

Supplementary method S1

Adsorption assay of KFS-EC3

Adsorption assay of KFS-EC3 was performed as previously described by Kim et al. (2018) with minor modification [1]. Briefly, KFS-EC3 was mixed with a culture of *E. coli* O157:H7 ATCC 10536 (10^8 CFU/mL) at an equivalent volume ratio to obtain a multiplicity of infection (MOI) of 0.001 and incubated at 37 °C for 8 min at 110 rpm. A 1 mL aliquot of the mixture was collected at every 2-min interval and centrifuged at $12,000 \times g$ for 30 s at 4 °C. The supernatant containing the non-adsorbed phage was immediately filtered using a 0.20- μ m cellulose acetate filter and the filtrate that was obtained was used for phage titer determination using a plaque assay as described in section 2.2. The experiment was conducted in triplicates and the adsorption rate was calculated using the following equation:

Adsorption rate (%) = (average phage titer at each time interval) / (average phage titer at time 0) \times 100

Supplementary method S2

Polyvalent lytic capacity of KFS-EC3 against various host strains

For comparing the polyvalent lytic capacity of KFS-EC3 phage against each target bacterium and bacterial cocktail, KFS-EC3 (10^7 PFU/mL) was added to each bacterial suspension of *E. coli* O157:H7 ATCC 10536, *Salmonella* Mission, and *Shigella sonnei* ATCC 9290 and the cocktail (1:1:1, v/v) at an MOI of 1.0. SM buffer was added in the control instead of using the phage. Following incubation at 37 °C with gentle shaking for 4 h, the bacterial number was counted using xylose lysine deoxycholate (XLD, Difco Laboratories Inc.) and eosin methylene blue (EMB, Difco Laboratories Inc.) agar plates for comparison.

[Supplementary data]

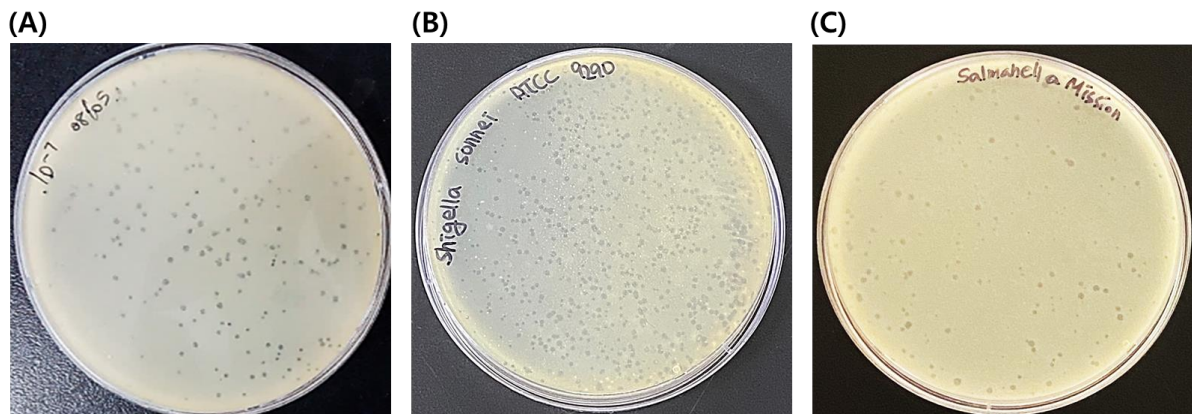


Figure S1. Plaque morphology of KFS-EC3 against (A) the indicator strain, (B) *Shigella sonnei*, and (C) *Salmonella* Mission.

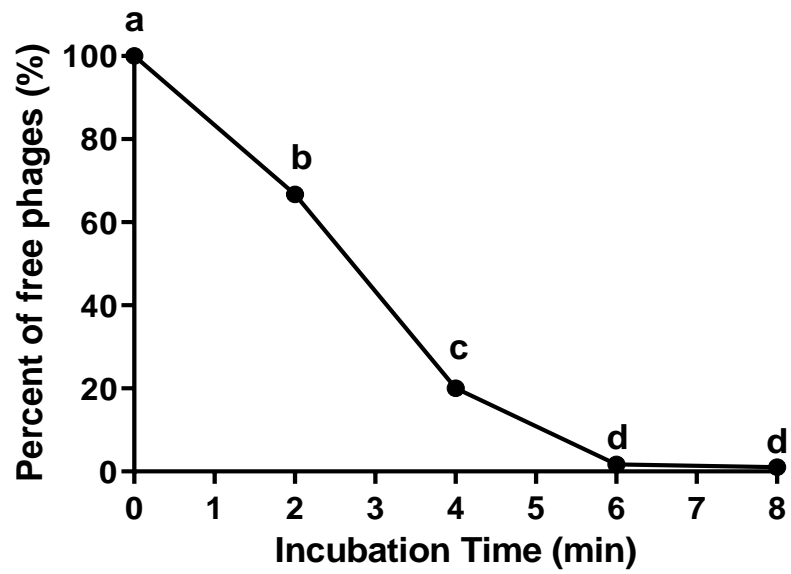


Figure S2. Adsorption assay of KFS-EC3.

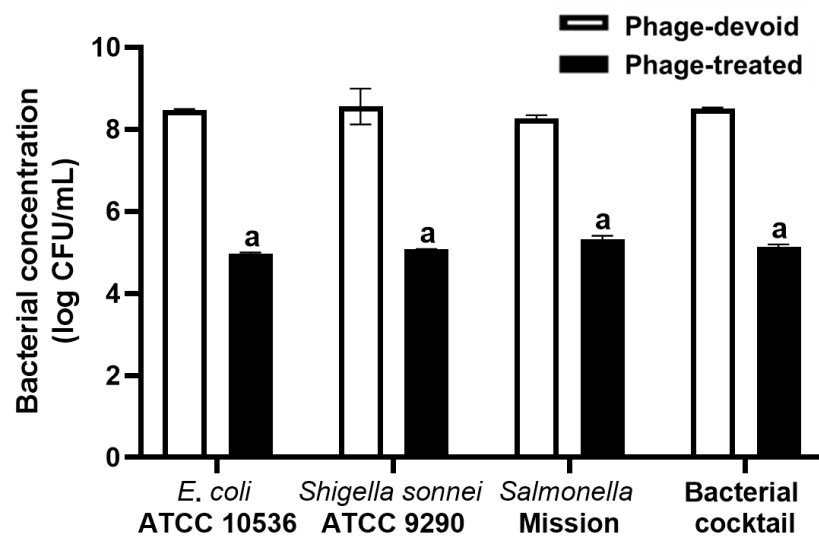


Figure S3. Polyvalent lytic capacity of KFS-EC3 after its exposure to each bacterium and their cocktail at an MOI of 1.0.

Table S1. Several reported broad and narrow spectrum phages infecting *E. coli*

Phage	Host strain	Classification	Size of length (nm)		Specificity	Eclipse period (min)	Latent period (min)	Burst size (PFU/cell)	Reference
			Head	Tail					
KFS-EC3	<i>E. coli</i> O157:H7 ATCC 10536	<i>Myoviridae</i>	96.35	68.42–133.48	Polyvalent (3 genera)	5	20	71	This study
SFP10	<i>E. coli</i> O157:H7 ATCC 43890	<i>Myoviridae</i>	68.75	41.67–131.25	Polyvalent (2 genera)	15	25	100	[2]
HY01	<i>E. coli</i> O157:H7 ATCC 43890	<i>Myoviridae</i>	100	100	Polyvalent (2 genera)	5	25	25	[3]
PS5	<i>S. Typhimurium</i> NBRC12529	<i>Myoviridae</i>	84	106	Polyvalent (2 genera)	-	25	204	[4]
PEf1	<i>E. coli</i> K-12	<i>Siphoviridae</i>	-	-	Polyvalent (2 genera)	-	50	99	[5]
phiC119	<i>E. coli</i> O157 EC-48	<i>Siphoviridae</i>	43	168	Polyvalent (2 genera)	-	20	210	[6]
SH6	<i>Shigella flexneri</i> SF1	<i>Siphoviridae</i>	62 ± 2	161 ± 2	Polyvalent (2 genera)	-	16	103 ± 16	[7]
vB_EcoM_swi3	<i>E. coli</i> K88	<i>Myoviridae</i>	80	120	Polyvalent (2 genera)	-	25	25	[8]
EcS1	<i>E. coli</i> BL21	<i>Myoviridae</i>	111 ± 5.5	110 ± 5.5	Polyvalent (3 genera)	-	-	-	[9]
SH7	<i>S. flexneri</i> SF1	<i>Myoviridae</i>	112 ± 5	116 ± 4	Polyvalent (3 genera)	-	23	26 ± 5	[7]
T4 Yer mutants	<i>E. coli</i> K-12	<i>Myoviridae</i>	-	-	Polyvalent (3 genera)	-	-	-	[10]
KFS-EC	<i>E. coli</i> O157:H7 ATCC 43895	<i>Myoviridae</i>	100	113	Narrow	5	30	150	[11]
CBA120	<i>E. coli</i> O157:H7 NCTC 12900	<i>Myoviridae</i>	90	105	Narrow	20	40	440	[12]
CEV1	<i>E. coli</i> O157:H7 NCTC 12900	<i>Myoviridae</i>	100	100	Narrow	18	26	150	[13]
FAHEc1	<i>E. coli</i> O157:H7 isolate ERL 022447	<i>Myoviridae</i>	99	108	Narrow	-	-	-	[14]
rV5	<i>E. coli</i> O157:H7 strain R508	<i>Myoviridae</i>	91	121	Narrow	-	-	-	[15]
vB_EcoS_ACG-C40	<i>E. coli</i> isolate Can 40	<i>Myoviridae</i>	110	114	Narrow	-	-	-	[16]
vB_EcoS_ACG-C91	<i>E. coli</i> isolate Can 91	<i>Podoviridae</i>	65–68	12	Narrow	-	-	-	[16]
vB_EcoS_ACG-M12	<i>E. coli</i> isolate MSHS1210	<i>Siphoviridae</i>	57	172	Narrow	-	-	-	[16]
Φ241	<i>E. coli</i> O157:H7 strain B0241	<i>Myoviridae</i>	80	33	Narrow	-	15	53	[17]
vB-EcoS_Rogue1	<i>E. coli</i> O157:H7 R508N	<i>Siphoviridae</i>	53	152	Narrow	-	-	-	[18]
vB_EcoS_HSE2	<i>E. coli</i> strain 40371	<i>Siphoviridae</i>	56	178	Narrow	-	30	86	[19]
Vb_EcoS_B2	<i>E. coli</i> BL21	<i>Siphoviridae</i>	48	143	Narrow	-	30	224	[20]
vB_EcoM_IME339	<i>E. coli</i> BL21	<i>Myoviridae</i>	-	-	-	-	-	91	[21]
Teqskov	<i>E. coli</i> K-12 MG1655	<i>Myoviridae</i>	-	-	-	-	-	-	[22]
Teqhal	<i>E. coli</i> K-12 MG1655	<i>Myoviridae</i>	-	-	-	-	-	-	[22]
Slur08	<i>E. coli</i> K-12 MG1655	<i>Myoviridae</i>	-	-	-	-	-	-	[23]
Slur03	<i>E. coli</i> K-12 MG1655	<i>Myoviridae</i>	-	-	-	-	-	-	[23]
phiLLS	<i>E. coli</i> O157:H7 CECT 4076	<i>Siphoviridae</i>	56	135	-	-	70	176	[24]

Table S2. General genomic characteristics of KFS-EC3 and phylogenetically related phages

Phage	Host	Genome (bp)	GC content (%)	Taxonomy (Family; Genus)	Identity (%)	Accession number
KFS-EC3	<i>E. coli</i> O157:H7 ATCC 10536	166,440	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	-	MZ065353
Slur13	<i>E. coli</i> K-12 MG1655	167,299	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.24	LN881737.1
Slur04	<i>E. coli</i> K-12 MG1655	167,298	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.24	NC042130.1
Slur11	<i>E. coli</i> K-12 MG1655	167,298	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.24	LN881734.1
Teqhal	<i>E. coli</i> MG1655 K-12	168,070	35.1	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.28	MN895435.1
Teqsoen	<i>E. coli</i> K-12 MG1655	166,468	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.00	MN895436.1
Kha5h	<i>E. coli</i> O103:H2	167,318	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.35	KT184312.1
Shfl2	<i>Shigella flexneri</i>	165,919	35.6	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	97.47	HM035025.1
ime09	<i>E. coli</i>	166,499	35.7	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	98.04	JN202312.1
vB_EcoM_IME339	<i>E. coli</i> BL21	164,366	35.6	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	97.71	MH051915.1
vB_EcoM_G50	<i>E. coli</i>	167,728	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	97.74	MK327942.1
vB_EcoM_KAW1E185	<i>E. coli</i>	164,987	35.4	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.56	MK373781.1
Teqskov	<i>E. coli</i> MG1655 K-12	165,017	35.4	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.69	MN895437.1
phiD1	<i>Yersinia pestis</i>	167,063	35.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.81	HE956711.1
vB_EcoM_Ozark	<i>E. coli</i> (STEC)	167,600	39.5	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.49	MT682713.1
Slur08	<i>E. coli</i> K-12 MG1655	167,467	35.4	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.12	LN881733.1
Slur14	<i>E. coli</i> K-12 MG1655	167,467	35.4	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.13	LN881736.1
Slur03	<i>E. coli</i> K-12 MG1655	167,467	35.4	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.12	NC042129.1
PhiZZ30	<i>Serratia</i> sp. ATCC 39006	167,484	35.3	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.25	MT176426.1
vB_EcoM_Lutter	<i>E. coli</i> (STEC)	170,054	35.4	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.39	MT682714.1
T4	<i>E. coli</i> B strain	168,908	35.3	<i>Myoviridae</i> ; <i>Tequatrovirus</i>	96.23	MT984581.1

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