonella typhimurium</i> DT204	—	51.3	35155	AY319521	√	√	√	√	1
4	3625_26581	NA	Bacteriophage sp. isolate 3625_26581	Japan	54.7	27828	OP075671	√	√	√*	√	—

5	K139	Longwoodvirus	<i>Vibrio cholerae</i> O139	NA	48.9	33106	NC_003313	√	√	√	√	1,24
6	Kappa	Longwoodvirus	<i>Vibrio cholerae</i> O1 biovar eltor	NA	48.8	33507	NC_010275					1,23
7	φ O18P	Bielevirus	<i>Aeromonas media</i>	NA	61.7	33985	NC_009542					1,24
8	HP1	Hpunavirus	<i>Haemophilus influenzae</i>	NA	40.0	32355	NC_001697					1,19,20,21
9	HP2	Hpunavirus	<i>Haemophilus influenzae</i>	NA	39.9	31508	NC_003315					1,21
10	F108	Irtavirus	<i>Pasteurella multocida</i>	NA	42.1	30505	NC_008193			—		1,22
Bacteriophages 3: genus <i>Peduvovirus</i>												
1	P2	Peduvovirus	<i>Escherichia coli</i>	NA	50.2	33593	NC_001895	√	√	√	√	1,2,4,12,13
2	P2_Hy_dis	Peduvovirus	Recombinant between P2 and a defective P2-like prophage in an <i>Escherichia coli</i> B strain	NA	—	—	AJ306907-c&cox	√	√	√	√	2,7,10,11
3	φ D124	Peduvovirus	<i>Escherichia coli</i> C, Clinical isolate	Los Angeles, Calif	—	—	AM159060-c&cox, AJ298558-ONML	√	√	√	√	1,2
4	W φ	Peduvovirus	<i>Escherichia coli</i> W str. ATCC9637	NA	51.7	32684	NC_005056	√	√	√	√	1,2
5	L-413C	Peduvovirus	<i>Yersinia pestis</i>	NA	52.1	30728	NC_004745	√	√	√	√	1,2,4
6	φ D160	Peduvovirus	<i>Escherichia coli</i> C, Clinical isolate	Los Angeles, Calif	—	—	AM159075-c&cox, AJ298560-ONML	√	√	√	√	1,2
7	φ D145	Peduvovirus	<i>Escherichia coli</i> C, Clinical isolate	Los Angeles, Calif	—	—	AM159077-c&cox, AM158280-int, AJ298559-ONML	√	√	√	√	1,2
8	P2-EC4	Peduvovirus	<i>Escherichia coli</i> str. ECOR4	NA	—	—	AM159080-c&cox	√	√	√	√	2
9	GMG73	Peduvovirus	<i>Yersinia pestis</i>	China	51.5	33804	OP880301	√	√	√	√	4
10	GMS190	Peduvovirus	<i>Yersinia pestis</i>	China	53.0	29462	OP880302	√	√	√	√	4
11	HQ103	Peduvovirus	<i>Yersinia pestis</i> EV76-CN	China	51.7	31962	NC_070908	√	√	√	√	4,6

12	Vb_YpM_22	Peduvovirus	<i>Yersinia pestis</i> EV76-CN	China	51.5	31809	NC_055844	√	√	√	√	3,4
13	Vb_YpM_46	Peduvovirus	<i>Yersinia pestis</i> EV76-CN	China	51.7	32336	NC_055845	√	√	√	√	3,4
14	Vb_YpM_50	Peduvovirus	<i>Yersinia pestis</i> EV76-CN	China	52.1	31096	NC_055846	√	√	√	√	3,4
15	vB_YenM_42.18	Peduvovirus	<i>Yersinia enterocolitica</i>	Germany	46.4	36481	NC_070913					5
Bacteriophages 4: Prophages												
	Name	Host strain/source	Location in host genome	GC (%)	Sequence Size (bp)	Sequence accession No.						Ref.
1	Φ ECA29	<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043	2935258-2966778	50.9	31521	NC_004547						1
2	φ ECO1	<i>Escherichia coli</i> HS	916812-948276	52.0	31465	NC_009800	√	√	√	√		1
3	φ ECO2	<i>Escherichia coli</i> CATCC 8739	3023202-3058101	50.5	34900	NC_010468	√	√	√	√		1
4	φ ECO3	<i>Escherichia coli</i> CFT073	908870-942351	50.3	33482	NC_004431	√	√	√	√		1
5	φ ECO4	<i>Escherichia coli</i> E22	1631226-1670396	51.7	39171	NZ_AAJV000000000						1
6	φ ECO5	<i>Escherichia coli</i> UTI89	903605-951760	53.5	32767	NC_007946						1
7	φ ECO6	<i>Escherichia coli</i> 101-1	908551-947403	52.6	38853	NZ_AAMK000000000						1
8	φ ECO7	<i>Escherichia coli</i> 53638	2139828-2172764	51.9	32927	NZ_AAKB000000000						1
9	φ ESP	<i>Enterobacter</i> sp. 638	3783460-3815505	53.1	32093	NC_009436	√	√	√	√		1
10	Φ YPS	<i>Yersinia pseudotuberculosis</i> IP 32953	3688279-3717980	49.2	29702	NC_006155						1
11	Φ YE98	<i>Yersinia enterocolitica</i> subsp. <i>enterocolitica</i> 8081	981219-1012614	48.8	31396	NC_008800						1
12	φ KPN	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> MGH 78578	3803150-3835929	52.0	32827	NC_009648	√	√	√	√		1
13	φ SEN1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi CT18	3515381-3549053	51.8	33673	NC_003198	√	√	√	√		1
14	φ SEN2	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi CT18	4473835-4507389	51.7	32767	NC_003198	√	√	√	√		1

notes: "NA" denotes not applicable, "—" indicates the absence of content, "-c&cox" refers to the accession numbers for the C and Cox genes, "-ONML" specifies the accession numbers for the O, N, M, and L genes, while entries without any suffix represent the accession numbers for the complete genome sequences.

Reference.

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7. Characterization of the developmental switch region of bacteriophage P2 Hy dis
8. Complete Genome Sequence of EtG, the First Phage Sequenced from *Erwinia tracheiphila*
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12. Studies on lysogenesis. I. The mode of phage liberation by lysogenic *Escherichia coli*
13. Characterization of five novel endolysins from Gram-negative infecting bacteriophages
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20. The complete nucleotide sequence of bacteriophage HP1 DNA
21. Bacteriophage HP2 of *Haemophilus influenzae*

22. Isolation and sequencing of a temperate transducing phage for *Pasteurella multocida*
23. Temperature-sensitive mutants of *Serratia* phage Kappa
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