

Supplementary Table S1. Genomic features of *E. coli* isolates.

Genome	Contigs	Genome Length (bp)	G-C content (%)	Coding Sequence (CDS)	tRNA
C072	115	5168708	50.37	4913	59
C2033	107	5243891	50.31	4920	63
C2-107	147	5086635	50.50	4954	63
C2-108	139	5042928	50.52	4890	57

Supplementary Table S2. Resistome of colistin-resistant *E. coli* isolates.

Antibiotics family	Isolates and antibiotic resistance genes <sup>a</sup>				
	C072	C2033	C2-107	C2-108	RC2-007
<b>Aminoglycosides</b>	<i>aac(3)-IV, aadA2, aadA5, aph(4)-Ia, aph(6)-Id aph(3'')-Ib, aph(3')-Ia</i>	<i>aac(3)-IV, aaC2-II-d, aadA2, aph(4)-Ia, aph(3')-Ia</i>	<i>aph(4)-Ia, aac(3)-IV, aph(3')-Ia, aadA2, aadA1</i>	<i>aph(4)-Ia, aac(3)-IV, aph(3')-Ia, aadA2, aadA1</i>	<i>aac(3)-IIa, aadA5, aph(3'')-Ib, aph(6)-Id</i>
<b>Tetracyclines</b>	<i>tetB</i>	<i>tetB</i>	-	-	<i>tetB</i>
<b>Florfenicol/chloramphenicol</b>	<i>cat, cmlA1, floR</i>	<i>cmlA1, floR</i>	<i>cmlA1, floR</i>	<i>cmlA1, floR</i>	<i>cat, floR</i>
<b>Trimethoprim</b>	<i>dfrA17</i>	<i>dfrA17</i>	-	-	<i>dfrA17</i>
<b>Fosfomycin</b>	<i>fosA3</i>	<i>fosA3</i>	<i>fosA3</i>	<i>fosA3</i>	-
<b>Macrolides</b>	<i>mphA</i>	<i>mphA</i>	<i>mphA, mdx(A)</i>	<i>mphA, mdx(A)</i>	<i>mphA</i>
<b>Sulfonamides</b>	<i>sul3</i>	<i>sul2, sul3</i>	<i>sul2, sul3</i>	<i>sul2, sul3</i>	<i>sul1, sul2, sul3</i>
<b>Lincosamide</b>	-	-	-	-	<i>inuF</i>
<b>-lactam</b>	CTX-M-14, TEM-1	CTX-M-14	CTX-M-14	CTX-M-14, TEM-116	CTX-M-55
<b>Colistin</b>	<i>mcr-1.1</i>	<i>mcr-1.1</i>	<i>mcr-1.1</i>	<i>mcr-1.1</i>	<i>mcr-1.1</i>
<b>Quinones/Fluoroquinolones</b>	Ser83Leu and Asp87Asn for GyrA, and Ser80Ile for ParC	Ser83Leu and Asp87Asn for GyrA, and Ser80Ile for ParC	Ser83Leu and Asp87Asn for GyrA, and Ser80Ile for ParC	Ser83Leu and Asp87Asn for GyrA, and Ser80Ile for ParC	Ser83Leu and Asp87Asn for GyrA, and Thr56Ala and Ser80Ile for ParC

<sup>a</sup>Both chromosomal mutations of gyrases and topoisomerase as acquired resistance genes (coverage greater than 90% identified) were determined in the Center for Genomic Epidemiology using the ResFinder tool (<http://www.genomic epidemiology.org>).

Supplementary Table S3. Phages and prophages carrying *mcr-1* identified on *E. coli* and *K. pneumoniae* genomes.

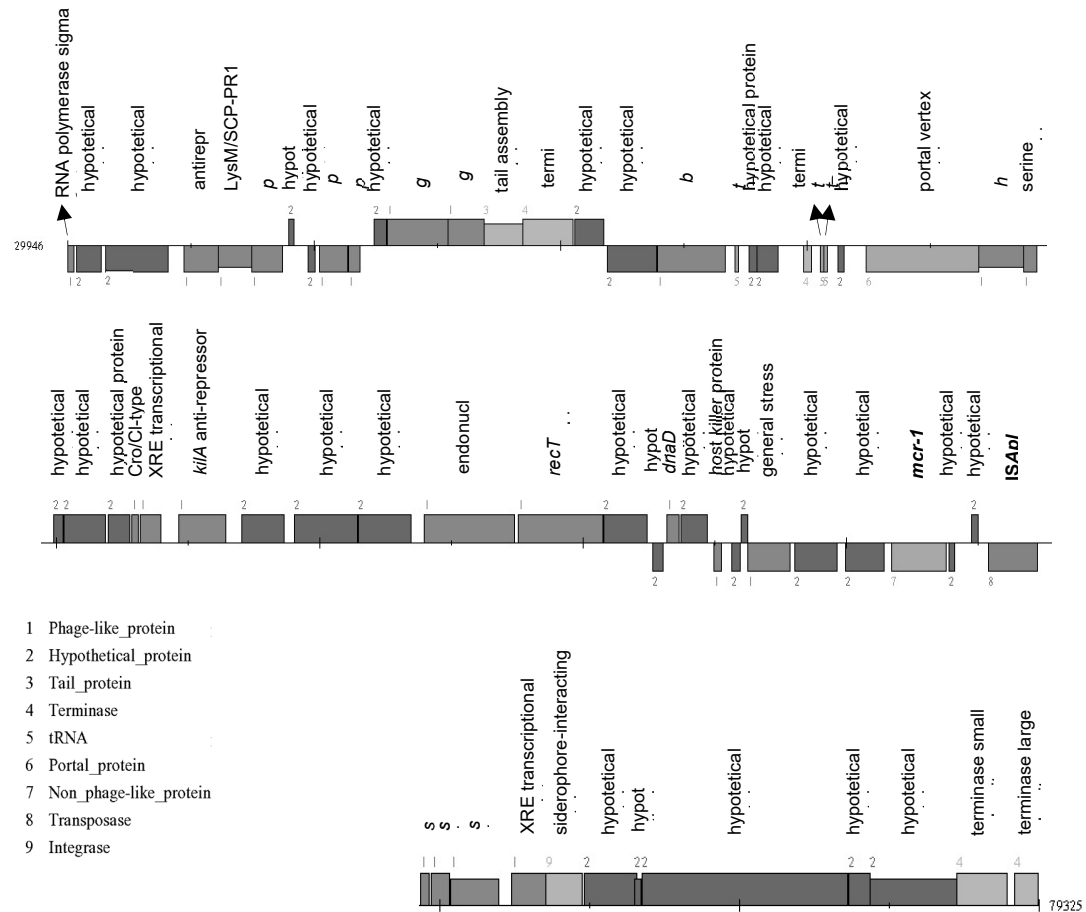
Bacterial species	Level	No. de genomes (%) <sup>a</sup>	<i>mcr-1</i> positive (%)	VirSorter <sup>b</sup>						Genomes with prediction of intact and incomplete phages or prophages
				Cat-1	Cat-2	Cat-3	Cat-4	Cat-5	Cat-6	
				Phage			Prophage			
<i>E. coli</i>										
	Complete	689 (5)	48	0	0	28	0	2	12	Cat-5 (EC590 and HS30-1)
	Draft	12,868 (95)	820	10	12	313	0	2	202	Cat-1 (2140, 2142, 3421, A351, B146, HU4, RC2-007, XJ4, YH17180 and YH17137), Cat-2 (A200, A215, A245, A246, A276, A26, A38, A415, A6, HEB3, HLJ8 and LN48) and Cat-5 (3768 and A432)
Total		13,557	868 (6.4)	10	12	341	0	4	214	
<i>K. pneumoniae</i>										
	Complete	306 (5)	3 (1)	0	0	2	0	0	1	no strains
	Draft	6,297 (95)	42 (0.7)	1	1	23	0	0	2	Cat-1 (SCKP-LL83) and Cat-2 (SCKP020138)
Total		6,603	45 (0.7)	1	1	25	0	0	3	

<sup>a</sup>Genomes obtained from RefSeq Database at November, 2019.

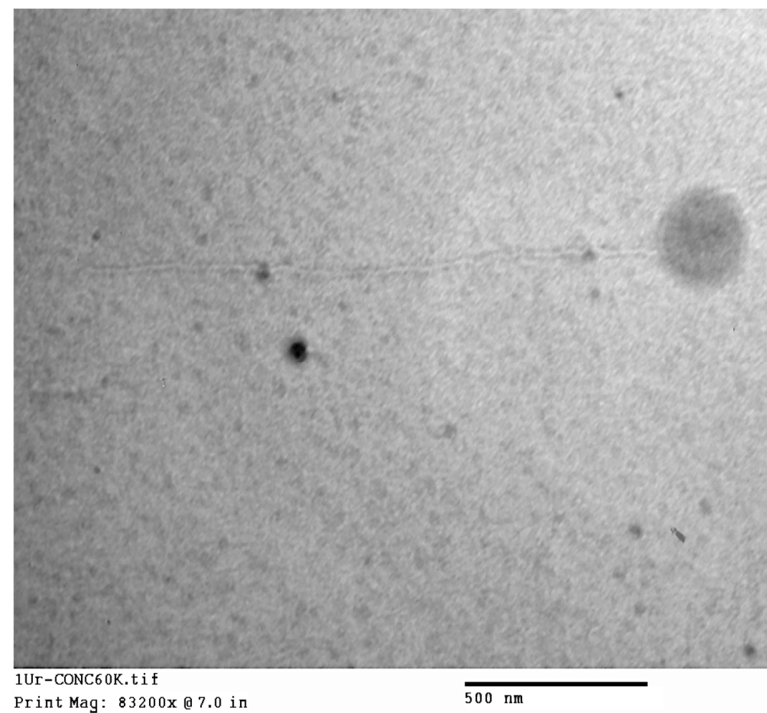
<sup>b</sup>Phages and prophages identified in the *E. coli* and *K. pneumoniae* using VirSorter program [40].

Supplementary Table S4. Primers used for *mcr*- and CTX-M-type genes identification.

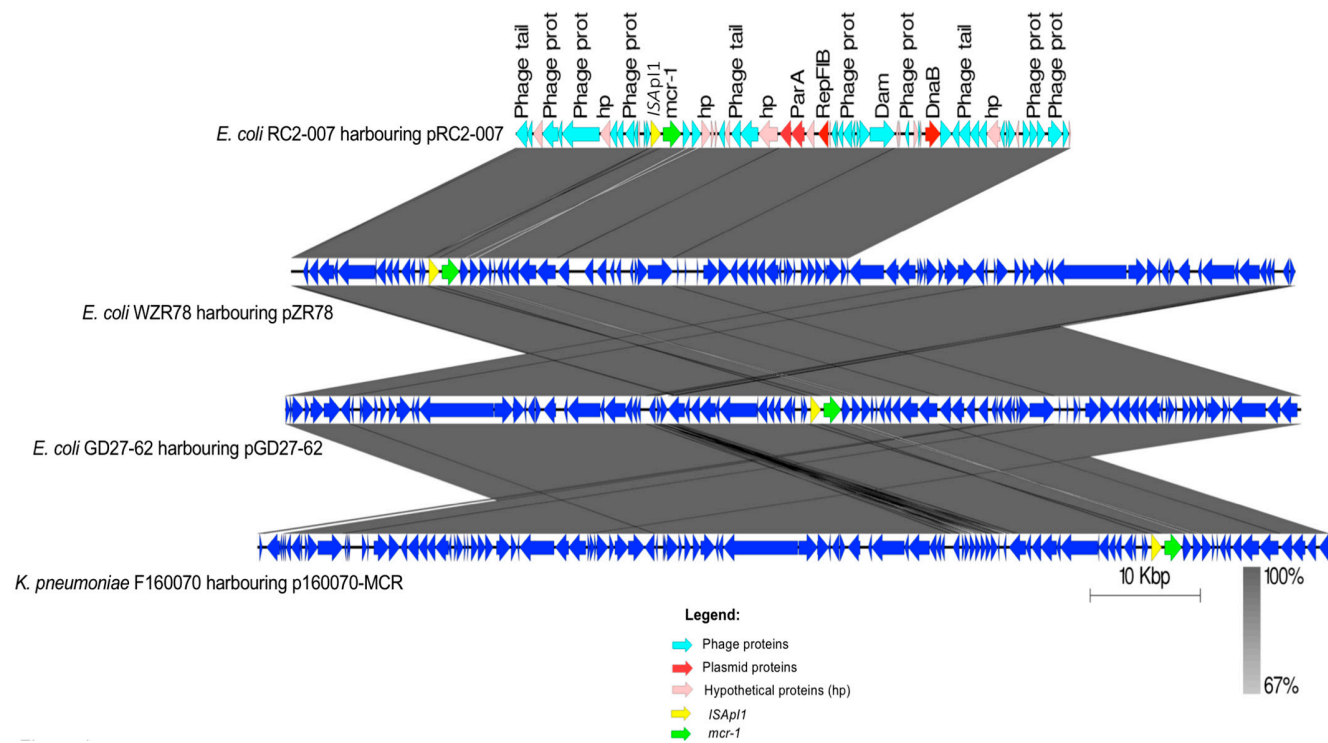
Gene target	Primer and Sequence (5' – 3')	Amplicon (bp)	Reference
<i>mcr-1</i>	CLR5-F: GGTCAGTCCGTTTGTTTC CLR5-R: CTTGGTCGGTCTGTAGGG	309	[8]
<i>mcr-2</i>	MCR-12-F: TGGTACAGCCCCTTTATT MCR-12-R: GCTTGAGATTGGGTTATGA	600 pb	This study
<i>mcr-3</i>	mcr3-F: TTGGCACTGTATTTTGCATTT mcr3-R: TTAACGAAATTGGCTGGAACA	542 pb	[42]
<i>mcr-4</i>	Mcr-4 FW: ATTGGGATAGTCGCCTTTTT Mcr-4RV: TTACAGCCAGAATCATTATCA	487 pb	[43]
<i>mcr-5</i>	MCR5_fw: ATGCGGTTGTCTGCATTTATC MCR5_rew: TCATTGTGGTTGTCCTTTTCTG	1644 pb	[44]
<b>CTX-M</b>	CTX-MF: GCTGTTGTTAGGAAGTGTG CTX-MR: GGTGACGATTTTAGCCGCC	811 bp	[30]



Supplementary Figure S1. Genome map of prophage as the genetic context of *mcr-1* gene. The predicted genes and the functions predicted by PHASTER program [41] are indicated as boxes with the superscript number in each box.



Supplementary Figure S2. Electronic microscopy of phage that contained no detectable *mcr-1* gene.



Supplementary Figure S3. Comparison of phage-like plasmid that contains the *mcr-1* gene in the pRC2-007 plasmid with other phage-like plasmids