REVIEW
ARTICLE

Conditionally lethal genes associated with bacterial plasmids

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Overview

Bacterial cells commonly serve as hosts for plasmids and bacteriophages. Since both plasmids and bacteriophages are not capable of proliferation without the machinery of the bacterial host, their stable coexistence with the host would be expected to be symbiotic. However, this is not always the case. Bacteriophages are good examples of parasites since often the killing and the lysis of their host is part of their life cycle. In contrast, bacterial plasmids are generally thought of as stable extrachromosomal elements (Nordström & Austin, 1989). During the course of co-evolution of bacteria and plasmids, many non-essential genes were concentrated on plasmids from which they could be utilized by the host bacterium. Thus, bacterial plasmids could be considered as temporary endosymbionts (Sonea, 1991). However, new observations indicate that several bacterial plasmids carry genes capable of killing their host in a seemingly spiteful manner. In addition, recent experiments have identified plasmid genes that are conditionally lethal in a host-specific manner. What all these systems have in common is that they kill their host from within (the killer plasmid is initially present in the target cell), unlike colicins, microcins or antibiotics. Whilst most killing genes were identified as such and only operationally at the time of their discovery, their study is revealing a variety of mechanisms of interaction between plasmids and their hosts. The focus of previous reviews has been on post-segregational plasmid stabilization systems (Nordström & Austin, 1989; Jensen & Gerdes, 1995). The intention here is to provide a broader description of reasonably well-studied killer mechanisms employed by various plasmids. The killing of susceptible cells by bacteriocins and type II restriction-modification systems has been described elsewhere (Naito et al., 1995; Konisky, 1982) and is beyond the scope of this article.

Post-segregational killing of plasmid-free cells

Plasmids are normally inherited by both daughter cells when their host bacterium divides. If, however, the plasmid DNA has not replicated prior to cell division or the plasmid copies are physically joined to each other at the time of cell division, a plasmid-free daughter cell can be produced. To prevent this segregational loss, several independent mechanisms that ensure the stable maintenance of plasmids in the population have evolved. Some of these systems increase the likelihood of both daughter cells receiving a copy of the plasmid by selectively positioning plasmid DNA molecules (Fig. 1a) and are often called ‘true’ partitioning systems (reviewed in Williams & Thomas, 1992; Hiraga, 1992). Other stabilization systems are involved in the resolution of plasmid multimers into monomers, thus increasing the probability of equal distribution of plasmid molecules into daughter cells (Fig. 1b) (Summers & Sherratt, 1984; Austin et al., 1981). Unlike these partitioning systems, the post-segregational killing systems found on some plasmids do not increase the likelihood of a daughter cell receiving the plasmid. Rather, plasmids carrying such genes are capable of selectively killing plasmid-free segregants after they are produced (Fig. 1c). This post-segregational killing was observed and described in the IncFII plasmids R1 and F (Loh et al., 1988; Gerdes et al., 1986b) and there is also evidence that plasmids of the incompatibility groups P[RK2; (Young et al., 1985)] and bacteriophage P1 (Lehnher et al., 1993) encode gene products that have an analogous role. Post-segregational killing systems always contain two components: a stable killer toxin and an unstable factor that prevents expression of the toxin or functions as an antidote to it. While the killer toxin is always a protein, the antitoxin is either antisense...
RNA or a protein. The latter has also been named the proteic killer gene system (Jensen & Gerdes, 1995).

**Systems in which both the killer and its antidote are proteins**

The ccd locus [coupled cell division (Jaffé et al., 1985); or control of cell death (Van Melderen et al., 1994)] of the F plasmid is probably the best characterized post-segregational killer system in which both components are proteins. The ccd region has two components: ccdA (also called H or letA), which is a suppressor of inhibition, and ccdB (also called G, letB or letD), which codes for a lethal protein (Fig. 2). Although it was originally thought that the function of ccd is to couple cell division to the proliferation of the plasmid (Ogura & Hiraga, 1983), it was later shown that the presumptive coupling is achieved by the killing of the plasmid-free segregants (Jaffé et al., 1985). Jaffé et al. (1985) and later Hiraga et al. (1986) showed that if the replication of the plasmid was prevented, the plasmid-free segregants became non-viable and formed long filaments. This phenomenon was explained by the non-viable segregant model. When the replication of a thermosensitive-replication derivative of the plasmid was inhibited by a temperature shift, plasmid molecules were diluted by cell division and eventually a plasmid-free subpopulation of cells arose. These were, however, inhibited in their growth, formed filaments and became non-viable. It was speculated (Jaffé et al., 1985) that this was due to the rapid decay of the CcdA protein, which enabled the toxic CcdB gene product to kill the cells. Hiraga et al. (1986) showed in a separate experiment that this must indeed be the case since the viability of the coexisting plasmid-free cells, which never carried the plasmid, was not affected. These experiments suggested that the killing action does not work by cell-to-cell contact and therefore the killing must be occurring from within.

Several studies have focused on the control and regulation of the ccd operon. It has been shown that expression of ccdA and ccdB is negatively controlled at the level of transcription (Tam & Kline, 1989a). The repression of the ccd operon is achieved only if both the CcdA and CcdB proteins are present. It was also shown (Tam & Kline, 1989b) that the CcdA and CcdB proteins form a complex even in the absence of the ccd operator. A recent study by Salmon et al. (1994) indicated that the domain of the CcdA protein responsible for autoregulation is different from the domain involved in the antidote effect; several missense CcdA polypeptides that lost their autoregulatory activities retained the ability to antagonize the lethal activity of CcdB. The same was shown for the CcdB toxin; mutants that inactivated CcdB killer activity retained their autoregulatory properties (Bahassi et al., 1995).

The CcdB protein (11700 Da) acts by poisoning DNA-gyrase complexes (Maki et al., 1992; Bernard & Couturier, 1992). The tetrameric A₂B₂ DNA-gyrase is an essential cellular enzyme that catalyses negative supercoiling of DNA. DNA-gyrase introduces a transient double-stranded nick in its substrate DNA and passes a double helix through the break in the direction that will decrease supercoiling of DNA. During the breaking and rejoining reaction, the 5'-ends of the substrate DNA are covalently linked to the A subunit of gyrase (Bernard & Couturier, 1992). CcdB stabilizes the cleaved DNA-gyrase complex and does not allow rescaling of the nicked DNA (Bernard et al., 1993). These induced complexes then interfere with replication and transcription, causing DNA lesions which in turn induce the SOS response and bacterial death (Salmon et al., 1994). In this respect, its action resembles that of the quinolone antibiotics and other antitumour drugs although the CcdB protein is less efficient (Jaffé et al., 1985). It was shown by in vitro and in vivo studies (Bernard & Couturier, 1992) that the CcdB protein is responsible for plasmid DNA linearization, which suggests that it can promote gyrase-mediated double-stranded DNA breakage. As expected, an Escherichia coli strain resistant to CcdB (ccdB') was found to have a mutation in the A subunit of the DNA-gyrase (Miki et al., 1992). In this strain, the ability of CcdB to induce linearization of the plasmid DNA as well as SOS induction was suppressed. Interestingly, the UV-light-triggered SOS induction was unaffected. Bernard & Couturier (1992) proposed a model in which CcdB-promoted SOS induction is a consequence of DNA damage produced by a CcdB-gyrase–DNA complex rather than inhibition of gyrase.

![Diagram](Image)

Fig. 1. Diagrammatic representation of three distinct plasmid stabilization mechanisms. (a) Some plasmids are selectively positioned inside the bacterial cell, thus ensuring that each of the daughter cells will receive a copy of a plasmid. (b) A multimer-resolution mechanism resolves plasmid multimers (when they are formed) into monomers, thus increasing the likelihood that both daughter cells will receive at least one copy of a plasmid. (c) Post-segregational killing systems selectively kill daughter cells that fail to receive a copy of a plasmid, thus enriching the subpopulation of plasmid-harbouring cells.
activity. However, Maki et al. (1992) reported that an increased dosage of the wild-type DNA-gyrase overcame the growth inhibition of the CcdB product. This observation suggested that the target of CcdB protein is the DNA-gyrase, particularly the A subunit. It was found that in the CcdB-overproducing strain the DNA supercoiling activity was decreased to a nondetectable level (Maki et al., 1992). This was due to the inactivation of DNA-gyrase activity since the free DNA-gyrase isolated from these strains was also completely inactivated. Addition of the CcdA protein (8700 Da) to the extract of the CcdB-overproducing strain led to full restoration of gyrase activity (Maki et al., 1992). These results indicated that the CcdA and CcdB proteins form an opposing pair in modulating the activity of DNA-gyrase. It is believed that CcdA interacts directly with CcdB, forming a complex of about 69000 Da (Tam & Kline, 1989b). DNA-gyrase plays a fundamental role in many cellular processes such as DNA replication, transcription, recombination and the resolution of daughter chromosomes. An interesting possibility is that the CcdB protein also causes the inability of the bacterial chromosome to decatenate or to position the daughter chromosome, which could lead to the observed filamentation and formation of anucleated cells (Miki et al., 1992; Bernard & Couturier, 1992). Certain conditional mutations in the gyrA gene have essentially the same phenotype (Kato et al., 1989; Hussain et al., 1987). It is possible that the CcdB protein preferentially inhibits the decatenation activity of the DNA-gyrase and the resulting higher topological order of the chromosomal DNA might interfere with proper chromosome segregation.

**Differential stability of toxin and antidote is critical for post-segregational killing**

For proper functioning as a post-segregational killing system, the stabilities of the CcdA and CcdB proteins must be different. It was proposed by Jaffé et al. (1985)
that in the plasmid-free cells, de novo synthesis of the Ccd proteins ceases and the CcdA protein is diluted, enabling the CcdB protein to kill the cell. In more recent work, Van Melderen et al. (1994) obtained evidence that the half-life of the CcdA protein is shorter than that of the CcdB protein. Using pulse-chase experiments, the half-life of the CcdA protein was estimated to be about 1 h whilst the CcdB protein remained stable for over 2 h. A number of proteases were suggested to play critical roles in fast turnover of proteins in the prokaryotic cell. The two best-characterized ATP-dependent serine proteases in *E. coli* are Lon and Clp (Gottesman & Maurizi, 1992). Interestingly, the stability of the CcdA protein improved in a Lon- strain, suggesting that Lon is the major protease responsible for the degradation of CcdA. It was found that under conditions in which the CcdB protein is also produced, the stability of CcdA improved (Van Melderen et al., 1994). This partial resistance to proteolysis was shown for other unstable proteins degraded by the Lon protease and may be due to the fact that the motifs recognized by the protease are also involved in protein–protein interactions (Van Melderen et al., 1994). Another interesting observation is that the half-life of the CcdA protein is long when compared with other Lon targets such as the SulA, RcsA or N protein (Van Melderen et al., 1994). This, however, might be necessary considering the essential function of the antidote. Since Lon is a heat-shock protein, rapid changes in the surrounding environment could lead to the degradation of the antidote even in the plasmid-harbouring cells and eventually to the killing of the cells. Degradation of the antidote that is too slow would, on the other hand, lead to dilution of the toxin protein and thus the system would not be efficient.

**ccd-like operons are found on many unrelated plasmids**

The *ccd* operon of the F plasmid is not the only plasmid-borne post-segregational system with both the toxin and antidote occurring as proteins. The *parD* stability system of the R1 plasmid also codes for two genes: cytotoxin Kid (12 kDa) and the antidote protein Kis (9.3 kDa) (Ruiz-Echevarria et al., 1991b). The ParD system is exactly conserved in the closely related R100 plasmid where it has been described as the Pem system (Van Melderen et al., 1994). Another interesting observation is that the ParD system has the organization of a *ccd* operon improved in a Lon- strain, suggesting that Lon is the major protease responsible for the degradation of CcdA. It was found that under conditions in which the CcdB protein is also produced, the stability of CcdA improved (Van Melderen et al., 1994). This partial resistance to proteolysis was shown for other unstable proteins degraded by the Lon protease and may be due to the fact that the motifs recognized by the protease are also involved in protein–protein interactions (Van Melderen et al., 1994). Another interesting observation is that the half-life of the CcdA protein is long when compared with other Lon targets such as the SulA, RcsA or N protein (Van Melderen et al., 1994). This, however, might be necessary considering the essential function of the antidote. Since Lon is a heat-shock protein, rapid changes in the surrounding environment could lead to the degradation of the antidote even in the plasmid-harbouring cells and eventually to the killing of the cells. Degradation of the antidote that is too slow would, on the other hand, lead to dilution of the toxin protein and thus the system would not be efficient.

A functionally similar system was also found in the bacteriophage P1. As in the case of the *ccd* locus, there are two proteins involved in the post-segregational killing system of P1. The action of the toxic protein Doc (126 amino acids) is prevented in cells that retain P1 by the antidote protein Phd (73 amino acids) (Lehnerr et al., 1993). These two genes are organized in an operon (called addiction module) and the synthesis of Doc is translationally linked to that of Phd. Unlike killing by CcdB, expression of *doc* does not trigger SOS induction. Also, whilst killing by *ccd* or *pem* (*parD*) leads to filamentation, cells that have lost P1 show a reduced size and a decreased capacity for SOS induction (Lehnerr et al., 1993). There is no evidence to suggest that DNA-gyrase is the target of Doc protein; moreover, since the expression of *doc* does not trigger the SOS response, it seems unlikely that DNA-gyrase is the target. As in the case of *ccd* and *pem* (*parD*), the shorter half-life of the antidote protein is due to its preferential degradation by protease. However, unlike the CcdA and PemL proteins, Doc protein is degraded by the ATP-dependent serine protease ClpXp and not Lon protease (Lehnerr & Yarmolinsky, 1995). Despite these differences, the *doc/phd* addiction module shares the same organizational features as the *ccd* or *pem* systems (Fig. 2).

The *parDE* operon of the broad-host-range plasmid RK2 also contributes to stabilization through the post-segregational killing of plasmid-free cells (Roberts et al., 1994). The *parDE* operon has the organization of a proteic killer system and encodes toxic ParE protein (83 amino acids) and an antidote protein ParD (103 amino acids) (Fig. 2). It has been shown that ParE exists as a dimer, which binds to dimeric ParD to form a tetramer (Johnson et al., 1996). In addition to its antidote function, ParD protein also acts as a negative regulator of the *parDE* operon (Roberts et al., 1993; Johnson et al., 1996). Similarly to killing by *ccd* or *pem*-specified proteins, killing by ParE leads to growth inhibition accompanied by filamentation (Roberts et al., 1994). While the *parDE* operon is necessary for cell filamentation, a region outside *parDE* and called *psa* (post-segregational arrest) is required for cell-growth arrest in the absence of filamentation (Jovanovic et al., 1994). The *parDE* operon has been shown to stabilize RK2 in a
Conditionally lethal bacterial plasmid genes

100 bp

R1

\[ \text{mok} \quad \text{sok} \quad \text{hok} \]

F

\[ \text{srnB} \quad \text{srnC} \]

F

\[ \text{flmA} \quad \text{flmB} \]

R483, R16

\[ \text{pndB} \quad \text{pndA} \]

E. coli chromosome

\[ \text{orf69} \quad \text{gef} \]

E. coli chromosome

\[ \text{sof} \quad \text{relF} \]

Fig. 3. Genetic organization of the hok/sok and related systems associated with plasmids and the E. coli chromosome (indicated on the left). Cross-hatched boxes represent killer genes; open boxes, overlapping regulatory genes; black boxes, antisense RNAs; bent arrows, transcription start sites; asterisks, transcription termination points; and short black bars, inverted repeats which can form stem-loop structures. (Adapted from Nielsen et al., 1991).

broad spectrum of hosts, suggesting the importance of this locus for broad-host-range or RK2 plasmids (Sia et al., 1995).

Recently, a novel killer system has been suggested for plasmid Rts1 (Tian et al., 1996). The hig locus (host inhibition of growth) consists of higA (encoding an 11.7 kDa antidote protein) and higB (encoding a 10.7 kDa killer protein). Contrary to other proteic killer systems, the toxic part of the hig locus is located upstream of the antidote (Fig. 2). The interaction between HigA and HigB, as well as the molecular target of HigB, is yet to be characterized.

Systems in which the killer is a protein, the synthesis of which is controlled by antisense RNA

In other post-segregational killing systems the role of the antidote is played by antisense RNA. The best understood and characterized system of this type is the parB locus of the plasmid R1 (Gerdes et al., 1990a). When the parB region was inserted into a plasmid with a temperature-sensitive replicon, stabilization in the inheritance of such a construct at non-permissive temperatures was observed (Gerdes et al., 1986b). Moreover, a large fraction of the population of plasmid-free cells was found to be non-viable. These non-viable cells, however, differed significantly from those observed with the ccd locus. The presence of parB did not induce filamentation; on the contrary, ghost cells were formed. The parB region was mapped to within a 580 bp region and consists of two genes: hok (host killing) and sok (suppressor of killing) (Fig. 3) (Gerdes et al., 1986a). The product of the hok gene is a small 52 amino acid hydrophobic polypeptide associated with the cellular membrane which, when overexpressed, causes cell death. It was observed that shortly after the synthesis of the Hok product, there is a rapid decrease in the rate of oxygen consumption and a decrease in the membrane electrochemical potential (Gerdes et al., 1986a). However, short-circuiting of membrane potential did not lead to inhibition of respiration and, vice versa, inhibition of respiration did not lead to the collapse of the membrane potential. It was therefore proposed that the Hok polypeptide interacts with a component of the membrane, the inactivation of which simultaneously leads to the observed changes in respiration and membrane potential (Gerdes et al., 1986a). The potential target for the Hok polypeptide was proposed to be some component of the respiratory chain since the inhibition of this function should lead to an inhibition of electron transport and proton pumping. The morphological changes associated with the expression of hok (ghost cell appearance) could be due to the permeabilization of the cell membrane (Gerdes et al., 1986a). Due to the osmotic...
pressure and loosening of the peptidoglycan layer, water accumulates in the cell, resulting in the expansion of the cell volume and dilution of the intracellular material.

**hok RNA is regulated by antisense RNA**

The expression of *hok* is regulated at the post-transcriptional level by the *sok*-encoded 67 nucleotide antisense RNA which is transcribed in the opposite direction to *hok* (Fig. 3) (Thisted *et al.*, 1994b). It was shown that the target for Sok RNA is in the Hok mRNA leader region (SokT) (Thisted *et al.*, 1994b). This region overlaps with the translation initiation region (TIR) of the third open reading frame *mok* (mediation of killing). It is likely that Sok RNA inhibits *mok* translation by obstructing the *mok* TIR and preventing the entry of ribosomes to this region. The *mok* gene starts upstream of the *hok* gene and overlaps with *hok* out-of-frame. Translation of *mok* is very tightly regulated by Sok RNA and the translation of *mok* is also a prerequisite for *hok* translation (Thisted & Gerdes, 1992). This genetical arrangement allows for the regulation of *hok* expression indirectly via *mok*.

Gerdes *et al.*, (1990b) found that *hok* mRNA is very stable but *sok* RNA decays rapidly. Also, a new truncated *hok* mRNA species was found and its formation was found to be negatively regulated by Sok RNA. The truncated *hok* mRNA was found when the *sok* promoter was inactivated by site-specific mutagenesis or if rifampicin was added to cells containing the *hok/sok* locus. Addition of rifampicin also led to efficient expression of the Hok protein. On the other hand, addition of streptolydigin, which also led to the rapid decay of Sok RNA, had no effect on the truncation of

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**Fig. 4.** Schematic illustration of proposed model of post-transcriptional regulation of *hok/sok* genes. In plasmid-carrying cells, binding of either the *fbi* region or the Sok RNA to the *mok* TIR region prevents translation of the Hok protein by targeting Hok RNA for degradation by RNase III. The absence of Sok RNA in plasmid-free cells leads to eventual translation of the Hok protein and cell death. A similar mode of regulation was proposed for other members of the *hok/sok* family. See text for details. (Adapted from Thisted *et al.*, 1994a).
is highly unstable. The full-length Hok mRNA is slowly
the pool of Sok RNA decays rapidly since the Sok RNA
expected. However, binding of FBI to
essential for the proper functioning of this system. Since
Hok mRNA from being degraded. In plasmid-free cells,
fast turnover of the
region will prevent translation of the Hok protein. On
antisense RNA is significantly slower and ensures the
activation of translation of these genes in a fashion
similar to that of the Hok mRNA. It seems clear that
these genes constitute a family of Hok-homologous killer
genes.

**Conditionally lethal genes associated with the E. coli chromosome**

Surprisingly, homologues of the Hok family killer genes have also been found on the chromosome of E. coli. The relF gene of the relB operon is related to the Hok gene both structurally and functionally (Fig. 3) (Gerdes et al., 1986a). It encodes a 51 amino acid residue polypeptide that has 40% homology to the Hok protein. Induction of the relF gene leads to the same physiological response as the expression of the Hok gene: cessation of respiration, dissipation of the membrane potential, appearance of ghost cells and cell death (Gerdes et al., 1986a). Another chromosomai gene, gef, was identified on the chromosome of E. coli K-12 (Poulsen et al., 1989), the protein product of which was found to be structurally and functionally similar to the proteins encoded by Hok and relF. The Gef protein is a toxin of 50 amino acid residues and was found associated with the bacterial membrane (Poulsen et al., 1991b). It was found that this protein forms dimers. However, the mutation which prevented the dimer formation had only a small effect on the toxicity of Gef protein (Poulsen et al., 1991b). It has been shown that even though the gef gene is transcribed constitutively, Gef protein cannot be detected in cells (Poulsen et al., 1991a). The regulatory model for the control of the expression of gef was proposed to be similar to that of the regulation of the expression of Hok (Poulsen et al., 1991a). According to this model, translation of gef is coupled to the translation of the upstream open reading frame called orf69 which is negatively regulated by the antisense RNA Sof. This Sof RNA can bind to the first three codons and the ribosome-binding site of the orf69
mRNA and thus prevent translation of gef (Poulsen et al., 1991a). Two chromosomal mutations in E. coli were identified that rendered cells resistant to the Gef protein (Poulsen et al., 1992). The function of the proteins involved in the Gef E phenotype is at present unknown. Even though relF and gef share structural and functional homology with the plasmid-borne killing systems of the hok family, the chromosomal killer genes, unlike their plasmid counterparts, were not shown to be able to stabilize plasmid inheritance (Poulsen et al., 1989).

An entirely different killing system was also found to be associated with the chromosome of E. coli. Two genes, kicA and kicB, were identified upstream of mukB, a gene essential for chromosome partitioning (Fig. 2) (Feng et al., 1994). KicA (antidote) and KicB (toxin) were found to be non-essential for the normal function of the cell. The kicA and kicB genes were cloned onto a cloning vector and their effect on the physiology of the host was investigated. Similarly to the ccd system of F, KicA can prevent killing by KicB, presumably by protein–protein interaction with KicB. Preliminary experiments suggested that KicB interferes with protein synthesis, resulting in the killing of the cell (Feng et al., 1994). Unlike other chromosome-borne killing systems, when kicA and kicB were transferred from the chromosome to a plasmid they were able to act in a 'true' post-segregational killing manner by killing plasmid-free segregants (Feng et al., 1994). Recently, another operon of the E. coli chromosome was identified to be homologous to the ccd/pem family. The functional and structural homologue of the pem locus was located at 60 min (chpA) and at 100 min (chpB) (Fig. 2) (Masuda et al., 1993). chpA is located within the relA operon and chpB is located in close proximity to the ppa region. Both of these regions are believed to be involved in the stringent response, suggesting a possible role of chpA and chpB in this response (Masuda et al., 1993).

## kil/kor genes of plasmids of incompatibility groups P and N

Bacterial plasmids of the incompatibility groups P and N have been found to carry an entirely different set of genes that are potentially lethal to their host. It was found that certain regions of the IncP plasmid RK2 (indistinguishable from RP4) could not be cloned unless there were other regions of the same plasmid present in cis or in trans (Figurski et al., 1982). These genes were designated kil and genes that can prevent killing were called kor (killing override). Later experiments showed that the kil/kor genes constitute a network of coregulated genes that are also involved in the control of replication (Schreiner et al., 1985; Motallebi-Veshareh et al., 1992) and conjugation (Motallebi-Veshareh et al., 1992). Four kil operons have been identified: kilA, consisting of the genes klaA, klaB and klaC (Saltman et al., 1991; Goncharoff et al., 1991); kilB, consisting of trbB and trbC (Thomson et al., 1993; Larsen & Figurski, 1994); kilC, consisting of klcA, klcB and korB (Larsen & Figurski, 1994); and kilE, consisting of kleA–F (Kornacki et al., 1993). At least five kor genes (-A, -B, -C, -E and -F) have been identified to date (Larsen & Figurski, 1994). The kil and kor genes are organized into a kil-kor regulon which resides within a 26 kb region of RK2 (Larsen & Figurski, 1994). It is not known whether these genes are involved in the post-segregational killing of plasmid-free cells or whether they contribute to plasmid stability by some other mechanism. It was shown (Saltman et al., 1991; Goncharoff et al., 1991; Thomson et al., 1993; Kornacki et al., 1993; Larsen & Figurski, 1994) that unregulated expression of the kil genes leads to killing of the host cells. The cells overexpressing the Kil proteins became elongated, had distorted outer membranes and their electron-dense materials were visible in the periplasmic spaces (Saltman et al., 1991). This cell killing was always prevented if the corresponding kor region was present.

Incompatibility group N plasmids pKM101 and pCU1 were also shown to carry genes that are potentially lethal to their host. Even though there is no sequence homology to the kil/kor genes of RK2 and kor genes of these plasmids cannot inhibit lethality of RK2 kil genes, Winans & Walker (1985) used the same terminology for pKM101 genes. Two kil genes (kilA and kilB) and two kor genes (korA and korB) were identified in the sequence of pKM101 (Winans & Walker, 1985) and a third kil gene (kilC) was identified in the sequence of pCU1 (M. Holčík, M. Rodriguez, A. Couse, G. Cherton-Horvat & V. N. Iyer, unpublished). Recently, kilA and kilB were found to be allelic with traL and traE, respectively (Moré et al., 1996). Both kil genes are required for conjugation and are homologous to transfer genes of Agrobacterium tumefaciens (vir operon) and toxin export genes (ptl) of Bordetella pertussis (Pohlman et al., 1994).

Several studies indicated that the function of kor genes is to regulate expression of kil genes at the level of transcription (Williams & Thomas, 1992; Motallebi-Veshareh et al., 1992; Thomson et al., 1993; Kornacki et al., 1993; Moré et al., 1996). Detailed study of korA and korB of pKM101 indicated that KorA and KorB together repress transcription from the kil promoter region as well as their own transcription. Interestingly, neither protein alone was capable of repression. DNase I footprinting and gel retardation assays identified 29 nucleotide kor boxes located upstream of kil or kor promoters where the KorA/KorB heterodimers bind (Moré et al., 1996). This type of regulation, however, is not expected for a system which would preferentially kill plasmid-free segregants since it cannot function as a molecular memory. Interestingly, the kilA and korA sequences of RK2 are part of the cryptic tellurite resistance transposon Tn521 (Grewal, 1990), and the korA and korB sequences of RK2 are conserved throughout the incompatibility group P plasmids (Figurski et al., 1982; Thomas et al., 1995).

As mentioned above, the kil/kor regulatory system of pKM101 is superficially similar to that of plasmid RK2. Furthermore, both systems are located within the
conjugal transfer system regions of the respective plasmids. Tight regulation of transfer genes may be required to achieve a fine balance between appropriate expression of these genes for plasmid transfer and their potentially negative effects such as zygotic induction or susceptibility to bacteriophages (Moré et al., 1996).

Plasmid genes lethal in Klebsiella oxytoca but not in E. coli

All known conjugative plasmids of the incompatibility groups N, P and W confer a phenotype called Kik*. This phenotype was characterized by marked reduction of the viability of K. oxytoca recipients, but not of E. coli recipients, following matings with the donor host (Rodriguez & Iyer, 1981). This phenotype is called Kik (killing of Klebsiella) to distinguish it from kil which is manifested in E. coli and has been described in detail in the IncN group plasmid pCU1. Transposon insertions defined a region that abolished this phenotype. This region was called kikA and subsequent studies showed that intracellular expression of kikA in K. oxytoca was lethal whilst expression in E. coli was not (Hengen et al., 1992). Two other loci, kikB (Thatte et al., 1983) and kikC (Rodriguez et al., 1995), have also been implicated in reducing the viability of K. oxytoca and remain to be analysed. The kikA locus consists of two separate genes, orf70 and pep (PRD1 entry protein), and their co-expression causes reversible growth inhibition without any apparent morphological changes (Holčík & Iyer, 1996b). Even though the kikA locus lies outside the N tra region as it was defined in E. coli, mutations in pep resulted in reduced frequency of transfer in K. oxytoca and abolished susceptibility to N-plasmid-specific bacteriophage PRD1 in both K. oxytoca and E. coli (Holčík & Iyer, 1996a). Pep is an 8.9 kDa protein located in the periplasmic space, suggesting that pep (or kikA) is part of an extended tra region of pCU1. No plasmid region that overrides the lethality of kikA has been found. However, it was found that K. oxytoca cells that survived mating with pCU1 had acquired a chromosomal mutation (kik-immune) that protected them against killing by pCU1 in subsequent matings (Rodriguez et al., 1995). Mating experiments using prototrophic E. coli donors carrying pCU1: lacZ with auxotrophic K. oxytoca recipients demonstrated that the plasmid pCU1 is deleterious to the K. oxytoca host when it is present in the cell (Rodriguez et al., 1995). The observed lethality was therefore not a consequence of segregational plasmid loss followed by the killing of plasmid-free cells as has been observed in E. coli with a number of plasmids (see above). Analysis of lacZ expression from pCU1: lacZ in developing colonies following conjugation suggested that the mutation conferring immunity to the Kik* phenotype occurs late during the development of a bacterial colony. These observations led to the proposal of a hypothesis whereby the expression of K. oxytoca-lethal genes arrests the growth of the recipient, thus allowing for a rare secondary chromosomal mutation which renders the cell immune to killing by kik genes (Rodriguez et al., 1995). The mutation induced in K. oxytoca is likely to be specific as the screening of several Kik-immune strains did not indicate that they had acquired other identifiable mutations (Rotheim et al., 1991). This suggests that the mutation induced by pCU1 is site-specific. The nature of this mutation, as well as the mechanism of its occurrence, is at present unknown.

Lethal genes in Streptomyces plasmids

While the majority of the killer genes described above were studied in E. coli, at least two distinct and species-specific killer systems have been described. Plasmid transfer in Gram-positive Streptomyces is associated with the formation of `pocks’ corresponding to areas of growth inhibition in the recipient strain (Bibb & Hopwood, 1981). Genetic studies with the plasmid pIJ101 identified four genes, traA (formerly kilA), kikB, spdB and spdB, which are necessary for conjugal transfer and pock formation in Streptomyces lividans (Kendall & Cohen, 1988). Similarly to the kil/kor genes from RK2 or pKM101, kil genes of pIJ101 cannot be cloned unless their corresponding kor genes are present in cis or in trans. The spdB and spdB genes are responsible for the spreading of the plasmid in the mycelium after transfer (Kendall & Cohen, 1988). The traA gene is negatively regulated by the divergently transcribed korA gene, the promoter of which overlaps the control region of kilA (Stein et al., 1989). A second regulatory gene, korB, represses its own expression as well as the expression of kilB (Zaman et al., 1992). KorB is synthesized as a 10 kDa protein which is subsequently processed to its active 6 kDa form. The footprint of KorB was found to overlap the sti locus, which is involved in plasmid incompatibility, copy number and pock formation during mating, suggesting that KorB is likely to be involved in plasmid DNA replication during or after mating (Tai & Cohen, 1993). Mutational analysis of KorB also suggested its central importance for plasmid transmission (Tai & Cohen, 1994). Analogous kil/kor genes were also identified in the plasmid pSAM2 from Streptomyces ambofaciens and the multicopy plasmid pSN22 from Streptomyces nigrifaciens (Kataoka et al., 1991). Conservation of these genes in Streptomyces plasmids and their involvement in conjugal transfer strongly suggests that they are involved in the regulation of the transfer processes.

Other phenotypes associated with bacterial plasmids

Two further lethal phenomena are connected with conjugative plasmids: lethal zygosis (Gross, 1963) and zygotic induction (Hayes, 1965) are associated with plasmid transfer by conjugation. Lethal zygosis was first observed as reduced viability of the recipients under conditions where F- bacteria were used in matings with an excess of Hfr donor cells (carrying F factor integrated into their chromosome). Recipients were inhibited in the synthesis of macromolecules and active transport across the membrane, and leakage of the cytoplasm was
observed (Skurray & Reeves, 1973). Lethal zygosis is attributed to the fact that during prolonged mating, membrane rearrangement, which occurs to facilitate plasmid transfer, can cause permeability of the recipient membrane followed by cell death (Skurray & Reeves, 1973; Ou, 1980). Bacterial cells that survive killing by lethal zygosis are immune. This immunity is, however, dependent on the presence of the F plasmid; curing of F from immune cells rendered them subsequently sensitive to lethal zygosis. Immunity to lethal zygosis is caused by entry (surface) exclusion, which is a mechanism by which a plasmid-carrying population of E. coli reduces the acceptance of a second, closely related plasmid of the same exclusion group (Ou, 1980). The surface exclusion genes of plasmid F were identified as traT and traS. TraS is a small inner-membrane protein that is believed to block DNA transfer after a mating pair has been established. In contrast, TraT is an outer-membrane lipoprotein that acts primarily to inhibit the initial steps in mating formation (for a review see Frost et al., 1994). Zygotic induction is, on the other hand, caused by the transfer of a lysogenic bacteriophage inserted in the chromosome of the Hfr donor strain into a non-lysogenic recipient (Hayes, 1963). The transfer of the phage genome from the donor to a non-lysogenic recipient results in the induction of phage development in the recipient followed by cell lysis and the release of phage particles. The induction of lysogenic prophage is due to the lack of the repressor protein, which maintains the prophage in its lysogenic state in the donor. The production of phage particles has been shown to be inhibited by transfer of the rac locus from the E. coli chromosome into a RacI* recipient (Feinstein & Low, 1982). However, evidence suggests that the rac locus is a cryptic, and possibly defective prophage that is excised during the induction process. Zygotic induction has also been implicated in the induction of expression of specific plasmid genes such as psiB and ssb, suggesting they have a role in plasmid conjugation (Jones et al., 1992).

**Concluding discussion**

Bacterial plasmid genes often encode optional characteristics that are selectively advantageous to bacteria in some environments but not others. The best known example of such genes are probably the antibiotic resistance determinants carried on R plasmids. At the end of the twentieth century, when almost all infectious diseases are treated with natural or synthetic antibiotics, R plasmids still represent a serious threat due to their abilities to spread rapidly between different bacterial species, many of which are human or animal pathogens. Bacterial genes move between chromosomes and plasmids as well as from one plasmid to another. It is therefore not surprising that the same, or very similar sets of lethal genes, are found on different plasmids and that some of these genes are also shared with the chromosome (Table 1). Interestingly, some plasmids carry genes of more than one system on the same replicon (e.g. ccd, srnB and flmA on F). This may seem superfluous since one stability system should be sufficient to ensure inheritance of a given plasmid. In addition to the lethal genes, many, especially large, plasmids carry other, non-lethal stability determinants (for reviews see Williams & Thomas, 1992; Nordström & Austin, 1989). It is interesting then that the presence of multiple stability determinants on a given plasmid is often paralleled by the presence of multiple replicons on the same plasmid. While there is no direct evidence to support this, a plausible hypothesis could be that these plasmids arose by the recombination of multiple, initially separate plasmids, each with its own replication and maintenance systems. If true, a common origin of plasmid replicons and stability determinants could be inferred by their relative location on the new plasmid. A similar hypothesis has been proposed for the origin of the bacterial chromosome that would emerge as a gradual concentration of smaller replicons with all the essential genes for bioenergetic activity (Sonea, 1991). Interestingly, gef and ref analogues are conserved in several bacterial species including E. coli B and C, Agrobacterium and Rhizobium, suggesting that these genes play an important role in the physiology of the cell (Poulson et al., 1989). It has been shown recently that hok/sok genes are involved in phage exclusion of bacteriophage Τ4 and this mechanism could play an important role in the evolution of hok/sok-like genes found on bacterial chromosomes (Pecota & Wood, 1996).

The origin of lethal genes is open to speculation. An attractive hypothesis is that they emerged early during the evolution of prokaryotic cells, as a means to ensure co-segregation of self-replicating DNA molecules. These replicons carried different groups of essential genes and their stability and co-segregation was essential for cell survival. As these independent replicons fused together to form a bacterial chromosome the function of lethal genes became redundant. Lethal genes may, however, have been acquired by autonomously replicating DNA molecules and gave rise to a variety of stability determinants found on bacterial plasmids. Alternatively, they may have evolved on plasmids in the course of establishing opportunistic relationships with bacterial cells and this was followed by the evolution of a system to control the kil system, either as a cognate kor system of the same plasmid, or appropriate changes on the bacterial chromosome. Some of the plasmid lethal genes (kil-kor regulons) play a critical role in the regulation of plasmid replication and conjugal transfer. These genes may thus not be "true" lethal genes. Rather, their lethality could be a consequence of unregulated gene expression. Since many of these kil genes are part of the plasmid transfer region it is possible to imagine that overexpression of membrane or pilus proteins would be detrimental to the cell. The function of the cognate kor loci is then to control expression of the kil genes. We have nevertheless included a discussion of these genes in this review to demonstrate the wide variety of conditionally lethal genes associated with bacterial plasmids, and to emphasize that other classes of such genes may remain to be uncovered. As suggested here, the presence
of these genes is important at several levels of plasmid biology: (i) they will ensure selective killing of plasmid-free cells and thus effectively ensure stable inheritance of plasmids (as in the case of post-segregational killing systems e.g. bok/sok or ccd); (ii) they are involved in controlling the expression and regulation of complicated networks of replication and transfer genes (such as kil/kor genes of RK2 and pKM101); (iii) the existence of kik (killing of Klebsiella) genes in some plasmids such as pCU1 and pKM101 suggests that they have a role in determining or modulating the host range of plasmids; the kikA gene was shown to be involved in modifying host range of conjugal transfer as well as susceptibility to bacteriophages (Holčík & Iyer, 1996a); (iv) a gene (klaA) of the kilA operon of RK2 has been reported to affect septum formation in E. coli (Saltman et al., 1991); (v) the chromosomal kilB gene has been reported to interfere with protein synthesis (Feng et al., 1994) and a novel killer system has been suggested for plasmid Rts1 (Tian et al., 1996); and (vi) the indication that carriage of pCU1 by K. oxytoca results in a specific chromosomal mutation hints at the possible involvement of plasmids in directly modifying the genetic diversity of bacterial hosts (Rodriguez et al., 1995). It is likely that future investigations will identify as yet unknown functions associated with these systems. It seems clear that the discovery of families of such genes as operationally-defined kil genes followed by their characterization will continue to provide useful insights into the plasmid–bacterium relationship.

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