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This family of 50 to 60 kDa pore-forming bacterial toxins (sulfhydryl-activated cytolysins) comprises 19 structurally and antigenically related, chromosomally encoded single-chain soluble proteins endowed with potent lethal and lytic properties resulting from the disruption of the cytoplasmic membrane of eukaryotic cells and that of certain cell organelles. Membrane cholesterol appears as a specific binding site of these toxins and is thought to contribute to their oligomerization in target membranes.

The 19 toxins identified to date are produced by gram-positive aerobic or anaerobic, sporulating or non-sporulating bacteria from the genera *Streptococcus*, *Bacillus*, *Clostridium*, and *Listeria* (Smyth and Duncan 1978, Alouf and Geoffroy 1991) listed below in Table 1.

Except for PLY, which is intracytoplasmic, the other toxins are secreted in culture medium during bacterial growth. Among the toxin-producing bacteria, only *Listeria* are intracellular pathogens which grow and release their toxins in host phagocytes or possibly in other cells.

The lethal (cardiotoxic) and cytolytic properties of the toxins are suppressed by oxidants or by thiol-group block-

ing agents and restored by reducing agents. The toxins share common epitopes and elicit in humans or in animals neutralizing and precipitating cross-reacting antibodies. The biological properties are irreversibly lost in the presence of very low concentrations of cholesterol and other related 3β-hydroxysterols which interfere with toxin binding on target cells (Alouf and Geoffroy 1991).

A considerable progress in our understanding of structure-activity relationship resulted from the cloning, sequencing, and expression of *tox* genes of 8 out of the 19 toxins of the family.

Table 1

Bacterial genus	Species	Toxin name	Established or suggested ^b toxin and gene acronyms	
<i>Streptococcus</i>	<i>S. pyogenes</i>	Streptolysin O ^a	SLO	<i>sio</i>
	<i>S. pneumoniae</i>	Pneumolysin ^a	PLY	<i>ply</i>
	<i>S. suis</i>	Suilyisin ^a	SUI	<i>sui</i>
<i>Bacillus</i>	<i>B. cereus</i>	Cereolysin O ^a	CLO	<i>clo</i>
	<i>B. alvei</i>	Alveolysin ^a	ALV	<i>alv</i>
	<i>B. thuringiensis</i>	Thuringiolysin O ^a	TLO	<i>tlo</i>
	<i>B. laterosporus</i>	Laterosporolysin	LSL	<i>lsi</i>
<i>Clostridium</i>	<i>C. tetani</i>	Tetanolysin [*]	TTL	<i>ttl</i>
	<i>C. botulinum</i>	Botulinolysin	BTL	<i>btl</i>
	<i>C. perfringens</i>	Perfringolysin O ^a	PFO	<i>Pfo</i>
	<i>C. septicum</i>	Septicolysin O	SPL	<i>spl</i>
	<i>C. histolyticum</i>	Histolyticolysin O	HTL	<i>htl</i>
	<i>C. novyi A (oedematiens)</i>	Novyilysin	NVL	<i>nvl</i>
	<i>C. chauvoei</i>	Chauveolysin	CVL	<i>cvl</i>
	<i>C. bifermentans</i>	Bifermentolysin	BFL	<i>bfl</i>
	<i>C. sordellii</i>	Sordellilysin	SDL	<i>sdl</i>
<i>Listeria</i>	<i>L. monocytogenes</i>	Listeriolysin O ^a	LLO	<i>llolisA</i>
	<i>L. ivanovii</i>	Ivanolysin ^a	ILO	<i>ilo</i>
	<i>L. seeligeri</i>	Seeligerolysin	LSO	<i>lso</i>

Some strains of streptococci of groups C and G also produce streptolysin O.

^aNative toxins reported to be purified to apparent homogeneity ^bAuthor's proposal.

The deduced number of amino acid residues and mol. wt. of mature toxins are the following: SLO (538 AA, 60151 Da; databank accession number M18638; see preceding entry p. 5), PLY (471 AA, 52800 Da, databank accession number: M17717; Walker *et al.* 1987), PFO (472 AA, 52469 Da; databank accession number: M36704; Tweten 1988b), ALV (469 AA, 51766 Da; databank accession number M62709; Geoffroy *et al.* 1990), LLO (504 AA, 55842 Da; databank accession number M24199; Mengaud *et al.* 1988; Domann and Chakraborty 1989), ILO (505 AA, 55961 Da; databank accession number X60461; Haas *et al.* 1992), and LSO (505 AA, 56371 Da; databank accession number X60462; Haas *et al.* 1992) Cereolysin gene (*clo*) has been cloned and expressed in *E. coli* and *B. subtilis* (Kreft *et al.* 1983) but to our knowledge no sequence has been so far reported. A considerable AA sequence homology (stronger at the C-terminal part) was found. It was more pronounced when structurally related AA were taken into account. At the nucleotide sequence level, the homology was lower although detectable, indicating that *tox* genes have undergone extensive divergence from a common ancestor (Boulnois *et al.* 1991).

An 11 AA sequence (—ECTGLAWEWWR—) was the longest common motif conserved in each protein (except for single amino acid change in seeligerolysin). It contained the unique Cys residue of the toxins (except for ILO which possesses a second Cys residue beyond the consensus sequence closer to the C-terminus). The thiol group of the Cys residue of the conserved undecapeptide was logically considered as an 'essential' group required for lytic activity as supported by its abrogation by thiol blocking agents. This contention was not supported by site-directed mutagenesis undertaken on PLY, SLO, and

LLO (see Michel *et al.* 1990; Boulnois *et al.* 1991; Sheehan *et al.* 1994). Changing the Cys residue to either alanine, serine, or glycine did not affect or only reduced lytic activity suggesting that there is no absolute requirement for the thiol group in the *in vitro* activity of the toxins. In contrast, the overall structure of the motif appears important (at least in part) for interaction with cholesterol and pore-formation. On the other hand, the use of genetically truncated recombinant PLY showed that the deletion of the six C-terminal AA reduced binding by 96 per cent as also found for PFO (Owen *et al.* 1994).

The genetic regulation of toxin expression has been particularly investigated for LLO and PFO. The former was shown to be positively regulated by a 27.1 kDa protein encoded by *prfa* gene the deletion of which besides LLO affects at least four other virulence factors (Schwan *et al.* 1994; Sheehan *et al.* 1994). PFO expression was also under positive control of a regulatory gene (*pfor*) which also affected the expression of clostridal collagenase and hemagglutinin (Shimizu *et al.* 1994).

■ Purification and sources

The native toxins purified so far are isolated to apparent homogeneity by standard protein chemistry techniques from culture supernatants (except for PLY obtained from disrupted pneumococci) of appropriate toxin-producing strains, grown under culture conditions specific for each bacterial species described in the hereafter cited publications. Most procedures comprise a combination of crude material concentration (ultrafiltration and/or salting-out by ammonium sulfate), then ion-exchange column chromatography, followed by gel molecular

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sieving and (or) hydrophobic (low- or high-pressure) column chromatography. Covalent thiopropyl gel chromatography has been widely used taking advantage of toxin cysteinyl residue. Appropriate purification techniques have been described for PLY (Kancierski and Möllby 1987; Rubins *et al.* 1994), PFO (Tweten 1988a), ALV (Geoffroy and Alouf 1983), LLO (Geoffroy *et al.* 1987; Kreft *et al.* 1989), ILO (Kreft *et al.* 1989; Vazquez-Boland *et al.* 1989), BTL (Haque *et al.* 1992), and suilysin (Jacobs *et al.* 1994). The production and purification of fully bioactive recombinant PFO expressed in *E. coli* (Tweten 1988a) or of PLY expressed in this microorganism (Mitchell *et al.* 1989; Rubins *et al.* 1994) and *B. subtilis* (Taira *et al.* 1989) has been reported. The toxins are not commercially available to our knowledge.

The pH optimum for the lytic activity of the various toxins so far studied falls between 6.5 and 7.4 except for LLO with a pH optimum about 5 (no activity at pH 7.0) which may reflect the acid nature of the phagolysosome where it acts (Geoffroy *et al.* 1987; Sheehan *et al.* 1994).

■ Toxicity

Microgram quantities of the toxins are lethal for mice, rabbits, and other laboratory animals. The LD₅₀ (i.v. route) ranges from 0.2 to 0.8 µg (Smyth and Duncan 1978; Geoffroy *et al.* 1987).

Hemolytic activity on sheep or rabbit erythrocytes ranges from 0.5 to 2 × 10⁶ hemolytic units/mg of protein (Alouf and Geoffroy 1991). The use of the toxins is safe for operators following normal safety recommendations for bacterial manipulations.

■ Use in cell biology

The lytic properties of the toxins and their specific binding of cholesterol on to eukaryotic cells and organelle membranes have been used for the permeabilization of these structures for the analysis of various cell functions and metabolism, the introduction of exogenous molecular effectors and the generation of limited lesions in various cells for the isolation of membrane receptors intracellular enzymes or organelles which could not be easily obtained by other methods (see Alouf and Geoffroy 1991; Berthou *et al.* 1992; Launay *et al.* 1992; Ahnert-Hilger *et al.* 1993).

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