

41<sup>th</sup> ANNUAL MEETING  
of the  
Society for  
**INVERTEBRATE  
PATHOLOGY**  
and  
9<sup>TH</sup> INTERNATIONAL CONFERENCE ON  
*BACILLUS THURINGIENSIS*  
Incorporating COST862 Action: Bacterial  
Toxins for Insect Control

**PROGRAM and ABSTRACTS**

3-7 August 2008  
University of Warwick,  
Coventry, UK

Poster / Bacteria. Tuesday, 10:30. **B-29****Characterization of environmental isolates of *Bacillus thuringiensis* from northeastern Poland harbouring vip3A gene homologues**Izabela Swiecicka<sup>1</sup>; Dennis K. Bideshi<sup>2</sup>; Magdalena Czajkowska<sup>1</sup>; Sylwia Kotowicz<sup>1</sup><sup>1</sup>Department of Microbiology, University of Białystok, Swierkowa 20B, PL15-950 Białystok, Poland, <sup>2</sup>Department of Natural and Mathematical Science, California Baptist University, 8432 Magnolia Ave, Riverside, California 92504, USA.

Address for correspondence: izabelas@uwb.edu.pl

Various strains of *Bacillus thuringiensis* have been used effectively as biological insecticides due to their production of highly specific crystalline proteins, the so-called Cry or d-endotoxins. Recently, vegetative insecticidal proteins (VIPs) secreted during vegetative growth of certain *B. thuringiensis* strains have been described. As VIPs, particularly VIP3A, are known to be active against lepidopteran larvae, there is significant interest in identifying or developing strains with novel Cry and VIP combinations for applied use. To this end, the purpose of this study was to determine (i) the presence of vip3A homologues in *B. thuringiensis* collected in northeastern Poland; (ii) the correlation between the vip3A and cry genes contents, as well as the diversity in chromosomal DNA patterns; and in particular, (iii) the diversity of vip3A. Of 166 *B. thuringiensis* isolated from small wild mammals, soil, and milk products, 16 (~10%) harboured vip3A homologues with high levels of sequence conservation. These vip3A-positive isolates were shown to contain genes encoding known lepidopteran-active toxins, such as cry1 (11 isolates), cry2 (8 isolates), and cry9 (2 isolates). Finally, PFGE analysis of DNA profiles demonstrated marked diversity among these isolate. As such, further studies are required to determine whether these isolates vary in toxicity against lepidopterans.

Poster / Bacteria. Tuesday, 10:30. **B-30****Characterization of a novel Cry9Bb  $\delta$ -endotoxin from *Bacillus thuringiensis***Joseilde O. Silva-Wemeck<sup>1</sup>; David J. Ellar<sup>2</sup><sup>1</sup>Embrapa Recursos Genéticos e Biotecnologia, Parque Estação Biológica, Final W5 Norte, Brasília, DF, 70.770-900, Brazil,<sup>2</sup>Department of Biochemistry, University of Cambridge, 80 Tennis Court Road, Cambridge CB2 1GA, UK.

Address for correspondence: joseilde@cenargen.embrapa.br

The *Bacillus thuringiensis* serovar japonensis strain S725 produces spherical crystals harboring a major protein of about 130 kDa. This protein showed immunoaffinity and high level of N-terminal sequence identity with Cry9 delta-endotoxins. A cry9-like gene from Bt S725 was cloned, sequenced and expressed in Bt. The cloned gene sequence contains a 3492 bp ORF, which encodes a polypeptide of 1163 amino acids, with a predicted molecular mass of 131.4 kDa. The deduced amino acid sequence was unique and showed 73% identity with Cry9Ba. The novel d-endotoxin was assigned to a new subclass, Cry9Bb, by the Bt Toxin Nomenclature Committee. The 130 kDa Cry9Bb protein formed crystals and produced two fragments around 69 and 58 kDa upon trypsin activation. It exhibited activity against the lepidopterans *Manduca sexta* and *Anticarsia gemmatilis*. The biological effect of an amino acid residue substitution, A84P, was investigated. The LC<sub>50</sub> for the Cry9Bb crystals against *M. sexta* neonate larvae was 6.84  $\mu\text{g}/\text{cm}^2$ , while the LC<sub>50</sub> for Cry9BbA84P crystals was 0.78  $\mu\text{g}/\text{cm}^2$ . PCR screening revealed that, in addition to cry9Bb, Bt strain S725 also contains cry11 and vip3 genes. Transcription analysis, using RT-PCR, showed that the cry11 gene was transcribed at T<sub>2</sub> and T<sub>5</sub> stages of sporulation.

Poster / Bacteria. Tuesday, 10:30. **B-31 STU****Identification and cloning of novel cry genes from *Bacillus thuringiensis* strain Y41**Changlong Shu<sup>1</sup>; Xudong Su<sup>1</sup>; Jie Zhang<sup>1</sup>; Dafang Huang<sup>2</sup>; Fuping Song<sup>1</sup><sup>1</sup>Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, 100193, P. R. China, <sup>2</sup>Biotechnology Research Institute, Chinese Academy of Agricultural Sciences, Beijing, 100081, P. R. China.

Address for correspondence: jzhang@ippcaas.cn, fpsong@ippcaas.cn

Four novel cry genes were cloned by PCR-RFLP method from *Bacillus thuringiensis* isolate Y41, which was isolated from Hainan Province. The toxins accumulating within the cells consisted of major proteins of 66 and 140 kDa and forming spherically shaped crystals. Compared the sequences of these fragments with known holotype cry genes, the result indicated that three of them are similar with cry40Aa1, cry30Aa1, and cry19Aa1 respectively, and one of them is not distinct similar with any reported cry genes. All toxins have typical characteristic of delta-endotoxin and containing five homology blocks (1-5) which present in most *B. thuringiensis* delta-endotoxins. These four novel cry genes were deposited in GenBank and named by the *B. thuringiensis* delta-endotoxin nomenclature committee as cry40Ca1, cry30Da1, cry52Aa1 and cry53Aa1 respectively.

Poster / Bacteria. Tuesday, 10:30. **B-32 STU****The characterization of novel Bt toxins**Zenas George<sup>1</sup>; Neil Crickmore<sup>1</sup><sup>1</sup>University of Sussex, Falmer, Brighton, BN1 9QG, UK.

Address for correspondence: zg21@sussex.ac.uk

Despite the large numbers of Bt toxins already discovered there remains the potential for the discovery of new toxins or the creation of variants with improved activities through traditional or directed evolution techniques. Although many techniques now exist for the directed evolution of new proteins the screening of variant toxins for improved activities remains a labour-intensive and resource heavy activity. Using the toxins Cry1Ac, Cry1Ah and Cry1Ie we have investigated the possibility of using an in vivo method for the selection of improved recombinants. We will describe the basis of this selection procedure and present the results of initial feasibility studies.

Poster / Bacteria. Tuesday, 10:30. **B-33 STU****Identification of new cry genes of *Bacillus thuringiensis* through the use of a system of universal primers**Pedro A. Noguera<sup>1</sup>; Jorge E. Ibarra<sup>1</sup><sup>1</sup>Departamento de Biotecnología y Bioquímica, CINVESTAV-IPN, Apartado postal 629, Irapuato, GTO. Mexico.

Address for correspondence: pnoguera@ira.cinvestav.mx

Based on the known cry gene sequences of *B. thuringiensis*, three pairs of primers were designed from the 5 conserved blocks found in the delta-endotoxin coding region. Designed primer pairs amplify the regions between blocks 1 and 5, 2 and 5, and 1 and 4, respectively. *In silico* analyses indicated that up to 96% of the known sequences can be amplified by one or more of these pairs. Their ability to detect new cry genes was tested when DNA from *B. thuringiensis* strains showing atypical crystal morphology was used as template. Some 175 strains recorded as "atypical" in the CINVESTAV-IPN (LBIT-series) collection log were further selected by phase contrast microscopy, SDS-PAGE, and SEM analyses. After a systematic amplification and sequencing of amplicons obtained from 27 strains, 5 putative cry genes showed