

Supplementary information

The bacteriophage pEp_SNUABM_08 is a novel singleton siphovirus with high host specificity for *Erwinia pyrifoliae*

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Table S1 Functional categories of the identified open reading frames (ORFs) in pEp_SNUABM_08.

Functional group	Locus tag	Identified protein	Protein ID	Related bacteriophage	Coverage (%)	Identity (%)
Nucleotide regulation	pEpSNUABM08_01	Putative primase	QEQ94748.1	<i>Salmonella</i> phage FSL SP-019	97	37.1
Hypothetical protein	pEpSNUABM08_02	Hypothetical protein	QEQ94749.1	N/A ^a	N/A	N/A
Hypothetical protein	pEpSNUABM08_03	Hypothetical protein	QEQ94750.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_04	Hypothetical protein	QEQ94751.1	N/A	N/A	N/A
Nucleotide regulation	pEpSNUABM08_05	Cas4-like protein	QEQ94752.1	<i>Burkholderia</i> phage AH2	95	39.37
Hypothetical protein	pEpSNUABM08_06	DUF2815 domain-containing protein	QEQ94753.1	<i>Providencia</i> phage Redjac	85	37.24
Nucleotide regulation	pEpSNUABM08_07	Putative DNA polymerase I	QEQ94754.1	<i>Salmonella</i> virus FSLSP088	95	48.02
Nucleotide regulation	pEpSNUABM08_08	VRR-NUC domain-containing protein	QEQ94755.1	<i>Burkholderia</i> phage AH2	84	39.33
Nucleotide regulation	pEpSNUABM08_09	Putative DEAD-like helicase	QEQ94756.1	<i>Achromobacter</i> phage phiAxp-2	91	41.88
Packaging	pEpSNUABM08_10	Putative terminase small subunit	QEQ94757.1	<i>Proteus</i> phage PM87	90	38.07
Packaging	pEpSNUABM08_11	Putative terminase large subunit	QEQ94758.1	<i>Proteus</i> phage PM87	98	54.91
Structure	pEpSNUABM08_12	Putative head completion protein	QEQ94759.1	<i>Klebsiella</i> phage Seifer	87	49.38
Structure	pEpSNUABM08_13	Putative portal protein	QEQ94760.1	<i>Serratia</i> phage JS26	95	52.01
Structure	pEpSNUABM08_14	Putative capsid assembly protease	QEQ94761.1	<i>Serratia</i> phage JS26	94	43.29
Structure	pEpSNUABM08_15	Putative head decoration	QEQ94762.1	<i>Burkholderia</i> phage AH2	94	42.17

		protein				
Structure	pEpSNUABM08_16	Putative major capsid protein	QEQ94763.1	<i>Klebsiella</i> phage Seifer	96	42.41
Hypothetical protein	pEpSNUABM08_17	Hypothetical protein	QEQ94764.1	<i>Serratia</i> phage JS26	98	33.59
Structure	pEpSNUABM08_18	Putative head-tail joining protein	QEQ94765.1	<i>Salmonella</i> phage KFS-SE1	99	50.28
Structure	pEpSNUABM08_19	Putative tail completion protein	QEQ94766.1	<i>Proteus</i> phage PM87	96	54
Structure	pEpSNUABM08_20	Putative tail tube terminator protein	QEQ94767.1	<i>Enterobacter</i> phage Enc34	95	38.18
Structure	pEpSNUABM08_21	Ig-like domain-containing tail protein	QEQ94768.1	<i>Salmonella</i> virus SPN19	82	42.9
Structure	pEpSNUABM08_22	Putative tail assembly chaperone	QEQ94769.1	<i>Klebsiella</i> phage Seifer	72	31.03
Hypothetical protein	pEpSNUABM08_23	Hypothetical protein	QEQ94770.1	<i>Serratia</i> phage JS26	81	46.15
Structure	pEpSNUABM08_24	Putative tape measure protein	QEQ94771.1	<i>Salmonella</i> virus iEPS5	82	32.71
Structure	pEpSNUABM08_25	Putative lambda tail tip M like protein	QEQ94772.1	Unidentified phage	95	35.82
Structure	pEpSNUABM08_26	Putative lambda tail tip L like protein	QEQ94773.1	Unidentified phage	99	46.91
Structure	pEpSNUABM08_27	Putative lambda tail tip I like protein	QEQ94774.1	<i>Burkholderia</i> phage BcepNazgul	76	56.45
Hypothetical protein	pEpSNUABM08_28	Hypothetical protein	QEQ94775.1	<i>Xanthomonas</i> phage Xoo-sp2	83	36.67
Structure	pEpSNUABM08_29	Putative lambda tail tip J like protein	QEQ94776.1	<i>Salmonella</i> phage Season12	92	40.46

Hypothetical protein	pEpSNUABM08_30	Hypothetical protein	QEQ94777.1	<i>Salmonella</i> virus FSLSP088	99	38.62
Hypothetical protein	pEpSNUABM08_31	Hypothetical protein	QEQ94778.1	<i>Enterobacter</i> phage Enc34	97	32.01
Hypothetical protein	pEpSNUABM08_32	Hypothetical protein	QEQ94779.1	<i>Proteus</i> phage PM87	99	38.79
Hypothetical protein	pEpSNUABM08_33	Hypothetical protein	QEQ94780.1	<i>Salmonella</i> virus Chi	99	49.86
Hypothetical protein	pEpSNUABM08_34	Hypothetical protein	QEQ94781.1	<i>Salmonella</i> phage 118970_sal1	44	31.64
Hypothetical protein	pEpSNUABM08_35	Hypothetical protein	QEQ94782.1	<i>Serratia</i> phage JS26	100	28.44
Hypothetical protein	pEpSNUABM08_36	Hypothetical protein	QEQ94783.1	<i>Salmonella</i> phage Season12	82	23.99
Hypothetical protein	pEpSNUABM08_37	Hypothetical protein	QEQ94784.1	N/A	N/A	N/A
Lysis	pEpSNUABM08_38	Putative virion protein (lysis protein A like)	QEQ94785.1	<i>Salmonella</i> phage FSL SP-099	97	63.52
Lysis	pEpSNUABM08_39	Hypothetical protein (Rz-like)	QEQ94786.1	<i>Providencia</i> phage Redjac	96	35.44
Hypothetical protein	pEpSNUABM08_40	Hypothetical protein	QEQ94787.1	<i>Enterobacter</i> phage Enc34	69	50.85
Hypothetical protein	pEpSNUABM08_41	Hypothetical protein	QEQ94788.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_42	Hypothetical protein	QEQ94789.1	<i>Escherichia</i> phage vB_EcoM_ECO1230-10	25	56.98
Hypothetical protein	pEpSNUABM08_43	Hypothetical protein	QEQ94790.1	N/A	N/A	N/A
Nucleotide regulation	pEpSNUABM08_44	Putative N-6-adenine- methyltransferase	QEQ94791.1	<i>Klebsiella</i> phage Seifer	98	45.64
Hypothetical protein	pEpSNUABM08_45	Hypothetical protein	QEQ94792.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_46	Hypothetical protein	QEQ94793.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_47	Hypothetical protein	QEQ94794.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_48	Hypothetical protein	QEQ94795.1	<i>Proteus</i> phage PM87	79	38.75
Hypothetical protein	pEpSNUABM08_49	Hypothetical protein	QEQ94796.1	<i>Serratia</i> phage JS26	46	32.32
Hypothetical protein	pEpSNUABM08_50	Hypothetical protein	QEQ94797.1	<i>Serratia</i> phage JS26	35	39.62
Structure	pEpSNUABM08_51	Putative tail fiber protein	QEQ94798.1	<i>Klebsiella</i> phage KPN N137	76	43.33

Nucleotide regulation	pEpSNUABM08_52	Putative exonuclease	QEQ94799.1	<i>Enterobacter</i> phage Enc34	66	28.67
Hypothetical protein	pEpSNUABM08_53	Hypothetical protein	QEQ94800.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_54	Hypothetical protein	QEQ94801.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_55	Hypothetical protein	QEQ94802.1	<i>Serratia</i> phage JS26	95	35.51
Hypothetical protein	pEpSNUABM08_56	Hypothetical protein	QEQ94803.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_57	Hypothetical protein	QEQ94804.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_58	Hypothetical protein	QEQ94805.1	N/A	N/A	N/A
Nucleotide regulation	pEpSNUABM08_59	Putative cytosine C5-specific methylase	QEQ94806.1	<i>Escherichia</i> phage K1-ind(2)	97	46.4
Hypothetical protein	pEpSNUABM08_60	Hypothetical protein	QEQ94807.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_61	Hypothetical protein	QEQ94808.1	<i>Klebsiella</i> phage YMC16/01/N133_KPN_BP	80	37.97
Hypothetical protein	pEpSNUABM08_62	Hypothetical protein	QEQ94809.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_63	Hypothetical protein	QEQ94810.1	<i>Klebsiella</i> phage KPN N137	57	53.41
Hypothetical protein	pEpSNUABM08_64	DUF1382 domain-containing protein	QEQ94811.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_65	Hypothetical protein	QEQ94812.1	<i>Klebsiella</i> phage YMC16/01/N133_KPN_BP	56	38.24
Hypothetical protein	pEpSNUABM08_66	Hypothetical protein	QEQ94813.1	<i>Pseudomonas</i> phage Psp6	22	50
Nucleotide regulation	pEpSNUABM08_67	Putative DnaQ-like exonuclease	QEQ94814.1	<i>Pectobacterium</i> phage MA11	76	39.06
Hypothetical protein	pEpSNUABM08_68	Hypothetical protein	QEQ94815.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_69	Hypothetical protein	QEQ94816.1	<i>Salmonella</i> phage BSPM4	72	68.75
Hypothetical protein	pEpSNUABM08_70	Hypothetical protein	QEQ94817.1	<i>Salmonella</i> phage FSL SP-124	98	52.2
Hypothetical protein	pEpSNUABM08_71	Hypothetical protein	QEQ94818.1	<i>Salmonella</i> phage 118970_sal1	99	53.03

Hypothetical protein	pEpSNUABM08_72	Hypothetical protein	QEQ94819.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_73	Hypothetical protein	QEQ94820.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_74	Hypothetical protein	QEQ94821.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_75	Hypothetical protein	QEQ94822.1	<i>Escherichia</i> phage vB_EcoM-Ro121c4YLVW	43	46.22
Hypothetical protein	pEpSNUABM08_76	Hypothetical protein	QEQ94823.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_77	Hypothetical protein	QEQ94824.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_78	Hypothetical protein	QEQ94825.1	N/A	N/A	N/A
Hypothetical protein	pEpSNUABM08_79	Hypothetical protein	QEQ94826.1	N/A	N/A	N/A

^aN/A, Not available.

Fig. S1 ERIC-PCR genotyping of *Erwinia* spp. used in this study for host range analysis; M, 1kb plus size marker; -, negative control; 1-26, *E. amylovora* strains; 27-51, *E. pyrifoliae* strains; 1, YKB 14715; 2, YKB 14740; 3, YKB 14742; 4, YKB 14748; 5, YKB 14750; 6, RA0030; 7, RA0031; 8, RA0032; 9, RA0033; 10, RA0034; 11, RA0035; 12, RA0041; 13, RA0042; 14, RA0043; 15, RA0044; 16, RA0045; 17, RA0051; 18, RA0052; 19, RA0053; 20, RA0054; 21, RA0055; 22, RA0062; 23, RA0063; 24, RA0064; 25, RA0065; 26, RA0066; 27, KACC13945; 28, KACC13946; 29, KACC13948; 30, KACC13949; 31, KACC13952; 32, RP0100; 33, RP0101; 34, RP0102; 35, RP0103; 36, RP0104; 37, RP0105; 38, RP0108; 39, RP0109; 40, RP0110; 41, RP0111; 42, RP0112; 43, RP0113; 44, RP0114; 45, RP0115; 46, RP0116; 47, RP0117; 48, RP0118; 49, RP0119; 50, RP0120; 51, RP0121.

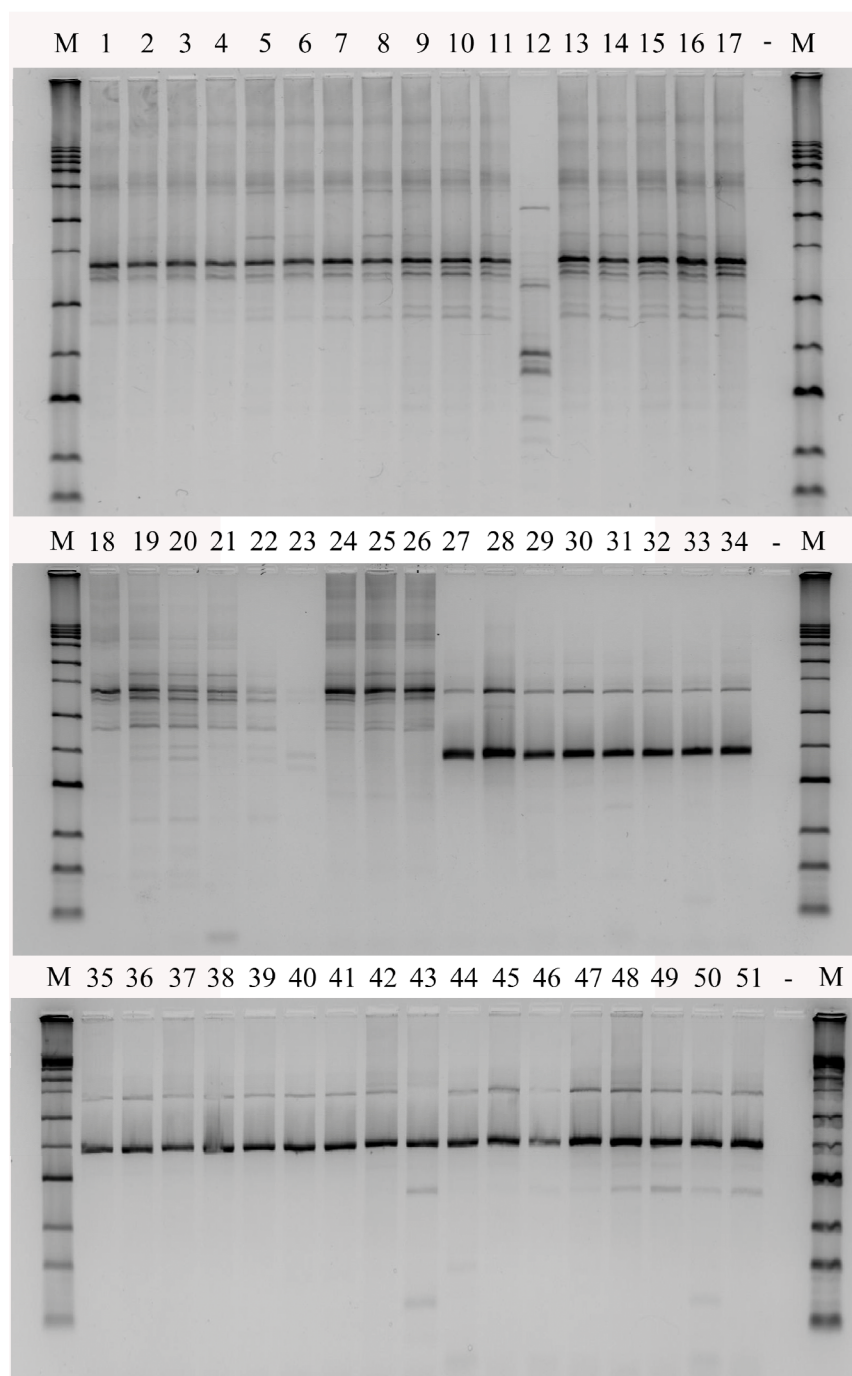


Fig. S2 Comparative genome analysis of *Erwinia* phage pEp_SNUABM_08 with *Salmonella* phage Chi. The tBLASTx comparison result was represented in blue and red by their direction and the intensity of color represents the % identity.

