

Electronic Supplementary Material

Characterization and complete genome sequence of vB_EcoP-Bp4, a novel polyvalent N4-like bacteriophage that infects chicken pathogenic *Escherichia coli*

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Supporting information to DOI: 10.1007/s12250-016-3787-4

Table S1. *E. coli* strains used for determination of vB_EcoP-Bp4 host range in this study

Number*	Strain	Sero-type	Infec-tivity	Inhibition zone to drugs (mm)							
				Cepha-zolin	Strepto-mycin	Amika-cin	Genta-mycin	Ciproflo-xacin	Norflox-acin	Tobra-mycin	Erythro-mycin
1	HL041025A	O24	N ^a	7	13	22	15	7	-	-	-
2	CH041025A	O15	N	-	12	8	12	16	14	9	7
3	ZC041025A	O78	N	22	12	30	26	13	14	16	-
4	H041027A	O88	C ^b	18	-	22	20	8	-	18	11
5	C041027B	X	C	-	7	19	25	8	7	15	7
6	EC041029A	O78	C	24	7	24	26	14	7	30	-
7	EH041029B	O78	N	21	10	25	30	10	7	24	-
8	C041029A	O78	C	22	-	24	24	15	10	25	-
9	H041029	O78	N	24	-	26	22	17	11	20	10
10	L041030A	O78	N	23	8	27	-	15	8	21	-
11	Z041030B	O1	N	26	-	26	26	14	12	21	-
12	EZ041122A	O73	N	-	12	24	17	-8	8	14	-
13	EZ041030B	O78	N	22	20	27	24	-	8	22	-
14	L041030B	O78	N	18	15	23	28	13	-	22	-
15	L041030C	O78	N	20	-	20	-	14	14	17	-
16	H041103A	O23	N	16	13	18	19	-	-	20	-
17	H041103D	O88	N	13	8	23	8	7	-	17	-
18	H041104A	O24	N	23	-	21	-	9	-	13	-
19	Z041108E	O15	C	24	11	7	-	-	-	-	10
20	EH041110D	X	C	22	10	26	-	17	-	18	8
21	ER041118B	X	C	-	-	25	10	12	-	17	-
22	G041126A	O93	N	22	12	20	15	11	13	13	-
23	ER041118C	X	C	17	-	22	18	11	9	15	-
24	ER041118B	X	N	19	14	19	19	13	11	17	-
25	BL21	/	N	U	U	U	U	U	U	U	U
26	JM109	/	N	U	U	U	U	U	U	U	U
27	JM110	/	N	U	U	U	U	U	U	U	U
28	DH5 α	/	C	U	U	U	U	U	U	U	U

Note: * Strains that numbered 1-24 were isolated from diseased chicken organs and identified as *E. coli* in 2004 and were multi-resistant to antibiotics at different levels. Strains that numbered 25–28 are laboratory *E. coli* strains used widely in gene engineering operation. -: no Inhibition zone to the drug. U: drug sensitivity test on these strains was not done; N^a: no lysis; C^b: clear lysis.

Table S2. Genome annotation of phage vB_EcoP-Bp4

ORF	Start	Stop	Size(bp)	Hypothetical protein	Molecular mass (kDa)	No. of amino acids	Identities (%)						
							KBNP21	IME11	pSb-1	EC1-UPM	vB_EcoP-G7C	N4	phAPEC5
1	2	268	267	hypothetical protein	9.65	89	100	96.6	90.4	97.8	94.4	82	-
2	470	796	327	hypothetical protein	12.71	109	93.9	72.7	59.1	56.8	-	-	68.7
3	793	948	156	hypothetical protein	6.17	52	96.1	-	-	-	-	-	96.1
4	1076	1249	174	hypothetical protein	6.26	58	90.9	-	87.3	85.5	80.8	-	90.7
5	1396	1698	303	hypothetical protein	11.6	101	86	82	86.9	88	89	-	85
6	1685	2074	390	hypothetical protein	15.05	130	93.9	90.8	88.5	84.6	90	-	90.8
7	2274	2564	291	hypothetical protein	11.17	97	91.7	93.5	97.8	96.7	91.3	54.1	91.3
8	2734	3423	690	hypothetical protein	25.62	230	100	100	100	-	99.1	78	99.6
9	3416	5005	1590	terminase subunit A	60.77	530	100	99.6	99.8	99.8	99.6	92.3	99.6
10	5012	5722	711	putative tail protein	27.04	237	100	74.4	100	99.6	100	69.9	99.6
11	5713	7515	1803	tail fiber protein	64.65	601	75.3	57.1	79.1	93.4	85.9	-	90.5
12	7521	8435	915	hypothetical protein	31.9	305	-	-	-	-	-	-	-
13	8484	10598	2115	tail spike protein	74.33	705	98.7	-	86.4	98.3	63.3	-	86.5
14	10629	11282	654	hypothetical protein	23.52	218	96.7	-	95.2	-	-	-	-
15	11380	11709	330	tail length tape-measure protein	12.43	110	99.1	89.1	98.2	96.8	87.9	83.9	87.1
16	11694	11954	261	putative holin protein	10.04	87	-	95.3	97.7	98.8	90.7	82.9	-
17	11944	12579	636	putative N-acetylmuramidase	22.82	212	99.5	98.4	100	-	97.8	85.2	98.4
18	12842	13066	225	putative Rz/RzI spanin protein	8.61	75	100	98.6	-	100	98.6	88.9	98.6
19	13069	15339	2271	portal protein	85.18	757	99.7	98.7	99.5	99.7	98	85.8	98.8
20	15353	15697	345	hypothetical protein	12.83	115	100	96.5	-	-	99.1	70.5	96.5
21	15717	16937	1221	tape measure protein	44.45	407	100	97	98.7	98.3	97.8	71.5	97
22	16954	18156	1203	major coat protein	44.13	401	100	99.3	99.3	100	99.8	94	99.5
23	18230	18865	636	hypothetical protein	23.65	212	99.5	98.1	99	98.6	97.6	75	96.2
24	18942	19778	837	putative structural protein	30.4	279	100	89.6	99.3	97.8	97.8	76.5	99.3
25	19780	20916	1137	hypothetical protein	41.78	379	98.4	98.4	98.9	99.2	96.5	66.6	98.4
26	21108	22433	1326	hypothetical protein	48.07	442	99.8	95.9	98.4	96.6	95.7	73.4	97.7
27	22447	22890	444	structural protein	15.63	148	98.6	98	97.6	88.6	82.4	68.7	98.6

To be continued

ORF	Start	Stop	Size(bp)	Hypothetical protein	Molecular mass (kDa)	No. of amino acids	Identities (%)						
							KBNP21	IME11	pSb-1	EC1-UPM	vB_EcoP-G7C	N4	phAPEC5
28	22903	23769	867	structural protein	31.25	289	83.3	89.2	82.3	83	88.9	67.7	90
29	23766	24029	264	structural protein	9.52	88	81.5	97.5	81.5	81.5	100	86.4	97.5
30	24026	24862	837	structural protein	30.3	279	66.8	97.1	67.5	64.2	100	58.9	97.5
31	24956	35668	10713	virion RNA polymerase	389.53	3571	98.5	97.5	99.2	94.4	93.8	82.3	97.3
32	35703	36194	492	hypothetical protein	18.87	164	99.4	84.8	-	-	-	94.3	95.1
33	36313	36693	381	hypothetical protein	13.79	127	100	67.5	-	96.8	-	69.9	98.4
	37083	37010		tRNA									
	37862	37787		tRNA									
34	38611	38811	201	hypothetical protein	7.5	67	100	-	98.1	-	94.4	-	-
35	39046	39486	441	hypothetical protein	15.92	147	100	97.9	95.9	95.9	94.5	-	94.5
36	39488	40042	555	hypothetical protein	20.03	185	100	98.9	99.5	-	98.9	81.9	99.5
37	40042	40845	804	ssDNA-binding protein	28.83	268	100	98.7	98.4	98.7	95.7	73.2	95.7
38	40885	41637	753	hypothetical protein	28.57	251	100	99.2	-	99.2	99.2	88.8	99.2
39	41694	43586	1893	DNA primase	72.36	631	98.7	98.6	-	98.6	98.3	88	98.1
40	43583	43726	144	DNA primase	4.76	48	93.5	93.5	93.5	93.5	93.5	93.5	93.5
41	43843	44823	981	hypothetical protein	37.65	327	100	98.5	98.6	99.4	97.5	82.4	97.5
42	44820	45317	498	HNH homing endonuclease	19.02	166	100	-	-	96.9	99.4	-	63.3
43	45389	45865	477	hypothetical protein	18.5	159	100	72.6	98.7	98.7	80.8	89.3	82.6
44	45865	46170	306	hypothetical protein	11.6	102	100	100	100	100	98	73	98
45	46167	46661	495	DNA polymerase	18.61	165	100	99.4	99.4	100	100	92	100
46	46948	48633	1686	DNA polymerase	-	-	100	99.8	100	99.4	99.6	81.3	99.6
47	48753	49283	531	hypothetical protein	64.9	562	100	99.4	100	98.9	97.7	7108	96.6
48	49294	50604	1311	DNA helicase	19.95	177	100	99.3	99.3	99.5	99.3	81.9	99.3
49	50638	50976	339	hypothetical protein	48.93	437	100	99.1	80	79.8	76.4	98.5	69.9
50	51023	51418	396	hypothetical protein	12.1	113	100	100	99.1	97.7	95.4	87	96.2
51	51481	53529	2049	rIB-like protein	14.96	132	99.4	92.3	94	90.7	90.9	67.4	92.3
52	53534	53779	246	rIIA-like protein	75.73	683	96.3	95.1	96.3	92.6	86.3	-	86.3

ORF	Start	Stop	Size(bp)	Hypothetical protein	Molecular mass (kDa)	No. of amino acids	Identities (%)						
							KBNP21	IME11	pSb-1	EC1-UPM	vB_EcoP-G7C	N4	phAPEC5
53	53881	55263	1383	riIA-like protein	-	-	98.5	93.9	93.9	96.1	90.4	54.3	92.4
54	55281	56099	819	riIA-like protein	-	-	97	97.7	95.8	97.3	95.4	75.8	94.7
55	56127	56318	192	hypothetical protein	29.86	273	100	-	-	-	-	-	100
56	56311	56637	327	hypothetical protein	7.23	64	100	98.1	99.1	89.9	87.4	75.9	88
57	56630	56842	213	hypothetical protein	11.54	109	100	100	100	100	97.1	62.2	70.7
58	56902	57117	216	hypothetical protein	7.85	71	100	88.7	65.7	98.6	65.7	-	65.7
59	57137	58081	945	thymidilate synthase	8.6	72	97.5	94.9	96.4	93.6	88.9	81.4	90.4
60	58081	58524	444	hypothetical protein	35.89	315	99.3	98	98.6	95.9	95.2	51.7	96.6
61	58524	58904	381	hypothetical protein	17.17	148	87.5	85.2	66.9	89.7	-	62.3	86.7
62	59060	59263	204	putative membrane immunity protein	14.88	127	96.9	96.9	98.5	100	98.4	-	98.4
63	59337	59546	210	hypothetical protein	7.52	68	95.7	91.3	67.2	-	66.7	-	53.8
64	59556	60062	507	dCTP deaminase	18.81	169	97.6	98.8	98.8	70	98.8	76.2	69.3
65	60062	60580	519	hypothetical protein	19.76	173	99.4	98.8	98.8	98.8	99.4	77.8	98.8
66	60635	61234	600	hypothetical protein	22.97	200	100	96.5	95.1	97.7	97.7	72	97.1
67	61234	61545	312	hypothetical protein	11.66	104	-	-	60.4	-	74.8	-	-
68	61720	61953	234	hypothetical protein	8.88	78	97.4	100	98.7	97.4	98.7	68.1	98.7
69	61965	62771	807	hypothetical protein	-	-	100	100	100	99.5	100	85.5	100
70	62806	63135	330	hypothetical protein	11.78	110	96.5	98.8	98.8	98.8	61	-	58.5
71	63136	63321	186	hypothetical protein	6.62	62	100	98.4	96.7	98.4	98.4	-	95.1
72	63318	63527	210	hypothetical protein	7.62	70	98.6	98.6	-	98.6	-	-	-
73	63524	63784	261	hypothetical protein	10.09	87	90.6	-	-	90.7	-	-	-
74	63781	63969	189	hypothetical protein	6.91	63	100	-	65.6	98.4	98.4	-	93.5
75	64030	64290	261	hypothetical protein	8.93	87	-	95.3	-	-	-	-	-
76	64428	65261	834	capsid decorating protein	28.54	278	95.8	95.3	96.4	92.8	88.3	82.1	95.7
77	65335	65517	183	hypothetical protein	6.78	61	100	90	96.7	-	85.76	-	85.7
78	65575	66792	1218	RNAP2	45.9	406	100	99.5	100	99.5	93.6	81.2	93.8
79	66848	67009	162	hypothetical protein	6.19	54	98.1	100	-	-	-	-	98.1
80	66999	67817	819	RNAP1	31.99	273	99.3	99.3	98.1	98.2	98.5	81	98.2

ORF	Start	Stop	Size(bp)	Hypothetical protein	Molecular mass (kDa)	No. of amino acids	Identities (%)						
							KBNP21	IME11	pSb-1	EC1-UPM	vB_EcoP-G7C	N4	phAPEC5
81	67871	68131	261	hypothetical protein	10.29	87	90.7	90.7	-	90.7	-	-	96.5
82	68128	68511	384	hypothetical protein	14.04	128	66.1	67	67.8	67	67.8	82.5	96
83	68588	68692	105	hypothetical protein	3.98	35	-	-	-	-	-	100	93.3
84	68689	68832	144	hypothetical protein	5.39	48	-	-	-	-	-	-	95.7
85	68930	69310	381	hypothetical protein	14.09	127	94.4	95.2	95.2	-	91.3	95	95
86	69307	69621	315	hypothetical protein	12.09	105	97.1	-	97.1	97.1	89.4	90.3	91.3
87	69618	69809	192	hypothetical protein	7.07	64	100	-	-	-	-	-	-
88	69806	70063	258	hypothetical protein	9.77	86	100	94	95.2	91.7	76.2	-	77.4
89	70060	70281	222	hypothetical protein	8.71	74	100	91.8	91.8	93.2	94.5	-	97.3
90	70287	70517	231	hypothetical protein	8.67	77	100	-	-	-	-	-	88.2
91	70510	70818	309	hypothetical protein	11.44	103	99	96	96.1	96.1	95	82.4	-
92	70897	71025	129	hypothetical protein	4.94	43	100	59.6	92.9	90.5	90.5	66	62.1
93	71010	71192	183	hypothetical protein	7.25	61	100	77.2	98.3	98.3	96.4	-	-
94	71189	71377	189	hypothetical protein	7.55	63	100	63.9	-	100	-	-	61.3
95	71518	71898	381	RNAP1 subunit A	14.03	127	99.2	94.5	92.8	100	94.5	84.4	94.5