

International Congress on Invertebrate Pathology and Microbial Control &

52nd Annual Meeting of the Society for  
Invertebrate Pathology &

17th Meeting of the IOBC-WPRS Working Group  
“Microbial and Nematode Control of Invertebrate Pests”

28th July - 1st August



VALENCIA  
**SIP/IOBC**  
2019

Programme and Abstracts

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tein toxins (Crickmore *et al.* 2016, <http://www.btnomenclature.info/>). In the present study, the molecular taxonomy of monosporic cultures of *B. thuringiensis* collected from south and south-east region of Kazakhstan was investigated.

A partial sequence of the pyruvate carboxylase encoding *pycA* gene and the glycerol uptake facilitator protein *glpF* gene were sequenced as molecular-taxonomic markers to determine the systematic position of the isolates with respect to the *Bacillus cereus sensu lato* complex as part of the multilocus sequence analysis (MLSA) scheme introduced by Priest *et al.* (2004, J. Bacteriol 186: 7959-7970).

Phylogenetic reconstruction located all isolates within the *Bacillus cereus* complex and with firm bootstrap support in the clade representing the *B. cereus* sub-species *Bacillus thuringiensis*. Importantly, isolates were thereby unambiguously differentiated from human both pathogenic *B. cereus* and *B. anthracis*. Moreover, Kazakh isolates were shown to belong to the Bt lineages "sotto" and "kurstaki".

POSTER SESSION. Wednesday, 16:30 **PB-23**

**Molecular characterization of a new *Bacillus thuringiensis* strain from Argentina toxic against Lepidoptera and Coleoptera base on its whole-genome analysis**

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The insecticidal proteins of *Bacillus thuringiensis* are used as formulations of spore-crystal complexes and their genes have been incorporated into several crops, which has provided a model for genetic engineering in agriculture. Despite the variability of the Cry proteins described so far, it is still necessary to look for toxins with a broad spectrum of action, since a significant number of pests are not controlled with the available Cry proteins. It is also important to provide alternatives to address the problem of insect resistance, which has already appeared with the use of formulations and in transgenic plants that express *cry* genes that code for insecticidal proteins. We report the characterization of a novel *B. thuringiensis* isolate native to Argentina (FCC7) toxic against lepidoptera and coleoptera insects. The strain shows a rounded crystal harboring mainly a protein of about 130 kDa. Through the whole-genome sequencing by Illumina Miseq 1500 platform we detected two crystal protein genes with *cry8*-like genes homology, three vegetative insecticidal protein (Vip) genes and multiple virulence factors such as phospholipases, proteases, enhancins, chitinases, among others. The two *cry8*-like genes, homologous to the sequences Cry8Ac1 and Cry8Qa1 with 73,4 % and 88,9 % identity respectively, were cloned and expressed into the 4Q7/pSTAB system and the larvicidal activity were tested against *Spodoptera frugiperda* and *Tenebrio molitor*. Two of the Vip genes were identified as Vip1-like with an identity of 74,9% and 70,3% respectively while the third Vip gene was 82% identical to Vip2 sequences.

Supported by ANPCyT (PICT N° 2015-0575) and Universidad Nacional de Mar del Plata (15/E793 EXA840/17).

POSTER SESSION. Wednesday, 16:30 **PB-24**

**The impact of the absence of the *Bacillus cereus* siderophore Bacillibactin and the FeuA siderophore binding protein on iron acquisition and in insect virulence**

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The ability of *B. cereus* and *B. thuringiensis* to colonize hosts is linked to several adaptation factors, including iron acquisition from host iron sources like hemoglobin, ferritin. Previously, we showed that the surface protein IIsA is expressed in the insect haemocoel and takes part in virulence. IIsA binds host ferritin and the iron stored in this molecule can be mobilized

for bacterial growth by the combined action of IIsA and the siderophore Bacillibactin (BB) encoded by "Ent" operon. To enter the bacteria the BB/Iron complex binds to a Siderophore Binding Proteins (SPB) at the cell surface. To get insight into the role of the SPB "FeuA" in iron uptake from ferritin a *Bc* ATCC 14579 mutant  $\Delta$ feuA and a  $\Delta$ feuA $\Delta$ entA double mutant along with complemented strains were analysed. The results indicate that the  $\Delta$ feuA mutant is affected *in vitro* almost similarly to the entA-mutant with ferritin as the sole iron source. Interestingly, *in vivo* infection (injection into the hemocoel of *G. mellonella*) shows that the feuA mutant and particularly the double mutant  $\Delta$ feuA $\Delta$ entA were as virulent as the wildtype strain, while the FeuA complemented double mutant resulted in the less virulent EntA mutant phenotype. In addition, a *in trans* plasmid born transcriptional *iIsA* fusion was analyzed in the various strains and in different growth media. IIsA was significantly expressed in the double mutant background but absent from the wild type and the single mutants when ferritin was the only iron source. This suggests, that in the absence of BB/FeuA *B. cereus* can modulate expression of iron acquisition and/or virulence factors to maintain host colonisation.

POSTER SESSION. Wednesday, 16:30 **PB-25**

**Populational and Genetic Analysis of *Wolbachia* Symbionts in some Pests of Russia**

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Maternally-inherited symbionts of *Wolbachia* genus are extremely widespread among insects. These symbionts can affect biology of their hosts in different ways, including sex ratio shift, contribution to essential metabolite synthesis, suppress host mutations, protection against viruses and etc. However, there are few information of *Wolbachia* effect on the most infected hosts. Indeed such experiments are rather laborious and should imply multidimensional and integral design. Here we present data on *Wolbachia* prevalence and its genetic diversity in populations of different pests. In particular, we studied native and invasive populations of *Polygraphus proximus* (Coleoptera; Curculionidae: Scolytinae), Siberian and European populations of *Aporia crataegi* (Lepidoptera; Pieridae), Far-Eastern and Siberian populations of *Dendrolimus sibiricus* and *Dendrolimus pini* (Lepidoptera; Lasiocampidae), East European populations of *Ostrinia nubilalis* and *Ostrinia scapularis* (Lepidoptera; Crambidae), and other species. As a result, we observed cases of high *Wolbachia* prevalence in populations, recent *Wolbachia* horizontal transmission, and *Wolbachia* loss. High *Wolbachia* prevalence in pest populations over broad territory is likely to indicate an important role of these symbionts in host biology. Finally, we aim to confer the ways of experimental tests of *Wolbachia* role in certain species and applying *Wolbachia* infection as an agent for pest control.

This study was supported by the Russian Foundation for Basic Research RFBR №18-316-00099 and №19-04-00983.

POSTER SESSION. Wednesday, 16:30 **PB-26 STU**

**No synergism of Cry1Ca and Vip3Aa by Lepidoptera and Coleoptera fragments of cadherin in *Spodoptera exigua* and *Grapholita molesta***

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96 *Bacillus thuringiensis* (Bt) is a gram positive bacteria used as a biope-