



Research Article

Isolation of Novel Carbapenem-Resistant *Klebsiella pneumoniae* (CRKP) ST 147 Phage RMN1

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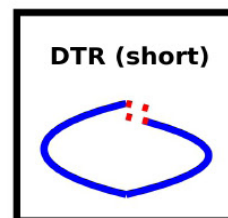
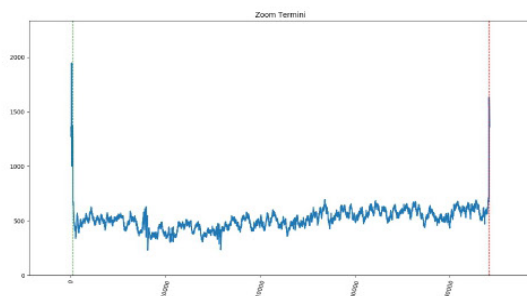
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Keywords | *Klebsiella pneumoniae*, Carbapenem-resistant *K. pneumoniae*, Bacteriophage, Phage therapy, Whole genome sequence



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PhageTerm Method

Ends	Left (red)	Right (green)	Permuted	Orientation	Class	Type
Redundant	44162	213	No	NA	DTR (short)	T7

*Direct Terminal Repeats: 278 bp

Strand	Location	T	pvalue	T (Start. Pos. Cov. / Whole Cov.)
+	44162	0.61	3.75e-163	
	7951	0.44	1.79e-79	
	15667	0.32	2.97e-42	
	10662	0.26	1.41e-31	
	23535	0.16	8.17e-25	
-	213	0.57	3.13e-15	
	7948	0.05	2.56e-01	
	7945	0.05	1.42e-01	
	361	0.04	1.00e+00	
	7950	0.03	1.00e+00	

Li's Method

Packaging	Termini	Forward	Reverse	Orientation
COS	Fixed	Obvious Termini	Obvious Termini	Forward

*Direct Terminal Repeats: 276 bp

Strand	Location	SPC	R	SPC
+	44162	904	3.0	
	7951	288	-	
	15667	155	-	
	10662	117	-	
	23535	93	-	
-	213	609	24.0	
	205	25	-	
	201	22	-	
	7945	19	-	
	7948	18	-	

Supplementary Figure S1: Determination of phage RMN1 termini and packaging based on PhageTerm.

Supplementary Table S1: *Phenotypic and genotypic characterization of clinical CRKP host isolate 032U (ST147).*

No	Isolate report	Result		
Phenotypic characterization				
1	Antimicrobial re- sistance profile	Antibiotic (Code)	Interpretation (S/I/R)	Resistance (%)
		AK	S	0
		AMC	I	100
		AMP	R	100
		AZT	R	100
		CAZ	R	100
		CIP	R	100
		CRO	R	100
		CTX	R	100
		FEP	R	100
		GEN	S	0
		IMI	S	0
		MEM	S	0
		KZ	R	100
		LEV	R	100
		MXF	R	100
		PIP	R	100
		PTZ	S	0
		SAM	R	100
		SCF	I	100
		SXT	R	100
		TET	R	100
		TGC	R	100
		NITRO	R	100
Genotypic characterization				
2	K locus	KL 128		
3	O locus	OL3y		
4	Predicted O type	O3y		
5	wzi	Wzi99		
6	Antimicrobial resist- ance	Drug/Class	Resistance genes	
		Aminoglycosides	strB, aph3-Ia, strA, aadA2	
		Carbapenems	OmpK35:p.Thr67fs	
		Cephalosporins (3 rd gen.)	CTX-M-15	
		Fluoroquinolones	qnrB1, GyrA:p.Ser83Ile, ParC:p.Ser80Ile	
		Penicillins	CTX-M-15, SHV-11	
		Phenicol	catII.2 (homolog)	
		Sulfonamides	sul1, sul2	
		Tetracycline	tet(A)	
		Trimethoprim	dfrA12, dfrA14 (homolog)	

Where; AK: Amikacin, AMC: Amoxicillin-Clavulanic Acid, AMP: Ampicillin, AZT: Aztreonam, CAZ: Ceftazidime, CIP: Ciprofloxacin, CRO: Ceftriaxone, CTX: Cefotaxime, FEP: Cefepime, GEN: Gentamicin, IMI: Imipenem, MEM: Meropenem, KZ: Cefazolin, LEV: Levofloxacin, MXF: Moxifloxacin, PIP: Piperacillin, PTZ: Piperacillin-Tazobactam, SAM: Ampicillin-Sulbactam, SCF: Cefoperazone-Sulbactam, SXT: Trimethoprim-Sulfamethoxazole (Cotrimoxazole), TET: Tetracycline, TGC: Tigecycline, NITRO: Nitrofurantoin, S: Sensitive, I: Intermediate, R: Resistant.

Supplementary Table S2: *Similarity percentage of phage RMN1 with other Drulisvirus phages based on NCBI analysis.*

No	ID Phage	Query coverage	Percent identity	Accession number
1	<i>Klebsiella</i> phage vB_KpnP_Dlv622	80%	93.73%	MT939252.1
2	<i>Klebsiella</i> phage P252	82%	93.39%	PP934443.1
3	<i>Klebsiella</i> phage vB_KpP_AttikonH1	82%	92.49%	PP974225.1
4	<i>Klebsiella</i> phage Pune	81%	91.80%	MT701589.1
5	<i>Klebsiella</i> phage VLC5	81%	91.73%	MT197175.1

Supplementary Table S3: *Genome annotations of phage RMN1.*

ORFs	Start	Stop	Strand	Predicted protein function
1	1523	1738	+	Hypothetical protein
2	1817	2398	+	Hypothetical protein
3	2395	2619	+	Hypothetical protein
4	2691	2864	+	Hypothetical protein
5	2914	3147	+	Hypothetical protein
6	3140	3403	+	Hypothetical protein
7	3411	3596	+	Hypothetical protein
8	3600	3779	+	Hypothetical protein
9	3776	3994	+	Hypothetical protein
10	3982	4326	+	Hypothetical protein
11	4373	6061	+	Hypothetical protein
12	6061	7095	+	Phage peptidase
13	7098	7526	+	Hypothetical protein
14	7523	7741	+	Hypothetical protein
15	7741	8532	+	Phage primase
16	8513	8950	+	HNH endonuclease
17	8951	10231	+	Phage DNA helicase
18	10284	10550	+	Hypothetical protein
19	10602	10757	+	Hypothetical protein
20	10754	11203	+	HNH endonuclease
21	11172	13550	+	Phage DNA-directed DNA polymerase
22	13547	13768	+	Hypothetical protein
23	13936	14364	+	HNH endonuclease
24	14357	15337	+	Phage phosphoesterase
25	15460	15654	+	Hypothetical protein
26	15710	16552	+	Hypothetical protein
27	16617	16871	+	Hypothetical protein
28	16872	17150	+	Hypothetical protein
29	17150	17524	+	Hypothetical protein
30	17521	17685	+	Hypothetical protein
31	17688	17885	+	Hypothetical protein
32	17888	18046	+	Hypothetical protein
33	18046	19014	+	Phage exonuclease
34	18971	19171	+	Hypothetical protein

Table continues on next column.....

ORFs	Start	Stop	Strand	Predicted protein function
35	19165	19395	+	Hypothetical protein
36	19392	19814	+	Phage endonuclease
37	19811	20272	+	Phage nucleotide kinase
38	20414	22882	+	Phage DNA-directed RNA polymerase
39	22906	23346	+	Hypothetical protein
40	23343	23606	+	Hypothetical protein
41	23616	25211	+	Phage collar, head-to-tail connector protein
42	25226	26068	+	Phage capsid assembly scaffolding protein
43	26094	27116	+	Phage major capsid protein
44	27128	27310	+	Hypothetical protein
45	27400	27960	+	Phage non-contractile tail tubular protein
46	27970	30330	+	Phage non-contractile tail tubular protein
47	30332	30919	+	Phage internal virion protein A
48	30937	33621	+	Phage internal virion protein B
49	33672	37370	+	Phage DNA ejectosome component
50	37372	39864	+	Phage non-contractile tail fiber protein
51	39875	40093	+	Hypothetical protein
52	40093	40395	+	Phage terminase small subunit
53	40395	42251	+	Phage terminase large subunit
54	42251	42625	+	Hypothetical protein
55	42637	42819	+	Hypothetical protein
56	42819	43223	+	Putative spanin
57	43216	43467	+	Phage holin
58	43451	44059	+	Phage endolysin

Where; ORFs: Open reading frames, +: indicates positive strain.