

Supplementary Materials

Table S1. *E. coli* strains and 4HA13 Host Range.

	Serotype	AMR	Strain Number	Isolation Source	Source	Host Range	
						PHIDA	EOP
Generic <i>E. coli</i>	O2:H7	N/A	HA2018074	Human UTI	AAFC	N	0%
	O25:H4	N/A	HA2018075	Human UTI	AAFC	N	0%
	O28:NM	N/A	HA2018076	Human UTI	AAFC	N	0%
	O82:DM3Na	N/A	HA2018076	Unknown	AAFC	N	0%
	O114:H4	N/A	HA2018078	Human UTI	AAFC	N	0%
	DH5- α	N/A	HA2018027	Unknown	AAFC	D	0%
STEC	O26:H11	N/A	HA2018016	Bovine feces	PHAC-NML at Guelph	N	0%
	O26:H11	N/A	HA2018085	Human	PHAC-NML at Guelph	N	0%
	O45:H2	N/A	HA2018020	Bovine feces	PHAC-NML at Guelph	N	0%
	O103:H2	N/A	HA2018017	Bovine feces	PHAC-NML at Guelph	N	0%
	O103:H2	N/A	HA2018084	Human	PHAC-NML at Guelph	N	0%
	O111:NM	N/A	HA2018015	Bovine feces	PHAC-NML at Guelph	D+, 13 h	100%
	O111:H8	N/A	HA2018083	Bovine	PHAC-NML at Guelph	NL++, 18%	1%
	O121:H19	N/A	HA2018019	Human	PHAC-NML at Guelph	N	0%
	O145:NM	N/A	HA2018018	Bovine feces	PHAC-NML at Guelph	N	0%
	O157:H7	N/A	HA2018013		ATCC700927	N	0%
	O157:H7	N/A	HA2018079	Human UTI	AAFC	N	0%
Antimicrobial-resistant <i>E. coli</i>	N/A	AMP, CHL, SIX, STR, SXT, TET	HA2018155	Unknown	PHAC-NML at Guelph	N	0%
	N/A	AMP, CHL, CIP, GEN, NAL, SIX, SXT, TET	HA2018160	Unknown	PHAC-NML at Guelph	N	0%
	N/A	AMP, CRO, GEN, STR, SIX, SXT, TET	HA2018163	Unknown	PHAC-NML at Guelph	N	0%
	N/A	AMC, AMP, FOX, CRO, CHL, GEN, SIX, STR, SXT, TET	HA2018164	Unknown	PHAC-NML at Guelph	N	0%

	N/A	TET	HA2018166	Unknown	PHAC-NML at Guelph	N	0%
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*Antibiotics: AMC=amoxicillin/clavulanic acid, AMP=Ampicillin,
 CHL=Chloramphenicol, CIP=ciprofloxacin, CRO=ceftriaxone,
 FOX=cefoxitin, GEN=gentamicin, NAL=nalidixic acid, SIX= sulfisoxazole,
 STR=streptomycin, SXT=trimethoprim/sulphamethoxazole,
 TET=tetracycline

C=completion inhibition of bacterial growth, D+=more than a 5-hour delay
 in initial detection of bacterial growth, D=less than a 5-hour delay, NL+=no
 delay on detection, but final optical density is less than 40% of control,
 N=no effect.

Table S2. Protein identification of 4HA13 by tryptic digestion and LC MS/MS analyses.

Protein name	NCBI accession number	Predicted mass	Sequence coverage (90 min LC run)	Sequence coverage (180 min LC run)
hypothetical protein AC4HA13_0057	gi 1735348866 gb QEM4 3028.1	16478	100%*@	100%*@
hypothetical protein AC4HA13_0070	gi 1735348883 gb QEM4 3045.1	13788	80%	80%
tail tube protein	gi 1735348877 gb QEM4 3039.1	16516	77%	76%
tail completion protein	gi 1735348875 gb QEM4 3037.1	19408	76%§	76%§
major capsid protein	gi 1735348871 gb QEM4 3033.1	37186	71%§	86%§
major head subunit precursor	gi 2062562666 gb QEM4 3027.2	38825	69%	61%
tail sheath protein	gi 1735348876 gb QEM4 3038.1	51283	66%	66%
tail tape measure protein	gi 1735348880 gb QEM4 3042.1	128217	64%	67%
single-stranded DNA-binding protein	gi 1735348822 gb QEM4 2984.1	13146	62%	62%
hypothetical protein AC4HA13_0060	gi 1735348872 gb QEM4 3034.1	16555	60%	61%
head-tail adaptor protein	gi 1735348874 gb QEM4 3036.1	13877	60%	60%
baseplate wedge protein	gi 1735348885 gb QEM4 3047.1	13468	58%*@	57%*@
hypothetical protein AC4HA13_0029	gi 1735348838 gb QEM4 3000.1	12922	53%	53%
hypothetical protein AC4HA13_0050	gi 1735348859 gb QEM4 3021.1	15743	52%	38%
hypothetical protein AC4HA13_0041	gi 1735348850 gb QEM4 3012.1	9546	50%	50%

* The N-terminal methionine are deleted in the protein sequences.

@ Acetylation at the N-terminus of the protein

§ Lysine acetylation of proteins: major capsid protein (peptide 262-269 at residues IKGLNAIK at m/z 449.7904); tail completion protein (peptide 37-56 at residues GDYAAIKCVSSLNPGFDENR at m/z 1128.0223)