

## Online Research @ Cardiff

This is an Open Access document downloaded from ORCA, Cardiff University's institutional repository: http://orca.cf.ac.uk/81254/

This is the author's version of a work that was submitted to / accepted for publication.

Citation for final published version:

Palma, Leopoldo and Berry, Colin 2016. Understanding the structure and function of Bacillus thuringiensis toxins [Letter]. Toxicon 109, pp. 1-3. 10.1016/j.toxicon.2015.10.020 file

Publishers page: http://dx.doi.org/10.1016/j.toxicon.2015.10.020 <a href="http://dx.doi.org/10.1016/j.toxicon.2015.10.020">http://dx.doi.org/10.1016/j.toxicon.2015.10.020</a>

## Please note:

Changes made as a result of publishing processes such as copy-editing, formatting and page numbers may not be reflected in this version. For the definitive version of this publication, please refer to the published source. You are advised to consult the publisher's version if you wish to cite this paper.

This version is being made available in accordance with publisher policies. See <a href="http://orca.cf.ac.uk/policies.html">http://orca.cf.ac.uk/policies.html</a> for usage policies. Copyright and moral rights for publications made available in ORCA are retained by the copyright holders.



Letter to the editor

1
 2
 3

Understanding the structure and function of *Bacillus thuringiensis* toxins.

4

5 Dear editor,

6

7 "If you want to understand function, study structure" (Francis Crick, 1988).

8

9 As biological control agents take an expanding share of the pesticides market and the 10 production of insect-resistant crops increases, it is essential to understand the structure and 11 function of the active agents, the invertebrate-active toxins that are the fundamental ingredients 12 of these control systems. The potential for these agents in industry, agriculture and medicine 13 necessitates a thorough investigation of their activity. The entomopathogenic bacterium Bacillus 14 thuringiensis (Bt) is an important biological source of insecticidal proteins, with many strains 15 bearing a wide variety of insecticidal genes. Bt delta-endotoxins (Cry and Cyt) (Figure 1) are 16 synthesized during the stationary growth phase as crystalline parasporal inclusions, highly 17 active against a wide range of insects (Schnepf, Crickmore et al. 1998). This bacterium also 18 synthesizes other proteins during vegetative growth that are secreted into the culture medium. 19 These have been designated as vegetative insecticidal proteins (Vips) (Estruch, Warren et al. 20 1996, Warren, Koziel et al. 1998) and secreted insecticidal protein (Sip) (Donovan, Engleman et 21 al. 2006), and exhibit insecticidal activity against some coleopteran (the two-component 22 Vip1/Vip2 toxin, and Sip) and lepidopteran pests (Vip3) (Estruch, Warren et al. 1996, Warren, 23 Koziel et al. 1998). The insecticidal proteins of Bt are highly specific for their hosts and have 24 gained worldwide importance as environmentally desirable alternatives to chemical insecticides. 25 Bt products have the biggest market share of biological insecticides and are used successfully in 26 crop protection and vector control programmes worldwide. Moreover, Bt strains are also the 27 major source for insect resistance transgenes in transgenic plants. Despite the importance of a 28 wide variety of toxins in the action of this entomopathogenic bacterium, structural information 29 has only been published on a subset of toxin classes: (i) the 3-domain Cry toxins (eg (Li, Carroll 30 et al. 1991)), (ii) the binary Cry34Ab/Cry35Ab toxin ((Kelker, Berry et al. 2014)), (iii) the Cyt 31 toxins (eg (Li, Koni et al. 1996)); (iv) the Vip2Aa protein (an ADP-ribosyl transferase (Han, 32 Craig et al. 1999)) and (v) aerolysin-like structures such as the Cry45 (anticancer parasporin 33 protein), Cry46 (anticancer parasporin protein), and Cry51 insecticidal toxin (Akiba, Higuchi et 34 al. 2006, Akiba, Abe et al. 2009, Xu, Chinte et al. 2015). The 3-domain Cry toxins (Figure 1) 35 are the best-characterized group of insecticidal proteins and are toxic after crystal solubilisation 36 and proteolytic activation by midgut proteases of susceptible insects (Schnepf, Crickmore et al. 37 1998). Even though different 3-domain Cry toxins display clear differences in their amino acid 38 sequences and biological activities, the activated toxins all share in common a remarkably 39 similar and conserved 3-domain structure (de Maagd, Bravo et al. 2003, Bravo, Gill et al. 2007). 40 The availability of structures for 3-domain Cry proteins (Figure 1) has opened the field for 41 extensive mutagenesis to retarget toxins (Pigott and Ellar 2007) and to overcome resistance to 42 the most used toxins to date (e.g. Cry1A) (Ferré and Van Rie 2002). The structures of the 43 components for the binary Cry34/Cry35 toxin show similarities to the aegerolysin (Cry34) and 44 aerolysin (Cry35) families of proteins, which are able to interact with cell membranes to form 45 pores and kill coleopterans (Kelker, Berry et al. 2014). Although the roles of the two 46 components in toxicity are not clear, Cry35 may be a beta-pore forming toxin and/or may 47 interact with receptor via its lectin-like domain. The similarity of this protein with the better 48 studied Bin toxins may also help in the elucidation of its activity. Cyt toxins directly interact 49 with saturated membrane lipids and kill by causing cell lysis (Xu, Wang et al. 2014). Even 50 though Cyt toxins are usually considered to be active against mosquitoes and black flies (de Maagd, Bravo et al. 2003), low activity has been reported against Chironomus larvae (Hughes, 51 52 Stevens et al. 2005) and aphids (Porcar, Grenier et al. 2009) and the knowledge of Cyt toxin 53 structure facilitated modification to enhance Cyt2Aa binding and toxicity against hemipteran 54 pests (Chougule, Li et al. 2013). Hemipterans may show a general interaction in this class of 55 toxins since related proteins from the bacterium Dickeya dadantii have been shown also to kill 56 pea aphids (Loth, Costechareyre et al. 2015). However, despite the importance of increasing our 57 knowledge of the structure of insecticidal toxins, a significant number of them do not share the 58 3-domain structure and for many of these, structural information still is not available. 59 Consequently, our ability to carry out similar studies to exploit these toxins is severely limited, 60 thereby inhibiting their development. Amongst the classes of other toxins lacking basic 61 biochemical and structural characterisation are the following, important examples: (i) 62 Vegetative insecticidal proteins Vip1 and Vip3 (Figure 1). Vip1 and Vip2 proteins together 63 constitute a binary toxin and are commonly toxic against coleopteran and homopteran pests (Warren, Koziel et al. 1998). Vip2 exhibits homology with the enzymatic ADP-64 ribosyltransferase toxin and its structure has been already elucidated (Han, Craig et al. 1999). 65 66 No structure-function studies have been developed for Vip1, the specificity-determining B 67 component of the toxin. In addition, the mode of action of Vip3 toxins remains unclear and 68 would be significantly enriched by studying the structure-activity relationships for this protein 69 class with increasing interest in its development for use in transgenic plants. Variations in the 70 insecticidal toxicity profiles of natural Vip3 sequences from different Bt strains will provide a 71 background of sequence diversity with which to understand specificity and to map the variant 72 amino acids with the structural data. (ii) Cry6 is a ~ 54-kDa protein exhibiting features of the 73 Smc chromosome segregation protein family (Palma, Muñoz et al. 2014) showing activity 74 against nematodes and coleopterans (van Frankenhuyzen 2013). (iii) Cry22 is active against

coleopteran pests and ants (Payne, Kennedy et al. 1997, Isaac, Krieger et al. 2003). It has regions of homology with cadherins and lectins but again, its structure has not been published.

iv) The small Cry37 protein (~14 kDa) that acts as a member of a two-component toxin that kills coleopterans (Donovan, Donovan et al. 2000). (v) Cry55 is active against coleopteran pests and nematodes (van Frankenhuyzen 2009) and, although some regional similarities to Toxin\_10 family proteins are predicted, its overall fold and mechanism of action are unknown. Bringing new toxins to market involves numerous regulatory hurdles and structure function data greatly enhance our ability to address safety and target specificity issues. In addition, a deeper knowledge of structure and mechanism will be crucial in our efforts to avoid insect resistance (for example through understanding toxin-receptor interactions) and to be able to retarget toxins against new pests (as achieved previously with 3-domain toxins and dipteran active Cyt2Aa toxin). Therefore, a comprehensive understanding of the modes of action along with the understanding of structure will revolutionise our ability to exploit these proteins by providing new paradigms for the action of insect toxins and will assist the agri-business sector in their attempts to exploit new toxin types.

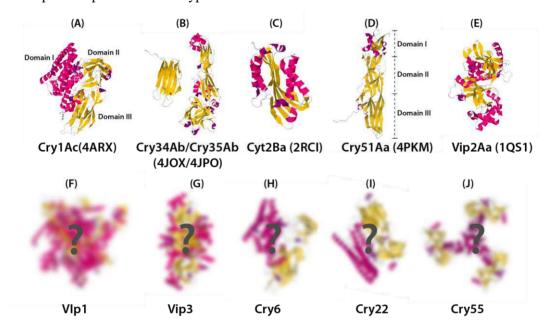


Figure 1. Bt toxin structures

Known three-dimensional structures of insecticidal toxins from Bt: (A) Three-domain Cry toxin Cry1Ac, Domain I (in pink) is the pore-forming domain whereas domains II and III (in yellow) have roles in toxin-receptor interactions. (B) Binary Cry34Ab/Cry35Ab toxin. (C) Cyt2Ba toxin (monomer). (D) Cry51 toxin (monomer) exhibits an aerolysin-like architecture that can be considered as 3-domains. (E) Vip2Aa protein from *Bacillus cereus*. Unknown toxin structures for insecticidal proteins of interest are represented by defocussed structural images: Vip1 (F) and Vip3 (G) and for insecticidal (crystal) toxins Cry6 (H), Cry22 (I) and Cry55 (J). Codes in parenthesis correspond to Protein Data Bank accession numbers.

- 101 References
- Akiba, T., Y. Abe, S. Kitada, Y. Kusaka, A. Ito, T. Ichimatsu, H. Katayama, T. Akao, K.
- Higuchi, E. Mizuki, M. Ohba, R. Kanai and K. Harata (2009). "Crystal Structure of the
- 104 Parasporin-2 Bacillus thuringiensis Toxin That Recognizes Cancer Cells." Journal of Molecular
- 105 <u>Biology</u> **386**(1): 121-133.
- Akiba, T., K. Higuchi, E. Mizuki, K. Ekino, T. Shin, M. Ohba, R. Kanai and K. Harata (2006).
- 107 "Nontoxic crystal protein from Bacillus thuringiensis demonstrates a remarkable structural
- similarity to beta-pore-forming toxins." Proteins **63**(1): 243-248.
- Bravo, A., S. S. Gill and M. Soberon (2007). "Mode of action of *Bacillus thuringiensis* Cry and
- 110 Cyt toxins and their potential for insect control." <u>Toxicon</u> **49**(4): 423-435.
- 111 Chougule, N. P., H. Li, S. Liu, L. B. Linz, K. E. Narva, T. Meade and B. C. Bonning (2013).
- "Retargeting of the *Bacillus thuringiensis* toxin Cyt2Aa against hemipteran insect pests." Proc
- 113 Natl Acad Sci U S A **110**(21): 8465-8470.
- de Maagd, R. A., A. Bravo, C. Berry, N. Crickmore and H. E. Schnepf (2003). "Structure,
- diversity, and evolution of protein toxins from spore-forming entomopathogenic bacteria."
- 116 Annu Rev Genet **37**: 409-433.
- Donovan, W. P., J. C. Donovan and A. C. Slaney (2000). "Bacillus thuringiensis CryET33 and
- 118 CryET34 compositions and uses thereof " <u>US Patent 6063756</u>.
- Donovan, W. P., J. T. Engleman, J. C. Donovan, J. A. Baum, G. J. Bunkers, D. J. Chi, W. P.
- 120 Clinton, L. English, G. R. Heck, O. M. Ilagan, K. C. Krasomil-Osterfeld, J. W. Pitkin, J. K.
- Roberts and M. R. Walters (2006). "Discovery and characterization of Sip1A: a novel secreted
- protein from Bacillus thuringiensis with activity against coleopteran larvae." Appl Microbiol
- 123 <u>Biotechnol</u> **72**(4): 713-719.
- Estruch, J. J., G. W. Warren, M. A. Mullins, G. J. Nye, J. A. Craig and M. G. Koziel (1996).
- "Vip3A, a novel *Bacillus thuringiensis* vegetative insecticidal protein with a wide spectrum of
- activities against lepidopteran insects." Proc Natl Acad Sci USA 93(11): 5389-5394.
- Ferré, J. and J. Van Rie (2002). "Biochemistry and genetics of insect resistance to Bacillus
- thuringiensis." Annu Rev Entomol 47: 501-533.
- Han, S., J. A. Craig, C. D. Putnam, N. B. Carozzi and J. A. Tainer (1999). "Evolution and
- mechanism from structures of an ADP-ribosylating toxin and NAD complex." Nat Struct Biol
- 131 **6**(10): 932-936.
- Han, S., J. A. Craig, C. D. Putnam, N. B. Carozzi and J. A. Tainer (1999). "Evolution and
- mechanism from structures of an ADP-ribosylating toxin and NAD complex." Nature structural
- 134 biology **6**(10): 932-936.

- Hughes, P. A., M. M. Stevens, H.-W. Park, B. A. Federici, E. S. Dennis and R. Akhurst (2005).
- 136 "Response of larval Chironomus tepperi (Diptera: Chironomidae) to individual Bacillus
- thuringiensis var. israelensis toxins and toxin mixtures." J. Invertebr. Pathol. 88: 34-39.
- 138 Isaac, B., E. K. Krieger, L. Mettus and F. M. Sakuntala (2003). "Polypeptide compositions toxic
- to anthonomus insects, and methods of use." US Patent 6541448.
- Kelker, M. S., C. Berry, S. L. Evans, R. Pai, D. G. McCaskill, N. X. Wang, J. C. Russell, M. D.
- Baker, C. Yang, J. W. Pflugrath, M. Wade, T. J. Wess and K. E. Narva (2014). "Structural and
- Biophysical Characterization of Bacillus thuringiensis Insecticidal Proteins Cry34Ab1 and
- 143 Cry35Ab1." PLoS One **9**(11): e112555.
- Li, J., P. A. Koni and D. J. Ellar (1996). "Structure of the mosquitocidal delta-endotoxin CytB
- from Bacillus thuringiensis sp. kyushuensis and implications for membrane pore formation." <u>J.</u>
- 146 <u>Mol. Biol.</u> **257**(1): 129-152.
- Li, J. D., J. Carroll and D. J. Ellar (1991). "Crystal structure of insecticidal delta-endotoxin from
- 148 Bacillus thuringiensis at 2.5 A resolution." Nature 353(6347): 815-821.
- Loth, K., D. Costechareyre, G. Effantin, Y. Rahbe, G. Condemine, C. Landon and P. da Silva
- 150 (2015). "New Cyt-like delta-endotoxins from Dickeya dadantii: structure and aphicidal
- 151 activity." Sci Rep 5: 8791.
- Palma, L., D. Muñoz, C. Berry, J. Murillo and P. Caballero (2014). "Bacillus thuringiensis
- toxins: an overview of their biocidal activity." Toxins (Basel) **6**(12): 3296-3325.
- Payne, J. M., K. Kennedy, J. B. Randall, H. Meier, H. J. Uick, L. Foncerrada, H. E. Schnepf, G.
- 155 E. Schwab and J. Fu (1997). "Bacillus thuringiensis toxins active against hymenopteran pests."
- 156 <u>US Patent 5596071</u>.
- Pigott, C. R. and D. J. Ellar (2007). "Role of receptors in Bacillus thuringiensis crystal toxin
- 158 activity." Microbiol Mol Biol Rev **1**(2): 255-281.
- Porcar, M., A. M. Grenier, B. Federici and Y. Rahbe (2009). "Effects of Bacillus thuringiensis
- delta-endotoxins on the pea aphid (Acyrthosiphon pisum)." Appl Environ Microbiol 75(14):
- 161 4897-4900.
- Schnepf, E., N. Crickmore, J. Van Rie, D. Lereclus, J. Baum, J. Feitelson, D. R. Zeigler and D.
- H. Dean (1998). "Bacillus thuringiensis and its pesticidal crystal proteins." Microbiol Mol Biol
- 164 <u>Rev</u> **62**(3): 775-806.
- van Frankenhuyzen, K. (2009). "Insecticidal activity of Bacillus thuringiensis crystal proteins."
- 166 J Invertebr Pathol **101**(1): 1-16.
- van Frankenhuyzen, K. (2013). "Cross-order and cross-phylum activity of *Bacillus thuringiensis*
- pesticidal proteins." J Invertebr Pathol **114**(1): 76-85.
- Warren, G. W., M. G. Koziel, M. A. Mullins, G. J. Nye, B. Carr, N. M. Desai, K. Kostichka, N.
- B. Duck and J. J. Estruch (1998). "Auxiliary proteins for enhancing the insecticidal activity of
- pesticidal proteins." <u>US patent 5770696.</u>

- 172 Xu, C., U. Chinte, L. Chen, Q. Yao, Y. Meng, D. Zhou, L. J. Bi, J. Rose, M. J. Adang, B. C.
- Wang, Z. Yu and M. Sun (2015). "Crystal structure of Cry51Aa1: A potential novel insecticidal
- aerolysin-type beta-pore-forming toxin from Bacillus thuringiensis." Biochem Biophys Res
- 175 <u>Commun</u> **462**(3): 184-189.
- 176 Xu, C., B. C. Wang, Z. Yu and M. Sun (2014). "Structural insights into Bacillus thuringiensis
- 177 Cry, Cyt and parasporin toxins." <u>Toxins (Basel)</u> **6**(9): 2732-2770.

178

- 179 Leopoldo Palma\*
- 180 Facultad de Ciencias Agrarias, Universidad Nacional del Litoral, Esperanza, Santa Fe,
- 181 Argentina.
- 182 Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina.
- 183 Colin Berry.
- 184 Cardiff School of Biosciences, Cardiff University, Park Place, Cardiff CF10 3AT, UK.

185

- 186 \*Corresponding author.
- 187 Facultad de Ciencias Agrarias, Universidad Nacional del Litoral, Esperanza, Santa Fe,
- 188 Argentina. E-mail address: <u>lpalma@fca.unl.edu.ar</u> (L. Palma)

189