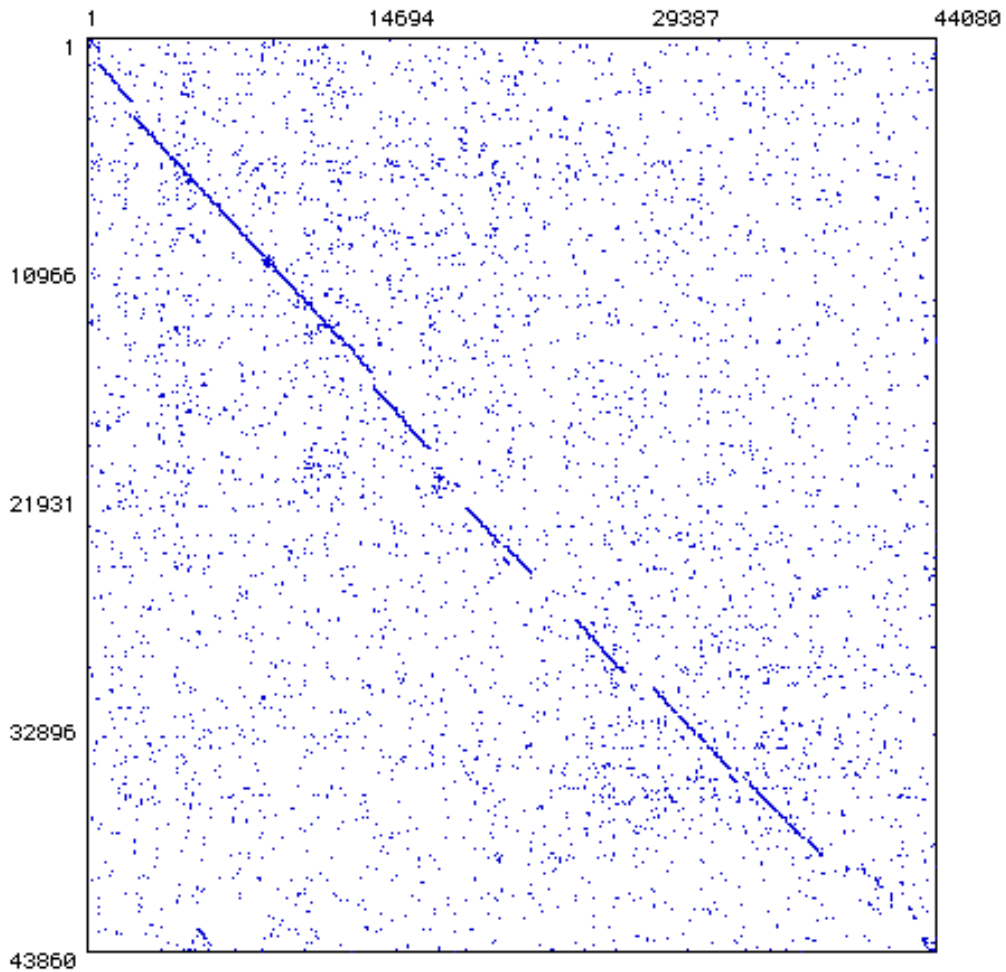


Supplemental Fig. S1. Morphology of Cp1 and Cp2 particles. The purified particles of Cp1 and Cp2 were negatively stained and examined by transmission electron microscopy. Cp1 particles had an icosahedral capsid of 60 ± 5 nm in diameter with a long non-contractile tail of 135 ± 10 nm long by 12 ± 2 nm wide ($n=20$). Cp2 particles showed an icosahedral capsid of 60 ± 5 nm in diameter with a short tail of 15 ± 5 nm long ($n = 20$).

File: Cp1
Mode: Normal 1 - 43860 5'→3'
File: phiL7
Mode: Normal 1 - 44080 5'→3'
Plotting Mode: Left Up Check Size: 65 Matching Size: 33



Supplemental Fig. S2. Matrix comparison of the nucleotide sequences between Cp1 and phiL7 genomes.

Supplemental Table S1 Predicted ORFs found in the Cp1 genome

Coding sequence	Strand	Position (5' to 3')	G+C (%)	Length (aa)	Mass (kDa)	Amino acid identity/similarity to best homologs	FASTA score (E value)
ORF1	+	106-333	59.3	76	7.94	p01 phiL7	43 (0.025)
ORF2	+	392-628	52.5	78	8.44	P02 phiL7- hypothetical protein	84 (8e-13)
ORF3	+	635-1315	53.9	226	25.06	group 1 intron GIY-YIG endonuclease (<i>Pseudomonas stutzeri</i> Kos6)	123 (1e-30)
ORF4	+	1349-3054	54.6	568	61.58	p03 phiL7-Terminase large sub unit	730 (0.0)
ORF5	+	3079-3723	50.4	214	23.71	group 1 intron GIY-YIG endonuclease (<i>Pseudomonas stutzeri</i> Kos6)	109 (9e-26)
ORF6	+	3734-5029	55.1	431	46.65	p04 phiL7-Putative head portal protein	652 (0.0)
ORF7	+	5026-5745	50.6	239	25.23	p05 phiL7-Protease of the ClPp family	288 (5e-76)
ORF 8	+	5760-6944	59.6	394	41.7	p06 phiL7- Head protein	641 (0.0)
ORF9	+	7029-7526	49.1	165	18.51	p07 phiL7- HNH endonuclease	180 (1e-43)
ORF10	+	7528-7863	53.8	111	12.6	p08 phiL7- Phage coat protein	111 (6e-23)
ORF11	+	7863-8237	52.1	124	13.16	p09 phiL7- Head- tail Joint	187 (8e-46)
ORF12	+	8227-8694	49.1	156	17.17	p10 phiL7-Conserved phage protein I	172 (6e-52)
ORF13	+	8691-9047	50.1	118	13.17	p11 phiL7- Phage coat protein	177 (7e-43)
ORF14	+	9057-9695	55.6	212	22.24	p12 phiL7- Major tail	288 (3e-76)
ORF15	+	9695-9997	55.0	100	10.9	p13 phiL7- Hypothetical protein	170 (8e-41)
ORF16	+	10102-10311	57.2	69	8.05	p14 phiL7-Conserved phage protein II	79.1(7e-25)
ORF17	+	10406-11917	50.8	503	56.34	p15 phiL7- Hypothetical Protein	590(0.0)
ORF18	+	11963-14827	55.4	953	99.34	p16 phiL7-Tail length tape measure protein	992 (0.0)
ORF19	+	14827-15189	48.7	121	13.81	p17 phiL7- Tail protein I	179 (2e-43)
ORF20	+	15189-15647	52.1	152	16.79	p18 phiL7- Tail protein II	225 (3e-57)
ORF21	+	15665-16051	54.2	129	14.62	Xop411 phage, p21, Peptidoglycan hydrolase	174 (7e-42)
ORF22	+	16064-16669	52.0	201	23.05	Bacillus phage G, G3MAX5 (Gp595)	62 (9e-08)
ORF23	+	16710-21431	53.8	1573	167.72	- OP1_ORF21,Putative tail component protein.	2048(0.0)
ORF24	+	21478-22554	51.7	358	37.68	- p20 phiL7- Tail protein III OP1_ORF25,Deduced tail fiber protein	1496(0.0) 77 (6e-12)
ORF25	+	22556-22855	49.3	98	10.48	p22 phiL7- hypothetical protein	125 (2e-27)
ORF26	+	22857-23543	46.8	228	23.91	p23 phiL7- Conserved Phage protein	253 (23-65)
ORF27	-	23540-23908	51.3	122	13.39	p24 phiL7- Hypothetical protein	200 (1e-63)
ORF27.1	+	24387-24587	50.9	66	7.046	P27 phiL7- putative holin	48 (7e-5)
ORF28	+	24591-25130	53.9	179	19.83	p28 phiL7- Phage type lysozyme	265 (2e-69)
ORF29	+	25099-25467	51.0	122	13.5	p29 phiL7- Hypothetical protein	110 (7e-23)
ORF30	-	25676-26327	53.2	200	22.27	group I intron endonuclease (D6TZN2)	71 (1e-10)

Supplemental Table S1 continued

Coding sequence	Strand	Position (5' to 3')	G+C (%)	Length (aa)	Mass (kDa)	Amino acid identity/similarity to best homologs	BLAST score (E value)
ORF31	-	26558-27104	50.8	181	19.39	<i>Hemophilus parasuis</i> SH0165 (Interrupted gp229, phage associated)	160 (8e-45)
ORF32	-	27100-27534	53.7	144	14.35	F7T9I5(Putative uncharacterized protein)	69 (3e-10)
ORF33	-	27912-30327	53.6	804	91.43	p35 phiL7- RNA polymerase	1212 (0.0)
ORF34	-	30601-31164	54.3	187	21.14	<i>Pantoea</i> phage LIMEzero (F4N9T4), Putative uncharacterized protein	86 (3e-15)
ORF35	-	31175-32026	50.4	283	32.35	p39 phiL7- Putative DNA polymerase III	456 (e-126)
ORF36	-	32013-32408	53.5	131	14.64	p40 phiL7- Endonuclease VII	134 (4e-30)
ORF37	-	32405-33334	56.0	309	34.35	p41 phiL7- Exonuclease	312 (5e-83)
ORF38	-	33334-34215	57.1	293	32.02	ADQ2- <i>Caulobacter</i> Cd1 Phage, Putative Uncharacterized protein	133 (4e-11)
ORF39	-	34229-34936	55.3	235	26.6	unknown	
ORF40	-	35296-37014	53.2	572	63.96	p46 phiL7- DNA polymerase lacking N-terminal exonuclease	550(e-154)
ORF41	-	37073-38365	55.5	430	48.35	p47 phiL7- Replicative helicase of the DnaB family	408 (e-113)
ORF42	-	38350-39177	52.0	275	30.6	p48 phiL7-DNA primase of the DnaG family	239 (4e-61)
ORF43	-	39758-40066	43.8	102	12.21	Xop411_p 45 Hypothetical protein	74 (1e-11)
ORF44	-	40063-40263	42.1	66	7.46	Xp10_45L, 7K protein; inhibitor of transcription initiation and anti-terminator	35.8(0.13)
ORF45	+	41309-41626	53.2		11.55	unknown	-----
ORF46	+	42546-43075	46.9	175	20.24	p07 phiL7- HNH endonuclease	166 (4e-50)
ORF47	+	43111-43425	45.6	104	12.38	p57 phiL7	57 (1e-06)

Supplemental Table S2 Predicted ORFs found in the Cp2 genome

Coding sequence	Strand	Position (5' to 3')	G+C (%)	Length (aa)	Mass (kDa)	Amino acid identity/similarity to best homologs	FASTA score (E value)
ORF1	+	454-1398	66.8	314	34.88	phage protein Gp37/Gp68.	329(3e-108)
ORF2	+	1364-1945	63.2	193	18.1	hypothetical protein F116p34 (<i>Pseudomonas</i> phage F116)	106 (6e-26)
ORF3	+	2262-2717	66.8	151	16	holliday junction resolvase , RUSA	112 (2e-28)
ORF4	+	2836-3952	73.9	372	32.71	no similarity	----
ORF5	+	4030-4632	70.5	200	21.46	phage lysozyme (<i>Burkholderia multivorans</i> CF2)	127(1e-32)
ORF6	+	4635-5108	64	157	16.46	hypothetical protein SSKA14_3083 (<i>Stenotrophomonas</i> sp. SKA14)	51 (3e-06)
ORF7	+	5105-5662	67.3	185	20.37	hypothetical protein SSKA14_2891 (<i>Stenotrophomonas</i> sp. SKA14)	80 (1e-12)
ORF8	+	5665-5979	67.6	104	11.61	hypothetical protein XVE_1166 (<i>Xanthomonas vesicatoria</i> ATCC 35937)	59(1e-09)
ORF9	+	6031- 6360	67.3	109	11.45	No similarity	----
ORF10	+	6712-7149	65.8	145	16.1	hypothetical protein Pden_3755 (<i>Paracoccus denitrificans</i> PD1222)	59 (4e-09)
ORF11	+	7289-8815	67	508	56.21	putative phage terminase B protein [<i>Enterococcus</i> phage phiEf11]	196 (7e-53)
ORF12	+	8820-9158	65.3	112	11.95	Bbp20 (<i>Bordetella</i> phage BPP-1)	58(4e-09)
ORF13	+	9234 -11294	67.6	686	74.87	bacteriophage head to tail connecting protein	300 (2e-89)
ORF14	+	11629-12354	65.8	241	25.11	endoprotease (<i>Pantoea</i> sp. aB)	84 (1e-16)
ORF15	+	12398-13411	63.1	337	36.38	putative major capsid protein (<i>Pseudomonas</i> phage AF)	257 (8e-80)
ORF16	+	13447-13893	66.6	148	15.35	hypothetical protein AF_009 (<i>Pseudomonas</i> phage AF)	73 7e-14)
ORF17	+	13947-14537	59.5	196	19.98	no similarity	---
ORF18	+	14607-15290	67.3	227	24.71	putative tail tubular protein A (<i>Pseudomonas</i> phage AF)	89(1e-18)
ORF19	+	15292-16683	65.7	463	49.5	putative phage protein p13 (<i>Hydrogenophaga</i> sp. PBC)	155 (9e-38)
ORF20	+	16683-18395	65.1	570	61.81	<i>Salmonella</i> phage epsilon15	350(5e-07)
ORF21	+	18392-18868	64.5	158	17.7	hypothetical protein PhiV10p16 (<i>Escherichia</i> phage phiV10)	112 (3e-28)
ORF22	+	18868-19371	67.5	167	17.11	hypothetical protein Q5W_4240 (<i>Hydrogenophaga</i> sp. PBC)	64 (2e-12)
ORF23	+	19371-21563	68.8	730	79.04	putative structural lysozyme (<i>Pseudomonas</i> phage AF)	94(4e-17)
ORF24	+	21566-29002	68.2	2478	267.54	hypothetical protein AF_016 (<i>Pseudomonas</i> phage AF)	506(9e-143)
ORF25	+	29002-30111	63.5	369	40.13	endo-N- acetylneuraminidase (Endosialidase) family protein,	79 (4e-13)
ORF26	+	30289-31314	64.2	341	35.78	end_tail_spike LysM domain protein (<i>Xanthomonas citri</i> <i>pv. mangiferaeindicae</i>)	115(1e-24)
ORF27	+	31311-32243	60.9	310	33	putative tail fiber protein (<i>Pseudomonas</i> phage PT2)	64(9e- 09)
ORF28	+	32233-32808	61.0	191	21.69	tail fibre protein (<i>Pseudomonas</i> phage LUZ19)	74 (2e-13)
ORF29	-	33018-33584	67.6	188	21.26	hypothetical protein YPK_2318 (<i>Yersinia</i> <i>pseudotuberculosis</i> YPIII)	70 (6e-12)
ORF30	-	33829-34191	63.8	120	12.84	N4 Gp49/Sf6 protein 66 phage family protein (<i>Acinetobacter baumannii</i> OFCO211)	110 (6e-29)
ORF31	-	34225-34710	64.9	161	17.68	Orf76(<i>Pseudomonas</i> phage D3)	73 (2e-13)
ORF32	-	34723-35160	62.7	145	16.35	Single-stranded DNA binding protein (<i>Xanthomonas translucens</i> <i>pv. graminis</i> ART-Xtg29)	173 (5e-52)
ORF33	-	35157-35534	65.3	125	13.27	- hypothetical protein Bphy_1919 (<i>Burkholderia phymatum</i> STM815) - bacteriophage-like protein (<i>Ralstonia</i> <i>solanacearum</i> GMI1000]	106 (2e-26) 103(2e-25)

Supplemental Table S2 continued

Coding sequence	Strand	Position (5' to 3')	G+C (%)	Length (aa)	Mass (kDa)	Amino acid identity/similarity to best homologs	BLAST score (E value)
ORF30	-	33829-34191	63.8	120	12.84	N4 Gp49/Sf6 protein 66 phage family protein (<i>Acinetobacter baumannii</i> OFCO211)	110 (6e-29)
ORF31	-	34225-34710	64.9	161	17.68	Orf76(Pseudomonas phage D3)	73 (2e-13)
ORF32	-	34723-35160	62.7	145	16.35	Single-stranded DNA binding protein (<i>Xanthomonas translucens</i> pv. <i>graminis</i> ART-Xtg29)	173 (5e-52)
ORF33	-	35157-35534	65.3	125	13.27	- hypothetical protein Bphy_1919 (<i>Burkholderia phymatum</i> STM815)	106 (2e-26)
ORF34	-	35534-36157	65.5	207	23.36	- bacteriophage-like protein (<i>Ralstonia solanacearum</i> GMI1000)	103(2e-25)
ORF35	-	36385-37227	64.4	280	30.33	YqaJ-like viral recombinase domain; pfam09588 (<i>Xanthobacter autotrophicus</i> Py2)	207(7e-64)
ORF36	-	37496-39031	69.3	511	56.94	ERF family protein (<i>Burkholderia glumae</i> BGR1)	179 (7e-51)
ORF37	-	39072-39896	65.9	274	29.27	hypothetical protein F116p18 (<i>Pseudomonas</i> phage F116)	73(4e-11)
ORF38	-	39951-40325	63.4	124	13.04	protein of unknown function (DUF2303)(Vibrio phage VvAW1)	190 (2e-55)
ORF39	+	41829-42176	66.7	115	12.48	hypothetical protein VvAW1_00024c (Vibrio phage VvAW1)	76 (3e-15)
ORF40	+	42178-231	62.6	338	36.7	Predicted: DNA polymerase subunit gamma-1 (<i>Callithrix jacchus</i>)	35 (2.2)
						- hypothetical protein (<i>Escherichia</i> phage TL-2011b) "PhdYeFM_antitox"	140(1e-35)
						- Pyocin large subunit-like protein [<i>Pseudomonas</i> sp. R81]	127(3e-31)