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Immunity proteins to pore-forming colicins: structure–function relationships

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Summary

Colicin A and B immunity proteins (Cai and Cbi, respectively) are homologous integral membrane proteins that interact within the core of the lipid bilayer with hydrophobic transmembrane helices of the corresponding colicin channel. By using various approaches (exchange of hydrophilic loops between Cai and Cbi, construction of Cbi/Cai hybrids, production of Cai as two fragments), we studied the structure–function relationships of Cai and Cbi. The results revealed unexpectedly high structural constraints for the function of these proteins. The periplasmic loops of Cai and Cbi did not carry the determinants for colicin recognition although most of these loops were required for Cai function; the cytoplasmic loop of Cai was found to be involved in topology and function of Cai. The immunity function did not seem to be confined to a particular region of the immunity proteins.

Introduction

Pore-forming colicins form voltage-dependent ion-channels in the cytoplasmic membrane of sensitive bacteria (Konisky, 1982). After these channels have formed, the cells are depleted of their intracellular K^+ (Bourdinaud *et al.*, 1990), active transport is inhibited (Cramer *et al.*, 1983), and inorganic phosphate leaks out of the cells. The leakage causes intracellular ATP to be hydrolysed into ADP and AMP (Guihard *et al.*, 1993).

Like many toxins, colicins are made up of functional domains, each of which is associated with particular functions in the overall activity (Baty *et al.*, 1988). The *N*-terminal and the central domains of pore-forming colicins are involved in their transport through the *Escherichia coli* envelope; the *C*-terminal domain carries the ionophoric activity (Lazdunski *et al.*, 1988; Pattus *et al.*, 1990).

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The crystal structure of the pore-forming domain of colicin A (ColA) in aqueous solution was obtained at 2.4 Å resolution (Parker *et al.*, 1989; 1992). This domain consists of a hydrophobic hairpin (helices 8 and 9) surrounded by eight amphipathic α -helices. *In vitro* experiments performed on model membranes at low pH indicate that if the membrane potential is missing, the pore-forming domain of ColA remains embedded at the surface of the membrane (Géli *et al.*, 1992; Lakey *et al.*, 1993; Duché *et al.*, 1994). The hydrophobic hairpin of the homologous colicin E1 (ColE1) seems to assume a transmembrane orientation (Merrill *et al.*, 1990; Rath *et al.*, 1991; Zhang and Cramer, 1992; Shin *et al.*, 1993). The structure of the membrane-spanning ion-channel has not been determined. It probably includes the hydrophobic hairpin and an amphiphilic hairpin that was identified in ColE1 as the voltage-sensitive region (Merrill and Cramer, 1990; Abrams *et al.*, 1991; Song *et al.*, 1991; Zhang and Cramer, 1992).

To prevent the colicin they release in the extracellular medium from killing them, colicin-producing strains also synthesize immunity proteins (Géli *et al.*, 1986). According to their respective homologies, immunity proteins were classified into two groups (Schramm *et al.*, 1988; Géli *et al.*, 1989; Song and Cramer, 1991). The first group comprises immunity proteins to colicins A, B, and N, and the second comprises immunity proteins to colicins E1, Ia, and Ib. Colicin A and B immunity proteins show 38% identity and 39% conservative substitutions; their sequences can be aligned with the introduction of very few gaps.

Immunity proteins are integral inner membrane proteins (Goldman *et al.*, 1985; Mankovich *et al.*, 1986; Schramm *et al.*, 1988; Géli *et al.*, 1988; Pugsley, 1988). They interact with the pore-forming domain of the corresponding colicin (Mankovich *et al.*, 1984; Bishop *et al.*, 1985; Bénédicti *et al.*, 1991; Géli and Lazdunski, 1992a). The topologies of colicin A and E1 immunity proteins (Cai and Cei, respectively) are known: Cai has four transmembrane regions and its *N*- and *C*-termini face the cytoplasm (Géli *et al.*, 1989); Cei crosses the membrane bilayer three times (Song and Cramer, 1991).

The hydrophobic hairpin of the ColA pore-forming domain is the main determinant recognized by Cai; it was proposed that immunity protein function required helix–helix recognition within the lipid bilayer, involving the ColA hydrophobic hairpin (Géli and Lazdunski, 1992a, b). Another amphiphilic region of ColE1, defined

as a transmembrane helix of the channel in the open state, appears to be involved in the interaction between ColE1 and Cei (Zhang and Cramer, 1993). This is consistent with membrane helix-helix interactions being the basis for the immunity function.

Recently, we have found that a fusion protein comprising the pore-forming domain of ColA attached to a yeast mitochondrial sorting sequence was cytotoxic for the producing cell and that the lethality was inhibited within the membrane by Cai (Espeset *et al.*, 1994, accompanying paper).

In this study, we addressed the role of the small hydrophilic loops (20 to 30 residues in length) of Cai in the protective function. These loops may interact directly with the hydrophilic loops of the membrane-spanning pore-forming domain of ColA or may influence the way in which the transmembrane helices of Cai functionally assemble. We also showed that Cai produced as two independent fragments did not assemble into a functional structure and that it was not possible to combine hydrophobic segments of two homologous immunity proteins to form a functional entity.

Results

Overproduction of Cai confers immunity to colicin B

We have previously observed that Cai conferred partial immunity to colicin B (ColB); in contrast, Cbi is highly specific for ColB (Géli and Lazdunski, 1992a). In order to determine the regions of Cai that are involved in ColA recognition,

we performed NH_2OH mutagenesis on plasmid pIA1 (carrying the *cai* gene) and selected transformants insensitive to ColB (see the *Experimental procedures*). Three such clones were obtained whose insensitivities to ColB were correlated with the mutated pIA1 plasmid. The clones were also immune to high concentrations of ColA and sensitive to ColE1. Sequencing of the plasmid DNA of each immune clone showed that all mutations were located near to or in the Pribnow box of the *cai* promoter (Fig. 1A) (Llobès *et al.*, 1986); they were predicted to increase the promoter strength (Mulligan *et al.*, 1984). Because no antibody directed against Cai was available, it was not possible to confirm that Cai had been overproduced from the mutated variants of pIA1. To determine whether cells overproducing Cai became immune to ColB, we used a Cai derivative (EpCai, encoded by plasmid pEpCai) whose production was inducible. In EpCai, the first 12 residues of Cai are replaced with a 30-amino-acid epitope recognized by the monoclonal antibody (mAb) 1C11 (Géli *et al.*, 1993). We then analysed the kinetics with which C600 pEpCai acquired immunity to ColA and ColB after the gene fusion had been induced (Fig. 1B): after 40 min, 100% of the cells were immune to ColA and 20% were immune to ColB; after 120 min, 90% of the cells were immune to ColB (Fig. 1B). By immunoblot analysis with the 1C11 mAb, we calculated that the amount of Ep-Cai required to protect the cells against ColB was 20-fold higher than that required to protect against ColA (not shown). The results indicated that cells overproducing Cai became immune to ColB and confirmed that Cai and Cbi were functionally related.

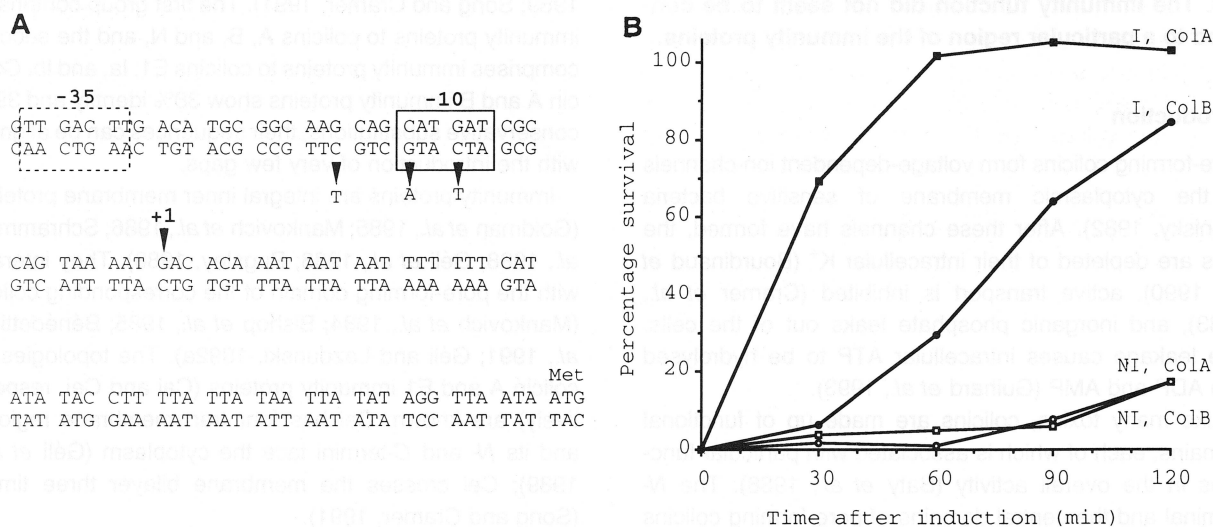


Fig. 1. A. Nucleotide sequence of the *cai* promoter region in NH_2OH -mutated pIA1 selected for insensitivity to ColB. The transitions are shown by arrows. The recognition and binding sequences for RNA polymerase are boxed with dotted lines (-35 sequence) and solid lines (Pribnow box), and +1 shows the start point of transcription (Llobès *et al.*, 1986).

B. Kinetics of acquisition of immunity to ColA and ColB after induction of EpCai production. C600 (pEpCai) was treated with mitomycin C (300 ng ml^{-1}) to induce the synthesis of EpCai and assayed for colicin sensitivity at the indicated times. The percentage of survival was expressed as the ratio of the absorbance (at 600 nm) of the culture incubated with ColA or ColB (1 mg ml^{-1}) to that of the control culture incubated with the dilution buffer. I, induced cells, NI, non-induced cells; ColA, percentage survival to ColA; ColB, percentage survival to ColB.

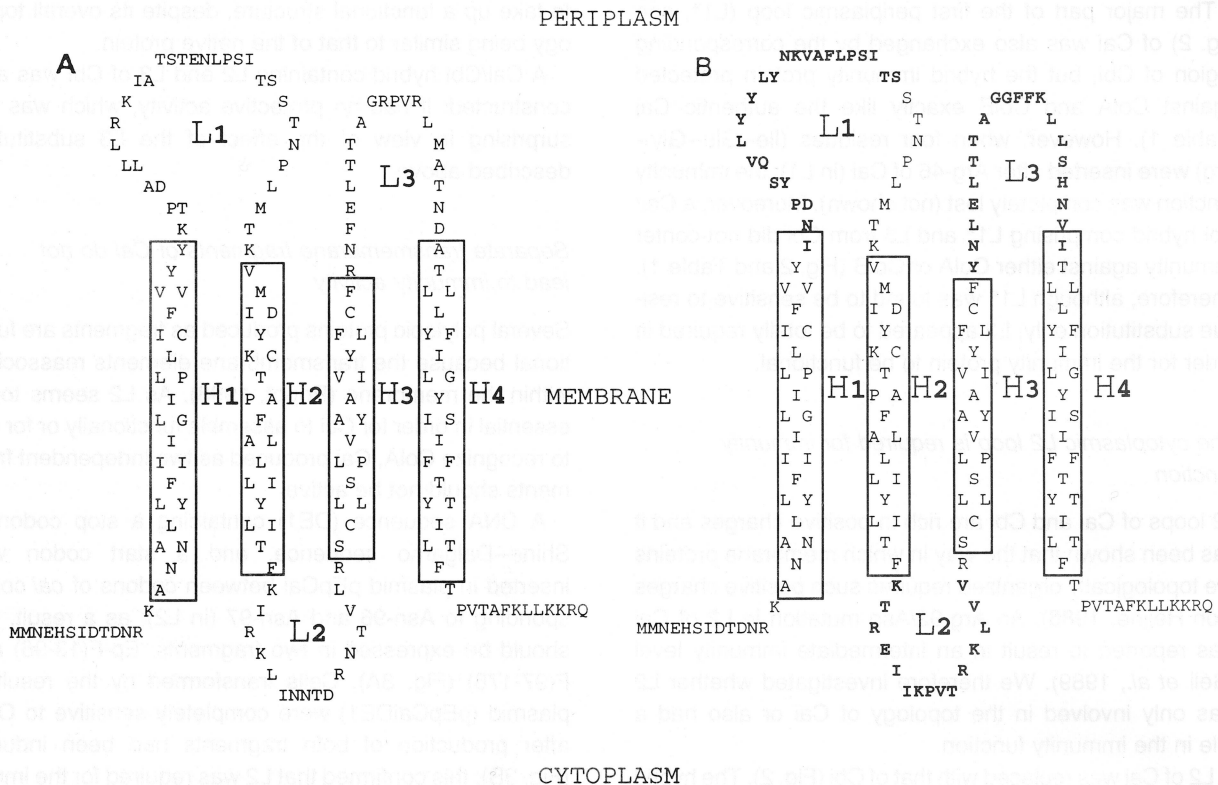


Fig. 2. Sequence and topology of Cai and its mutant forms.

A. Wild-type Cai.

B. Mutant forms of Cai; the bold sequences indicate the Cbi regions.

Five mutants were obtained in which L1, L2, L3, L1 + L3, and L2 + L3 were exchanged.

Immunity is lost when the periplasmic L3 loop is exchanged between Cai and Cbi

An Arg-136/Asp substitution in the second periplasmic loop (L3) of Cai abolishes the immunity function (Géli *et al.*, 1989) and the main ColA determinant for immunity recognition is located in the hydrophobic hairpin of ColA

(Géli and Lazdunski, 1992a). To investigate whether L3 was involved in the specificity of colicin recognition, L3 of Cai was substituted for that of Cbi (Cai and Cbi sequences are aligned in Fig. 5 — see later). The resulting hybrid protein did not protect cells against low concentrations of either ColA or ColB (Fig. 2 and Table 1).

Table 1. Exchange of hydrophilic loops between Cai and Cbi and correlation with the immunity activity.

Immunity proteins and mutant forms ^b	ColA Concentration (mg ml ⁻¹) ^a					ColB Concentration (mg ml ⁻¹) ^a						
	1	10 ⁻¹	10 ⁻²	10 ⁻³	10 ⁻⁴	10 ⁻⁵	1	10 ⁻¹	10 ⁻²	10 ⁻³	10 ⁻⁴	10 ⁻⁵
No immunity	+	+	+	+	+	-	+	+	+	+	+	+
Cai	+	+	±	-	-	-	+	+	+	+	-	-
Cbi	+	+	+	+	±	±	-	-	-	-	-	-
Cai + Cbi	+	+	-	-	-	-	-	-	-	-	-	-
Cai (L1*)	+	+	-	-	-	-	+	+	+	±	-	-
Cai (L2)	+	+	+	±	-	-	+	+	+	+	±	±
Cai (L3)	+	+	+	+	+	-	+	+	+	+	+	+
Cai (L1* + L3)	+	+	+	+	+	+	+	+	+	+	+	+
Cai (L2 + L3)	+	+	+	+	+	+	+	+	+	+	+	+

a. One microlitre of each colicin dilution was spotted onto a lawn of the indicator strain; + indicates a plaque of growth inhibition and thus a lack of activity of immunity protein, - indicates no clearing corresponding to active immunity protein, and ± indicates a turbid plaque of growth inhibition.

b. Brackets indicate the replaced regions of Cai (see Fig. 2). The immunity gene and its variants were carried by a pBR derivative (pIA2) in C600.

The major part of the first periplasmic loop (L1*, see Fig. 2) of Cai was also exchanged by the corresponding region of Cbi, but the hybrid immunity protein protected against ColA and ColB exactly like the authentic Cai (Table 1). However, when four residues (Ile–Glu–Gly–Arg) were inserted after Arg-46 of Cai (in L1), the immunity function was completely lost (not shown). Moreover, a Cai/Cbi hybrid comprising L1* and L3 from Cbi did not confer immunity against either ColA or ColB (Fig. 2 and Table 1). Therefore, although L1* was found to be sensitive to residue substitution only, L3 appeared to be totally required in order for the immunity protein to be functional.

The cytoplasmic L2 loop is required for immunity function

L2 loops of Cai and Cbi are rich in positive charges and it has been shown that the way in which membrane proteins are topologically organized requires such positive charges (von Heijne, 1986). An Arg-92/Asp mutation in L2 of Cai was reported to result in an intermediate immunity level (Géli *et al.*, 1989). We therefore investigated whether L2 was only involved in the topology of Cai or also had a role in the immunity function.

L2 of Cai was replaced with that of Cbi (Fig. 2). The hybrid protein protected against 100-fold less ColA than did the native Cai (Table 1). To study the topology of this hybrid protein, a tagged inducible fusion protein (EpVBG7) was constructed: it consisted of EpCai fused to alkaline phosphatase (PhoA) in L3 (see the *Experimental procedures*). L2 of EpVBG7 was then replaced with that of Cbi. The PhoA activities of cells producing each protein, EpVBG7 and the modified EpVBG7, were compared: the activities were found to be identical for both proteins (not shown) and reflected the fact that L2 was able to promote the export of the PhoA moiety of EpVBG7. This identity indicated that the gross organization of the protein in the membrane was probably not affected when L2 was replaced with that of Cbi. Nevertheless, the hybrid immunity protein was unable

to take up a functional structure, despite its overall topology being similar to that of the native protein.

A Cai/Cbi hybrid containing L2 and L3 of Cbi was also constructed: it had no protective activity, which was not surprising in view of the effect of the L3 substitution described above.

Separate transmembrane fragments of Cai do not lead to immunity activity

Several polytopic proteins produced as fragments are functional because the transmembrane elements reassociate within the membrane (Popot, 1993). As L2 seems to be essential in order for Cai to assemble functionally or for Cai to recognize ColA, Cai produced as two independent fragments should not be active.

A DNA sequence (DE1) containing a stop codon, a Shine–Dalgarno sequence, and a start codon was inserted in plasmid pEpCai between codons of *cai* corresponding to Asn-96 and Asn-97 (in L2); as a result, Cai should be expressed in two fragments: Ep-F(13-96) and F(97-178) (Fig. 3A). Cells transformed by the resulting plasmid (pEpCaiDE1) were completely sensitive to ColA after production of both fragments had been induced (Fig. 3B); this confirmed that L2 was required for the immunity protein to be functional. To check that the fragments were expressed and membrane associated, we transferred the DE1 sequence into pEpVBG7: the modified plasmid (pEpVBG7DE1) encoded Ep-F(13-96) and a hybrid protein in which the PhoA protein was fused to the F(97-133) fragment (F(97-133)-PhoA) (Fig. 4A). The two fragments were produced; Ep-F(13-96) was found to be membrane associated but we were not able to probe its orientation by protease treatment because L1 and L3 of Cai are fully resistant to externally added protease in EDTA-treated cells (V. Géli, unpublished). PhoA activity was detected when F(97-133)-PhoA was produced (Fig. 4B); thus, at least the first transmembrane fragment of F(97-178) was correctly assembled into the membrane.

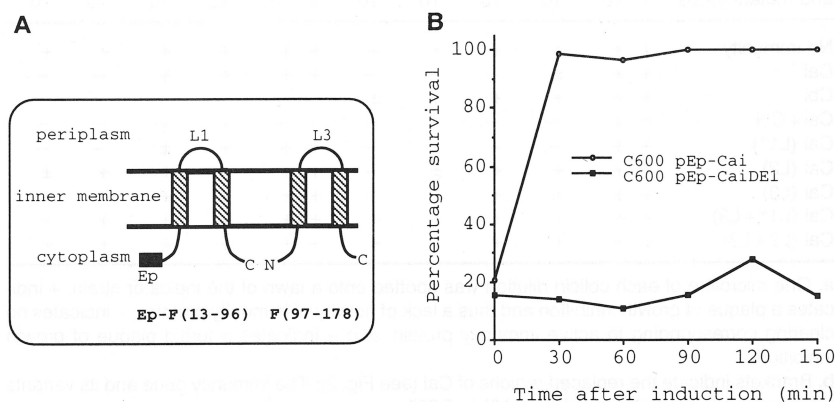


Fig. 3. Cai produced in two independent fragments is not functional. **A.** Position and predicted transmembrane disposition of the two Cai fragments. In Ep-F(13-96) the first 12 N-terminal residues of Cai were replaced by the 1C11 epitope. **B.** Kinetics of acquisition of immunity to ColA after induction of the production of both Cai fragments.

Table 2. Immunity activity of Cbi/Cai hybrid proteins.

Immunity protein	Fusion site ^b	ColA (mg ml ⁻¹) ^a					ColB (mg ml ⁻¹)						
		1	10 ⁻¹	10 ⁻²	10 ⁻³	10 ⁻⁴	10 ⁻⁵	1	10 ⁻¹	10 ⁻²	10 ⁻³	10 ⁻⁴	10 ⁻⁵
No immunity		+	+	+	+	+	+	+	+	+	+	+	
Cai		+	+	±	-	-	-	+	+	+	+	-	-
Cbi		+	+	+	+	+	±	-	-	-	-	-	-
Cai + Cbi		+	+	-	-	-	-	-	-	-	-	-	-
Cbi/Cai	(19/23)	-	-	-	-	-	-	+	+	+	-	-	-
Cbi/Cai	(22/26)	-	-	-	-	-	-	+	+	+	-	-	-
Cbi/Cai	(24/28)	-	-	-	-	-	-	+	+	+	-	-	-
Cbi/Cai	(26/30)	-	-	-	-	-	-	+	+	+	-	-	-
Cbi/Cai	(57/61)	+	+	+	+	±	-	+	+	+	+	+	+
Cbi/Cai	(75/79)	+	+	+	+	±	-	+	+	+	+	+	±
Cbi/Cai	(129/133)	+	+	+	+	+	±	+	+	+	+	+	±
Cbi/Cai	(168/172)	+	+	+	+	+	±	-	-	-	-	-	-

a. The colicin activity was analysed as described for Table 1.

b. Brackets indicate the positions of the fusion sites in the hybrid immunity proteins (see Fig. 4).

clones carried plasmids encoding perfect hybrid immunity proteins; the fusion sites of these inactive Cbi/Cai hybrids were located in L1, H2 and L3, respectively (Fig. 5, Table 2).

Only two transformants insensitive to ColB were obtained; the fusion sites were located in the extreme C-terminal part of Cbi (Fig. 5). These hybrid proteins displayed the same immunity activities as Cbi (Table 2).

These results indicated that only the first two-thirds of H1 of Cai were able to be replaced by the corresponding region of Cbi to give an active immunity protein. Interestingly, immunity was conserved when the regions Cai(1-30) or L1* were exchanged, although immunity was lost when the region Cai(1-60) was exchanged (see above and Fig. 5, Table 1). This suggested that the region Cai(30-Leu-Cys-Ile-Phe-Val-Val-Tyr-37) contained determinants for ColA recognition or that this region was specifically required for interaction with another transmembrane hydrophobic helix of Cai.

Discussion

It has been previously shown that it was possible to replace the N- and C-terminal cytoplasmic ends of Cai by unrelated amino acid sequences without affecting its function (Géli *et al.*, 1988). Various single point mutations in the polar loops of Cai, L2, and L3 decrease the immunity function (Géli *et al.*, 1989), whereas those of the ColE1 immunity protein (Cei) tolerate a high degree of substitution (Song and Cramer, 1991; Zhang and Cramer, 1993). However, the main determinant necessary for colicins A, B, and E1 to be recognized by immunity proteins is located in the transmembrane regions of their pore-forming domains (Géli and Lazdunski, 1992a; Zhang and Cramer, 1993). Thus it was suggested that colicin transmembrane helices are recognized by the immunity protein within the lipid bilayer. In addition, it was proposed that the immunity proteins function independently of colicin translocation systems (Géli

and Lazdunski, 1992a; Bénédicti *et al.*, 1992; Zhang and Cramer, 1993). Lateral diffusion of the immunity proteins in the membrane would ensure rapid recognition of colicin molecules (Zhang and Cramer, 1993).

Moreover, we have recently shown that, when produced in *E. coli*, a chimeric protein comprising the ColA pore-forming domain fused to a mitochondrial intermembrane space sorting sequence formed a channel in the inner membrane of the cells; the channel formed independently of the Tol proteins and it was inhibited by Cai (Espesset *et al.*, 1994, accompanying paper). Thus, it appears that immunity proteins interact within the core of the lipid bilayer with the channel in the open state (Géli and Lazdunski, 1992a; Zhang and Cramer, 1993). However, this does not exclude a role for the polar regions of Cai.

The results reported in this study indicated that: (i) Cai overproducing cells became immune to ColB; (ii) L1* and L3 of Cai and Cbi did not carry, by themselves, the determinants for colicin recognition, although most of these loops were required for Cai function; (iii) when L2 of Cai was replaced with that of Cbi the immunity function was lost but this was not due to modified topology; (iv) Cai produced as two membrane fragments was not functional; and (v) fusion sites of functional Cbi/Cai hybrids were located upstream of Leu-30 of Cai. These results showed that although Cai and Cbi are homologous (38% identity and 39% conservative substitutions), only limited regions were able to be exchanged without affecting function.

Two roles can be proposed for the hydrophilic loops of Cai and Cbi: (i) they may interact on both sides of the cytoplasmic membrane with different parts of the colicin molecule to prevent the pore-forming helices from assembling; (ii) they may allow the transmembrane helices of Cai to assemble functionally. These two roles may or may not be mutually exclusive.

The first proposition implies that assembly of Cai into the membrane would not be perturbed if its hydrophilic loops

were exchanged. When L2 of Cai was replaced with that of Cbi, the PhoA activity of the modified EpVBG7 protein was not affected; thus it seemed that the topology of Cai was not affected when its polar regions were replaced with those of Cbi. Furthermore, if the polar regions of Cai interacted with the ColA pore-forming domain in the open state, this domain would be expected to expose regions on the cytoplasmic side of the inner membrane to interact with L2 of Cai. However, studies on the gating of ColE1 channels (Slatin *et al.*, 1986; Raymond *et al.*, 1986; Jakes *et al.*, 1990; Abrams *et al.*, 1991) and ColE1 topographic studies (Song *et al.*, 1991; Zhang and Cramer, 1992) indicate that the loops of ColE1 connecting the four putative transmembrane helices on the cytoplasmic side of the inner membrane are very short and uncharged. As ColA is homologous to ColE1, it is unlikely that its cytoplasmic loops interact with L2 of Cai. Thus we favour the second proposition: the hydrophilic loops may allow the transmembrane helices of Cai to assemble functionally.

Conversely, the periplasmic loops of Cai may interact with ColA on the periplasmic side of the inner membrane. Indeed, Cai was inactivated when both L1 and L3 were replaced with those of Cbi. However, the activity of Cei is not affected even if its peripheral domains are extensively modified. This suggests that these regions are not critical for activity (Zhang and Cramer, 1993). In contrast, hydrophobic intramembrane helix-helix interactions are important for both ColA and ColE1 (Géli and Lazdunski, 1992a; Zhang and Cramer, 1993).

The differences in permissivity with regard to alterations of peripheral loops in Cai and Cei may reflect structure-function relationships. The structures of these proteins require that: (i) the transmembrane helices assemble either into a three- α -helix bundle (Cei) or four- α -helix bundle (Cai), and (ii) these bundles should be able to interact with hydrophobic helices of colicins. The structural constraints imposed on helix orientation should be much less marked with a three- α -helix bundle than with a four- α -helix bundle. Thus the bundle of Cai helices may be destabilized when its peripheral loops are modified, whereas the Cei α -helix bundle may be more robust.

Cai produced as two membrane fragments was unable to assemble into a functional protein. Transmembrane fragments of several proteins behave as autonomous folding domains (Köster and Braun, 1990; Popot and Engelman, 1990; Bibi and Kaback, 1990; Lemmon *et al.*, 1992; Kahn and Engelman, 1992; Maggio *et al.*, 1993). These transmembrane regions may undergo tight intermolecular associations that may not be modified when the domains function. In contrast, because intramembrane hydrophobic interactions are involved in the function of immunity proteins (Géli and Lazdunski, 1992a; Zhang and Cramer, 1993), inter-helix affinities within immunity proteins may not be very high so that the helices can interact with the

hydrophobic helical hairpins of the pore-forming colicins. This is consistent with independent membrane fragments of Cai not being able to assemble into a functional complex and with L2 being required. Alternatively, proteins with only four transmembrane segments may have a reduced probability of assembling correctly when produced as two separate fragments.

The protective function of the Cbi/Cai hybrids indicates that the hydrophobic regions of Cai and Cbi cannot be combined although they are homologous. The results also suggest that the last seven amino acids of H1 of Cai (residues 30 to 36) are specifically required for function. These data suggest that either the functional packing of Cai requires H1 to interact with another Cai transmembrane region or that H1 specifically recognizes ColA.

Immunity protein mutants able to protect against colicin mutants which bypass the wild-type immunity protein may help better define how Cai and pore-forming helices interact.

Experimental procedures

Strain and plasmids

E. coli C600 was the recipient strain for all plasmids and was also used as a sensitive indicator strain for colicin cytotoxicity. Plasmids pIA1, pIB1, and pIAB carry *cai*, *cbi*, and both *cbi* and *cai* in tandem, respectively (Géli and Lazdunski, 1992a). Plasmid pVL1 (Géli *et al.*, 1988) was cut by *Nco*I–*Sma*I, treated with *E. coli* polymerase Klenow fragment, and re-ligated to give pEpCai. Plasmid pEpCai carries the *cai* gene under the control of the ColA gene-inducible promoter (Llobès *et al.*, 1986); the protein encoded by pEpCai (EpCai) also carries an amino-terminal 'tag' recognized by mAb 1C11 (Géli *et al.*, 1988; 1993); EpCai is fully functional (Géli *et al.*, 1993). Plasmid pEpVBG7 was constructed by replacing the *Bgl*II–*Hind*III DNA fragment of pEpCai with the *Bgl*II–*Hind*III DNA fragment of pVBG7 (Géli *et al.*, 1989); the protein encoded by pEpVBG7 has the PhoA enzyme fused to L3 of EpCai. ColA and ColB are encoded by pE4 and pUCB19, respectively (Duché *et al.*, 1993; Géli and Lazdunski, 1992a).

Hydroxylamine mutagenesis of pIA1 and selection of ColB-immune clones

Hydroxylamine mutagenesis was performed as described (Silhavy *et al.*, 1984). Briefly, 5 μ g of purified plasmid pIA1 DNA was incubated for 3 h at 65°C in a total volume of 500 μ l containing 100 mM phosphate buffer, pH 6, 1 mM EDTA, and 0.5 M NH₂OH. The reaction was stopped by passing the mix through a spun column of Sephadex G50 (Pharmacia). The DNA was precipitated and resuspended in H₂O at a concentration of 200 ng ml⁻¹. C600 competent cells (0.1 ml) were transformed by electroporation with 200 ng of mutagenized plasmid. The cells were incubated for 45 min in 500 μ l of LB medium and then 2 μ g of purified ColB was added. Cells were incubated for 10 more min and were plated on ampicillin Luria–Bertani plates. Plasmids were isolated from selected transformants and used to transform C600 cells. The killing

activity of ColB was tested on the transformants to check that the immune phenotype was plasmid-linked. Plasmids of immune clones were sequenced.

Substitution of *Cai* hydrophilic loops L1, L2, and L3 for the homologous loops of *Cbi*

The *Clal* restriction site of pIA1 was destroyed to obtain pIA2. *AccI*, *Clal*, *AflIII*, and *Eco47III* restriction sites were created by site-directed mutagenesis in pIA2 at codons 35, 56, 89, and 144 of the *cai* gene, respectively. Pairs of oligonucleotides (5'-A TAC ATT AAT GAG CCG TAT TCA CAA GTA CTG TAT TAC CTG TAC AAC AAA GTC GCA TTC CTG CCA T-3', 5'-CGA TGG CAG GAA TGC GAC TTT GTT GTA CAG GTA ATA CAG TAC TTG TGA ATA CGG CTC ATT AAT GT-3'); (5'-TTA AGA ACT CGC GAT ATC ATT AAA CCG GTA ACG CGT AAA TTA GTC GTC A-3', 5'-GA TCT GAC GAC TAA TTT ACG CGT TAC CGG TTT AAT GAT ATC GCG AGT TC-3'), and (5'-A ACT ACA GCT GGC GGA TTT TTC AAA ATA TTA AGT CAT AAT GTT ATA GC-3', 5'-GC TAT AAC ATT ATG ACT TAA TAT TTT GAA AAA TCC GCC AGC TGT AGT T-3') were used to replace the sequences encoding L1, L2, and L3 of *Cai* by those of *Cbi*, respectively. Plasmid pIA2 was cut either by *AccI*+*Clal*, *AflIII*+*BglII*, or *HpaI*+*Eco47III*. *BglII* and *HpaI* are natural sites of pIA2. Pairs of oligonucleotides were hybridized and ligated into pIA2 cut with the appropriate restriction enzymes. DNA encoding the hybrid immunity proteins was sequenced. The region encoding the complete L3 of *Cai* was replaced with that of *Cbi* by site-directed mutagenesis. Arg-124 and Phe-126 were substituted for Tyr and Leu, respectively, by using the following mutagenic oligonucleotide: 5'-C TGT AGT TAA CTC GAG ATT GTA GAA GCA GAA TAG-3'.

Production of *Cai* as two independent fragments

A pair of oligonucleotides (5'-TTA AGA ATC AGA AAA TTA ATC AAC TTA GAG GTA AAT ATG AAC AGC GAC AGG AAC ACT GTA CTT A-3', 5'-GATC AAG TAG AGT GTT CCT GTC GCT GTT CAT ATT TAC CTC TTA GTT GAT TAA TTT TCT GAT CT-3') was introduced into pIA2 cut with *AflIII* and *BglII*. This synthetic DNA fragment contains a stop codon followed by a Shine-Dalgarno sequence and an ATG codon (see underlined sequences above) after the codon corresponding to Asn-96 of *Cai*. This DNA modification was also transferred into pEpCai and pEpVBG7.

Construction of *Cbi/Cai* hybrid proteins

Plasmid pIAB (5 µg) carrying *cbi* and *cai* in tandem was linearized with *EcoRV* (this restriction site is located between the two genes), treated with exonuclease III and mung-bean nuclease as previously described (Géli and Lazdunski, 1992a), and used to transform strain C600. Transformants were tooth-picked onto plates on which 100 µl of purified ColA or ColB solution (20 µg ml⁻¹) had been spread. ColA- or ColB-sensitive and -insensitive clones were identified. Their DNAs were analysed by restriction mapping. Homologous recombination between *cbi* and *cai* resulted in a fixed deletion (Tomassen *et al.*, 1985). The hybrid genes resulting from homologous recombination were selected and sequenced.

Miscellaneous

Published methods were used for ColA and ColB purification (Cavard and Lazdunski, 1979; Pressler *et al.*, 1986), liquid and plate assays for colicin cytotoxicity (Cavard and Lazdunski, 1979; Géli and Lazdunski, 1988; 1992a), site-directed mutagenesis (Baty *et al.*, 1987), DNA sequencing (Sequenase sequencing kit protocol), and the alkaline phosphatase assay (Manoil and Beckwith, 1985). EpCai and EpVBG7 were expressed as described by Géli *et al.* (1988).

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References

- Abrams, C.K., Jakes, K.S., Finkelstein, A., and Slatin, S.L. (1991) Identification of a translocated gating charge in a voltage-dependent channel. *J Gen Phys* **98**: 77–93.
- Baty, D., Knibiehler, M., Verheij, H., Pattus, F., Shire, D., Bernadac, A., and Lazdunski, C. (1987) Site-directed mutagenesis of the COOH-terminal region of colicin A: effect on secretion and voltage-dependent channel activity. *Proc Natl Acad Sci USA* **84**: 1152–1156.
- Baty, D., Frenette, M., Llobès, R., Géli, V., Howard, S.P., Pattus, F., and Lazdunski, C. (1988) Functional domains of colicin A. *Mol Microbiol* **2**: 807–811.
- Bénédicti, H., Frenette, M., Baty, D., Knibiehler, M., Pattus, F., and Lazdunski, C. (1991) Individual domains of colicins confer specificity in colicin uptake, in pore-properties and in immunity requirements. *J Mol Biol* **217**: 429–439.
- Bénédicti, H., Letellier, L., Llobès, R., Géli, V., Baty, D., and Lazdunski, C. (1992) Study of the import mechanisms of colicins through protein engineering and K⁺ efflux kinetics. In *Bacteriocins, Microcins and Lantibiotics*. Nato ASI Series. Vol. H65. James, R., Lazdunski, C., and Pattus, F. (eds). Berlin: Springer Verlag, pp. 215–223.
- Bibi, E., and Kaback, H.R. (1990) *In vivo* expression of the *lacY* gene in two segments leads to functional lac permease. *Proc Natl Acad Sci USA* **87**: 4325–4329.
- Bishop, L.J., Bjes, E.S., Davidson, V.L., and Cramer, W.A. (1985) Localization of the immunity protein reactive domain in unmodified and chemically modified COOH-terminal peptides of colicin E1. *J Bacteriol* **164**: 237–244.
- Bourdineaud, J.P., Boulanger, P., Lazdunski, C., and Letellier, L. (1990) *In vivo* properties of colicin A: channel activity is voltage dependent but translocation may be voltage independent. *Proc Natl Acad Sci USA* **87**: 1037–1041.
- Cavard, D., and Lazdunski, C. (1979) Purification and molecular properties of a new colicin. *Eur J Biochem* **96**: 519–524.
- Cramer, W.A., Dankert, J.R., and Uratani, Y. (1983) The membrane channel-forming bacteriocidal protein, colicin E1. *Biochim Biophys Act* **737**: 173–193.

- Duché, D., Parker, M.W., Gonzalès-Manas, S.M., Pattus, F., and Baty, D. (1994) Uncoupled steps of the colicin A pore-formation demonstrated by disulfide bond engineering. *J Biol Chem* **269**: 6332–6339.
- Espeset D., Corda, Y., Cunningham, K., Bénédicti, H., Llobès, R., Lazdunski, C., and Géli, V. (1994) The colicin A pore-forming domain fused to mitochondrial intermembrane space sorting signals can be functionally inserted into the *Escherichia coli* plasma membrane by a mechanism that bypasses the Tol proteins. *Mol Microbiol* **13**: 1121–1131.
- Géli, V., and Lazdunski, C. (1992a) An α -helical hydrophobic hairpin as a specific determinant in protein–protein interaction occurring in *Escherichia coli* colicin A and B immunity systems. *J Bacteriol* **174**: 6432–6437.
- Géli, V., and Lazdunski, C. (1992b) Immunity protein to pore forming colicins. In *Bacteriocins, Microcins and Lantibiotics*. Nato ASI Series. Vol. H65. James, R., Lazdunski, C., and Pattus, F. (eds). Berlin: Springer Verlag, pp. 171–179.
- Géli, V., Baty, D., Crozel, V., Morlon, J., Llobès, R., Pattus, F., and Lazdunski, C. (1986) A molecular genetic approach to the functioning of the immunity protein to colicin A. *Mol Gen Genet* **202**: 455–460.
- Géli, V., Baty, D., and Lazdunski, C. (1988) Use of a foreign epitope as a 'tag' for the localization of minor proteins: the case of the immunity protein to colicin A. *Proc Natl Acad Sci USA* **85**: 689–693.
- Géli, V., Baty, D., Pattus, F., and Lazdunski, C. (1989) Topology and function of the integral membrane protein conferring immunity to colicin A. *Mol Microbiol* **3**: 679–687.
- Géli, V., Koorengel, M.C., Demel, R.A., Lazdunski, C., and Killian, A. (1992) Acidic interaction of the colicin A pore-forming domain with model membranes of *E. coli* lipids results in a large perturbation of acyl chain order and stabilization of the bilayer. *Biochemistry* **31**: 11089–11094.
- Géli, V., Llobès, R., Zaat, S.A.J., van Spaendonk, R.M.L., Rollin, C., Bénédicti, H., and Lazdunski, C. (1993) Recognition of the colicin A N-terminal epitope 1C11 *in vitro* and *in vivo* in *Escherichia coli* by its cognate monoclonal antibody. *FEMS Microbiol Lett* **109**: 335–342.
- Goldman, K., Suit, J., and Kayalar, C. (1985) Identification of the plasmid-encoded immunity protein for colicin E1 in the inner membrane of *Escherichia coli*. *FEBS Lett* **190**: 319–323.
- Guihard, G., Bénédicti, H., Besnard, M., and Letellier, L. (1993) Phosphate efflux through the channels formed by colicins and phage T5 in *Escherichia coli* cells is responsible for the fall in cytoplasmic ATP. *J Biol Chem* **268**: 17775–17780.
- von Heijne, H. (1986) The distribution of positively charged residues in bacterial inner membrane proteins correlates with the transmembrane topology. *EMBO J* **5**: 3021–3027.
- Jakes, K.S., Abrams, C.K., Finkelstein, A., and Slatin, S.L. (1990) Alteration of the pH-dependent ion selectivity of the colicin E1 channel by site-directed mutagenesis. *J Biol Chem* **265**: 6984–6991.
- Kahn, W.T., and Engelman, D.M. (1992) Bacteriorhodopsin can be refolded from two independently stable transmembrane helices and the complementary five-helix fragment. *Biochemistry* **31**: 6144–6151.
- Konisky, J. (1982) Colicins and other bacteriocins with established modes of action. *Annu Rev Microbiol* **36**: 125–144.
- Köster, W., and Braun, V. (1990) Iron (III) hydroxamate transport of *Escherichia coli*: restoration of iron supply by coexpression of the N- and C-terminal halves of the cytoplasmic membrane protein FhuB cloned on separate plasmids. *Mol Gen Genet* **223**: 379–384.
- Lakey, J.H., Duché, D., Gonzalès-Manas, J.M., Baty, D., and Pattus, F. (1993) Fluorescence energy transfer distance measurements. The hydrophobic helical hairpin of colicin A in the membrane bound state. *J Mol Biol* **230**: 1055–1067.
- Lazdunski, C., Baty, D., Géli, V., Cavard, D., Morlon, J., Llobès, R., Howard, S.P., Knibiehler, M., Chartier, M., Varenne, S., Frenette, M., Dasseux, J.L., and Pattus, F. (1988) The membrane channel-forming colicin A: synthesis, secretion, structure, action and immunity. *Biochim Biophys Acta* **947**: 445–464.
- Lemmon, M.A., Flanagan, J.M., Treutlein, H.R., Zhang, J., and Engelman, D.M. (1992) Sequence specificity in the dimerization of transmembrane α -helices. *Biochemistry* **31**: 12719–12725.
- Llobès, R., Baty, D., and Lazdunski, C. (1986) The promoters of the genes for colicin production, release and immunity in the ColA plasmid: effects of convergent transcription and LexA. *Nucl Acid Res* **14**: 2621–2636.
- Maggio, R., Vogel, Z., and Wess, J. (1993) Reconstitution of functional muscarinic receptors by co-expression of amino- and carboxy-terminal receptor fragments. *FEBS Lett* **319**: 195–200.
- Mankovich, J.A., Lai, P.H., Gokul, N., and Konisky, J. (1984) Organization of the colicin Ib gene. *J Biol Chem* **259**: 8764–8768.
- Mankovich, J.A., Hsu, C., and Konisky, J. (1986) DNA and amino acid sequence analysis of structural and immunity genes of colicin Ia and Ib. *J Bacteriol* **168**: 228–236.
- Manoil, C., and Beckwith, J. (1985) *ThpA*: a transposon probe for protein export signals. *Proc Natl Acad Sci USA* **82**: 8129–8133.
- Merrill, A.R., and Cramer, W.A. (1990) Identification of a voltage-responsive segment of the potential-gated colicin E1 ion channel. *Biochemistry* **29**: 8529–8534.
- Mulligan, M.E., Hawley, D.K., Entriken, R., and McClure, W.R. (1984) *Escherichia coli* promoter sequences predict *in vitro* RNA polymerase selectivity. *Nucl Acids Res* **12**: 789–800.
- Parker, M.W., Pattus, F., Tucker, A.D., and Tsernoglou, D. (1989) Structure of the membrane-pore-forming fragment of colicin A. *Nature* **337**: 93–96.
- Parker, M.W., Pastman, J.P.M., Pattus, F., Tucker, A.D., and Tsernoglou, D. (1992) Refined structure of the pore-forming domain of colicin A at 2.4 Å resolution. *J Mol Biol* **224**: 639–657.
- Pattus, F., Massotte, D., Wiulmsen, H.U., Lakey, J., Tsernoglou, D., Tucker, A., and Parker, M. (1990) Colicins: prokaryotic killer pores. *Experientia* **46**: 180–192.
- Popot, J.-L. (1993) Integral membrane protein structure. *Curr Opin Struct Biol* **3**: 532–540.
- Popot, J.-L., and Engelman, D.M. (1990) Membrane protein folding and oligomerization: the two-stage model. *Biochemistry* **29**: 4031–4033.

- Pressler, V., Braun, V., Wittmann-Liebold, B., and Benz, R. (1986) Structural and functional properties of colicin B. *J Biol Chem* **261**: 2654–2659.
- Pugsley, A.P. (1988) The immunity and lysis genes of ColN plasmid pCHAP4. *Mol Gen Genet* **211**: 325–341.
- Rath, P., Bousche, O., Merrill, A.R., Cramer, W.A., and Rothschild, K.J. (1991) Fourier transform infrared evidence for a predominantly α -helical structure for the membrane-bound channel-forming COOH-terminal peptide of colicin E1. *Biophys J* **59**: 516–522.
- Raymond, L., Slatin, S.L., Finkelstein, A., Liu, Q.R., and Levinthal, C. (1986) Gating of a voltage-dependent channel (colicin E1) in planar lipid bilayers: translocation of regions outside the channel-forming region. *J Membr Biol* **92**: 255–268.
- Schramm, E., Olschlager, T., Troger, W., and Braun, V. (1988) Sequence, expression and localization of the immunity protein for colicin B. *Mol Gen Genet* **211**: 176–182.
- Shin, Y.K., Levinthal, C., Levinthal, F., and Hubbell, W.L. (1993) Colicin E1 binding to membranes: time-resolved studies of spin-labeled mutants. *Science* **259**: 960–963.
- Silhavy, T.J., Bennam, M.L., and Endquist, L.W. (1984) *Experiments with Gene Fusions*. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press.
- Slatin, S.L., Raymond, L., and Finkelstein, A. (1986) Gating of a voltage-dependent channel (colicin E1) in planar lipid bilayers: the role of protein translocation. *J Membr Biol* **92**: 247–254.
- Song, H.Y., and Cramer, W.A. (1991) Membrane topography of ColE1 gene products: the immunity protein. *J Bacteriol* **173**: 2935–2943.
- Song, H.Y., Cohen, F.S., and Cramer, W.A. (1991) Membrane topography of ColE1 gene products: the hydrophobic anchor of the colicin E1 channel is a helical hairpin. *J Bacteriol* **173**: 2927–2934.
- Tomassen, J., van der Ley, P., van Zeil, M., and Agteberg, M. (1985) Localization and functional domains in *E. coli* K12 outer membrane porins. *EMBO J* **4**: 1583–1587.
- Zhang, Y.L., and Cramer, W.A. (1992) Constraints imposed by protease accessibility on the trans-membrane and surface topography of the colicin E1 ion channel. *Prot Sci* **1**: 1666–1676.
- Zhang, Y.L., and Cramer, W.A. (1993) Intramembrane helix-helix interactions as the basis of inhibition of the colicin E1 ion channel by its immunity protein. *J Biol Chem* **268**: 1–9.