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REVISED**Partition locus-based classification of selected plasmids in *Klebsiella pneumoniae*, *Escherichia coli* and *Salmonella enterica* spp: an additional tool.**

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1. Introduction

Plasmids are extrachromosomal DNA molecules capable of autonomous replication and are the main vectors of resistance and virulence genes, especially in Enterobacteriaceae. Tracing plasmids conferring drug resistance is important for analysis of evolution, epidemiology and spread of antibacterial resistance. The epidemic plasmids belong to the most frequently occurring plasmid families, however antibiotic resistance gene are not always associated with one particular replicon, transfer or partition system. Therefore is difficult to construct phylogenies of plasmids or to track the spread of particular markers.

Incompatibility (Inc) group identification has been frequently used to classify plasmids. Identification methods include the initial technique based on conjugation (Novick, 1987), hybridization with cloned replication regions (Couturier et al., 1988), PCR-based replicon typing (PBRT) (Carattoli et al., 2005) and relaxase typing (Compain et al., 2014). Moreover MLST schemes for plasmids were developed to assign plasmids to STs, in analogy to the typing developed for bacterial genomes (García-Fernández et al., 2008).

Mitotic segregation of plasmids, termed partition in bacteria, is a fundamental step of the cell cycle that ensures the transmission of the whole genome to daughter cells. It is governed by specific genetic loci named *par*, first identified in low-copy-number plasmids and later found to be present as homologues in most bacterial chromosomes. *par* loci are organized into operons encoding two proteins, an ATPase and a DNA-binding protein, and including a centromeric site. These components interact with each other to direct the subcellular localization that ensures stability of their replicons. Three types of partitioning ATPases are known (Gerdes et al., 2010): the Walker-type ATPases encoded by the *par/sop* gene family (type I partitioning loci which are the most common of the *par* systems), the actin-like ATPase encoded by the *par* locus of plasmid R1 (type II partitioning locus) and the tubulin-like GTPases encoded by plasmids from *Bacillus* sp. (type III partitioning loci). Despite their similarities in genetic organization, these three *par* types use entirely different molecular mechanisms (Guynet and de la Cruz, 2011).

While the acquisition of plasmids often enables bacteria to survive in the presence of antibiotics, it is possible that plasmids also confer vulnerabilities that may be exploited in tailored antibacterial therapy (Williams and Hergenrother, 2008). In order to control the spread of multiresistance plasmids, we need to determine many more variables that affect their replication, maintenance and movement.

Recently we developed a multiplex PCR method called “plasmid relaxase gene typing” (PRaseT). This classification scheme is based on the relaxase, a key protein which is part of the mobilization region of transmissible plasmids. The aim of the present study was to identify different partition systems located on multiresistance plasmids and to design a multiplex PCR method here called “plasmid partition gene typing” (PAR-T). This method could further the classification of plasmids in *Klebsiella pneumoniae*, *Escherichia coli* and *Salmonella enterica spp.* and will constitute another option for characterising plasmids.

2. Materials and methods

2.1. Database search, primer design and *in silico* primer assay

An *in silico* analysis was carried out using GenBank BLAST (<http://blast.ncbi.nlm.nih.gov/>) on plasmids >40 kb from *K. pneumoniae* and *E. coli* conferring multidrug resistance. Due to a low number of plasmids IncHI, IncI1 from *K. pneumoniae*, the *in silico* analysis was extended to some plasmids from *Enterobacter cloacae* and *Citrobacter freundii*. For the eight Inc groups studied (IncF, IncA/C, IncL/M, IncN, IncHI, IncR, IncI1, IncX), the *par* operon was used as template; the presence of partition-specific multidomains was searched for using CD-Search (<http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi/>). Multiple alignments were performed with ClustalW2 software (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>). Primer pairs covering most sequences in each family were designed using FastPCR (<http://primerdigital.com/fastpcr.html>) and Primerblast (<http://www.ncbi.nlm.nih.gov/tools/primer-blast>) software, while minimizing codon degeneracy (Table 1). Oligonucleotide primers were tested *in silico* for hybridization with plasmids from Enterobacteriaceae referenced in GenBank.

2.2. Bacterial strains and plasmids

For validation of the PCR assays, experiments were conducted with 136 *Escherichia coli* transconjugants (Tc) or transformants (Tf) of Enterobacteriaceae (Table 2). All strains carried plasmids belonging to diverse Inc groups that encoded β -lactamases conferring resistance to third-generation cephalosporins and/or carbapenems (ESBLs, acquired cephalosporinases, carbapenemases). They were part of four collections of, respectively, (i) *E. coli* strains isolated between 1997 and 2002 in various French university hospitals (Marcadé et al., 2009) (Branger et al., 2005), (ii) *K. pneumoniae* strains from various geographical regions collected since the 1980s (D. Decré and G. Arlet, personal collection), (iii) *Salmonella enterica* subsp. *enterica* strains representing various serovars (collection of the French National Reference Center for *E. coli*, *Shigella* sp., and *Salmonella* sp., Institut Pasteur), (iv) *E. coli*, *S. enterica*, *K. pneumoniae* strains isolated during 2013 in various Argentina University Hospitals (M. Jure, personal collection). All Tc, Tf and clinical strains used in this study were analyzed in parallel with the PAR-T and PRaseT methods. The IncR plasmids which do not encode relaxases were analyzed only by using PBRT (Carattoli et al., 2005). The Tc used as positive controls in PAR-T reactions are given in Table 2. After optimization using Tc or Tf carrying replicons of various types according to PRaseT, we applied the PAR-T method to a panel of 30 clinical strains (17 *E. coli*, 11 *K. pneumoniae* and 2 *S. enterica*) carrying replicons of one to four different types (Table 3).

2.3. DNA extraction and PCR conditions

Lysis by boiling was used for total DNA extraction as previously described (Dallenne et al., 2010). Multiplex PCR was carried out using the Qiagen Multiplex PCR kit (Qiagen, Courtaboeuf, France). The master mix contained pre-optimized concentrations of HotStarTaq DNA polymerase and MgCl₂, deoxynucleotide triphosphate and buffer. To all multiplex PCRs, solution Q (Qiagen) that facilitates the reaction with difficult-to-amplify templates by modifying DNA melting was added. Total DNA in 2 μ L of bacterial lysate was subjected to multiplex PCR in a 50 μ L volume. The conditions for multiplex PCR were optimized to ensure that all targets were sufficiently amplified for amplicons to be easily visible on 1.5% agarose gels. The optimal primer concentrations are reported in Table 1. PCR conditions consisted of an initial activation at 95°C for 5 min, followed by 35 cycles of 95°C for 30 s, 57°C for 90 s and 72°C for 90 s with a final extension at 68°C for 10 min; for Multiplex I and Multiplex II annealing temperature was elevated to 60°C for 90 s. Simplex PCRs were

performed in a 50 μ L mix with 2U of Taq DNA polymerase (Roche Diagnostics), 10 \times PCR buffer/MgCl₂ (Roche Diagnostics, Meylan, France), 200 μ M of each deoxynucleotide triphosphate (dNTP Mix, Eurobio, Courtaboeuf, France), 0.2 pmol/ μ L of each primer, 40 μ L of sterile water and 2 μ L of total DNA extract. PCR conditions consisted in 30 cycles [94°C for 1 min, 55°C for 40 s, 72°C for 1 min], preceded by 1 cycle at 94°C for 5 min and followed by 1 cycle at 72°C for 5 min. PCR products were separated at 100 V for 90 min (180 min for Multiplex IV) on 1.5% agarose gel electrophoresis containing ethidium bromide and visualized using GelDoc (Biorad, Marnes-La-Coquette, France). PCR products were purified using the Exosap purification kit (Illustra Exostar-1 Step, Dutscher, Brumath, France) and subjected to bidirectional DNA sequencing using the BigDye terminator v3.1 cycle sequencing kit (Applied Biosystems, Foster City, CA, USA) and an Applied Biosystems 3730 XL capillary sequencer. Sequence analysis was carried out using Sequence scanner (Applied Biosystems), GeneDoc (www.psc.edu/biomed/genedoc) and GenBank BLAST software.

3. Results and discussion

3.1. *In silico* analysis

We mainly focused on plasmid families previously found to be involved in the spread of resistance genes in Enterobacteriaceae (Carattoli, 2013). The majority of plasmids contain a single *par* locus, with the exception of some plasmids such as pR55 plasmid which include two *par* loci (type I *parAB* and type II *parMR*). The type I partitioning loci are the most common of the *par* systems (74%). The partition loci are often close to *rep* gene. In contrast, some of them are located at some distance, e.g. the *parAB* locus of pCTX-M-360 which is 30000 bp away from RepA. Different designations are used in the annotated sequences for *par* loci: *par*, *sop*, *stb*. *In silico* analysis showed that some Inc groups are relatively homogeneous with respect their partition systems, such as IncL/M, N, A/C, II or R. The high sequence similarity within these groups (99-100%) allowed designation of a pair of primers for each group. The study of the genetic environment (500 nucleotides on either side of the *par* genes or their equivalent) of the same groups showed high similarity (75 to 100%). In contrast, other groups such as IncF showed more divergent *par* sequences. In addition, IncX plasmids from *K. pneumoniae* (e.g. pIncX-SHV, accession number JN247852 or pKPC-NY79, accession number JX104759) carried a *parA* gene encoding a Walker-type ATPase near the *rep* region and an annotated *parB* gene 25 kb apart from *parA* without a partition-specific multidomain. *In silico* analysis of IncX plasmids in *E. coli* showed a different

organization from that found in *K. pneumoniae*, with *parA* and *parB* organized in an operon. *In silico* analysis of IncHI plasmids did not show any correlation between *par* loci and IncHI1 and HI2. Furthermore, the phylogram of *K. pneumoniae* in Fig. 1 reveals partition proteins form distinct subgroups and are connected to Inc group with the exceptions of plasmids IncF. *In silico* analysis led to the design of 18 pairs of primers targeting the *par* operons of plasmids from *K. pneumoniae*, *E. coli* and *Salmonella enterica* spp. belonging to Inc groups A/C, F, HI, I1, L/M, N, R. For plasmids belonging to the IncX group we decided to target only the *parA* gene (Table 1). The primer names for IncF (F1 to F9) and IncHI (HIa and HIb) groups were arbitrarily chosen.

3.2. Primer evaluation using transconjugants and transformants

In order to assess the sensitivity and specificity of each PCR, primers were tested using a collection of 136 recipient cells, with PRaseT as the reference method (Table 2). Each primer pair was validated using all recipient cells, first in a simplex and then a multiplex PCR and target DNA of either single cells or cell mixtures was used. PCR conditions were optimized and all amplicons were sequenced. *E. coli* strain J53 was used as negative control in PCR experiments to test for possible cross-hybridization with chromosomal DNA. An example of the results is shown in Fig S1. No non-specific amplification was observed. PAR-T results were largely consistent with the PRaseT results (98.6%) except for two strains which carried an IncX replicon (*E. coli* strains 64 and 110). These results were surprising. If the study of IncX plasmids indicates a diversity in their backbones, no data allow an explanation as to why the *par* loci are organized differently in *K. pneumoniae* and *E. coli* and why there are differences in the *parA* genes between these two species. A complete analysis of all IncX replicon present in the databases will be required (all Enterobacteriaceae).

3.3. Evaluation of PAR-T using clinical strains

Thirty clinical strains, each carrying replicons of one to four different types, were tested by PAR-T to confirm the specificity of the designed primers (Table 3). An example of the results is shown in Fig S1. For 24 strains (80%) there was a perfect correlation between the results obtained with PAR-T and PRaseT. Six strains were positive with PRaseT but negative with PAR-T. Among these, five carried IncX replicons (four *E. coli* strains, i.e. 17, 19, 28 and 34, and one *K. pneumoniae* strain, KpS20) and one (*E. coli* strain 105) carried an IncI1 replicon. As shown by *in silico* analysis, *par* loci in IncX plasmids are organized differently between *K. pneumoniae* and *E. coli*. It is likely that our analysis targeting plasmids >40 kb of *K. pneumoniae* and some *E. coli* did not allow the study of all the *par* loci of IncX plasmids. A complete analysis of all IncX replicon present in the databases will be required (all the Enterobacteriaceae). The strain (*E. coli* 105) that carried an IncI1 plasmid was negative with PAR-T. We considered three possibilities: (i) a divergent IncI1 *par* locus that could not hybridize with our primers was present, (ii) the *par* locus was truncated or (iii) the gene locus was absent. *In silico* analysis has shown that the *par* sequences of IncI1 replicons are well conserved and form a homogen group, thus making the first possibility (i) unlikely.

Overall the specificity were very high (>90%) for all Inc groups studied except IncX.

Finally, four strains (*E. coli* 19 and 34, and *K. pneumoniae* KpS5 and KpS26) which were negative with PRaseT were found to contain IncF and IncR plasmids, respectively, when PAR-T was used. For the *K. pneumoniae* strains, the results were not unexpected as IncR plasmids do not encode relaxases. The two *E. coli* were positive with PBRT with IncFIA, IncFIB and IncFII replicons found in both. Moreover, PCR targeting the genes of the type IV secretion system was negative and the plasmids from neither strain could be transferred to a recipient cell by conjugation (Compain et al., 2014). We considered the possibility of the loss of genes for conjugative transfer.

4. Conclusions

Considering the complexity of constant plasmid evolution and the unavailability of full-length plasmid sequencing in most laboratories, the combined use of several complementary classification methods should be a practical value. Our set of seven multiplex PCRs allowed classification of the most frequently encountered transmissible plasmids in *Klebsiella pneumoniae*, *Escherichia coli* and *Salmonella enterica spp.* by targeting their *par* loci, with the exception of IncX replicons. For this group, *in silico* analysis of all plasmids present in the databases must be carried out to design new primers and to improve the value of the method described here.

Conflicting interest

The authors declare that they have no conflicting interests.

References

- Branger, C., Zamfir, O., Geoffroy, S., Laurans, G., Arlet, G., Thien, H.V., Gouriou, S., Picard, B., Denamur, E., 2005. Genetic background of *Escherichia coli* and extended-spectrum beta-lactamase type. *Emerg. Infect. Dis.* 11, 54–61.
- Carattoli, A., 2013. Plasmids and the spread of resistance. *Int. J. Med. Microbiol. IJMM* 303, 298–304.
- Carattoli, A., Bertini, A., Villa, L., Falbo, V., Hopkins, K.L., Threlfall, E.J., 2005a. Identification of plasmids by PCR-based replicon typing. *J. Microbiol. Methods* 63, 219–228.
- Compain, F., Poisson, A., Le Hello, S., Branger, C., Weill, F.-X., Arlet, G., Decré, D., 2014. Targeting relaxase genes for classification of the predominant plasmids in Enterobacteriaceae. *Int. J. Med. Microbiol. IJMM* 304, 236–242.
- Couturier, M., Bex, F., Bergquist, P.L., Maas, W.K., 1988. Identification and classification of bacterial plasmids. *Microbiol. Rev.* 52, 375–395.
- Dallenne, C., Da Costa, A., Decré, D., Favier, C., Arlet, G., 2010. Development of a set of multiplex PCR assays for the detection of genes encoding important beta-lactamases in Enterobacteriaceae. *J. Antimicrob. Chemother.* 65, 490–495.
- García-Fernández, A., Chiantto, G., Bertini, A., Villa, L., Fortini, D., Ricci, A., Carattoli, A., 2008. Multilocus sequence typing of IncI1 plasmids carrying extended-spectrum beta-lactamases in *Escherichia coli* and *Salmonella* of human and animal origin. *J. Antimicrob. Chemother.* 61, 1229–1233.
- Gerdes, K., Howard, M., Szardenings, F., 2010. Pushing and pulling in prokaryotic DNA segregation. *Cell* 141, 927–942.
- Guynet, C., de la Cruz, F., 2011. Plasmid segregation without partition. *Mob. Genet. Elem.* 1, 236–241.
- Marcadé, G., Deschamps, C., Boyd, A., Gautier, V., Picard, B., Branger, C., Denamur, E., Arlet, G., 2009. Replicon typing of plasmids in *Escherichia coli* producing extended-spectrum beta-lactamases. *J. Antimicrob. Chemother.* 63, 67–71.
- Novick, R.P., 1987. Plasmid incompatibility. *Microbiol. Rev.* 51, 381–395.
- Williams, J.J., Hergenrother, P.J., 2008. Exposing plasmids as the Achilles' heel of drug-resistant bacteria. *Curr. Opin. Chem. Biol.* 12, 389–399.

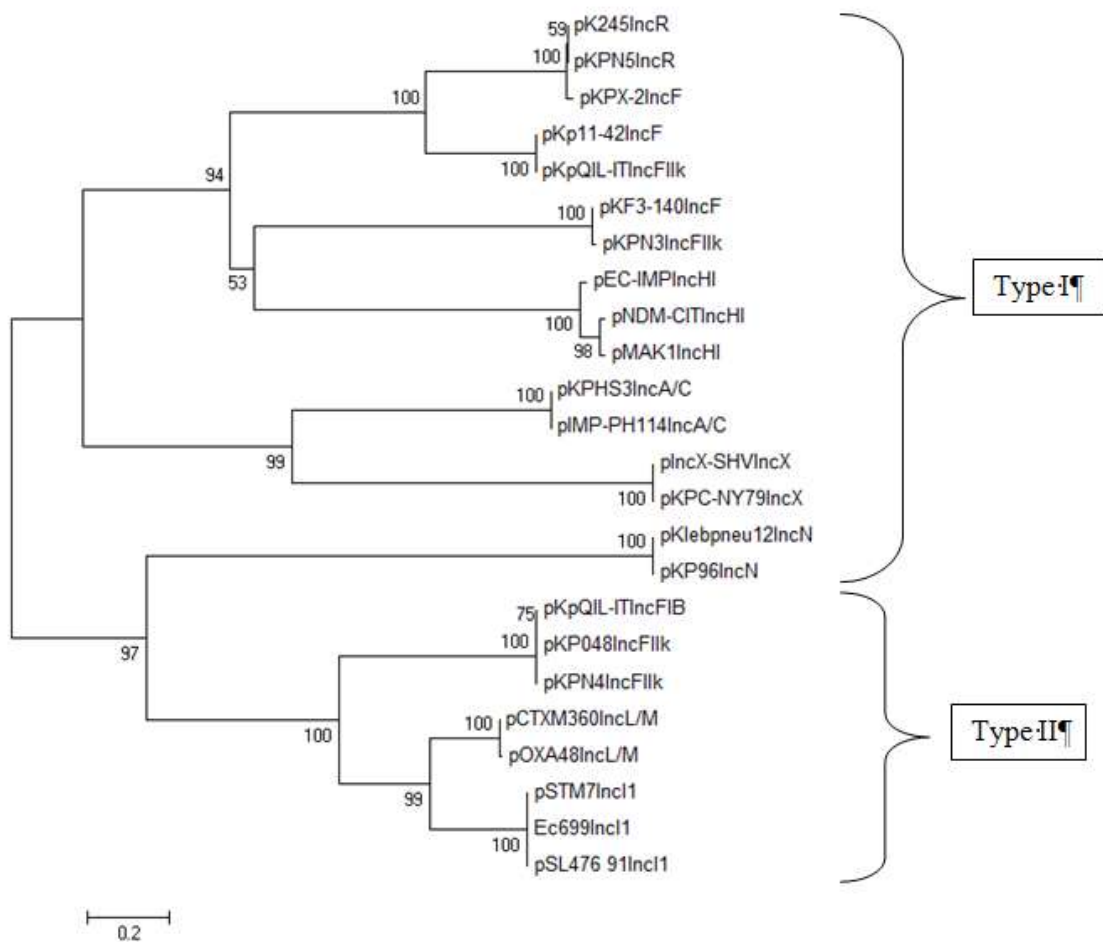


Figure 1. Phylogram of the partition proteins. Unrooted evolutionary tree showing 24 ParA and ParB proteins (or equivalent) from plasmid of *K. pneumoniae*, *E. coli*, *Salmonella spp.*, *C. freundii*, *E. cloacae*. pKpQIL-IT include two *par* loci. Types I and II refer to the two types of plasmid-encoded partitioning loci shown in Fig. 1 and described in the text. The phylogram was constructed using Mega5 (Neighbor-Joining algorithm, bootstrap: 1000 replication).

Table 1. Primers used in this study.

PCR name and plasmid type detected	Primer name	Sequence (5' - 3')	Length (bp)	Plasmid prototype	EMBL accession number	Target site	Amplicon size (bp)	Primer concentration (μ M)
Multiplex I, II, III: IncFIA, IncFIB, IncFIC, IncFII, IncFIIk	SopAB	CAACCAGTG	23	pKPN 3	CP00064 8.1	<i>sopA</i> <i>sopB</i>	1370	0,4
	-F1-for	CATAAGTGCT GGTC						
	SopAB	ACCATACGC	24					
	-F1-rev	GTGAGGCGC TCTCAA						
	SopAB	TAAACGCTG	21	pKF3- 140	FJ876827	<i>sopA</i> <i>sopB</i>	1130	0,4
	-F2-for	GTC						
	SopAB	GCGTGGTTTA	24					
	-F2-rev	ATCAGACGA TCGAA						
	SopAB	GGCTATTGCC	24	pKP18 7	CP00096 5.1	<i>sopA</i> <i>sopB</i>	720	0,4
	-F3-for	ATTGC						
SopAB	GCGCATACG	24						
-F3-rev	ACATTGATCG TGCCA							
Multiplex I : <i>sop</i> systems <i>E. coli</i> , <i>K. pneumoniae</i> , <i>S. enterica</i>	SopAB	CTATCGCCAT	22	pKPN-CZ	JX424424 .1	<i>sopA</i> <i>sopB</i>	928	0,4
	-F4-for	TGC						
	SopAB	ATGCTTCCCC	22					
	-F4-rev	AGGCATCCC GAA						
	SopAB	TAAACGCTG	21	pH233 2-166	KJ484626 .1	<i>sopA</i> <i>sopB</i>	1533	0,4
-F5-for	GTC							
SopAB	CTGTAAGTGC	24						
-		AGCAGCTTTA						

Multiplex II : <i>stb</i> systems <i>K. pneumoniae</i>	F5_rev	CGAC						
	KP-	TTTGAAGGC						
	StbAB	GATGAGCTTC	24	pKP04	FJ628167	<i>stbA</i>	1211	0,2
	-F2-for	AGACC	8			<i>stbB</i>		
	KP-							
	StbAB	GCCCCACCAT						
	-F2-	TTTCGGGCTC						
	rev	CATCC	24					
	KP-	GTCACGGTAT						
	StbAB	TTGTTGTACA	24	pKpQI	JN233705	<i>stbA</i>	453	0,2
	-F4-for	CTCC	L-IT			<i>stbB</i>		
	KP-							
StbAB	GTTGATACG							
-F4-	GTTTTGGATA							
rev	CGCCA	24						
EC-	GAACGTATA							
StbAB	CTGCGATGAT	21	pEC14	GQ39808	<i>stbA</i>	905	0,2	
-F1-for	GG	_114	6		<i>stbB</i>			
EC-								
StbAB	CTTTTTGCC							
-F1-	AAGATGGTG							
rev	CCA	22						
EC-	CCGGAATGG							
StbAB	TCTATGACGC	23	pKPC-	KC78840	<i>stbA</i>	1061	0,2	
-F2-for	TGCA	LKEc	5		<i>stbB</i>			
EC-								
StbAB	ATCAGGAAC							
-F2-	GGCAATCGTT							
rev	CATCC	24						
EC-	GCGGTCGCA							
StbAB	AAATTGCCG	24	pO145	CP00626	<i>stbA</i>	1194	0,2	
-F3-for	AAGCTG	-13516	3.1		<i>stbB</i>			
EC-								
StbAB	GAATTTTGCT							
-F3-	TGTTTCCCAG							
rev	AC	22						
Multiplex IV : IncA/C, L/M, N	ParAB							
	-AC-	AGGCCTTTTA	20	pKPH	CP00322	<i>parA</i>		
	for	TCTGGCGTTA	S3	5		<i>parB</i>	1817	0,4
	ParAB	GACAGTAGA						
	-AC-	CGGAACCAG						
	rev	AG	20					
	ParAB	CCACCAACA						
	-LM-	TCAAACCTGG	19	pOXA	JN626286	<i>parA</i>	1378	0,1
	for	C	-48			<i>parB</i>		
	ParAB	CAGATGCTG						
-LM-	GACGTTCTTA							
rev	C	20						
StbAB	TCCCGGCATT			EU19544	<i>stbA</i>			
C-N-	ATTGATAAA	24	pKP96	9	<i>stbB</i>	1093	0,1	

	for	GAGTT				<i>stbC</i>		
	StbAB	ACGGGTT-						
	C-N-	AAACGTCTC						
	rev	AGC	18					
Multiplex V : IncHI	ParAB	AAGATCGCC						
	-Hla-	CTCGTTGGTC		pEC-	EU85578	<i>parA</i>		
	for	AG	21	IMP	8	<i>parB</i>	2020	0,4
	ParAB	CAACTTTTTG						
	-Hla-	AGCAACCTG						
	rev	GAG	22					
	ParAB	AAGATCGCC						0,4
	-Hlb-	CTTGTCGGTC		pMAK	AB36644	<i>parA</i>		
for	AACG	23	1	0	<i>parB</i>	1765		
ParAB	TGGTAACAA							
-Hlb-	ATCCATGCTC							
rev	TTCCA	24						
Multiplex VI : IncR, IncII		TC-ACGA-						
	ParAB	CCAGCAAAA			CP00096	<i>parA</i>		
	-R-for	AGAGGAA	20	pKP91	6	<i>parB</i>	2032	0,4
		GCTAAACTC						
	ParAB	ATAAGTCAG						
	-R-rev	CGT	20					0,4
		GACGGCGAG						
	ParAB	AAGTTTTTCAT			Replicols	<i>parA</i>		
-II-for	T	20	Ec699	cope	<i>parB</i>	1227		
ParAB	TTCAGCGTTT							
-II-rev	CTTCTGGTCT	20						
Simplex VII : IncX		GAGCTTCAA						
	ParA-	CAGCAGAAC		pIncX-				
	X-for	AG	21	SHV	JN247852	<i>parA</i>	633	0,2
	ParA-	ATTGCATCAT						
X-rev	GTCTGGCTTG	20						

Table 2. Recipient cells used in validation experiments. Tc : transconjugants, Tf : transformant, PRaseT : plasmid relaxase gene typing, PBRT : PCR-based replicon typing, PAR-T : plasmid partitioning genes typing. † : Tc used as a positive control in partitioning genes typing.

N°	Parental strain	Tc/Tf	β -Lactamase	Plasmid classification	
				PRaseT (and/or PBRT)	PAR-T
48	<i>E. coli</i>	Tc	TEM-52	X1	X
51	<i>E. coli</i>	Tc	TEM-3	L/M	X
52	<i>E. coli</i>	Tf	TEM-52	X1	X
57	<i>E. coli</i>	Tc	SHV-12	F	F
62	<i>E. coli</i>	Tc	SHV-2	FIB	F
64	<i>E. coli</i>	Tc	SHV-5	X4	-
73	<i>E. coli</i>	Tc	SHV-4	FIIK	FIIK
85	<i>E. coli</i>	Tf	CTX-M-1	FIA	F
91	<i>E. coli</i>	Tc	CTX-M-3	N	N
94†	<i>E. coli</i>	Tc	CTX-M-9	FII	F
98	<i>E. coli</i>	Tc	CTX-M-1	X1	X
100	<i>E. coli</i>	Tc	CTX-M-1	FIA, FII	F
102	<i>E. coli</i>	Tc	CTX-M-1	HI2	HIa
104	<i>E. coli</i>	Tf	CTX-M-1	FIA, FIB, FII	F
105	<i>E. coli</i>	Tc	CTX-M-1	L/M	L/M
108	<i>E. coli</i>	Tf	CTX-M-1	FIA	F
110	<i>E. coli</i>	Tc	CTX-M-1	X4	-
111†	<i>E. coli</i>	Tc	CTX-M-1	FIA	F
114	<i>E. coli</i>	Tc	CTX-M-1	L/M	L/M
115	<i>E. coli</i>	Tc	CTX-M-9	FII	F
118	<i>E. coli</i>	Tc	CTX-M-1	FIA, FIB	F
120	<i>E. coli</i>	Tc	CTX-M-3	FIB	F
122	<i>E. coli</i>	Tc	CTX-M-9	FII	F
125	<i>E. coli</i>	Tc	CTX-M-1	FII	F
126	<i>E. coli</i>	Tc	CTX-M-1	N	N
127	<i>E. coli</i>	Tc	CTX-M-3	FIB	F
Levy	<i>E. coli</i>	Tc	OXA-48	L/M	L/M
AD-48	<i>E. coli</i>	Tc	OXA-48	L/M	L/M
AD-50	<i>E. coli</i>	Tc	OXA-48	L/M	L/M
AD-17	<i>E. coli</i>	Tc	OXA-48	L/M	L/M
AD-44-2	<i>E. coli</i>	Tc	NDM-1	N	N
AD-2	<i>E. coli</i>	Tc	OXA-48	L/M	L/M
Goe-137	<i>E. coli</i>	Tc	VIM	HI2	HIa
Goe-132	<i>E. coli</i>	Tc	VIM	A/C	A/C
KATS	<i>E. coli</i>	Tc	NDM-1, CTX-M-1	F	F
M-2	<i>E. coli</i>	Tc	KPC-2	L/M	L/M
M-3	<i>E. coli</i>	Tc	KPC-2	L/M	L/M
M-5	<i>E. coli</i>	Tc	KPC-2	L/M	L/M
Ec50	<i>E. coli</i>	Tc	TEM-52	II	II
S1	<i>K. pneumoniae</i>	Tc	CMY-4	A/C	A/C

S3	<i>K. pneumoniae</i>	Tc	FOX-3	A/C	A/C
S4	<i>K. pneumoniae</i>	Tc	DHA-1	A/C	A/C
S6	<i>K. pneumoniae</i>	Tc	SHV-5	A/C	A/C
S8	<i>K. pneumoniae</i>	Tc	CMY-2	A/C	A/C
S9	<i>K. pneumoniae</i> †	Tc	SHV-4	FIIk	F
S10	<i>K. pneumoniae</i>	Tc	ACC-1	A/C	A/C
S11	<i>K. pneumoniae</i>	Tc	CMY-4	A/C	A/C
S12	<i>K. pneumoniae</i>	Tc	SHV-2, DHA-1	FIIk, R	F, R
S13	<i>K. pneumoniae</i>	Tc	SHV-1	A/C	A/C
S14†	<i>K. pneumoniae</i>	Tc	CTX-M-15, CMY-4, VIM-4	A/C	A/C
S16	<i>K. pneumoniae</i>	Tc	CTX-M-3	A/C	A/C
S18	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	F	F
S19†	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	N	N
S20	<i>K. pneumoniae</i>	Tc	OXA-1, SHV-2a, CTX-M-15	F	F
S21	<i>K. pneumoniae</i>	Tc	TEM-3	A/C	A/C
S23	<i>K. pneumoniae</i>	Tc	CTX-M-3	N, A/C	N, A/C
S24	<i>K. pneumoniae</i>	Tc	TEM-3	A/C	A/C
S26	<i>K. pneumoniae</i>	Tc	SHV-12	N	N
S28	<i>K. pneumoniae</i>	Tc	DHA-1	L/M	L/M
S30†	<i>K. pneumoniae</i>	Tf	OXA-1, DHA-1	R	R
S33	<i>K. pneumoniae</i>	Tf	DHA-1	R	R
S34†	<i>K. pneumoniae</i>	Tc	DHA-1	L/M	L/M
S36	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-3	FII	F
S43	<i>K. pneumoniae</i>	Tc	CTX-M-3	N	N
S45	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	L/M	L/M
S46	<i>K. pneumoniae</i>	Tc	CTX-M-15	L/M	L/M
S47	<i>K. pneumoniae</i>	Tc	CTX-M-3	L/M	L/M
S48	<i>K. pneumoniae</i>	Tc	CTX-M-15	L/M	L/M
S49	<i>K. pneumoniae</i>	Tc	CTX-M-15	L/M	L/M
S51	<i>K. pneumoniae</i>	Tc	SHV-12	FIIk	F
S53	<i>K. pneumoniae</i>	Tc	SHV-12	R	R
S55	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	FIIk	F
S56	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	FIIk R	F, R
S61	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	F	F
S68	<i>K. pneumoniae</i>	Tc	TEM-129	A/C	A/C
S72	<i>K. pneumoniae</i>	Tc	SHV2a	F	F
S73	<i>K. pneumoniae</i>	Tc	SHV-4	A/C	A/C
S75†	<i>K. pneumoniae</i>	Tc	OXA-1, CTX-M-15	FIIk	F
S76	<i>K. pneumoniae</i>	Tc	TEM-12	F	F
S77	<i>K. pneumoniae</i>	Tf	SHV-12	R	R
S78	<i>K. pneumoniae</i>	Tc	CTX-M-15	FII	F

S79	<i>K. pneumoniae</i>	Tc	CTX-M-15	F	F
S82	<i>K. pneumoniae</i>	Tc	CTX-M-15	FII	F
S83	<i>K. pneumoniae</i>	Tc	TEM-3	A/C	A/C
S86	<i>K. pneumoniae</i>	Tc	CMY-4	A/C	A/C
S88	<i>K. pneumoniae</i>	Tc	SHV-2a	FIIIk	F
S89	<i>K. pneumoniae</i>	Tc	TEM-21	A/C	A/C
S90†	<i>K. pneumoniae</i>	Tc	KPC	X3	X
FM1	<i>K. pneumoniae</i>	Tc	OXA-48, CTX-M-15	L/M	L/M
FM2	<i>K. pneumoniae</i>	Tc	OXA-48, CTX-M-15	L/M	L/M
FUR-STA	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
CLE-TN	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
PET-TN	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
MUR-STA	<i>K. pneumoniae</i>	Tc	NDM-1	FIIIk	F
2966	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
LD-1131	<i>K. pneumoniae</i>	Tc	VIM	R	R
LD-3856	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
Z-19760	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
Z-45518	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
Z-16300	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
Z-47994	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
Z-4359	<i>K. pneumoniae</i>	Tc	OXA-48	L/M	L/M
MIKH	<i>K. pneumoniae</i>	Tc	OXA-48, CTX-M9	HI1	HIb
BHR	<i>K. pneumoniae</i>	Tc	VIM-4, CTX-M-1	HI1	HIb
M-4	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-6	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-7	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-14	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-20	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-32	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-40	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-41	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-50	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-52	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
M-53	<i>K. pneumoniae</i>	Tc	KPC-2	L/M	L/M
TNDHA-5	<i>K. pneumoniae</i>	Tc	DHA-1, SHV-12	HI2	HIb
TNDHA-6	<i>K. pneumoniae</i>	Tc	DHA-1, SHV-12	HI2	HIb
TNDHA-7	<i>K. pneumoniae</i>	Tc	DHA-1, SHV-12	HI2	HIb
TNDHA-8	<i>K. pneumoniae</i>	Tc	DHA-1, SHV-12	HI2	HIb
S00056	<i>S. enterica</i> Typhimurium	Tc	CTX-M-2	HI2	HIa
S00319†	<i>S. enterica</i> Havana	Tc	CTX-M-15	HI2	HIa

S01331	<i>S. enterica</i> Tel el kebir	Tc	CTX-M-15	HI2	HIa
S01477†	<i>S. enterica</i> Typhimurium	Tc	CTX-M-1/CMY-2	HI1, I1	I1, HIb
S01650	<i>S. enterica</i> Brandenburg	Tc	CTX-M-14	FrepB	F
S03207	<i>S. enterica</i> Typhimurium	Tf	CTX-M-15	FIA, FIB	F
S03663	<i>S. enterica</i> Grumpensis	Tc	CTX-M-15	HI2	HIa
S03664	<i>S. enterica</i> Typhimurium	Tc	CTX-M-15	N	N
S04662	<i>S. enterica</i> Virchow	Tc	CTX-M-32	N	N
S05343	<i>S. enterica</i> Concord	Tc	CTX-M-15	HI2	HIa
S07364	<i>S. enterica</i> Miami	Tc	SHV-2	N	N
S09118	<i>S. enterica</i> Keurmassar	Tc	SHV-12	HI2, FI	F, HIa
S27078	<i>S. enterica</i> Carmel	Tc	CTX-M-15	FrepB	F
S7917	<i>S. enterica</i> Derby	Tc	ND	FIA	F
S7981	<i>S. enterica</i> Saintpaul	Tc	OXA-48	L/M	L/M
M-1	<i>S. enterica</i> Enteritidis	Tc	KPC-2	L/M	L/M
S1106†	<i>S. enterica</i> Virchow	Tc	SHV-12	I1	I1

Table 3. Plasmid partition gene typing of 30 clinical strains of Enterobacteriaceae.

N°	Parental species	β -Lactamase	PRase T	PAR-T				
				Multiplex I and II	Multiplex III	Multiplex IV	Multiplex V	Simple x VI
3	<i>E. coli</i>	TEM-24	A/C		A/C			
15	<i>E. coli</i>	TEM-24	A/C, II		A/C		II	
17	<i>E. coli</i>	TEM-24	A/C, F, HI2, X4	F	A/C	HI		-
19	<i>E. coli</i>	TEM-21	A/C, N, X1	F	A/C, N			-
23	<i>E. coli</i>	TEM-24	A/C, F, II	F	A/C		II	
26	<i>E. coli</i>	TEM-24	A/C, F, HI1	F	A/C	HIa		
28	<i>E. coli</i>	TEM-21	A/C, X1		A/C			-
33	<i>E. coli</i>	TEM-24	A/C		A/C			
34	<i>E. coli</i>	TEM-24	A/C, N, X1	F	A/C, N			-
40	<i>E. coli</i>	TEM-24	A/C, F	F	A/C			
50	<i>E. coli</i>	TEM-52	II				II	
84	<i>E. coli</i>	CTX-M-1	F HI1, N	F	N	HIb		
88	<i>E. coli</i>	CTX-M-1	F, HI1, N	F	N	HIa		
101	<i>E. coli</i>	CTX-M-2	HI2			HIa		
105	<i>E. coli</i>	CTX-M-1	L/M, II		L/M		-	
106	<i>E. coli</i>	CTX-M-1	F, HI1, N	F	N	HIa		
107	<i>E. coli</i>	CTX-M-2	II, F	F			II	
KpS 5	<i>K. pneumoniae</i>	DHA-1	FIK, L/M	F	L/M		R	
KpS 19	<i>K. pneumoniae</i>	CTX-M-15, DHA-1	FIK, F, L/M, N	F	L/M, N			
KpS 20	<i>K. pneumoniae</i>	CTX-M-15, SH	F, X4	F				-

		V-2a						
KpS 26	<i>K. pneumoniae</i>	SHV- 12	FIIK, N	F	N		R	
KpS 47	<i>K. pneumoniae</i>	CTX- M-3	HI2, L/M		L/M	HIa		
KpS 63	<i>K. pneumoniae</i>	DHA-1	FIIK, L/M	F	L/M			
KpS 83	<i>K. pneumoniae</i>	TEM-3	A/C, F, N		A/C, N			
KpS 88	<i>K. pneumoniae</i>	SHV- 2a	FIIK	F				
KpS 92	<i>K. pneumoniae</i>	CTX- M-14, VIM-1	F, FIIK, II	F			II	
FM- 2	<i>K. pneumoniae</i>	OXA- 48	FIIK, L/M, N	F	L/M, N			
FM- 10	<i>K. pneumoniae</i>	OXA- 48	A/C, L/M		A/C, L/M			
S10- 1477	<i>S. enterica</i> Typhimurium	CTX- M-1, CMY- 2	HI1, II			HIb	II	
S10- 1526	<i>S. enterica</i> Typhimurium	CTX- M-1, CMY- 2	HI1, II			HIb	II	

Highlights

-Low-copy-number plasmids utilize partition systems for plasmid maintenance.

-*par* loci are organized into operons encoding two proteins, an ATPase and a DNA-binding protein, and including a centromeric site.

-The method called “plasmid partition gene typing” showed high specificity for the classification of resistance plasmids (IncA/C, FIA, FIB, FIC, FIIk, FII, HI1, HI2, I1, L/M, N) except for IncX replicons.

ACCEPTED MANUSCRIPT