

Supplementary materials

Table S1. Several reported phages with broad host range capable of infecting *E. coli*

Phage	Host strain	Morphology	Size (nm)		Host range	Reference
			Head	Tail		
KFS-EC3	<i>E. coli</i> O157:H7 ATCC 10536	Myophage	~97	~67-136	3 genera: <i>E. coli</i> , <i>Salmonella</i> , and <i>Shigella</i>	-
EcS1	<i>E. coli</i> BL21	Myophage	~111	~110	3 genera: <i>E. coli</i> , <i>Salmonella</i> , and <i>Shigella</i>	(Saad et al., 2019)
SH7	<i>S. flexneri</i> SF1	Myophage	~112	~116	3 genera: <i>E. coli</i> , <i>Salmonella</i> , and <i>Shigella</i>	(Hamdi et al., 2017)
SFP10	<i>E. coli</i> O157:H7 ATCC 43890	Myophage	~69	~42-131	2 genera: <i>E. coli</i> and <i>Salmonella</i>	(Park et al., 2012)
PS5	<i>S. Typhimurium</i> NBRC12529	Myophage	~84	~106	2 genera: <i>E. coli</i> and <i>Salmonella</i>	(Duc et al., 2020)
phiC119	<i>E. coli</i> O157 EC-48	Siphophage	~43	~168	2 genera: <i>E. coli</i> and <i>Salmonella</i>	(Amarillas et al., 2016)
vB_EcoM_swi3	<i>E. coli</i> K88	Myophage	~80	~120	2 genera: <i>E. coli</i> and <i>Salmonella</i>	(Sui et al., 2021)
HY01	<i>E. coli</i> O157:H7 ATCC 43890	Myophage	~100	~100	2 genera: <i>E. coli</i> and <i>Shigella</i>	(Lee et al., 2016)
SH6	<i>Shigella flexneri</i> SF1	Siphophage	~62	~161	2 genera: <i>E. coli</i> and <i>Shigella</i>	(Hamdi et al., 2017)

Table S2. Annotated functional genes in KFS-EC3 genome

No	Start	Stop	Strand	Function	Group
1	870	1331	+	Phage endonuclease	Nucleotide metabolism
2	1877	2218	+	Valyl-tRNA synthetase	Nucleotide metabolism
3	3443	4024	+	Thymidine kinase	Additional functions
4	4292	4585	+	Phage <i>rl</i> lysis inhibition regulator	Host lysis
5	6600	7379	+	Phage-associated homing endonuclease	Nucleotide metabolism
6	7363	8373	+	Thioredoxin, phage-associated	Additional functions
7	8489	9457	+	Thioredoxin, phage-associated	Additional functions
8	9559	9861	+	Thioredoxin, phage-associated	Additional functions
9	9922	10449	+	Thioredoxin, phage-associated	Additional functions
10	10505	10912	+	Thioredoxin, phage-associated	Additional functions
11	10920	11810	+	Thioredoxin, phage-associated	Additional functions
12	11819	12841	+	Thioredoxin, phage-associated	Additional functions
13	12869	13825	+	Thioredoxin, phage-associated	Additional functions
14	13822	14190	+	Thioredoxin, phage-associated	Additional functions
15	14192	14434	+	Thioredoxin, phage-associated	Additional functions
16	14436	14699	+	Thioredoxin, phage-associated	Nucleotide metabolism
17	15095	15415	+	Nucleotide reductase subunit C	Nucleotide metabolism
18	15539	15985	+	Pin protease inhibitor	Additional functions
19	16035	16508	+	Phage endonuclease	Nucleotide metabolism
20	16505	18322	+	Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)	Nucleotide metabolism
21	18319	18789	+	Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)	Nucleotide metabolism
22	19120	19428	+	Glutaredoxin	Additional functions
23	21330	21887	+	T4-like phage RNA polymerase sigma factor for late transcription	Nucleotide metabolism
25	22824	24026	+	a-gt alpha glucosyl transferase	Additional functions
26	24203	25222	+	Phage recombination-related endonuclease Gp47	Nucleotide metabolism
27	25708	27348	+	Phage recombination-related endonuclease Gp46	Nucleotide metabolism
28	27602	27991	+	RNA polymerase binding protein	Nucleotide metabolism
29	28047	28733	+	Sliding clamp DNA polymerase accessory protein, phage associated	Nucleotide metabolism
30	28785	29744	+	Replication factor C small subunit / phage DNA polymerase clamp loader subunit	Nucleotide metabolism
31	29746	30309	+	Phage DNA polymerase clamp loader subunit Gp62	Nucleotide metabolism
32	30311	30679	+	Phage endoribonuclease translational repressor of early genes, <i>regA</i>	Nucleotide metabolism
33	31007	33703	+	DNA polymerase (EC 2.7.7.7), phage-associated	Nucleotide metabolism
34	34143	34523	+	Phage immunity	Additional functions
35	34531	34782	+	Phage immunity	Additional functions
36	36305	37147	+	Glucosyl transferase	Additional functions
37	37225	38406	+	Recombination protein	Nucleotide metabolism

(continued)

No	Start	Stop	Strand	Function	Group
38	38399	38743	+	Phage capsid and scaffold	Phage packaging
39	38753	40180	+	Phage DNA primase/helicase	Nucleotide metabolism
40	40239	40421	+	Discriminator of mRNA degradation, phage-associated	Nucleotide metabolism
41	42437	43465	+	DNA primase (EC 2.7.7.-) / DNA helicase (EC 3.6.1.-), phage-associated	Nucleotide metabolism
42	44675	44920	+	Phage capsid and scaffold	Phage packaging
43	46233	46397	+	Molybdenum ABC transporter	Additional functions
44	46390	46860	+	Molybdenum ABC transporter	Additional functions
45	46869	47051	+	Molybdenum ABC transporter	Additional functions
46	47119	47742	+	NAD--protein ADP-ribosyltransferase modA (EC 2.4.2.-)	Additional functions
47	47739	48341	+	NAD--protein ADP-ribosyltransferase modA (EC 2.4.2.-)	Additional functions
48	48458	49204	+	Putative anti-sigma factor	Nucleotide metabolism
49	49514	50833	+	DNA helicase (EC 3.6.1.-)	Nucleotide metabolism
50	51087	51332	+	Phage exonuclease	Nucleotide metabolism
51	51325	51567	+	Phage exonuclease	Nucleotide metabolism
52	51567	52250	+	Exonuclease	Nucleotide metabolism
53	52483	52971	+	Transcriptional regulator	Nucleotide metabolism
54	52988	53407	+	Transcriptional regulator	Nucleotide metabolism
55	53798	54013	+	cef modifier of suppressor tRNAs, phage-associated	Nucleotide metabolism
56	55320	57137	+	Phage DNA topoisomerase large subunit (EC 5.99.1.3)	Nucleotide metabolism
57	57192	57395	+	Phage rIIA lysis inhibitor	Host lysis
58	57406	59583	+	Phage rIIA lysis inhibitor	Host lysis
59	60565	60759	+	Phage endonuclease	Nucleotide metabolism
60	61139	61615	+	Phage endonuclease	Nucleotide metabolism
61	62907	63362	+	Phage nucleoid disruption protein Ndd (ACLAME 1102)	Nucleotide metabolism
62	63912	65240	+	DNA topoisomerase, phage-associated	Nucleotide metabolism
63	65237	65386	+	Transcriptional regulator	Nucleotide metabolism
64	65512	66147	+	Phage transcriptional regulator of middle promoters	Nucleotide metabolism
65	66158	66487	+	Phage anti-restriction nuclease	Nucleotide metabolism
66	67526	67804	+	Phage anti-restriction nuclease	Nucleotide metabolism
67	67966	68238	+	Phage anti-sigma factor	Nucleotide metabolism
68	68239	68895	-	Phage holin	Host lysis
69	68927	69712	-	Phage tail fibers	Structure
70	69743	73639	-	Phage tail fiber	Structure
71	73648	74313	-	Phage tail fibers	Structure
72	74376	75491	-	Phage long tail fiber	Structure
73	75500	79369	-	Phage long tail fiber	Structure

(continued)

No	Start	Stop	Strand	Function	Group
74	79474	80391	+	Phage ribonuclease H (EC 3.1.26.4)	Nucleotide metabolism
75	80400	80669	+	Phage double-stranded DNA binding protein	Nucleotide metabolism
76	80647	80985	+	Transcriptional regulator	Nucleotide metabolism
77	80982	81635	+	Phage DNA helicase loader	Nucleotide metabolism
78	81736	82644	+	Single stranded DNA-binding protein, phage-associated	Nucleotide metabolism
79	84044	84625	+	Dihydrofolate reductase, phage-associated	Additional functions
80	85037	85897	+	Thymidylate synthase (EC 2.1.1.45)	Additional functions
81	86455	88719	+	Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)	Nucleotide metabolism
82	88771	89949	+	Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1)	Nucleotide metabolism
83	89977	90387	+	Phage endonuclease	Nucleotide metabolism
84	90440	91564	+	RNA ligase	Nucleotide metabolism
85	91626	92132	+	Phage alc transcription terminator (ACLAME 1242)	Nucleotide metabolism
86	92473	92772	+	Phage outer membrane lipoprotein Rz1	Structure
87	93314	94222	+	3'-Phosphatase, 5'-polynucleotide kinase, phage-associated	Additional functions
88	96042	96623	+	dCMP deaminase (EC 3.5.4.12)	Additional functions
89	96623	96859	+	Phage tail fibers	Structure
90	96860	97168	+	Phage tail fibers	Structure
91	97225	97560	+	Phage head assembly chaperone protein	Phage packaging
92	98151	98327	+	1,4-alpha-Glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)	Additional functions
93	101343	102806	+	DNA ligase, phage-associated	Nucleotide metabolism
94	103044	105137	+	RNA polymerase-ADP-ribosyltransferase Alt	Nucleotide metabolism
95	107578	108543	-	Tail assembly protein	Phage packaging
96	108543	109637	-	Phage baseplate tail tube cap (T4-like gp48)	Structure
97	109646	111418	-	Phage baseplate hub	Structure
98	111415	111873	-	Phage baseplate hub	Structure
99	111893	113068	-	Baseplate hub subunit	Structure
100	113068	113817	-	Phage baseplate	Structure
101	113868	114494	+	Phage baseplate hub	Structure
102	114494	114892	+	Phage baseplate wedge subunit (T4-like gp25)	Structure
103	114959	115372	+	Single stranded DNA-binding protein, phage-associated	Nucleotide metabolism
104	115845	116075	-	Phage DNA helicase	Nucleotide metabolism
105	116790	118298	-	Phage DNA helicase	Nucleotide metabolism
106	118301	118918	-	Phage-associated homing endonuclease	Nucleotide metabolism
107	119658	121076	+	Capsid and scaffold protein	Phage packaging
108	121655	122659	+	RNA ligase	Nucleotide metabolism
109	122689	123972	-	Capsid vertex protein	Structure

(continued)

No	Start	Stop	Strand	Function	Group
110	124056	125621	-	Major capsid protein	Structure
111	125640	126449	-	Phage prohead assembly (scaffolding) protein	Phage packaging
112	126480	127118	-	Phage prohead assembly (scaffolding) protein	Phage packaging
113	127118	127543	-	Phage capsid and scaffold	Phage packaging
114	127543	127785	-	Phage prohead core protein	Phage packaging
115	127785	129359	-	Phage portal vertex of the head	Phage packaging
116	129443	129934	-	Phage tail tube protein	Structure
117	130051	132030	-	Phage tail sheath	Structure
118	132062	133894	-	Phage terminase, large subunit	Phage packaging
119	133878	134372	-	Phage terminase, small subunit	Phage packaging
120	134381	135199	-	Tail sheath stabilizer and completion protein	Phage packaging
121	135241	136011	-	Phage neck protein	Structure
122	136013	136942	-	Phage neck protein	Structure
123	136975	138438	-	Phage fibritin (wac) protein	Structure
124	138435	140018	-	Tail fiber	Structure
125	140015	140674	-	Baseplate wedge subunit and tail pin	Structure
126	142482	143348	-	Phage baseplate wedge tail fiber connector (T4-like gp9)	Structure
127	143412	144416	-	Phage baseplate wedge subunit (T4-like gp8)	Structure
128	144409	147507	-	Phage baseplate wedge initiator (T4-like gp7)	Structure
129	147504	149486	-	Phage baseplate wedge subunit (T4-like gp6)	Structure
130	149495	149788	-	Phage-encoded phospholipase (ACLAME 172)	Host lysis
131	150318	152045	-	Phage baseplate hub structural protein / phage lysozyme R (EC 3.2.1.17)	Host lysis/Structure
132	152029	152619	-	Baseplate wedge subunit	Structure
133	152667	153119	+	Phage head completion protein	Phage packaging
134	153119	153946	+	DNA end protector protein	Nucleotide metabolism
135	153943	154602	+	Phage-associated homing endonuclease	Nucleotide metabolism
136	154709	155239	+	Phage tail completion protein	Phage packaging
137	155289	156002	+	Deoxynucleoside monophosphate kinase	Additional functions
138	156002	156244	+	Phage tail fiber assembly protein	Phage packaging
139	157106	157339	+	Phage internal (core) protein	Structure
140	159476	160141	+	Phage-associated homing endonuclease	Nucleotide metabolism
141	162224	162817	+	Phage host specificity protein (ACLAME 1259)	Host lysis
142	164651	165091	+	Nudix hydrolase, phage-associated	Additional functions
143	165129	165623	+	Phage lysozyme R (EC 3.2.1.17)	Host lysis
144	167193	167438	+	Pyruvate formate-lyase (EC 2.3.1.54)	Additional functions

Supplementary references

- Amarillas L, Chaidez C, Gonzalez-Robles A, Lugo-Melchor Y, León-Félix J. Characterization of novel bacteriophage phic119 capable of lysing multidrug-resistant shiga toxin-producing *Escherichia coli* O157:H7. *PeerJ*, 4, e2423 (2016)
- Duc HM, Son HM, Yi HPS, Sato J, Ngan PH, Masuda Y, Honjoh KI, Miyamoto T. Isolation, characterization and application of a polyvalent phage capable of controlling *Salmonella* and *Escherichia coli* O157:H7 in different food matrices. *Food Res Int*, 131, 108977 (2020)
- Hamdi S, Rousseau GM, Labrie SJ, Tremblay DM, Kourda RS, Ben Slama K, Moineau S. Characterization of two polyvalent phages infecting *Enterobacteriaceae*. *Sci Rep*, 7, 1-12 (2017)
- Lee H, Ku HJ, Lee DH, Kim YT, Shin H, Ryu S, Lee JH. Characterization and genomic study of the novel bacteriophage HY01 infecting both *Escherichia coli* O157:H7 and *Shigella flexneri*: Potential as a biocontrol agent in food. *PLoS One*, 11, e0168985 (2016)
- Park M, Lee JH, Shin H, Kim M, Choi J, Kang DH, Heu S, Ryu S. Characterization and comparative genomic analysis of a novel bacteriophage, SFP10, simultaneously inhibiting both *Salmonella enterica* and *Escherichia coli* O157:H7. *Appl Environl Microbiol*, 78, 58-69 (2012)
- Saad AM, Soliman AM, Kawasaki T, Fujie M, Nariya H, Shimamoto T, Yamada T. Systemic method to isolate large bacteriophages for use in biocontrol of a wide-range of pathogenic bacteria. *J Biosci Bioeng*, 127, 73-78 (2019)
- Sui B, Han L, Ren H, Liu W, Zhang C. A novel polyvalent bacteriophage vB_EcoM_Swi3 infects pathogenic *Escherichia coli* and *Salmonella* Enteritidis. *Front Microbiol*, 12, 649673 (2021)