Bacterial partitioning proteins affect the subcellular location of broad-host-range plasmid RK2

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INTRODUCTION

Spatial organization, localization and appropriate distribution of genetic material are essential for all cellular organisms. Major advances in the understanding of DNA dynamics in bacteria have been achieved by using fluorescence microscopy to visualize the intracellular location of plasmids and bacterial chromosomes. These studies have shown that plasmids are not randomly distributed but are located at distinct sites within bacterial cells. The low-copy-number Escherichia coli plasmids P1 (Gordon et al., 1997; Li & Austin, 2002) and F (Gordon et al., 1997, 2004; Niki & Hiraga, 1997) as well as Salmonella enterica plasmid R27 (Lawley & Taylor, 2003) are found at the mid-cell of newborn cells or symmetrically at the ¼ and ¾ positions in older, pre-divisional cells. For some plasmids, it was proposed that plasmid particles could form clusters. Plasmid R1, with a copy number of four to five per cell, also forms symmetrically located clusters, although in older cells, R1 clusters are shifted towards the cell poles (Jensen & Gerdes, 1999; Weitao et al., 2000). The mid-cell, ¼ and ¾ cellular positioning of plasmid clusters has been observed for the broad-host-range plasmid RK2 (60 kb in size) in E. coli, Pseudomonas aeruginosa and Vibrio cholerae (Pogliano et al., 2001; Ho et al., 2002). This plasmid belongs to the IncP-1 incompatibility group, is present at five to eight copies per chromosome, and is stably maintained in almost all Gram-negative bacteria (Rosche et al., 2000; Thomas et al., 1980, 1984; Wilson et al., 1997). When plasmids RK2, F and P1 were localized simultaneously, the majority of plasmid foci were close to but separated from each other, demonstrating that compatible bacterial plasmids are in independent cellular locations in E. coli (Ho et al., 2002). The subcellular localization of these plasmids is thought to be mediated by the partitioning (Par) systems they encode. Plasmid partitioning loci function as a cassette containing genes for two trans-acting proteins and a cis-acting centromere-like site. The first gene of a par operon encodes a ParA-like protein, which is a Walker box or actin-like ATPase (Ebersbach & Gerdes, 2005; Funnell, 2005). The product of the second gene, a ParB-like protein, binds as a dimer to specific sequences within the cis site (Schumacher & Funnell, 2005). The formation of a partitioning complex and oscillations of the filament-forming ParA ATPase were proposed to result in localization of the plasmid to the mid-cell or the ¼ and ¾ positions, which represent the middle of the next cell generation (Ebersbach & Gerdes, 2004; Ebersbach et al., 2006). For plasmid RK2, the partitioning cassette consists of the genes encoding IncC, a Walker box ATPase, and KorB, a protein that interacts with a palindromic operator (O8) found 12 times in RK2 DNA (Kostelidou & Thomas, 2000; Rosche et al., 2000; Williams et al., 1998). The rules governing plasmid positioning in bacterial cells are not fully understood. It is not known, for example, what bacterial factors affect plasmid cluster formation, localization and partitioning. In this work we demonstrate that...
chromosomal partitioning genes affect the subcellular location of a plasmid mini-replicon.

METHODS

Plasmids and bacterial strains. The plasmids and bacterial strains used in this work are listed in Table 1. Plasmids were introduced into E. coli and Pseudomonas cells by transformation (Sambrook et al., 1989).

Media and growth conditions. Bacteria were grown at 30 °C in LB or M63/glucose media. Antibiotics were added to the following final concentrations: ampicillin 50 μg ml⁻¹ for liquid media or 100 μg ml⁻¹ for agar plates, chloramphenicol up to 150 μg ml⁻¹, kanamycin 30 μg ml⁻¹ for liquid media or 60 μg ml⁻¹ for agar plates, gentamicin up to 20 μg ml⁻¹, tetracycline up to 50 μg ml⁻¹.

Fluorescence in situ hybridization (FISH). Mini-RK2 specific Cy3-labelled probes for FISH were prepared essentially as described by Pogliano et al. (2001). The procedure was modified as follows. After incubation with the blocking solution, the cells were treated with lysozyme (1 mg ml⁻¹ in PBS) for 10 min at room temperature. The next step was the same as described by Jensen & Shapiro (1999). Chromosomal DNA was stained with 4′,6-diamidino-2-phenylindole (DAPI) at a concentration of 0.5 μg ml⁻¹.

Fluorescence microscopy. E. coli S17-1 and Pseudomonas strains were prepared for microscopy as described previously (Ho et al., 2002; Pogliano et al., 2001). The expression of tetR-eyfp from pKO10 and pKO15 was induced with 0.4 % arabinose for 1 h. The expression of para, parB and tetR-eyfp from pLAK15 in E. coli cells was induced with 0.4 % arabinose for 1.5 h. The expression of tetR-eyfp in E. coli MGTRY was induced as described by Verheust & Helinski (2007). The cells were stained with FM4-64 (0.5 μg ml⁻¹), immobilized on a poly-L-lysine-treated slide coverslip and observed using an Olympus BX51 fluorescence microscope with F-View-II CCD camera. Measurements and image analysis were conducted with AnalySIS software.

Gel filtration assay. Column gel filtration was used to fractionate the DNA–ParB complexes as described previously (Konieczny & Helinski, 1997). The reaction mixture (100 μl), containing P. putida ParB (4 μg) and the indicated supercoiled plasmid DNA (2 μg) in 40 mM HEPES/KOH, pH 8.0, 40 mM potassium glutamate, 10 mM magnesium acetate, 4 % sucrose, 4 mM dithiothreitol, and 2 mM ATP, was incubated for 20 min at 32 °C and then run through a Sepharose CL-4B (0.5 × 12 cm) column, equilibrated at room temperature with the incubation buffer and 0.01 % Brij 58. Fractions (80 μl) were collected and a portion of each (35 μl) was analysed by SDS-PAGE followed by silver staining, while another portion (35 μl) was analysed on agarose gel stained with ethidium bromide.

Formaldehye cross-linking and chromat immunoprecipitation. Cells were grown at 30 °C in LB medium. Samples were taken during exponential growth (OD₆₀₀ 0.6) and prepared as described by Lin & Grossman (1998). Protein–DNA complexes were immunoprecipitated with polyclonal anti-ParB antibodies (C. M. Thomas, University of Birghmingam, UK), followed by incubation with 30 μl of a 50 % Protein A-Sepharose slurry (Amersham Pharmacia). PCR was performed with Taq DNA polymerase (Fermentas) and oligonucleotide primers (O₁, 5′-TCGCGCCTGCCAACCACCTCGGC-3′; O₂, 5′-TTATGGCTCATATCGAAAGTCTC-3′; O₃, 5′-GCCCGCATACCTAACGAGTTGTTGCG-3′; O₄, 5′-GGACCAACAGAATGGAAGTGTTCGTGCTT-3′; oriV, 5′-AACCGGATCTGGAGAACACCCGC-3′; 5′-AAAGCAGGTTAGCCTGCGC-3′; 5′-CCGCTTCAGCTCCAACCCCAGAC-3′, 5′-CTTGGCAAGGCTTGGTCAAGTGTTACC-3′). PCR products were separated on agarose gels and stained with ethidium bromide.

Purification of ParB. The P. putida ParB protein was expressed from plasmid PETK1 (Table 1). The bacterial strain, the conditions of parB expression and the protein purification were the same as described for the P1 plasmid ParB homologue (Davis & Austin, 1988) with the exception that only a phosphocellulose column was used. Peak fractions were pooled and dialysed against P buffer (150 mM NaCl). The final product yielded 8 μg ml⁻¹ of >95 % homogeneous protein.

RESULTS AND DISCUSSION

The subcellular position of RK2 mini-replicons depends on the host bacterium

To test for the possibility that a host cell can affect plasmid positioning, a dual plasmid system was used allowing identification of the location of clusters of the mini-derivative pCVI of broad-host-range plasmid RK2 in the cells of different host bacteria. pCVI, which lacks partitioning genes but contains two centromere-like sites (O₃₁⁹ and O₉₁⁸), the gene for plasmid replication initiator protein (trfA), the origin for vegetative DNA replication (oriV), the origin for conjugational transfer (oriT), antibiotic resistance determinants and a tetO array, was tagged by the TetR-EYFP fusion protein expressed from pKO10, an RK2-compatible dual-origin broad-host-range plasmid. The subcellular location of pCVI was examined after arabinose induction of the tetR-eyfp gene and staining of the cell membrane with the fluorescent dye FM4-64. When both plasmids were introduced into E. coli cells, arabinose induction resulted in fluorescent signals mainly localized at one of the cell poles (Fig. 1A i, ii, iii; D). Fluorescent foci were observed in only approximately 50 % of the cells, the majority of which had only one focus. A small fraction of E. coli cells had two foci (Fig. 1A iv, E). A similar subcellular distribution of pCVI was obtained when the TetR-EYFP protein was expressed from the tetR-eyfp gene on the chromosome of E. coli MGTRY (data not shown). Polar positioning of pCVI was confirmed by FISH in E. coli cells containing only this plasmid (Fig. 1B). Plasmid fluorescent signals were observed on the edge of DAPI-stained E. coli nucleoids, suggesting that the plasmid was not located in the mid-cell or ¼, ¼ positions but at the cell poles. Similarly as we observed for pCVI, it was previously reported that F and R1 mini-derivatives lacking...
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the partitioning segments are distributed at the cell poles (Ebersbach & Gerdes, 2004; Niki & Hiraga, 1997). Polar localization of RK2 mini-replicons in *E. coli* cells has also been reported recently by Verheust & Helinski (2007), who showed that insertion of the RK2 *par* locus into pCVI restores the mid-cell, or *J*, *L* positions of plasmid foci.

When we examined the localization of pCVI in *P. putida*, the results differed substantially from those obtained in *E. coli*. Instead of a polar location, we observed that the plasmid formed foci at approximately mid-cell and the *J*, *L* positions (Fig. 1F i, J). Also FISH and DAPI co-staining demonstrated plasmid foci inside DAPI-stained *P. putida* nucleoids (Fig. 1G). Overall, the location of pCVI foci in *Pseudomonas* cells was similar to the location of intact RK2 (data not shown), although with a broader distribution in the case of the mini-derivative clusters. Also, as observed in *E. coli*, foci of the mini-derivative were detected in only a few *P. putida* cells

**Fig. 1.** Subcellular localization of the RK2 mini-derivative pCVI in *E. coli* S17-1 and *P. putida* KT2440, grown in LB medium at 30 °C. The subcellular position of pCVI was determined by tagging with TetR-EYFP (A, F) or FISH (B, G). The gene for TetR-EYFP was expressed from pKO10. Cell membranes were stained with FM4-64 (red) (A, Ci, ii, F, Hi, ii). Chromosomal DNA was stained with DAPI (blue) (B, G). Representative *E. coli* S17-1 and *P. putida* KT2440 cells with one or two foci of pCVI are shown in panels A, B, F and G. Panels D, E, I and J demonstrate the subcellular distribution of pCVI in *E. coli* (D, E) and *P. putida* (I, J) for cells containing one focus (D, I) or two foci (E, J). Each point represents the relative position of a single focus measured as the distance to the pole in relation to the cell length. The pole was chosen randomly. Cell length is plotted against position of foci given as a fraction of cell length. Negative controls for tagging with TetR-EYFP and FISH are shown in panels C and H: representative *E. coli* S17-1 and *P. putida* KT2440 cells containing just pCVI (C i, H i), pKO10 (C ii, H ii) or no plasmid DNA (C iii, H iii).

**Fig. 2.** ParB protein from *P. putida* forms a complex with plasmid RK2 and its mini-derivative in vitro. The reaction mixture contained the indicated supercoiled DNA (RK2, pCVI, pUC18, pUC18-O_{B_9}^{+}(RK2), pUC18-O_{B_10}^{-}(RK2), pUC18-IR2_{P. putida}) and ParB protein in the amounts and with the incubation conditions described in Methods. After incubation, the reaction mixtures were loaded on a Sepharose CL-4B column. Fractions were collected and analysed by SDS-PAGE followed by silver staining. Agarose gels were stained with ethidium bromide.
fraction of the *Pseudomonas* cells (60%). Our experiments were carried out in both LB and M63/glucose media and no substantial difference was observed regarding plasmid positioning and plasmid foci number. We have also analysed RK2 mini-derivative localization in *P. aeruginosa* (data not shown). Using either TetR-EYFP tagging or FISH experiments we demonstrated that pCVI localization in *P. aeruginosa* is similar to that in *P. putida*.

In control experiments, the expression of *tetR-eyfp* in *E. coli* and *P. putida* cells without pCVI resulted in yellow fluorescence of the whole cells (Fig. 1C ii, H ii). When *tetR-eyfp* was not expressed in the cells, no signal was detected (Fig. 1C i, H i). Also FISH and DAPI co-staining demonstrated no signal when bacterial cells did not contain pCVI (Fig. 1C iii, H iii).

**P. putida** ParB protein interacts with RK2 DNA by binding centromere-like sites

The fluorescence microscopy experiments indicated that the subcellular localization of an RK2 mini-derivative that lacks partitioning genes depends on the host bacterium. This raised the possibility that the subcellular position of an RK2 mini-derivative could be affected by host factors, including the host-encoded partitioning machinery. Some similarities between the RK2 and *Pseudomonas* partitioning systems have been described (Hayes, 2000). In addition, RK2 and *Pseudomonas*, but not *E. coli*, have a type I par locus (Mohl & Gober, 1997; Ogasawara & Yoshikawa, 1992). The ParB protein from *P. putida* shows high similarity to the RK2 KorB protein (Lin & Grossman, 1998): based on amino acid sequence, it is 27% identical with KorB. It has also been demonstrated that KorB of RK2 specifically interacts with the *P. putida* chromosomal *cis* site (Chiu & Thomas, 2004). We asked if the *P. putida* ParB protein could interact with RK2 DNA. Size-exclusion chromatography was used to investigate this possibility. Purified ParB protein was incubated with or without plasmid DNA and then fractionated using a Sepharose CL-4B column. The results demonstrated that *P. putida* ParB formed nucleoprotein complexes with RK2 DNA (Fig. 2). When the entire RK2 plasmid or its mini-derivative pCVI were present in the incubation mixture, the ParB protein was detected in the column void volume, indicating the

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**Fig. 3.** ParB interacts in live *P. putida* KT2440 cells with centromere-like sites of plasmid RK2 and its mini-derivative. The PCR-amplified products of immunoprecipitation (IP) with anti-ParB antibodies and lysates of *P. putida* KT2440 (A lane 2; B lane 2, C lane 1), *P. putida* KT2440(pCVI) (A lane 1, B lane 1) or *P. putida* KT2440(RK2) (C lane 2). Lanes 3, control reactions with isolated DNA (A, B) and negative control of immunoprecipitation with anti-ParB antibodies and *E. coli* S17-1(RK2) lysates (C). The PCR-amplified products were separated on 1% agarose gels and stained with ethidium bromide. Primers used in reactions were designed for RK2 plasmid sequences containing *O_b^3*, *O_b^10* and oriV regions and the IR-2 sequence of *P. putida* KT2440 chromosomal DNA as indicated. All primer sequences are listed in Methods.
formation of a nucleoprotein complex. In the absence of DNA or in the presence of pUC18 DNA, no ParB protein was found in void volume fractions (Fig. 2). This result indicated interaction of ParB with RK2 plasmid DNA. The pCVI plasmid used in our study did not contain incC or the korB genes; however, two RK2 centromere-like sites, O_B^10 and O_B^3, were still present adjacent to the trfA and oriT sequences. To investigate whether those sites are capable of interacting with *P. putida* ParB protein, DNA fragments containing O_B^10, O_B^3 or *P. putida* centromere site IR2 were introduced into pUC18 plasmid DNA. When incubations were carried out with these plasmid constructs, ParB was detected in the void fractions (Fig. 2). Since no ParB complex formation was observed with pUC18, we concluded that the observed nucleoprotein complexes are the result of ParB protein interaction with RK2 centromere-like sites. The RK2 O_B motifs differ from the *Pseudomonas* IR2 sequence; therefore we could not exclude the possibility that ParB possesses two domains for interaction with DNA.

To test the possibility that this interaction also occurs in *P. putida* cells, a chromatin immunoprecipitation with polyclonal anti-ParB antibodies followed by a PCR reaction with O_B^9-, O_B^10-, oriV-, or IR2-specific oligonucleotide primers was performed. The interaction of the ParB protein with RK2 O_B^3 and *P. putida* chromosomal IR2 was clearly detected when RK2 mini-derivative pCVI (Fig. 3A, B, lane 1 and Fig. 4 lane 1) was present in *P. putida* cells. Less intensive bands of O_B^10-specific PCR product detected in immuno-precipitation experiments suggest that ParB interaction with this site on RK2 mini-derivatives could be less efficient (Fig. 3A, lane 1 and Fig. 4 lane 1). When oriV-specific primers were used, we did not detect any signal, indicating that a ParB complex is not formed with the RK2 origin (Fig. 3A, lane 1 and Fig. 4 lane 1). When the RK2 mini-derivative was not present in *P. putida* cells, we were able to detect ParB interaction only with the chromosomal IR2 sequence (Fig. 3B, lane 2). Similar results indicating *P. putida* ParB interaction with both O_B^3 and O_B^10 sites were obtained when the entire RK2 plasmid was present in *P. putida* cells (Fig. 3C lane 2). When RK2 plasmid was present in *E. coli* cells, no signal was detected, indicating that anti-ParB antibodies did not interact with RK2 KorB protein (Fig. 3C lane 3). These data showed that in *P. putida* cells chromosomally encoded ParB protein interacts with centromere-like O_B sites of plasmid RK2 DNA.

**P. putida** ParAB affects the position of RK2 replicons

To further explore the possibility that the *Pseudomonas* partitioning machinery could affect the subcellular position of RK2 mini-derivatives, we investigated whether the expression of *P. putida* parAB could change the asymmetrical polar distribution of the RK2 mini-derivative in *E. coli* cells. Plasmid pLAK15 containing both the gene for TetR-EYFP and *P. putida* parAB under the control of the PBAD promoter was constructed and introduced into *E. coli* cells containing the RK2 mini-derivative pCVI. In control experiments, in *E. coli* cells, instead of pLAK15 we used pKO10, which expresses only tetR-eyfp. After arabinose induction, when only the tetR-eyfp gene was expressed, the pCVI localization was polar and asymmetric (Fig. 5A–C). Approximately 40% of the cells contained fluorescent plasmid foci and multiple signals were detected in only 3% of the cells (Fig. 5M). In contrast, when TetR-EYFP and both ParA and ParB *P. putida* proteins were expressed, the distribution of pCVI in *E. coli* cells was more or less symmetrical, with plasmid foci located in the proximity of the mid-cell or the ¼, ¼ positions (Fig. 5D–F). Also, the proportion of the cells containing plasmid foci increased (Fig. 5M). We detected plasmid foci in 60% of the cells and among them approximately 30% had more than one fluorescent signal. These data were very similar to those obtained in a control experiment where pCVI number and location were analysed in wild-type *P. putida* cells (Fig. 5G–I, M, N). Further, we asked if *P. putida* ParB protein interacted with pCVI centromere-like sites when both ParA and ParB
Fig. 5. ParA and ParB proteins from *P. putida* alter the location of RK2 plasmid. The subcellular position of pCVI (A–L, N, P) was determined by tagging with TetR-EYFP in *E. coli* S17-1 (A–F), *P. putida* KT2440 (G–I, N) and *P. putida* KT2440 ΔparAB Vkan (J–L, P). The subcellular position of pZZ15 was determined by tagging with LacI-GFP in *P. putida* KT2440 (O) and *P. putida* KT2440 ΔparAB Vkan (Q). Bacteria were grown in LB medium at 30 °C. Genes for TetR-EYFP, ParA and ParB were expressed from pLAK15, whereas only tetR-eyfp was expressed from pKO10 and lacI-gfp from pZZ15. Cell membranes were stained with FM4-64 (red). Representative cells with one (i, ii) and two (iii) foci of pCVI are shown in panels C, F, I and L. Panels A, D, G and J demonstrate the subcellular distribution of pCVI for cells containing one focus. In order to facilitate comparison, histograms have been used in which the distance of the plasmid focus to the nearest cell pole is shown as a fraction of cell length. Panels B, E, H and K demonstrate subcellular distribution of mini-RK2 for cells with two foci. Cell length (µm) is plotted against position of foci given as a fraction of cell length. (M) Table showing the percentage of cells containing no, one or two and more fluorescent foci when ParA and ParB proteins are or are not present in the cells.
were expressed from pLAK15 or pKO15 in E. coli cells. Chromatin immunoprecipitation demonstrated that indeed under those experimental conditions promoting the mid-cell or the ¼, ¼ positions of pCVI in E. coli cells (Fig. 5D–F), both O₉ and O₉,₁₀ sites were bound by P. putida ParB (Fig. 4, lanes 4 and 5). In a control reaction, no PCR products were observed when E. coli cells contained plasmid pKO10, without the P. putida parAB region (Fig. 4, lane 3).

We also analysed the subcellular location of pCVI in a P. putida ΔparABΔkan mutant. The lack of functional ParA and ParB proteins changed the localization of the pCVI foci from the approximately mid-cell and ¼, ¼ positions near the cell poles (Fig. 5J–L, P). We did not observe differences in the number of cells containing plasmid foci; however, the number of cells with a single signal was slightly increased compared to the wild-type P. putida (Fig. 5M). No O₉ and O₉,₁₀-specific PCR products were observed after immunoprecipitation of P. putida ΔparABΔkan(pCVI) extract with anti-ParB antibodies (Fig. 4, lane 2). In the control, when oriV-specific primers were used (Fig. 4, lane 2), no signal was detected either.

Interestingly, when the localization of the entire RK2 plasmid (pZZ15) was analysed in the P. putida ΔparABΔkan mutant, dispersed signals were observed compared with the localization of pZZ15 in P. putida wild-type cells (Fig. 5O, Q). This indicates that in P. putida disturbances in the chromosomally encoded partitioning system affect the subcellular position of RK2 plasmid.

Stability of RK2 and its mini-derivative pCVI in E. coli and P. putida strains

The data presented above clearly show that the expression of P. putida parAB genes affects the position of RK2 mini-deriplions. In E. coli, the expression of P. putida parAB genes compensates for the lack of the RK2 partitioning system with regard to the cellular location of the RK2 mini-derivative pCVI. In P. putida, the lack of chromosomal partitioning genes results in a shift of the position of pCVI towards the cell poles and disturbances of the localization of the entire RK2 plasmid. To test if the observed subcellular localizations of the RK2 plasmids affect their stabilities, we analysed the maintenance of pZZ15 and pCVI in the strains used in the course of this work. pZZ15 was stably maintained in both E. coli S17-1 and P. putida KT2440 (Fig. 6A, E). Although we observed disturbances in pZZ15 localization in P. putida KT2440ΔparABΔkan (Fig. 5Q), stability tests revealed that the plasmid is stably maintained in this mutant (Fig. 6A). This result could be explained by the compensating effect of the dispersed plasmid localization. Stabilities of RK2 mini-derivative pCVI in E. coli S17-1 and P. putida KT2440 were significantly reduced compared to the stabilities of pZZ15 in these strains (compare Fig. 6E with Fig. 6A and B). It must be pointed out that pCVI stability in P. putida KT2440, where the plasmid was found at approximately mid-cell and the ¼, ¼ positions (Fig. 1G), was better when compared to pCVI stability in E. coli S17-1, where it was located at the cell poles (Fig. 1B and compare Fig. 6E and B). The disruption of the P. putida parAB locus (mutant KT2440ΔparABΔkan) resulted in only a very limited reduction of pCVI stability (Fig. 6B). A similar effect was observed when pCVI stability was tested with pKO10 also present in the cell. The pCVI stability observed in P. putida KT2440ΔparABΔkan was slightly reduced in comparison with its stability in P. putida KT2440 (Fig. 6C).

Similarly, only a limited effect on chromosome stability was previously observed in P. putida KT2440ΔparABΔkan (Godfrin-Estevenon et al., 2002). Also, during our experiments the pCVI stability loss rate tested in E. coli in the presence of pKO15 or pKO10 was very similar, regardless of the expression of P. putida parAB genes (Fig. 6D). However, at the beginning of the experiment more cells contained pCVI in the strain where P. putida parAB was expressed (Fig. 6D).

Fig. 6. Stability of pCVI and pZZ15 in E. coli S17-1, P. putida KT2440 and P. putida KT2440ΔparABΔkan cells. Stability assays were performed as described in Methods. Stability of pZZ15 in E. coli (E) and P. putida (A). Stability of pCVI when the mini-derivative was present alone in the cells (B, E) or in the presence of another plasmid, pKO10 or pKO15, as indicated (C, D).
A limited effect of the parAB locus on RK2 mini-derivative stability could be a result of ParA and ParB, which may not support plasmid segregation as efficiently as IncC and KorB. It is also possible that the full stabilization of the plasmid mini-derivatives requires other factors such as additional O2 sites, or post-segregation killing (psk) and multimer resolution (msr) systems that are missing in RK2 mini-derivatives. Accordingly, when the RK2 par locus containing korB and incC genes was introduced into pCVI DNA, it restored the mid- and quarter-cell positions of the plasmid but did not stabilize the plasmid during cell growth (Verheust & Helinski, 2007).

In summary, the experiments reported here demonstrate, we believe for the first time, that the subcellular position of broad-host-range plasmid RK2 is affected by Pseudomonas partitioning machinery. The Pseudomonas partitioning module plays a role in chromosomal segregation (Godfrin-Estevenon et al., 2002; Lewis et al., 2002); however, it has also been speculated that it is a remnant of RK2-like plasmid integration (Chiu & Thomas, 2004). That may explain cross-talk between chromosomal and plasmid partitioning systems. Our results at least raise the possibility that in certain bacteria the chromosomally encoded partitioning machinery could affect the subcellular positioning of a specific plasmid element.

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