Supplementary Material

Table S1. Primers used in this study

Cana(a)	Saanaaa 51-22		Defenence
			Kelerence
KPC F	TGTCACTGTATCGCCGTC	Gene detection	
KPC R	CTCAGTGCTCTACAGAAAACC	Gene detection	
OXA-48 F	TTGGTGGCATCGATTATCGG	Gene detection	2
OXA-48 R	GAGCACTTCTTTTGTGATGGC	Gene detection	2
IMI F	GTTCCATTCACCCATCACAAC	Gene detection	This study
IMI R	CTACCGCATAATCATTTGCCG	Gene detection	This study
New IMI variant F	CTACGCTTTAGACACTGGC	Gene detection	This study
New IMI variant R	TTGGTACGCTAGCACGAATA	Gene detection	This study
VIM F	GATGGTGTTTGGTCGCCATA	Gene detection	3
VIM R	CGAATGCGCAGCACCAG	Gene detection	3
IMP F	GGAATAGAGTGGCTTAAYTCT	Gene detection	3
IMP R	CCAAACCACTACGTTATCT	Gene detection	3
FRI-1 F	TGAACTCATTCGCCTCTCAG	Gene detection	11
FRI-1 R	CTGCTTCGTCATGTTTGTCG	Gene detection	11
TEM F	CATTTTCGTGTCGCCCTTAT	Gene detection	4
TEM R	TCCATAGTTGCCTGACTCCC	Gene detection	4
CTX-M multiplex		Gene detection	5
SHV F	ATGCGTTATATTCGCCTG	Gene detection	6
SHV R	TTAGCGTTGCCAGTGCTC	Gene detection	6
GES F	TTCCGATCAGCCACCTCTCA	Gene detection	7
GES R	CTGGCAGGGATCGCTCACTC	Gene detection	7
ampC multiplex		Gene detection	8
ampC F	GACATCCCCTTGACTCGCTA	Whole gene amplification & sequencing	This study
ampC R	GTTTTACTGTAGCGCCTCGA	Whole gene amplification & sequencing	This study
ampR F	TTTCATCTTCTCCACCAGCC	Whole gene amplification & sequencing	This study
ampR R	ATAGCGAGTCAAGGGGATGT	Whole gene amplification & sequencing	This study
ampD F	ATGTTGTTAGAAAACGGATG	Whole gene amplification & sequencing	9
ampD R	TCATGTTATCTCCTTATCTG	Whole gene amplification & sequencing	9
ompC F	TGAGGAGAATGAAATTGCCGAC	Whole gene amplification & sequencing	This study
ompC R	GCGGCAAGAGTACACCAAAA	Whole gene amplification & sequencing	This study
ompF F	AGACACCAAACTCTCATCAATAGTTC	Whole gene amplification & sequencing	10
ompF R	CGCTATCAGGTTAACGGTA	Whole gene amplification & sequencing	10
rspL F	ACGTACAGCACCACGACG	Expression analysis	This study
rspL R	AGCGTGTCTTCCAGACTCAC	Expression analysis	This study
ampC F	GCATGGCGGTGGCCGTTAT	Expression analysis	10
ampC R	CTGCTTGCCCGTCAGCTGT	Expression analysis	10
ompF F	TAATGACAGCAACGATGGCGAC	Expression analysis	This study
ompF R	AGCGCCTTCAGAGTTGTTACC	Expression analysis	This study
ompC F	CGGCCAGTGGGAATACCAGA	Expression analysis	This study
ompC R	GAATGAACCCGCATCAGCGAA	Expression analysis	This study
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Figure S1: UPGMA tree of concatenated sequences of *ampC*, *ampR*, *ompF* and the corresponding amino acid changes of AmpC, AmpR, OmpF and OmpC and cephalosporin and carbapenem MIC



CTX: cefotaxime, CAZ: ceftazidime, FEP; cefepime, IM: imipenem, MEM: meropenem, ERP: ertapenem, MICs in mg/L, NCTC13405: reference wild type E-cloacae, NCTC13405: reference wild type E-cloacae, NCTC13405: network and for start codes, OTC 13405: and for start codes, OTC 13405: network and for start codes, and for start cod

	Amino acid	cnanges																													
							OmpF	;															OmpC								
	u		12		L3	L4						β.			A					15				L6		L7			L8		
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Pro17	7Ala			Leu211lle		Pro227Ala	Tyr229Phe	Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	lle338Val (Gin346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Pro17	7Ala			Leu211Ile		Pro227Ala	Tyr229Phe	Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Pro17	7Ala			Leu211Ile		Pro227Ala	Tyr229Phe	Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp	Glu220Asp					As	p189Glu			Ala222Asp	Pro227Met	Tyr229Ala	Phe230Tyr	Glu232Asn	Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Pro17	7Ala			Leu211Ile		Pro227Ala		Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp		Leu242X			IS1(-15) Pro17	7Ala			Leu211Ile		Pro227Ala		Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp	Glu220Asp				40-4851 Pro17	7Ala As	p189Glu			Ala222Asp	Pro227Met	Tyr229Ala	Phe230Tyr	Glu232Asn	Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					_	As	p189Glu	Arg191Cys		Ala222Asp	Pro227Met	Tyr229Ala	Phe230Tyr	Glu232Asn	Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (Gin346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp	Glu220Asp				Δ1-1218																	
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Δ1-54																	
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp	Glu220Asp				_					Ala222Asp	Pro227Met	Tyr229Ala	Phe230Tyr	Glu232Asn	Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp	Glu220Asp				Δ1-7																	
			Ala88Gly	Val140Ala							Val301X			Pro17	7Ala As	p189Glu		Leu211Ile		Pro227Ala		Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (Gin346Ala	Thr347Ala
			Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Pro17	7Ala As	p189Glu		Leu211lle		Pro227Ala		Phe230Tyr		Val265Ala	GIn268Leu	lle303leu	Asn305_Tyr306insGlu	lle311Leu	lle338Val (GIn346Ala	Thr347Ala
			Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		G	u199Asp					Pro17	7Ala As	p189Glu		Leu211lle		Pro227Ala		Phe230Tyr		Val265Ala	Gln268Leu	Ile303leu	Asn305_Tyr306insGlu	lle311Leu	Ile338Val (GIn346Ala	Thr347Ala
														1021-221																	
														(33(*35)																	
														_																	
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		Phe198Tyr				Ile306Val \	/al307ile	Pro17	7Ala As	p189Glu		Leu211lle		Pro227Ala		Phe230Tyr		Val265Ala	Gln268Leu	lle303leu	Asn305_Tyr306insGlu	lle311Leu	lle338Val (Gin346Ala	Thr347Ala
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp		Phe198Tyr				Ile306Val \	/al307ile							Pro227Ala		Phe230Tyr									
Asn47Tyr	Asp48Ala	Ser49Gly	Ala88Gly	Val140Ala	Ser146Ala	Thr180Asp	Val183Leu	Phe198Tyr		Lys223G	ŝlu	Ile306Val \	/al307lle							Pro227Ala		Phe230Tyr									
Asn47Tvr	Asp48Ala	Ser49Glv	Ala88Glv	Val140Ala	Ser146Ala	Thr180Asp		Phe198Tvr		Lvs223G	ŝlu	lle306Val \	/al307ile							Pro227Ala		Phe230Tvr									

Figure S2: UPGMA tree of concatenated sequences of the 7 DNA fragments of MLST. Isolate numbers (sequence types by MLST)



0.008 0.006 0.004 0.002 0.000 0.010

Figure S 3. Outer membrane profiles of selected isolates on 12% SDS-polyacrylamide gel



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