

Supplementary Table S1. Primers used for amplifying and sequencing *basRS*, *phoPQ* and *eptA*

Gene	Primer	Sequence (5' - 3')	Amplicon size (bp)	Gene length (bp)	Amino acid length (aa)
<i>basR</i>	Eco-basR_F	CGCAAACGCAACACTATTCA	975	669	223
	Eco-basR_R	ATGATGTGGCGATCGTTGTT			
<i>basS</i>	Eco-basS_F	GACAATGAACCCTCGACCAA	1,605	1,092	364
	Eco-basS_F1	GTGCGTTTGCATCTGGA ACT			
	Eco-basS_R	CGGCGTAACCATGAAAGAGA			
<i>phoP</i>	Eco-phoP_F	CCCCATAACCACATAATCG	794	672	224
	Eco-phoP_R	CGTTGCCAACAGAAAACGTA			
<i>phoQ</i>	Eco-phoQ_F	CGCGTTCGAATACACCATTA	1,774	1,461	487
	Eco-phoQ_F1	TGCTGAGTGGAGATCATTCG			
	Eco-phoQ_R	CAAGAAAATCGGGCCAGTTA			
<i>eptA</i>	Eco-eptA_F	CCAGAATCAGTCCCTGCAAT	1,797	1,644	548
	Eco-eptA_R	TCCCCTTAATCCAGCAAACA			

Supplementary Table S2. Primers for qRT-PCR

Gene	Primer	Sequence (5' - 3')	Amplicon size (bp)
<i>rrsH</i>	rrsH_F	GAATGCCACGGTGAATACGTT	64
	rrsH_R	ACCCACTCCCATGGTGTGA	
<i>basR</i>	basR_F	ATTGCAGGGACTGATTCTGG	134
	basR_R	CGTCGGGTAACCCTAAATCC	
<i>phoP</i>	phoP_F	GCAGAAGATGCCAAAGAAGC	143
	phoP_R	ACCAGAATCGGCAGTGAAAC	
<i>eptA</i>	eptA_F	TCCCTAATACCGCATCTTGC	124
	eptA_R	ATGATATCCAGCACGCCTTC	

Supplementary Table S3. Antimicrobial resistance profile of the *E. coli* strains.

<i>E. coli</i> strain	Minimum Inhibitory Concentration (mg/L) ^{a, b, c}									
	CL	IMI	AMK	CPM	CRO	CIP	TET	RIF	P/T	A/S
E015	0.25 (S)	0.125 (S)	16 (I)	64 (R)	>64 (R)	16 (R)	64 (R)	32	2/4 (S)	32/16 (R)
E139	0.25 (S)	0.125 (S)	8 (S)	>64 (R)	>64 (R)	64 (R)	4 (S)	16	64/4 (I)	>64/32 (R)
E154	0.25 (S)	0.125 (S)	4 (S)	>64 (R)	>64 (R)	32 (R)	4 (S)	32	4/4 (S)	>64/32 (R)
E015R	64 (R)	0.125 (S)	2 (S)	>64 (R)	>64 (R)	16 (R)	>64 (R)	32	4/4 (S)	64/32 (R)
E139R	>64 (R)	0.125 (S)	2 (S)	0.25 (S)	0.063 (S)	>64	2 (S)	32	4/4 (S)	64/32 (R)
E154R	64 (R)	0.125 (S)	2 (S)	0.125 (S)	0.063 (S)	0.063 (S)	64 (R)	8	2/4 (S)	64/32 (R)
QIA18	8 (R)	0.125 (S)	2 (S)	0.125 (S)	0.063 (S)	64 (R)	>64 (R)	64	4/4 (S)	64/32 (R)
QIA24	8 (R)	0.063 (S)	2 (S)	0.125 (S)	0.063 (S)	0.063 (S)	>64 (R)	64	8/4 (S)	64/32 (R)
QIA32	8 (R)	0.125 (S)	1 (S)	0.125 (S)	0.063 (S)	0.25 (S)	64 (R)	16	2/4 (S)	64/32 (R)
QIA33	16 (R)	0.063 (S)	2 (S)	0.125 (S)	0.063 (S)	0.25 (S)	32 (R)	16	2/4 (S)	32/16 (R)
EC006	8 (R)	0.125 (S)	2 (S)	>64 (R)	>64 (R)	16 (R)	>64 (R)	64	8/4 (S)	64/32 (R)
EC019	8 (R)	0.125 (S)	4 (S)	>64 (R)	>64 (R)	64 (R)	2 (S)	32	8/4 (S)	64/32 (R)
EC111	16 (R)	0.125 (S)	2 (S)	>64 (R)	>64 (R)	32 (R)	2 (S)	32	>256/4 (R)	>64/32 (R)
J53 _{pEC006}	4 (R)	0.25 (S)	2 (S)	0.25 (S)	0.063 (S)	0.063 (S)	2 (S)	32	4/4 (S)	32/16 (R)
J53 _{pEC019}	4 (R)	0.125 (S)	2 (S)	0.125 (S)	0.063 (S)	0.063 (S)	2 (S)	16	8/4 (S)	32/16 (R)
J53 _{pEC111}	4 (R)	0.125 (S)	2 (S)	0.125 (S)	0.063 (S)	0.063 (S)	2 (S)	32	8/4 (S)	32/16 (R)
MG1655	0.25 (S)	-	-	-	-	-	-	-	-	-
J53	0.25 (S)	-	-	-	-	-	-	-	-	-

^a CL, colistin; PB, polymyxin B; IMI, imipenem; AMK, amikacin; CPM, cefepime; CRO, ceftriaxone; CIP, ciprofloxacin; TET, tetracycline; RIF, rifampicin; P/T, piperacillin-tazobactam; A/S, ampicillin-sulbactam

^b S, susceptible; I, intermediate-resistant; R, resistant

^c There is no CLSI breakpoint for rifampicin

Supplementary Figure S1. The results of MALDI-TOF mass spectrometry. (A) Isogenic strains E015 and E015R, (B) a parental *E. coli* J53 and a transconjugant J53_{pEC019}, and (C) WT *mcr-I*-positive strains EC006, EC019, and EC111. Bis-phosphorylated and hexa-acylated lipid A peak (1797.2 EM) was identified in all isolates. An addition of PEtN to the hexa-acylated lipid A (1920 EM) was detected from strains displaying colistin resistance.

