# Actinobacillus pleuropneumoniae RTX-toxins: uniform designation of haemolysins, cytolysins, pleurotoxin and their genes

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The three different pore-forming RTX-toxins of Actinobacillus pleuropneumoniae are reviewed, and new and uniform designations for these toxins and their genes are proposed. The designation ApxI (for Actinobacillus pleuropneumoniae RTX-toxin I) is proposed for the RTX-toxin produced by the reference strains for serotypes 1, 5a, 5b, 9, 10 and 11, which was previously named haemolysin I (HlyI) or cytolysin I (ClyI). This protein is strongly haemolytic and shows strong cytotoxic activity towards pig alveolar macrophages and neutrophils; it has an apparent molecular mass in the range 105 to 110 kDa. The genes of the apxI operon will have the designations apxIC, apxIA, apxIB, and apxID for the activator, the structural gene and the two secretion genes respectively. The designation ApxII is proposed for the RTX-toxin which is produced by all serotype reference strains except serotype 10 and which was previously named App, HlyII, ClyII or Cyt. This protein is weakly haemolytic and moderately cytotoxic and has an apparent molecular mass between 103 and 105 kDa. The genes of the apxII operon will have the designations apxIIC for the activator gene and apxIIA for the structural toxin gene. In the apxII operon, no genes for secretion proteins have been found. Secretion of ApxII seems to occur via the products of the secretion genes apxIB and apxID of the apxI operon. The designation ApxIII is proposed for the nonhaemolytic RTX-toxin of the reference strains for serotypes 2, 3, 4, 6 and 8, which was previously named cytolysin III (ClyIII), pleurotoxin (Ptx), or macrophage toxin (Mat). This protein is strongly cytotoxic and has an apparent molecular mass of 120 kDa. The genes of the apxIII operon have the designations apxIIIC, apxIIIA, apxIIIB and apxIIID for the activator gene, the structural gene and the two secretion genes respectively.

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## Introduction

Actinobacillus pleuropneumoniae is a Gram-negative bacterium belonging to the family Pasteurellaceae. It is the aetiological agent of swine pleuropneumonia, a severe disease causing large economic losses in industrialized swine production (Shope, 1964; Nicolet, 1992). Among the twelve different serotypes, three different exotoxins which belong to the group of poreforming RTX-toxins (Welch, 1991) have been detected (Frey & Nicolet, 1988a, 1990; Frey et al., 1991b, 1992; Chang et al., 1989; Rycroft et al., 1991a; Kamp et al., 1991; Smits et al., 1991; Lalonde et al., 1989; Jansen et al., 1993, 1992b; Macdonald & Rycroft, 1992; van den Bosch, 1991; Gygi et al., 1990). Two of these RTX-toxins possess both haemolytic and cytotoxic activity (Frey & Nicolet, 1988 a; Rosendal et al., 1988; Kamp et al., 1991) while the third has cytotoxic, but not haemolytic activity (Rycroft et al., 1991a; Kamp et al., 1991). The RTXtoxins have molecular masses of 100-120 kDa and can be distinguished serologically by polyclonal and monoclonal antibodies (Frey et al., 1992; Kamp et al., 1991; Rycroft et al., 1991a; Kamp & van Leengoed, 1989). Reference and field strains of several serotypes produce two different RTX-toxins (Frey et al., 1992; Kamp et al., 1991; Rycroft et al., 1991a; Jansen et al., 1992a, b, 1993), a situation which is rather unusual among RTXtoxin-producing bacteria and which created confusions in the serological distinction of different RTX-proteins. All RTX-toxins of A. pleuropneumoniae have been shown to be major immunogenic factors in experimentally and

naturally infected pigs (Devenish *et al.*, 1990*a*, *b*; Ma & Inzana, 1990; Frey & Nicolet, 1991; Rycroft *et al.*, 1991*a*) and seem to be important virulence factors (Inzana *et al.*, 1991; Kamp *et al.*, 1991; Stine *et al.*, 1991; Rycroft *et al.*, 1991*a*, *b*; Udeze & Kadis, 1992; Devenish *et al.*, 1992; Dom *et al.*, 1992). They have also been shown to be involved in the induction of protective immunity and are suggested to be important components in vaccines against swine pleuropneumonia (Bosse *et al.*, 1992; Bhatia *et al.*, 1991; Inzana *et al.*, 1991; Rycroft *et al.*, 1991*a*; Rossi Campos *et al.*, 1992; van den Bosch *et al.*, 1992; van den Bosch, 1991; Devenish *et al.*, 1990*a*; Fedorka Cray *et al.*, 1990).

In general, the operons encoding RTX-toxins consist of four contiguous genes in the order C A B D. The A gene encodes the structural toxin protein, the C gene encodes an activator protein which is involved in fatty acylation in the conversion of the protoxin to active toxin, and the B and D genes encode membraneassociated proteins for secretion of the toxins (Issartel et al., 1991; Welch, 1991; Felmlee et al., 1985). While this is also true for several RTX-operons of A. pleuropneumoniae (Gygi et al., 1992; Jansen et al., 1993, 1992b), partial RTX-operons containing two genes have been found in A. pleuropneumoniae and Actinobacillus suis (Burrows & Lo, 1992; Frey et al., 1993; Chang et al., 1991; Jansen et al., 1992a, b; Smits et al., 1991). The presence of different combinations of the three RTXtoxins in strains from the same species originally led to considerable confusion, probably because of the very similar molecular masses of these toxins. Due to the

New designation		Synonyms*								
Name of toxin	Protein/ <i>gene</i> symbols	Name of toxin	Protein/ gene symbols	Name of toxin	Protein/ gene FCRsymbols	Name of toxin	Protein/ gene symbols	Name of toxin	Protein, gene symbols	
RTX-toxin I	ApxI apxIC apxIA apxIB apxID	Haemolysin I	HlyI <sup>e</sup> hlyIC <sup>f</sup> s hlyIA <sup>fg</sup> hlyIB <sup>g</sup> hlyID <sup>g</sup>	Cytolysin I	ClyI <sup>k</sup> clyIC <sup>i</sup> clyIA <sup>i</sup> clyIB <sup>i</sup> clyID <sup>i</sup>		appB <sup>d</sup> appD <sup>d</sup>			
RTX-toxin II	ApxII <i>apxIIC</i> apxIIA	Haemolysin II	HlyII <sup>e</sup> hlyIIC <sup>f</sup> hlyIIA <sup>f</sup>	Cytolysin II	ClyII <sup>k</sup> clyIIC <sup>i</sup> clyIIA <sup>i</sup>	Haemolysin	App <sup>e</sup> appC <sup>e</sup> appA <sup>e</sup>	Cytolysin	Cyt <sup>a</sup> cytC <sup>a</sup> cytA <sup>a</sup>	
RTX-toxin III	ApxIII apxIIIC apxIIIA apxIIIB apxIIID	Pleurotoxin	Ptx <sup>m</sup> ptxA <sup>t</sup>	Cytolysin III	ClyIII <sup>k</sup> clyIIIC <sup>hj</sup> clyIIIA <sup>hj</sup> clyIIIB <sup>k</sup> clyIIID <sup>h</sup>			Macrophage- toxin	Mat <sup>b</sup>	

Table 1. New designations and synonyms used for the various RTX-toxins found in A. pleuropneumoniae

\*References: a, Anderson et al. (1991); b, van den Bosch et al. (1992); c, Chang et al. (1989); d, Chang et al. (1991); e, Frey & Nicolet (1988a); f, Frey et al. (1992); g, Gygi et al. (1992); h, Jansen et al. (1992a); i, Jansen et al. (1992b); j, Jansen et al. (1993); k, Kamp et al. (1991); l, Macdonald & Rycroft (1992); m, Rycroft et al. (1991a). intense research efforts on A. pleuropneumoniae RTX toxins which have been made simultaneously by various groups during the last few years, several different toxin names and gene designations have been used. A combination of the results from the molecular characterization at the genetic level and serological and toxicity studies has resulted in the present understanding of RTX-toxins and genes in A. pleuropneumoniae strains. The researchers working on A. pleuropneumoniae RTX toxins therefore made the effort to agree upon a common, uniform nomenclature for these toxins which was proposed at the Fallen Leaf Lake Conference 1992 on 'Bacterial Virulence Mechanisms'. These new designations and their synonyms are listed in Table 1 and are briefly described below. They are abbreviated by Apx, standing for Actinobacillus pleuropneumoniae RTXtoxins. ApxI, ApxII and ApxIII will be used according to numbering used in previously published work (Jansen et al., 1992a; Smits et al., 1991; Kamp et al., 1991; Frey & Nicolet, 1988a, 1990). For RTX toxins from other species the same strategy for abbreviations could be used.

#### ApxI (previously HlyI or ClyI)

A. pleuropneumoniae-RTX-toxin I (ApxI) was initially described as the strongly haemolytic haemolysin I (HlyI), purified from serotype 1 type strain 4074 as an active protein with an apparent molecular mass of 105 kDa (Frey & Nicolet, 1988 a, b). ApxI was also found to be cytotoxic for alveolar macrophages and neutrophils and therefore it was also named cytolysin I (ClyI) (Kamp et al., 1991). ApxI was found to be present in the reference strains of serotypes 1, 5a, 5b, 9, 10 and 11 (Frey & Nicolet, 1990; Frey et al., 1992; Kamp et al., 1991). In these reference strains the operon of ApxI contains four genes: apxIC, the activator gene; apxIA, the structural toxin gene; and apxIB and apxID, the secretion genes (Table 2). These genes were previously named hlvIC, hlyIA, hlyIB and hlyID respectively in serotype 1 (Gygi et al., 1990, 1992; Frey et al., 1993) or clyIC, clyIA, clyIB and clyID in serotype 9 (Jansen et al., 1992a, b; Smits et al., 1991). The apxIA genes of serotypes 1, 9 and 11 are similar whereas they show allelic variation in serotypes 5a, 5b and 10 (Jansen et al., 1992b; Frey et al., 1993). The genes apxIB and apxID correspond to the genes appB and appD, which were initially believed to be the secretion genes of ApxII (initially named App) (Chang et al., 1991). The apxI operon is transcribed into two RNA species: a major one of 3.5 kb which is Ca<sup>2+</sup> inducible and contains apxIC and apxIA, and a minor transcript of 7.5 kb which is not induced by Ca<sup>2+</sup> and contains the whole operon apxICABD (Gygi et al., 1992). The reference strains of serotypes 2, 4, 6, 7, 8 and

12 do not possess apxIC and apxIA and therefore these serotypes do not produce ApxI. Instead these serotypes possess a truncated apxI operon containing apxIB and apxID and the C-terminal end of apxIA (Frey et al., 1993; Jansen et al., 1992b). The serotype 3 reference strain lacks the entire apxI operon (Frev et al., 1993; Jansen et al., 1992b). The structural gene apxIA has been sequenced and was shown to be similar to the Escherichia *coli* haemolysin gene hlvA and to a lesser extent to Pasteurella haemolytica leukotoxin gene lktA (Frey et al., 1991b, 1993). apxIA encodes the protein ApxIA, which has a molecular mass of 110.2 kDa as deduced from the DNA sequence. It contains 13 glycine-rich repeats and binds <sup>45</sup>Ca<sup>2+</sup> (Frey et al., 1991b). This binding is required for haemolytic activity and binding to neutrophils (van Leengoed & Dickerson, 1992; Devenish & Rosendal, 1991).

### ApxII (previously HlyII, ClyII, App or Cyt)

ApxII was initially described as the weakly haemolytic toxin HlyII (haemolysin II) with an apparent molecular mass of 105 kDa isolated from serotype 2 reference strain \$1536 (Frey & Nicolet, 1988a, 1990; Frey et al., 1991a). ApxII was identified as a 103 kDa protein by monoclonal antibodies in the reference strains of all serotypes except 10 (Kamp et al., 1991). Besides its haemolytic activity. ApxII was also found to be cytotoxic for alveolar macrophages and neutrophils and was designated cytolysin II (ClyII) (Kamp et al., 1991). The genes encoding the activator and the structural protein of ApxII were first cloned from serotype 5 and sequenced (Chang et al., 1989) and designated appC and appA respectively. These sequences appeared to be nearly identical to the apxIICA (clyIICA) genes of serotype 9 (Smits et al., 1991). Using PCR amplification, gene expression and monoclonal and polyclonal antibodies, the AppA protein was shown to be identical to ApxIIA and to be produced by all serotypes except 10 (Frey et al., 1992; Kamp et al., 1991; Jansen et al., 1992a; Smits et al., 1991). apxIIA is present in all serotype reference strains except 10 and shows no significant allelic variations (Frey et al., 1993; Jansen et al., 1992a). The apxII operon was shown to contain only the activator gene apxIIC and the gene for the structural protein apxIIA, but not the genes for the secretion proteins B and D (Jansen et al., 1992a; Frey et al., 1993; Chang et al., 1989; Smits et al., 1991) (Table 2). The secretion genes were probably deleted, since only short segments of B-like genes were found downstream of apxIIA (Chang et al., 1989; Smits et al., 1991). Secretion of the ApxIIA protein seems to occur by transcomplementation with apxIB and apxID gene products (Frey et al., 1993; Jansen et al., 1992a). DNA sequence

Serotype 1	apxI operon				apxII operon		apxIII operon				
	apxIC	apxIA	apxIB	apxID	apxIIC	apxIIA					
2	•	•		apxID	apxIIC	apxIIA	apxIIIC	apxIIIA	apxIIIB	apxIIID	
3			•	•	apxIIC	apxIIA			apxIIIB		
4			apxIB	apxID	apxIIC	apxIIA			apxIIIB		
5a	apxIC	apxIA	apxIB	apxID	apxIIC	-	1	1		-	
5b	-	•	apxIB	•	apxIIC	apxIIA					
6	1	1	-	apxID	apxIIC	-	apxIIIC	apxIIIA	apxIIIB	apxIIID	
7			apxIB	apxID	apxIIC	apxIIA				1	
8			*	apxID		apxIIA	apxIIIC	apxIIIA	apxIIIB	avxIIID	
9	apxIC	apxIA	apxIB	-	apxIIC	4					
10	•		apxIB	-	-1	-1					
11		-	apxIB		apxIIC	apxIIA					
12			-	apxID	apxIIC						

 Table 2. Presence of the different apx genes in the reference strains for the different serotypes of A. pleuropneumoniae

Data were compiled from: Jansen et al. (1992a, b); Frey et al. (1992, 1993); Gygi et al. (1992); Smits et al. (1991); Chang et al. (1989, 1991). See text for details.

analysis of apxIIA reveals that the ApxIIA protein has a calculated molecular mass of 102.5 kDa and contains eight glycine-rich repeats (Chang *et al.*, 1989; Smits *et al.*, 1991). ApxIIA resembles the *P. haemolytica* leukotoxin LktA, and to a lesser extent ApxIA and the *E. coli* haemolysin HlyA (Smits *et al.*, 1991; Chang *et al.*, 1989). apxIIC and apxIIA were also cloned from serotype 7 and were named cytC and cytA respectively (Anderson *et al.*, 1991; Rossi Campos *et al.*, 1992) and were shown by DNA sequence analysis to be identical with the apxIICA sequences of serotype 5 and 9 (Chang *et al.*, 1989; Smits *et al.*, 1991).

### ApxIII (previously Ptx, ClyIII, Mat)

The third RTX-toxin of A. pleuropneumoniae, ApxIII, is a protein with an apparent molecular mass of 120 kDa. ApxIII is present in the reference strains of serotypes 2, 3, 4, 6 and 8 and was initially named cytolysin III (ClyIII) (Kamp et al., 1991; Jansen et al., 1992b, 1993), or pleurotoxin (Ptx) (Rycroft et al., 1991a; Macdonald & Rycroft, 1992), or macrophage toxin (Mat) (van den Bosch et al., 1992; van den Bosch, 1991). ApxIII has no haemolytic activity but shows strong cytotoxic activity towards alveolar macrophages and neutrophils (Kamp et al., 1991; Rycroft et al., 1991a; Macdonald & Rycroft, 1992; van den Bosch, 1991). The gene apxIIIA for the structural protein ApxIIIA was cloned and expressed in E. coli and designated ptxA, or clyIIIA (Macdonald & Rycroft, 1992; Jansen et al., 1992b). It was found to be present in the reference strains of serotypes 2, 3, 4, 6 and 8 (Macdonald & Rycroft, 1992; Jansen et al., 1992b) (Table 2). In all these serotypes a complete operon consisting of the activator gene apxIIIC, the structural gene for the toxin apxIIIA, and two secretion genes apxIIIB and apxIIID were found (Table 2) and previously named clyIIIC, clyIIIA or ptxA, clyIIIB and clyIIID respectively (Jansen et al., 1992b; Macdonald & Rycroft, 1992). The DNA sequence of apxIIIC and apxIIIA from the serotype 8 reference strain has been established (Jansen et al., 1993). The derived amino acid sequence for ApxIIIA shows the typical features of RTX-toxins, with the three hydrophobic domains in the N-terminal half of the protein and 13 glycine-rich repeats in the C-terminal part of the protein (Jansen et al., 1993). The calculated molecular mass of ApxIIIA is 112-8 kDa (Jansen et al., 1993).

## **Concluding remarks**

Detailed genetic and biochemical data are now available on *A. pleuropneumoniae* RTX-toxins. Their exact functions and target cells still remain to be established. It is therefore most important that all research groups working on these toxins use the uniform designations ApxI, ApxII and ApxIII proposed here, in order to avoid confusion and to ensure rapid research progress in the field.

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