International Congress on Invertebrate Pathology and Microbial Control and the 48th Annual Meeting of the Society for Invertebrate Pathology

Vancouver, Canada
August 9-13, 2015
**SIP 2015 Vancouver**

**Meeting at a Glance**

- How sea stars get wasted: Evidence of a viral etiology and host response to sea star wasting disease – C. Burge
- Symbiont-mediated defense against parasitic nematodes in Drosophila – S. Perlman
- No nematode is an island: Interactions between entomopathogenic nematodes and other organisms – C. Griffin
- The ecology of virulence in insect associated bacteria: Field experiments and experimental evolution – B. Raymond

12:30 – 14:00

**LUNCH (on your own)**

J. Invertebr. Pathol. Board lunch meeting

Symposium: Microsporidia/Diseases of Beneficial Invertebrates

- Microsporidia as emerging pathogens
  - The complex relationship between microsporidia and fungi – P. Keeling
  - Fish microsporidians: Emerging pathogens or emerging knowledge? – M. Freeman
  - Understanding phylogenetic relationships among relationships among species in the Nosema/Vairimorpha clade: What does genetic similarity say about host switching in the microsporidia? – W.-F. Huang
  - Emergent pathogens of invertebrates: Environmental sampling to identify novel parasite lineages – B. Williams
  - Investigations into the composition of the microsporidian polar tube – L. Weiss

14:00 – 16:00

**Contributed Papers**

- Bacteria 1
- 2306/9
- Microbial Control 1
- 2311

16:00 – 16:30

**BREAK**

16:30 – 18:30

**Symposium: Fungi/Microbial Control**

- The (underestimated) value of applied research: Moving the theoretical to the practical
  - Why biopesticides sometimes fail – R. Gwynn, M. Brownbridge, T. Glare
  - Multiple roles, so what should we measure? An ecological approach to promote the contribution of fungal entomopathogens in pest management within the agro ecosystem – N. Meyling
  - Research and development of biological crop protection products – R. Royalty, D. Maker
  - Adapting field trials for microorganisms – in practice – E. Ladurner
  - How do we improve efficacy monitoring or biopesticides? – T. Glare, M. Brownbridge, R. Gwynn

16:30 – 20:00

**Contributed Papers**

- Viruses 1
- 2306/9
- Microsporidia
- 2311

20:00 – 22:00

**Division meetings**

- Microbial Control 2301
- Diseases of Beneficial Invertebrates 2306/9
- Workshop: Environmental DNA

**TUESDAY – August 11**

8:00 – 10:00

**Symposium: Bacteria**

- Mechanisms of field resistance to Bt pesticides and Bt-crops
  - Bt resistance in Plutella – too many trees? – N. Crickmore
  - Multiple resistance mechanisms selected in cabbage looper populations resistant to Dipel – P. Wang
  - Pink bollworm resistance to Bt cotton: Similar mechanisms in the lab and the field – J. Fabrick

**SATURDAY – August 8**

14:00 – 20:00

Registration

Gage Reception

**SUNDAY – August 9**

7:30 – 18:00

Registration

Gage Reception

OECD-CRP Symposium

‘Microsporidia in the animal to human food chain: An international symposium to address chronic epizootic disease’

9:00 – 17:00

SIP Council meeting

10:30 – 11:00

**BREAK**

12:20 – 13:30

LUNCH

13:00 – 17:00

Workshop: Bacteria Division

‘Regulatory considerations for the commercialization of new insecticidal proteins’

Current insights on Bt insecticidal protein specificity and future directions – J. Jurat-Fuentes, N. Crickmore

Proteins 101: structure, function, and evolution – J. Jeu

Protein sequences, structures and functions – rules for divergence and rules for conservation – Adam Godzik

Modelling of insecticidal toxins and their potential interactions: Challenges and aspirations – C. Berry, N. Crickmore

Safety considerations derived from Cry34/35Ab1 structure and function – K. Narra, N. Storer, R. Herman

14:40 – 15:00

**BREAK**

Case study of a novel wCRW insecticidal protein from Chromobacterium sp. – K. Sampson

Biochemical characterization of parasporin-4 and effects of the pro-parasporin-4 diet on the health of mice – S. Oshumura, H. Koga, K. Inouye, E. Mizuki

Considerations for the safety assessment of novel insect control proteins: A regulatory perspective – P. MacDonald

New insecticidal proteins: Optimization and specificity – W. Moor, J. Haas, A. Evdokimov, J. Baum, A. Silvanovich, Y. Yin, D. Bowen, K. Glenn, A. Evan

16:20 – 17:00

Mixer

18:00 – 21:00

Mixer

Sage Bistro

**MONDAY – August 10**

7:30 – 18:00

Registration

Outside Great Hall

Opening Ceremony

Great Hall

Todd Kabaluk & Mark Goettel – Organizing Committee

Peter Krell – President, SIP

Welcome Addresses; Award Presentations

Founders’ Lecture

James Becnel – Chair of Founders’ Lecture Committee

Honoree: Phyllis T. Johnson

Lecturer: G. Stentiford

10:00 – 10:30

**BREAK**

10:30 – 12:30

Plenary Symposium

Great Hall

‘Insect pathogens in nature: Ecology and evolution’

*All meetings are in The Nest*
10:45 Excursion+BBQ buses leave Gage Residence
15:00 BBQ only buses leave Gage Residence
18:00 5k race Cheakamus Center
19:00 BBQ Cheakamus Center

**WEDNESDAY – August 12**

8:00 – 10:00 **Symposium: Viruses** 2301

‘Advances in host and insect virus genomics’
- Macro- and Micro-evolutionary trends in baculoviruses – J. Jehle
- Alphabaculoviruses: Host transcriptome responses to infection – G. Blissard
- Polynodnaviruses: From discovery to current insights – M. Strand
- Dicistrovirus – hijacking the host translational machinery – E. Jan
- Insect metagenomics-based discovery of novel, small RNA viral genomes – S. Liu

8:00 – 9:45

**Contributed Papers**
- Microbial Control 2 2306/9
- Nematode 1 2311

10:00 – 10:30 **BREAK**

10:30 – 12:30

**Symposium: Nematodes/Bacteria** 2306/9

‘Intracellular response to bacteria and bacterial toxins’
- Insecticidal action, cellular interactions and response of combinations of Photorhabdus-insect related (Pir) and Bacillus thuringiensis Crystal (Cry) toxins – A. Castagnola
- Response to Cry1Ac intoxication in midgut cells of Heliothis virescens larvae – C. Oppert
- Syringe-like infection mechanism of bacterial ABC toxins revealed in molecular detail – C. Gatsogiannis
- Caenorhabditis elegans nck-1 plays a distinct and specific role in defense against bacterial pore-forming toxins – A. Sitaram
- The cell biology of Wolbachia - filarial nematode interactions and the dark side of symbiosis – W. Sullivan
- Photorhabdus: light without heat – N. Waterfield

10:30 – 12:30

**Contributed Papers**
- Fungi 1 2311
- Viruses 3 2301

12:30 – 14:00 **LUNCH (on your own)**

14:00 – 16:00

**Symposium: Fungi** 2301

‘Endophytic entomopathogenic fungi: “pro-biotic” microbial associates of plants?’
- Endophytic entomopathogenic fungi as “plant probiotics”: An important tool in protecting and promoting plant health – C. Keyser
- Entomopathogenic fungi as endophytes: Interactions with plants and herbivores – S. Vidal
- Trading insect nitrogen for photosynthate: Carbon translocation from a plant to an insect pathogenic, endophytic fungus – M. Bidochka

14:00 – 15:00 **Nematodes Workshop** 2311

14:00 – 16:00 **Contributed Papers** 2306/9
- Viruses 4

16:00 – 16:30 **POSTER SESSION** 2301

**BREAK**

16:30 – 18:30 **Division meetings:**
- Fungi 2311
- Viruses + Workshop: *Definition of virus species concept* 2301
- Microsporidia + Workshop: *War and Peace: the comparative impact of morphology- and sequence-based phylogenies on practical taxonomy and evolutionary history of microsporidia* 2314
- Bacteria 2306
- Nematodes 2309

**THURSDAY – August 13**

8:00 – 10:00 **Symposium: Nematodes** 2301

‘Recent advances in entomopathogenic nematode infection behavior: inside and outside’
- Advances in entomopathogenic nematode dispersal and host-finding behavior – D. Shapiro-Ilan
- Sex, age and following the leader drive infection dynamics of entomopathogenic nematodes – E. Lewis
- Impact of infection behavior on lethal male fighting in Steinernema – C. Griffin
- The stability of virulence in insect parasitic nematodes is determined by social interactions – B. Raymond

8:00 – 10:00

**Contributed Papers**
- Fungi 2 2306/9
- Microbial Control 3 2311

10:00 – 10:30 **BREAK**

10:30 – 12:30 **SIP Business Meeting**

12:30 – 14:00 **LUNCH (on your own)**

14:00 – 16:00

**Symposium: Microbial Control** 2301

‘Synergies enabling the registration & adoption of biological pest controls – the role of governments, academic programmes, and industry’
- Facilitating the registration and adoption of biological pest controls in Canada – T. Laengle
- The IR-4 biopesticide and organic support program – B. Barney
- How does academia contribute to registration and adoption of biological control agents – a European perspective – J. Ellenberg
- Perils and pitfalls of product development and commercialization: An industry perspective – R. Martin
- Panel Discussion

14:00 – 16:00

**Contributed Papers**
- Viruses 5 2306/9
- Bacteria 3 2311

16:15 - 18:00 **Student Affairs Business Meeting** 2311

18:00 – 1:00 **Banquet**

Great Hall
# Table of Contents

(sections are hyperlinked / click bottom of pages to return here)

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>UBC Campus Map</td>
<td>3</td>
</tr>
<tr>
<td>Meeting at a Glance</td>
<td>4</td>
</tr>
<tr>
<td>SIP Officers &amp; SIP Divisions</td>
<td>8</td>
</tr>
<tr>
<td>SIP Committees</td>
<td>9</td>
</tr>
<tr>
<td>SIP 2015 Organizing Committee</td>
<td>11</td>
</tr>
<tr>
<td>2015 PROGRAM</td>
<td></td>
</tr>
<tr>
<td>Sunday</td>
<td>13</td>
</tr>
<tr>
<td>Monday</td>
<td>14</td>
</tr>
<tr>
<td>Tuesday</td>
<td>17</td>
</tr>
<tr>
<td>Wednesday</td>
<td>19</td>
</tr>
<tr>
<td>POSTERS</td>
<td>22</td>
</tr>
<tr>
<td>Thursday</td>
<td>30</td>
</tr>
<tr>
<td>2015 ABSTRACTS</td>
<td>35</td>
</tr>
<tr>
<td>Monday</td>
<td>36</td>
</tr>
<tr>
<td>Tuesday</td>
<td>47</td>
</tr>
<tr>
<td>Wednesday</td>
<td>55</td>
</tr>
<tr>
<td>POSTERS</td>
<td>70</td>
</tr>
<tr>
<td>Thursday</td>
<td>102</td>
</tr>
<tr>
<td>Author Index</td>
<td>113</td>
</tr>
<tr>
<td>Acknowledgment</td>
<td>125</td>
</tr>
<tr>
<td>Sponsors of SIP</td>
<td></td>
</tr>
<tr>
<td>Back cover</td>
<td></td>
</tr>
</tbody>
</table>
Officers  Society for Invertebrate Pathology  http://www.sipweb.org

**President**  Peter Krell  University of Guelph, Department of Molecular and Cellular Biology  50 Stone Rd East, Guelph, ON N1G 2W1, CANADA  Phone: 519 824 4120 x53368  Email: p.krell@uoguelph.ca

**Vice President**  Johannes Jehle  Federal Research Center for Cultivated Plants, Julius Kuehn Institute, Institute for Biological Control, Heinrichstr. 243, Darmstadt, 64287, GERMANY,  Phone: +49 (6151) 407-220  Email: johannes.jehle@jki.bund.de

**Past President**  Jørgen Eilenberg  Department of Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, Frederiksberg C, DK 1871, DENMARK  Phone: +45 35 33 2692  Email: jei@plen.ku.dk

**Secretary**  Mary Barbercheck  Department of Entomology, Penn State University  University Park, PA 16802, USA  Phone: 814-863-2982  Email: meb34@psu.edu

**Treasurer**  Stefan Jaronski  PO Box 232  Sidney, MT 59270, USA  Phone: 406-863-6369  Email: thebugdoc01@gmail.com

**Trustees**
- Surendra Dara  UC Cooperative Extension, University of California  2156 Sierra Way, Ste., San Luis Obispo, CA 93402, USA  Phone: 805-788-2321  Email: skdara@ucdavis.edu
- Ed Lewis  Department of Entomology, University of California Davis  One Hutchison Ave, Davis, CA 95616, USA  Phone: 530-754-7659  Email: eelewis@ucdavis.edu
- Albrecht Köppenhofer  Entomology Dept., Blake Hall, 93 Lipman Drive  New Brunswick, NJ 08901-8524, USA  Phone: 848-932-9802  Email: koppenhofer@aesop.rutgers.edu
- Monique van Oers  Wageningen University, Lab. of Virology  Droevendaalsesteeg, Wageningen, 6708 PB, THE NETHERLANDS  Phone: 31-317-485082  Email: monique.vanoers@wur.nl

**Executive Secretary**  Cecelia Schmitt  Society for Invertebrate Pathology  P.O. Box 11, Marceline, MO 64658, USA  Toll Free in North America: 888-486-1505, Outside NA: 660-376-3586

---

**BACTERIA DIVISION**  Baltasar Escriche, Chair  Ken Narva, Chair Elect  Raffi Aroian, Secretary/Treasurer  Yu-Lin Gao, Member at Large  Govind T. Gujar, Member at Large  Juan Luis Jurat-Fuentes, Past Chair  Peter Kupferschmied, Student Rep.

**MICROBIAL CONTROL DIVISION**  Leon Rabinovitch, Chair  Travis Glare, Chair Elect  Stefan Jaronski, Past Chair  Michael Brownbridge, Secretary/Treasurer  Pasco Avery, Member at Large  Jarrod Leland, Member at Large  Patricia Golo, Student Representative

**NEMATODE DIVISION**  David Shapiro-Ilan, Chair  Glen Stevens, Chair Elect  Raquel Campos-Herrera, Sec/Treas  Fatma Kaplan, Member at Large  Vladimir Puza, Member at Large  Selcuk Hazir, Past Chair  John G. Mc Mullen, Student Rep.

**FUNGI DIVISION**  Ingeborg Klingen, Chair  Nicolai vitt Meyling, Chair Elect  Ann Hajek, Secretary/Treasurer  Tarryn Goble, Member at Large  Stefan Jaronski, Member at Large  Chad Keyser, Student Representative  Joanna Fisher, Student Representative

**MICROSPORIDIA DIVISION**  Carlos Lange, Chair  Susan Björnson, Chair elect  Wei-Fone Huang, Secretary/Treasurer  Grant Stentiford, Member at Large  Johny Shajahan, Member at Large  Dörte Goertz, Past Chair  Thomas Steele, Student Representative

**VIRUS DIVISION**  Martin Erlandson, Chair  Madoka Nakai, Chair Elect  Eric Haas-Stapleton, Sec/Treas  Elisabeth Herniou, Member at Large  Adly Abd-Alla, Member at Large  Lorena Passarelli, Past Chair  Yasumasa Saito, Student Rep.  Gianpiero Gueli Alelli, Student Rep.

**DIVISION OF BENEFICIAL INVERTEBRATES**  Kelly Bateman, Chair  Grant Stentiford, Member at Large  Sebastian Gisder, Member at Large

**DIVISION OF BENEFICIAL INVERTEBRATES**  Helen Hesketh, Chair Elect  Elke Genersch, Past Chair  Elke Genersch, Sec Treas  Dominic Wiredu-Boayake & Henriette Knispel, Student Representatives
### SIP COMMITTEES

#### NOMINATING COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lee Solter</td>
</tr>
<tr>
<td>Mark Goettel</td>
</tr>
<tr>
<td>Harry Kaya</td>
</tr>
<tr>
<td>Madoka Nakai</td>
</tr>
<tr>
<td>Just Vlak</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>James Becnel</td>
</tr>
<tr>
<td>Neil Crickmore</td>
</tr>
<tr>
<td>Zhihong (Rose) Hu</td>
</tr>
<tr>
<td>Harry Kaya</td>
</tr>
</tbody>
</table>

#### FOUNDER’S LECTURE COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Andreas Linde</td>
</tr>
<tr>
<td>Patricia Stock</td>
</tr>
<tr>
<td>Monique van Oers</td>
</tr>
<tr>
<td>Surendra Dara</td>
</tr>
<tr>
<td>Hyun-Woo Park</td>
</tr>
</tbody>
</table>

#### AWARDS & STUDENT CONTEST COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mark Goettel</td>
</tr>
<tr>
<td>Neil Crickmore</td>
</tr>
<tr>
<td>Patricia Stock</td>
</tr>
<tr>
<td>Monique van Oers</td>
</tr>
<tr>
<td>Surendra Dara</td>
</tr>
<tr>
<td>Hyun-Woo Park</td>
</tr>
</tbody>
</table>

#### MEETINGS COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nina Jenkins</td>
</tr>
<tr>
<td>Kelli Hoover</td>
</tr>
<tr>
<td>Zhizong (Rose) Hu</td>
</tr>
<tr>
<td>Johannes Jehle</td>
</tr>
<tr>
<td>Jean-Louis Schwartz</td>
</tr>
<tr>
<td>Brian Federici, ex officio</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Roma Gwynn</td>
</tr>
<tr>
<td>Michael Brownbridge</td>
</tr>
<tr>
<td>Mike Dimock</td>
</tr>
<tr>
<td>Jim Harper</td>
</tr>
<tr>
<td>Dirk Ave</td>
</tr>
<tr>
<td>Kelli Hoover (ex officio)</td>
</tr>
</tbody>
</table>

#### ENDOWMENT AND FINANCIAL SUPPORT COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Elizabeth Davidson</td>
</tr>
<tr>
<td>James Harper</td>
</tr>
<tr>
<td>Don Roberts</td>
</tr>
<tr>
<td>Harry Kaya</td>
</tr>
<tr>
<td>Fernando Vega</td>
</tr>
<tr>
<td>Juerg Huber</td>
</tr>
<tr>
<td>Mark Goettel</td>
</tr>
</tbody>
</table>

#### HISTORY COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nina Jenkins</td>
</tr>
<tr>
<td>Kelli Hoover</td>
</tr>
<tr>
<td>Zhizong (Rose) Hu</td>
</tr>
<tr>
<td>Johannes Jehle</td>
</tr>
<tr>
<td>Jean-Louis Schwartz</td>
</tr>
<tr>
<td>Brian Federici, ex officio</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Roma Gwynn</td>
</tr>
<tr>
<td>Michael Brownbridge</td>
</tr>
<tr>
<td>Mike Dimock</td>
</tr>
<tr>
<td>Jim Harper</td>
</tr>
<tr>
<td>Dirk Ave</td>
</tr>
<tr>
<td>Kelli Hoover (ex officio)</td>
</tr>
</tbody>
</table>

#### PUBLICATIONS COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>David Shapiro Ilan</td>
</tr>
<tr>
<td>Albrecht Koppenhofer</td>
</tr>
<tr>
<td>Bryony Bonning</td>
</tr>
<tr>
<td>Selcuk Hazir</td>
</tr>
<tr>
<td>Jørgen Eilenberg, ex officio</td>
</tr>
<tr>
<td>Eric Haas-Stapleton, ex officio</td>
</tr>
<tr>
<td>Brian Federici, ex officio</td>
</tr>
<tr>
<td>Lee Solter, ex officio</td>
</tr>
<tr>
<td>Cecilia Schmitt, ex officio</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gianpiero Gueli Alletti</td>
</tr>
<tr>
<td>Bacteria Division: Peter Kupferschmied</td>
</tr>
<tr>
<td>DBI: Dominic Wiredu-Boayake &amp; Henriette Knispel</td>
</tr>
<tr>
<td>Fungi: Chad Keyser &amp; Joanna Fisher</td>
</tr>
<tr>
<td>Microbial Control: Patricia Golo</td>
</tr>
<tr>
<td>Microsporidia: Thomas Steele</td>
</tr>
<tr>
<td>Nematodes: John G. McMullen</td>
</tr>
<tr>
<td>Virus Division: Yasumasa Saito &amp; Gianpiero Gueli Alletti</td>
</tr>
</tbody>
</table>

#### STUDENT AFFAIRS COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nina Jenkins</td>
</tr>
<tr>
<td>Robert Anderson</td>
</tr>
<tr>
<td>Robert Anderson</td>
</tr>
<tr>
<td>Steven Arthurs</td>
</tr>
<tr>
<td>Sassan Asgari</td>
</tr>
<tr>
<td>Susan Bornstein-Forst</td>
</tr>
<tr>
<td>Sunday Ekesi</td>
</tr>
<tr>
<td>Carrie Hauxwell</td>
</tr>
<tr>
<td>Kelli Hoover</td>
</tr>
<tr>
<td>Annette Jensen</td>
</tr>
<tr>
<td>Yasuhisa Kunimi</td>
</tr>
<tr>
<td>Nicolai Meyling</td>
</tr>
<tr>
<td>Helen Roy</td>
</tr>
<tr>
<td>Jean-Louis Schwartz</td>
</tr>
<tr>
<td>Steven Valles</td>
</tr>
</tbody>
</table>

#### MEMBERSHIP COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>David Shapiro Ilan</td>
</tr>
<tr>
<td>Albrecht Koppenhofer</td>
</tr>
<tr>
<td>Bryony Bonning</td>
</tr>
<tr>
<td>Selcuk Hazir</td>
</tr>
<tr>
<td>Jørgen Eilenberg, ex officio</td>
</tr>
<tr>
<td>Eric Haas-Stapleton, ex officio</td>
</tr>
<tr>
<td>Brian Federici, ex officio</td>
</tr>
<tr>
<td>Lee Solter, ex officio</td>
</tr>
<tr>
<td>Cecilia Schmitt, ex officio</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacteria Division: Peter Kupferschmied</td>
</tr>
<tr>
<td>DBI: Dominic Wiredu-Boayake &amp; Henriette Knispel</td>
</tr>
<tr>
<td>Fungi: Chad Keyser &amp; Joanna Fisher</td>
</tr>
<tr>
<td>Microbial Control: Patricia Golo</td>
</tr>
<tr>
<td>Microsporidia: Thomas Steele</td>
</tr>
<tr>
<td>Nematodes: John G. McMullen</td>
</tr>
<tr>
<td>Virus Division: Yasumasa Saito &amp; Gianpiero Gueli Alletti</td>
</tr>
</tbody>
</table>

#### SIP2015 ORGANIZING COMMITTEE

<table>
<thead>
<tr>
<th>Chair</th>
</tr>
</thead>
<tbody>
<tr>
<td>Todd Kabaluk &amp; Mark Goettel (Co-Chairs)</td>
</tr>
<tr>
<td>David Theilmann (Treasurer)</td>
</tr>
<tr>
<td>Jenny Cory &amp; Alida Janmaat (Scientific Program Co-Chairs)</td>
</tr>
<tr>
<td>Joan Cossentine (Registration Coordinator)</td>
</tr>
<tr>
<td>Deborah Henderson (Social Activities Co-ordinator)</td>
</tr>
<tr>
<td>Paul MacDonald (Event Mobi Program / SIP App)</td>
</tr>
<tr>
<td>Cheryl Erlandson (Companion Tours)</td>
</tr>
<tr>
<td>Beth McCannel, Karen Toohey (Members)</td>
</tr>
</tbody>
</table>
2015 PROGRAM

- Attendants shall not take pictures from projections during the presentations
- The abstracts included in this book should not be cited in print without the author's permission

STU Indicates STUDENT presentation
000 Indicates number of ORAL presentation
BA - 00 Indicates abstract number for POSTER presentation
Session 1: Microsporidia – a general Introduction
Chair: Grant Stentiford
8:30  Introduction – Grant Stentiford
8:40  Introduction to the OECD/CRP. Stressors in the global food chain and the importance of pathogens
  – Primal Silva, Animal Health Science Directorate, Canada and Member Scientific Advisory Body, OECD.
  8:50  Parasites in food chains – Kristina Rösel, International Livestock Research Institute, CGIAR Consortium.
  9:10  Introduction to Microsporidia – James Becnel, USDA-ARS, Gainesville, FL, USA.
  9:30  The Microsporidia: Where did they come from and where are they going – Patrick Keeling, Canadian Institute for Advanced Research.

Session 2: Microsporidiosis in humans
Chair: Louis Weiss
9:50  Microsporidiosis in humans – an emerging issue?
  – Louis Weiss, Albert Einstein College of Medicine, NY.
10:10  Is global immunosuppression linked to rising burdens of microsporidiosis in human and animal populations?
  – Elizabeth Didier, Tulane University.
10:30 – 11:00  BREAK

11:00  How do Microsporidia exploit the biochemistry and physiology of the host cell? – Bryony Williams, University of Exeter.

Session 3: Microsporidiosis in terrestrial animals
Chair: James Becnel
11:20  Microsporidiosis in farmed animals and terrestrial wildlife – their roles in zoonoses – Louis Weiss, Albert Einstein College of Medicine, NY.
11:40  Microsporidiosis in companion animals – their role in zoonoses – Karen Snowden, Texas A & M.
12:00  Microsporidia as regulators of insect populations and disease agents in mass-reared insects – a future threat to edible insect cultivation? – Susan Bjørnson, St. Mary’s University, Halifax, Canada.

12:20 – 13:30  LUNCH

Session 4: Microsporidiosis in aquatic animals
Chair: Grant Stentiford
13:50  Wild and cultured fish as potential sources of zoonotic infections in humans – Mark A. Freeman, University of Malaya.
14:10  Pathogens of aquatic arthropods – focus on the Enterocytozoonidae – Grant D. Stentiford, European Union Reference Laboratory for Crustacean Diseases, Cefas, UK.
14:30  Clues for multiple-taxa lifecycles from invertebrate research – Yuliya Sokolova, Louisiana State University.

14:50 – 15:20  BREAK

Session 5: Microsporidian role in pollinator health
Chair: Leelien Solter
15:50  Interactions of Microsporidia with the global honey bee population – Leelien Solter, Illinois Natural History Survey, University of Illinois.

Session 6: Future look and final discussion
Symposium Organizers
16:00  Current and future models for microsporidian research
  – Emily Troemel, University of California, San Diego.
16:30  Discussion panel

Workshop
Bacteria
Sunday 13:00 – 17:00 2306/9

Regulatory Considerations for the Commercialization of New Insecticidal Proteins
Moderators: William Moar and Ken Narva

13:00  Current insights on Bt insecticidal protein specificity and future directions – Juan Luis Jurat-Fuentes, Neil Crickmore, Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA; School of Life Sciences, University of Sussex, Brighton, UK.
13:20  Proteins 101: Structure, function, and evolution – J. Jez, Washington University, Department of Biology, St. Louis, MO 63130, USA.
13:40  Protein sequences, structures and functions – rules for divergence and rules for conservation – Adam Godzik, Bioinformatics and Structural Biology Program, Sanford-Burnham Medical Research Institute, La Jolla, CA, USA.
14:00  Modelling of insecticidal toxins and their potential interactions: Challenges and aspirations – Colin Berry, Cardiff School of BioSciences, Cardiff University, Cardiff, CF10 3AT, UK; School of Life Sciences, University of Sussex, Brighton, UK.
14:20  Safety considerations derived from Cry34/35Ab1 structure and function – Kenneth E. Narva, Nick Storer, Rod Herman, Dow AgroSciences, LLC, Indianapolis, IN, USA.
14:40 – 15:00  BREAK
15:00  Case study of a novel wCRW insecticidal protein from Chromobacterium sp. – Kimberly Sampson, Bayer CropScience, Raleigh-Durham, North Carolina, USA.
15:20  Biochemical characterization of parasporin-4 and effects of the pro-parasporin-4 diet on the health of mice – Shiro Okumura, Hironori Koga, Kunio Inouye, Eichi Mizuki, , Biotechnology and Food Research Institute, Fukuoka Industrial Technology Center, Fukuoka, Japan; Division of Gastroenterology, Department of Medicine, Kurume University School of Medicine, Fukuoka, Japan; Division of Food Science and Biotechnology, Graduate School of Agriculture, Kyoto University, Kyoto, Japan; Inouye Laboratory of Enzyme Chemistry (iLEC), Kyoto, Japan.
15:40  Considerations for the safety assessment of novel insecticidal proteins: A regulatory perspective – Phil MacDonald, Plant and Biotechnology Risk Assessment Unit, CFIA, Ottawa, Ontario, Canada.
16:00  New insecticidal proteins: Optimization and specificity – William J. Moar, Jeff Haas, Artem Evdokimov, Jim Baum, Andre Silvanovich, Yong Yin, Dave Bowen, Kevin Glenn, Adam Evan, Monsanto Company, St. Louis, Missouri, USA.
16:20 – 17:00  DISCUSSION

18:00 – 21:00  Mixer  Sage Bistro

**MONDAY – August 10**

7:30 – 18:00  Registration  Outside Great Hall

**Great Hall**  Monday 8:00 – 10:00

**Opening Ceremony and SIP Founders’ Lecture**

8:00  Opening Ceremonies  Welcoming addresses  Todd Kabaluk and Mark Goettel, Meetings Co-Chairs  Peter Krell, President, SIP
Award presentations  Andreas Linde, Chair, Awards and Student Contest Committee
Founders’ Memorial Lecture  James Becnel – Chair, Founders’ Lecture Committee  Honoree: Phyllis T. Johnson  Lecturer: Grant Stentiford
10:00 – 10:30  BREAK

Plenary Symposium  Monday 10:30 – 12:30  Great Hall

**Insect Pathogens in Nature: Ecology and Evolution**  Moderators: Jenny Cory and Alida Janmaat

10:30  1 How sea stars get wasted: Evidence of a viral etiology and host response to sea star wasting disease – Colleen A. Burg, Team SSWD, Team EIMD, The Institute of Marine and Environmental Technology, University of Maryland Baltimore County, Baltimore, MD, USA.
11:00  2 Symbiont-mediated defense against parasitic nematodes in Drosophila – Steve J. Perlman, Department of Biology, University of Victoria, BC, Canada.
11:30  3 No nematode is an island: Interactions between entomopathogenic nematodes and other organisms – Christine T. Griffin, Biology Department, Maynooth University, Maynooth, County Kildare, Ireland.
12:00  4 The ecology of virulence in insect associated bacteria: Field experiments and experimental evolution – Ben Raymond, Imperial College London, Silwood Park Campus, Ascot, Berks, SL5 7PY, UK.
12:30 – 14:00  LUNCH (on your own)

14:00  5 The complex relationship between microsporidia and fungi – Patrick J. Keeling, Department of Botany, University of British Columbia, Vancouver, BC, Canada V6T 1Z4.
14:20  6 Fish microsporidians: Emerging pathogens or emerging knowledge? – Mark A. Freeman, Institute for Experimental Pathology at Keldur, University of Iceland, Reykjavik, Iceland.
14:40  7 Understanding phylogenetic relationships among species in the Nosema/Vairimorpha clade: What does genetic similarity say about host switching in the microsporidia? – Wei-Fone Huang, James Becnel, Leellen Solter, , Illinois Natural History Survey, Prairie Research Institute at the University of Illinois at Urbana-Champaign, IL, USA; United States Department of Agriculture, Agricultural Research Service, Gainesville, FL, USA.
15:10  8 Emergent pathogens of invertebrates: Environmental sampling to identify novel parasite lineages – Bryony A. P. Williams, Kristina Hamilton, David Bass, , Biosciences, College of Life and Environmental Sciences, University of Exeter, Exeter, UK; Centre for Environment, Fisheries & Aquaculture Science, Weymouth, Dorset, UK.
15:30  9 Investigations into the composition of the microsporidian polar tube – Louis M. Weiss, Koya Ghosh, Bing Han, Departments of Medicine and Pathology, Albert Einstein College of Medicine, Bronx, NY, 10461, USA.

**Contributed Papers**  Monday 14:00 – 16:00  2306/9

**Bacteria 1**

Moderators: Ken Narva and David Heckel
14:00 18 Resistance to Bacillus thuringiensis Cry2Ab toxin in Helicoverpa spp. is conferred by mutations in a novel ABC transporter – Wee Tek Tay1, Rod J. Mahon2, Thomas K. Walsh3, Sharon Downes1, William J. James1, Siu Fai Lee1, Annette Reineke1, Adam K. Williams3, Karl J. H. Gordon1, David G. Heckel1, 1CSIRO, Black Mountain Laboratories, Canberra, ACT, Australia; 2CSIRO, Australian Cotton Research Institute, Narrabri, NSW, Australia; 3Department of Genetics, University of Melbourne, Parkville, VIC, Australia; 4Institute for Phytochemistry, Geisenheim University, Geisenheim, Germany; 5Department of Entomology, Max Planck Institute for Chemical Ecology, Jena, Germany.

14:15 11-STU Functional range of insect ABC transporters as a Cry toxin receptor – Hruba Endo1, Shinho Tanaka1, Ryoichi Sato1, 1Graduate School of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology, Koganei, Tokyo, Japan; 2Research Fellow of Japan Society for the Promotion of Science.

14:30 12-STU CryIA toxins cause rapid cell lysis in a clonal stable non-lytic expression system, expressing ABC-C2 and cadherin – Anne Karpinski1, Yannick Pauchet1, David Heckel1, 1Department of Entomology, Max Planck Institute for Chemical Ecology, Jena, Germany.

14:45 13 Expressing a lepidopteran ABC2C gene in transgenic Drosophila causes BT Cry1Ac susceptibility without requiring a cadherin-like protein receptor – Tristan Stevens2, Simon W. Baxter2, 2School of Biological Sciences, University of Adelaide, Australia.

15:00 14 Differential toxicity of Cry1Ca and Cry1AC to Spodoptera exigua (Lepidoptera: Noctuidae) – Youngjin Park1, Salvador Herrero2, Yongguyn Kim2, 1Department of Bioresource Sciences, Andong National University, Andong 760-749, Korea; 2Department of Genetics, Universidad de Valencia, Dr Moliner 50, 46100 Burjassot, Spain.

15:15 15-STU Models for the interaction between cadherin-like receptor BT-R1 and three Cry1A family toxins from Bacillus thuringiensis – Diogo Martins1,2, Anna G. Dias1,2, Godofredo M. Borges1,2, 1Department of Genetics, University of Agrobiological Sciences, Geisenheim, Germany; 2Department of Biology, University of Aveiro, Portugal.

15:30 16 A high-throughput, in vitro assay for Bacillus thuringiensis Cry proteins – Michi Iizumi Wilcoxon, Jaclyn Dennis, Sabina Lau, Weiping Xie, You You, Song Leng, Ryan Fong, Takashi Yamamoto, Plant Protection, Ag Biotechnology, DuPont Pioneer, Hayward, CA, USA.

15:45 17 Transcriptome response of Aedes aegypti against Bacillus thuringiensis and the pathway for enhancing the mosquitoicidal activity – Wu Songqiang1,2, Liu Zhaoxue1,2, Wang Yafang1,2, Xu Zheying1,2, Guo Yajie1,2, Xiong Yueling1,2, Mou Yani1,2, Zhu Xiaoli1,2, Zhang Feiping1,2, 1China Agricultural University, Beijing, China; 2China Agricultural University, Beijing, China.

14:00 18 Autodissemination strategy for field suppression of Bactrocera dorsalis (Diptera: Tephritidae) using Metarhizium anisopliae-based biopesticide on mango – Sunday Ekenyi1, Ngoyu K. Manyang1, International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya.

14:15 19 Development of granules based on the biomass of liquid fermented Metarhizium anisopliae, Isaria fumosorosea or Beauveria bassiana for control of soil dwelling pests – Dietrich Stephan2, Medea Buranjadze2, Tanja Bernhardt2, Juliana Peit2, Johannes Schäfer2, Christopher Seib2, 1Institute for Biological Control, Heinrichstrasse 243, 64287 Darmstadt, Germany; 2Agricultural University of Georgia, 240, D. Agmanshenebely Alley, Tbilisi 0159, Georgia, USA.

14:30 20-STU Can pheromone enhance the transmission of Metarhizium brunneum in Agriotes obscurus click beetles? – Joyce P. S. Leung1, Jenny S. Cory1, J. Todd Kabaluk2, Alida F. Janmaat2, 1Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada; 2Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Agassiz, BC Canada.

14:45 21 Less effort – more efficient: An attract and kill strategy for wireworm control in potato – Mario Schumann1,2, Anant Patil2, Stefan Vidal1, 1Geom-August-University Goettingen, Department of Crop Sciences, Goettingen, Germany; 2University of Applied Sciences, Department of Engineering and Mathematics, Bielefeld, Germany.

15:00 22 Drosophila suzukii fungal infections and transmissions: A potential field suppression strategy – Joan Cossentino, Mairi Robertson, Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, BC, Canada.


15:30 24 The importance of searching for appropriate strains for the control of leaf-cutting ants – Patricia J. Folgarait, Daniela Goffré, Laboratorio de Hormigas, Universidad Nacional de Cuyo, Mendoza, Argentina.

16:00 – 16:30 BREAK

Symposium Monday 16:30 – 18:30
2301

The (Underestimated) Value of Applied Research: Moving the Theoretical to the Practical
Moderators: Roma Gwynn, Michael Brownbridge, Travis Glare

16:30 25 Why biopesticides sometimes fail – Roma Gwynn, Michael Brownbridge, Travis Glare, 1National Ltd., Lintlaw Farm Cottages, Duns TD113SA, Scotland; 2Vineland Research and Innovation Centre, Vineland Station, ON, Canada; 3Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand.

16:54 26 Multiple roles so what should we measure? An ecological approach to promote the contribution of fungal entomopathogens in pest management within the agro-ecosystem – Nicolai V. Meyling, Department of Plant and Environmental Sciences, University of Copenhagen, 1971 Frederiksberg C, Denmark.
17:18 27 Research and development of biological crop protection products – bridging the gaps from discovery to field – Reed N. Royalty, Denise C. Marker, Bayer CropScience, Biologics. 890 Embarcadero Drive, West Sacramento, CA, USA 95605.

17:42 28 Adapting field trials for microorganisms – in practice – Edith L’Abbe, Massimo Benuzzi, Sergio Francescini, CBC (Europe) S.r.l. – AREA TECNICA, via Calcinaro 2085 Int. 7, 47521 Cesena (FC), Italy; 4 CBD (Europe) S.r.l. – BIOGARD Division, via XXV Aprile 44, 24050 Grassobbio (BG), Italy.

18:06 29 How do we improve efficacy monitoring of biopesticides? – Travis Glore, Michael Brownbridge, Roma Gwynn 1, 3 Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand; 2VineLand Research and Innovation Centre, Vineland Station, ON, Canada; 3Rationale Ltd., Lintlaw Farm Cottages, Duns TD113QA, Scotland.

18:15 30 Overexpression of two microRNAs enhances the infectivity of Sindbis virus TES/2J in mosquitoes – Ning Huang 1, Jessica Moffitt 2, Kayvan Etebari 3, Sassan Asgari 1, Alexander W. E. Franz 1, A. Lorena Passarelli 2, Rolle J. Clerk 3; 1Division of Biology, Kansas State University, Manhattan, KS USA; 2School of Biological Sciences, University of Queensland, St. Lucia, Queensland, Australia; 3Department of Veterinary Pathology, University of Missouri, Columbia, MO USA.

18:45 31 Microbial challenges and stress modify piRNA cluster abundance in the dengue mosquito, Aedes aegypti – Kayvan Etebari 3, Mazhar Hussain 4, Gregor J. Devine 1, Sassan Asgari 1, 2Australian Infectious Disease Research Centre, School of Biological Sciences, The University of Queensland, Brisbane QLD 4072, Australia; 2QIMR Berghofer Institute of Medical Research, Brisbane, QLD 4006, Australia.

19:00 32-STU A modified viral shuttle for exploring RNAi-related genes – David Neunemann 1, Heiko Vogel 2, David G. Heckel 2, Salvador Herrero 3, Agata K. Jakubowska 1; 1Entomology Department, Max Planck Institute for Chemical Ecology, Jena, Germany; 2Department of Genetics, Universitat de València, Burjassot, Spain.

19:15 33-STU Role of dsRNA-mediated mechanism in the establishment of “latent” Glossina hytrosavirus infections in the tsetse fly – Irene M. Manker 1,2,3,4,5; 1,2Henry M. Karinithi, 3Just M. Viak, 4Adly M. M. Abd-Alla, 5Monique M. van Oers 1; 1Laboratory of Virology, Wageningen University, The Netherlands; 2Insect Pest Control Laboratory, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Vienna, Austria; 3Biotechnology Research Institute, Kenya Agricultural & Livestock Research Organization, Kaptagat Rd, Loresho, Nairobi, Kenya.

19:30 34-STU New target sites in pest control: Examining the role of REPAT proteins in defence against baculoviruses – Ersenel Odedmir 1, Umut Toprak 2, Sibel Çavdar 3, Diana Bekkaoi 4, Dwanye Hegedus 5, 1Ankara University, Faculty of Agriculture, Dept. of Plant Protection, Ankara, Turkey; 2Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.

19:45 35-STU Wolbachia-mediated antiviral protection is life stage dependent – Alexei L. Stevanovich, Pieter A. Arnold, Kayrin N. Johnson, School of Sciences, The University of Queensland, Brisbane 4072, Australia.

18:00 36-STU A viral histone H4 modules host gene expression by down regulating chromatin remodeling machinery – Sunil Kumar, Yongyuan Kim, Department of Bioresource Sciences, Andong National University, Andong 760-749, Republic of Korea.

18:15 37-STU Infection studies of an Agrotis segetum granulovirus isolate from Europe in cell cultures of Aile1611T – Gianpiero Guelli Alletti 1, Jörg T. Wennmann 2, Marino Eigenbrod 3, Eric B. Carstens 4, Regina G. Kleesips 1, Johannes A. Jehle 1, Julius Kühn Institute, Heinrichstr. 243, D-64287 Darmstadt, Germany; 2Queen’s University, K7L 3N6 Kingston, ON, Canada.

Contributed Papers Monday 16:30 – 18:30 2306/9

Viruses 1

Moderators: Rollie Clem and Martin Erlanson

16:30 38 Overexpression of two microRNAs enhances the infectivity of Sindbis virus TES/2J in mosquitoes – Ning Huang 1, Jessica Moffitt 2, Kayvan Etebari 3, Sassan Asgari 1, Alexander W. E. Franz 1, A. Lorena Passarelli 2, Rolle J. Clerk 3; 1Division of Biology, Kansas State University, Manhattan, KS USA; 2School of Biological Sciences, University of Queensland, St. Lucia, Queensland, Australia; 3Department of Veterinary Pathology, University of Missouri, Columbia, MO USA.

16:45 39 Microbial challenges and stress modify piRNA cluster abundance in the dengue mosquito, Aedes aegypti – Kayvan Etebari 3, Mazhar Hussain 4, Gregor J. Devine 1, Sassan Asgari 1, 2Australian Infectious Disease Research Centre, School of Biological Sciences, The University of Queensland, Brisbane QLD 4072, Australia; 2QIMR Berghofer Institute of Medical Research, Brisbane, QLD 4006, Australia.

17:00 40 STU A modified viral shuttle for exploring RNAi-related genes – David Neunemann 1, Heiko Vogel 2, David G. Heckel 2, Salvador Herrero 3, Agata K. Jakubowska 1; 1Entomology Department, Max Planck Institute for Chemical Ecology, Jena, Germany; 2Department of Genetics, Universitat de València, Burjassot, Spain.

17:15 41 STU Role of dsRNA-mediated mechanism in the establishment of “latent” Glossina hytrosavirus infections in the tsetse fly – Irene M. Manker 1,2,3,4,5; 1,2Henry M. Karinithi, 3Just M. Viak, 4Adly M. M. Abd-Alla, 5Monique M. van Oers 1; 1Laboratory of Virology, Wageningen University, The Netherlands; 2Insect Pest Control Laboratory, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Vienna, Austria; 3Biotechnology Research Institute, Kenya Agricultural & Livestock Research Organization, Kaptagat Rd, Loresho, Nairobi, Kenya.

17:30 42 STU New target sites in pest control: Examining the role of REPAT proteins in defence against baculoviruses – Ersenel Odedmir 1, Umut Toprak 2, Sibel Çavdar 3, Diana Bekkaoi 4, Dwanye Hegedus 5, 1Ankara University, Faculty of Agriculture, Dept. of Plant Protection, Ankara, Turkey; 2Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.

17:45 43 STU Wolbachia-mediated antiviral protection is life stage dependent – Alexei L. Stevanovich, Pieter A. Arnold, Kayrin N. Johnson, School of Sciences, The University of Queensland, Brisbane 4072, Australia.

18:00 44 STU A viral histone H4 modules host gene expression by down regulating chromatin remodeling machinery – Sunil Kumar, Yongyuan Kim, Department of Bioresource Sciences, Andong National University, Andong 760-749, Republic of Korea.

18:15 45 STU Infection studies of an Agrotis segetum granulovirus isolate from Europe in cell cultures of Aile1611T – Gianpiero Guelli Alletti 1, Jörg T. Wennmann 2, Marino Eigenbrod 3, Eric B. Carstens 4, Regina G. Kleesips 1, Johannes A. Jehle 1, Julius Kühn Institute, Heinrichstr. 243, D-64287 Darmstadt, Germany; 2Queen’s University, K7L 3N6 Kingston, ON, Canada.

Contributed Papers Monday 16:30 – 17:30 2311

Microsporidia

Moderator: Yuliya Sokolova

16:30 46 Host-pathogen interactions and genome evolution in two generalist and specialist microsporidian pathogens of mosquitoes – James J. Becnel 1, Christopher A. Desjardins 1, Neil Sanscranze 2, Jonathan M. Goldberg 2, David Heiman 2, Sarah Young 2, Qiondong Zeng 2, Hiten D. Madhani 2, Christina A. Cuomo 1, 2USDA, ARS, Center for Medical, Agricultural and Veterinary Entomology, 1600 SW 23rd Drive, Gainesville, Florida 32608, USA; 3Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA; 4Department of Biochemistry and Biophysics, University of California-San Francisco, San Francisco, California 94158, USA.

16:45 47 Ultrastructural analysis and SSU rRNA gene sequencing of A.lunensis sp. and Agglomerata cladocera from Siberian microcrustaceans shed light on diversification within the “Aquatic Outgroup” – Yuliya V. Sokolova 1,2, Yuri S. Takarev 1, Georgiy I. Rusakovitch 1, Igor V. Senderskiy 1, Institute of Cytology; 2Institute for Plant Protection, Russian Academy of Sciences, St.Petersburg, Russia, School of Veterinary Medicine, Louisiana State University, Baton Rouge LA, USA.

17:00 48 STU Understanding the evolutionary role of glycolysis in intracellular crab microsporidia and the role of their highly mutated hexokinase in metabolism in their unusual habit – Dominic Wierdu Boekye 1,2,3,4, Hiten D. Madhani 2,3,4,5, Grant Stentiford 2, Thomas Williams 2, 5College of Life and Environmental Sciences, University of Exeter, Geoffrey Pope. Stocker Road, Exeter. EX4 4QD; 6Centre of Environment, Fisheries and Aquaculture Science, CEFAS. The Nothe, Barrack Road, Weymouth, UK; 7Institute for Cell and Molecular Tyne Biosciences, University of Newcastle, Newcastle upon Tyne, Tyne and Wear, UK.

17:15 49 STU Characterization of the spliceosome and large introns in microsporidia – Thomas A. Whelan, Cameron Grisdale, Naomi M. Fast, Dept of Botany, University of British Columbia, Vancouver, BC, Canada.
SIP Division Business Meetings  
Monday 20:00-22:00

Microbial Control
Diseases of Beneficial Invertebrates (+Workshop)  
Monday 20:00-22:00

Workshop
Diseases of Beneficial Invertebrates Workshop
Organizers: Grant Stentiford and David Bass

TUESDAY – August 11

7:30 – 18:00  Information & Registration  Outside Great Hall

Symposium
Bacteria

Mechanisms of Field Resistance to Bt Pesticides and Bt-crops
Moderator: Juan Luis Jurat-Fuentes

8:00  BT resistance in Plutella – too many trees? – Neil Crickmore, School of Life Sciences, University of Sussex, Brighton, UK.

8:22  Multiple resistance mechanisms selected in cabbage looper populations resistant to DiPel – Ping Wang. Department of Entomology, Cornell University, New York State Agricultural Experimental Station, Geneva, NY, USA.

8:44  Pink bollworm resistance to Bt cotton: Similar mechanisms in the lab and the field? – Jeffrey A. Fabrick, Jeyakumar Ponnuraj, Xianchun Li, Yves Carrière, Bruce E. Tabashnik, USDA-ARS, U.S. Arid Land Agricultural Research Center, Maricopa, Arizona, USA; National Institute of Plant Health Management, Rajendranagar, Hyderabad, Andhra Pradesh, India; Department of Entomology, University of Arizona, Tucson, Arizona, USA.

9:06  Mechanism of Spodoptera frugiperda resistance to Cry1Fa in Bt corn – Juan Luis Jurat-Fuentes, Siva R. K. Jakkal, Rahul Baneje, James Hauser, Fangning Huang, Robert Meagher, Rodney Nagoshi, Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA; Dow AgroSciences, Indianapolis, IN, USA; Department of Entomology, LSU AgCenter, Baton Rouge, LA, USA; USDA-ARS, Insect Behavior and Biocontrol Research Unit, Gainesville, FL, USA.

9:28  Characterization of Cry3Bb1 resistance in western corn rootworm (Diabrotica virgifera virgifera) – Jeffrey A. Haas, Monsanto Company, 700 Chesterfield Parkway West, Chesterfield, MO 63017, USA.

9:50  Discussion

8:30  Pathogens on the horizon: Enhancing understanding of invasive alien entomopathogens and impacts on biodiversity – Helen Hesketh, Jørgen Ellenberg, Monique van Oers, Helen Roy, Alison Dunn, Grant Stentiford, Beth Purse, Regina Kleespies, Anja Amtoft-Wyns, Centre for Ecology & Hydrology (CEH), Wallingford, United Kingdom; University of Copenhagen, Denmark; Wageningen University, Netherlands; University of Leeds, United Kingdom; Centre for Environment, Fisheries and Aquaculture Science (Cefas), United Kingdom; Julius Kühn-Institut, Federal Research Institute for Cultivated Plants, Germany.

8:45  The prevalence of multi-host pathogens in Bombay pascuorum is influenced by honeybee domestication – Ivan Meeus, Laurie Parmentier, Jafar Maharramov, Niall Piot, Dirk C. de Groof, Guy Smagghe, Department of Crop Protection, Ghent University, Coupure links 653, B-9000 Ghent, Belgium; Department of Biochemistry and microbiology, Ghent University, Ghent, Belgium.

9:00  From the mosquito model to the bumblebee: A different behaviour of Vago mediated cross-talk between the small interfering RNA and Jak/stat pathways upon virus infection – Jiezi Niu, Ivan Meeus, Guy Smagghe, Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Coupure links 653, B-9000 Ghent, Belgium.

9:15  Variations in disease profile of juvenile edible crabs (Cancer pagurus) sampled from 3 different locations in the UK – Kelly S. Bateman, Stuart Ross, Rose Kerr, Ruth Hicks, Nick Taylor, Grant D. Stentiford, European Union Reference Laboratory for Crustacean Diseases, Centre for Environment, Fisheries and Aquaculture Science (Cefas), Barrack Road, The Nothe, Weymouth, Dorset DT4 8UB, UK; Centre for Environment, Fisheries and Aquaculture Science (Cefas), Barrack Road, The Nothe, Weymouth, Dorset DT4 8UB, UK.

9:30  Apicomplexan parasites cause regular mass mortalities in commercial scallop populations – Mark A. Freeman, Susan Inglis, Árni Kristmundsson, Institute for Experimental Pathology at Keldur, University of Iceland, Reykjavik, Iceland; Institute of Ocean and Earth Sciences, University of Malaya, Kuala Lumpur, Malaysia; University of Massachusetts-Dartmouth, SMAST, Fairhaven, MA USA.

8:00  STU AcMNPV encoded RING domain protein AC141 (Exon0) is associated with the GP64 and ME53 budding complex at the plasma membrane – Siddhartha Biswas, Yang Liu, Peter J. Kreit, David A. Theilmann, Plant Science, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC Canada V6T 1Z4; Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada N1G 2W1; Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, British Columbia, Canada.

8:15  AcMNPV LEF-3 plays a critical role in both viral DNA replication and late gene expression – Mustapha El Ayoubi, Eric B. Carstens, Department of Biomedical and Molecular Sciences, Queen’s University, Kingston,
Ontario, Canada.

8:30 55 The ODV-66 of Helicoverpa armigera nucleopolyhedrovirus is involved in viral oral infection but is not essential for BV synthesis – Dianhui Hou, Sijiani Luo, Fengqiao Zhou, Ranran Wang, Yanfang Zhang, Manli Wang, Huailin Wang, Zhihong Hu, Fei Deng, State Key laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, P.R. China.

8:45 56 Phosphorylation induces structural changes in the Autographa californica nucleopolyhedrovirus P10 protein – Linda A. King, Farheen Raza, Leo Graves, Sarah Irons, Robert D. Passie, Department of Biological and Medical Sciences, Oxford Brooks University, Oxford OX3 0BP UK.

9:00 57-STU Bombyx mori nucleopolyhedrovirus ARIF-1 enhances systemic infection in B. mori larvae – Ryubel Kokusho, Toru Shimada, Susumu Katsumo, Department of Agricultural and Environment Science, Graduate School of Agricultural and Life Sciences, the University of Tokyo, Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan.

9:15 58 Effect of me3 in baculovirus transcriptional regulation – Yang Liu, Eva Nagy, Peter J. Kreil, 1Department of Molecular and Cellular Biology, 2Department of Pathobiology, University of Guelph, Guelph, ON, Canada.

9:30 59 Termination of invertebrate iridescent virus mRNA transcripts: The role of a CATTAn-containing hairpin – Ikbal Agha Inci1, Monique M. van Ders1, Gorben P. Pijman2, Just M. Vlak, Laboratory of Virology, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands; 3Medical Microbiology Dept., Acıbadem University Medical School, Istanbul, Turkey.

9:45 60 Post-translational modifications of the baculovirus proteasome-like protein P6.9 and regulation of its hyperphosphorylation – Ao Li, Haizhou Zhao, Qingying Lai, Zhihong Huang, MeiJin Yuan, Kai Yang, State Key Laboratory of Biocontrol, Sun Yat-sen University, Guangzhou 510275, China.

10:00 – 10:30 BREAK

Contributed Papers  Tuesday 10:30 – 11:30

Bacteria 2

Moderators: Baltasar Escriche and Neil Crickmore

10:30 61 Screening Bacillus thuringiensis strains with unapparent Crystals – Chengjiang Shu1, Xuewen Zhang2, Neil Crickmore2, Fujing Song1, Jie Zhang1, 1State Key Laboratory of Biology for Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, P. R. China; 2School of Life Science, Northeast Agricultural University, Harbin, P. R. China; 3School of Life Sciences, University of Sussex, Falmer, Brighton, UK.

10:45 62-STU In search for novel bioactive molecules: Genome mining of the entomopathogenic bacterium Photobacterium luminescenssorensis (Gamma-Proteobacteria: Enterobacteriaceae) – Rouel A. Orozo, S. Patricia Stock, Department of Entomology, University of Arizona, Tucson, AZ, USA.

11:00 63 Structural mutants of the anti-feeding prophage – Mark Hurst1, Daria Rybakova2, Alok Mitra2, 1Innovative Farm systems, AgResearch, Lincoln Research Centre, New Zealand; 2Institute of Environmental Biotechnology, Graz University of Technology, Austria; 3School of Biological Sciences, University of Auckland, Auckland, New Zealand.

11:15 64 Loops replacements in domain II of Cry1Ab toxin with gut binding peptides alter insecticidal activity against the rice brown planthopper, Nilaparvata lugens (Stål) – Shao Ensi1, Sijun Liu1, Lin Li2, Guan Xiong3, 1Key Laboratory of Biopesticide and Chemical Biology, Ministry of Education, Fujian Agriculture and Forestry University, 350002 Fuzhou, Fujian, PR China; 2Department of Entomology, Iowa State University, Ames, IA 50011, USA.

10:30 65-STU White spot syndrome virus (WSSV) infection: Understanding pathways of infection and opportunities for treatment from the perspective of a resistant species – Bas Van Bruggen1, Ako K. Bickley2, Eduardo M. Santos2, Charles R. Tyler2, Grant D. Stentiford1, Kelly S. Bateman1, Ronny van Aerle1, College of Life and Environmental Sciences, Exeter University, UK.

10:45 66 Using genomics to identify host-pathogen interactions following white spot syndrome virus infection – Lea K. Bickley1, Bas Van Bruggen1, Kelly S. Bateman1, Grant D. Stentiford1, Charles R. Tyler2, Eduardo M. Santos2, Ronny van Aerle1, 1College of Life and Environmental Sciences, Exeter University, UK; 2Centre for Environment, Fisheries and Aquaculture Science (CEFAS), Weymouth, UK.

11:00 67 Effect of temperature on the immune, clinical and tissue response of American Lobster (Homarus americanus) experimentally infected with White Spot Syndrome Virus – Louise-Marie D. Roux1,2,3, Philip J. Byrne4, K. Fraser Clark4, Spencer J. Greenwood4,5, Glenda M. Wright5, Dorota W. Wadowska6, 1Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada; 2Gulf Biocontainment Unit, Department of Fisheries and Oceans Canada, Charlottetown, PE, Canada; 3Centre for Environment, Fisheries and Aquaculture Science (CEFAS), Weymouth, UK; 4Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada; 5Department of Pathology and Microbiology, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada; 6Electron Microscopy, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada.

11:15 68 Paramyxoviruses: Emergence of an enigmatic class of invertebrate parasites – David Boss1, Georgia Ward2, Rose Kerr2, Martyn Bennett2, Rosaline Hulse2, Grant D. Stentiford1, 1Centre for Environment, Fisheries, and Aquaculture Science (Cefas), Barrack Road, The Nothe, Weymouth, Dorset DT4 8UB, UK; 2Department of Life Sciences, The Natural History Museum, London, UK.

11:45 Buses leave for EXCURSIONS+BBQ Gage Residence

15:30 Buses leave for BBQ ONLY (for those not going on Excursions) Gage Residence

18:00 5k Run/Walk Cheakamus Centre

19:00 BBQ Cheakamus Centre

21:00 Buses return from BBQ to Gage Residence
8:00 68 Macro- and micro-evolutionary trends in baculoviruses – Jayne A. Jelhe, Lourin R. Mohnheimer, Gianpiero Guell Alletti, Jörg T. Wennmann, Institute for Biological Control, Federal Research Centre for Cultivated Plants, Julius Kühn Institute, Darmstadt, Germany.

8:24 70 Alphabaculoviruses: Host Transcriptome Responses to Infection – Yun-Ru Chen1, Silin Zhong1, Zhangjun Fei1, Zhaoji Li1, Ping Wang1, Gary W. Blissard2, Boyce Thompson Institute at Cornell University, Ithaca, New York, USA; 3State Key Laboratory of Agrobiootechnology, The Chinese University of Hong Kong, Hong Kong, China; 4Key Laboratory for Applied Entomology, Northwest A&F University, Yangling, China; 5Department of Entomology, Cornell University, New York State Agricultural Experiment Station, Geneva, New York, USA.

8:48 73 Polydnaviruses: From discovery to current insights – Michael R. Strand, Department of Entomology, University of Georgia, Athens, GA, USA.

9:12 72 Dicistrovirus – hijacking the host translational machinery – Eric Jan, Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada.

9:36 73 Insect metagenomics-based discovery of novel, small RNA viral genomes – Sijun Liu, Yuting Chen, Bryony C. Bonning, Department of Entomology, Iowa State University, Ames, IA, USA.

8:00 74 Potential of Aprehend™ (Beauveria bassiana) as a bed bug control agent – Alexis M. Barbarin1, Nina E. Jenkins1, Giovanni Bellicant1, Matthew B. Thomas1, Coby Schaal1, Department of Entomology, North Carolina State University, 100 Derieux Pl. Campus Box 7613, Raleigh, NC, 27695, USA; 2Department of Entomology, Penn State University, Merle Lab University Park, PA 16802, USA; 3Center for Infectious Disease Dynamics, Penn State University, Merle Lab University Park, PA 16802, USA.

8:15 75 Beauveria bassiana for the control of stored grain pests – Austin B. Dillon1, Clare G. Storm1, Taro Saito, Angela Brommit3, Department of Entomology, Northwest A&F University, Ames, IA, USA; 3Molecular Biology, University of Victoria, Victoria BC, Canada.

Contributed Papers 8:00 – 9:45 2306/9

Microbial Control 2

Moderator: Travis Glare

8:00 76-StU Semi-field trials and tribulations – Brian Lovett1, Etienne Bilgo2, Abdoulave Diabate2, Raymond St. Leger1, 1University of Maryland, College Park; 2Centre Murax, Burkina Faso.

8:45 77 A clean start strategy for seasonal poinsettia cuttings – Michael Brownbridge1, Rose Buitenhuis1, Graeme Murphy1, Taro Saito, Angela Brommit1, 1Vineland Research and Innovation Centre, 4890 Victoria Avenue North, Box 4000, Vineland Station, Ontario L0R 2E0, Canada; 2Biological Control Solutions, Welland, Ontario, Canada.

9:00 78 Selection and characterization of Colombian entomopathogenic fungi against Ceratoma tingomariana – Erika Grijalba, Carlos Espinel, Adriana Santos, Cindy Mejia, Carolina Ruiz, Biological Control Laboratory, Colombian Corporation for Agriculture Research, CORPOICA. Mosquera, Colombia.

9:15 79 Obstacles and opportunities for the use of biopesticides in conventional agriculture – Surendra K. Dana, University of California Cooperative Extension, San Luis Obispo, CA, USA.

9:30 80-StU Evaluation of the entomopathogenic fungi Isaria sp. as a biocontrol agent against pest insects in greenhouses – Katharina Saar1, Jasmin Philipp2, Edgar Schliepke1, Andreas Leclerque2, Manuel Werner2, Johannes A. Jelhe1, Dietrich Stephan1, 1Institute for Biological Control, Julius Kühn Institute, Darmstadt, Germany; 2Institute for Resistance Research and Stress Tolerance, Julius Kühn Institute, Quedlinburg, Germany; 3Institute for Microbiology and Biochemistry, Heinheim University, Heilheim, Germany.

Contributed Papers 8:00 – 9:45 2311

Nematodes 1

Moderator: Luis Leite

8:00 81 Selection of lipid and protein sources for solid fermentation of entomopathogenic nematodes – Luis G. Leite1, David I. Shapiro-Ilan2, Selcuk Hazir1, Mark A. Jackson1, 1Instituto Biologico, APTA, CP 70, Campinas, SP 13001-970, Brazil; 2USDA-ARS, SEFTNRL, Byron, GA 30108, USA; 3Adnan Menders University, Faculty of Arts and Sciences, Department of Biology, Akyun-Turkey; 4USDA-ARS, NCAUR, Peoria, IL, 61604, USA.


8:30 83-StU Investigating Deladenus siricidicola Kamona (Tylenchida: Neolychnidae) to control Sirex noctilio (Hymenoptera: Siricidae) in North America – Luis A. L. Caetano, Ann E. Hajek, Cornell University, Department of Entomology, Comstock Hall, 129 Garden Ave, Ithaca, New York, USA.

8:45 84-StU Interactions between parasitic nematodes and bacteria in Drosophila – M. A. Hanson, S. J. Perlman, Biology Department, University of Victoria, Victoria BC, Canada.

9:00 85-StU Characterization of immune response genes in the parasitic nematode Brugia malayi – Silvia Libro, Jeremy Foster, Barton Slatko, New England Biolabs,
### Insecticidal action, cellular interactions and response of combinations of *Photorhabdus*-insect-related (Pir) and *Bacillus thuringiensis* Crystal (Cry) toxins – *Anolis* Castanops1, Rousel Orozco1, Kathy Teng-Nelson1, Don Lightner1, Patricia Stock2, 1Center for Insect Science, University of Arizona, Tucson; 2Entomology Department, University of Arizona, Tucson; 3School of Animal and Comparative Biomedical Sciences, University of Arizona, Tucson, AZ, USA.

### Response to Cry1Ac intoxication in midgut cells of *Heliothis virescens* larvae – *Cris Oppert*, Omaththage P. Perera1, Thomas Lane1, Margaret Stanton1, Heba M. Abdelgaffar1, Juan Luis Jurat-Fuentes2, 1Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA; 2USDA-ARS, Southern Insect Management Research Unit, Stoneville, MS, USA.

### Syringe-like injection mechanism of bacterial ABC toxins revealed in molecular detail – *Christos Gotsopoulos*1, Dominic Meusch1, Alexander E. Long1, Klaus Aktories1, Stefan Rausner1, 1Department of Structural Biochemistry, Max Planck Institute of Molecular Physiology, Dortmund, Germany; 2Institut für Experimentelle und Klinische Pharmakologie und Toxikologie, Albert-Ludwigs-Universität, Freiburg, Germany.

### Caenorhabditis elegans nck-1 plays a distinct and specific role in defense against bacterial pore-forming toxins – *Anand Sitaran*, Yunqiang Yin, Raffi V. Aroian, University of Massachusetts Medical School, Worcester, MA, USA.

### The cell biology of *Wolbachia*-filarial nematode interactions and the dark side of symbiosis – F. Landmann1, J. M. Foster1, M. L. Michalski1, B. E. Slak1, W. Sullivan1, 1Department of Molecular, Cell and Developmental Biology, Sinshemer Labs, University of California, Santa Cruz, California, USA; 2Centre de Recherche de Oskosh, Biochimie Macromoléculaire, CNRS, Montpellier, France; 3Molecular Parasitology, New England Biolabs, Ipswich, Massachusetts, USA; 4Department of Biology and Microbiology, University of Wisconsin Oskosh, Oshkosh, Wisconsin, USA.
### WEDNESDAY

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30</td>
<td>102 Insectidrial parameters for the baculovirus infecting Agrotis ipsilon neonates – Robert W. Behie, USDA-ARS-NCAUR, Crop Bioprotection Research Unit, Peoria, Illinois, USA.</td>
</tr>
<tr>
<td>10:45</td>
<td>103 Haemocytes from Cossusstria giga and Ost-1: A promising in vitro model to study host/virus interactions – Benjamin Margot, Nicole Faury, Tristan Renaut, 1Ifremer (Institut Français de Recherche pour l’Exploitation de la Mer) Laboratoire de Génétique et Pathologie des Mollusques Marins, La Tremblade, France; 2Ifremer Departement Ressources Biologiques et Environnement, Nantes, France.</td>
</tr>
<tr>
<td>11:00</td>
<td>104-STU Comparison of viral growth characteristic of two nucleopolyhedroviruses isolated from the genus Adoxophyes – Yasumasa Saito,2 Yasuhisa Kunimi, Maki N. Inoue,1 Madoka Nakai2, Laboratory of Biological Control, University Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology, 3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan; 2Japan Society for the Promotion of Science.</td>
</tr>
<tr>
<td>11:15</td>
<td>105-STU A novel type of resistance of the codling moth against Cydia pomonella granulovirus shows two different resistance mechanisms – Annette M. Sauer, Manuela M. Gebhardt, Eva Fritsch, Karin Undorf-Spahn, Johannes A. Jehle, Institute for Biological Control, Federal Research Center for Cultivated Plants, Julius Kühn Institute, Darmstadt, Germany.</td>
</tr>
<tr>
<td>11:30</td>
<td>106-STU Nucleopolyhedrovirus and microsporidia in winter moth (Operophtera brumata) and bruce spanworm (O. bruceata) populations in the northeastern U.S. – Hannah J. Broady, Joseph S. Elkinton, John P. Burand, Matt Boucher, Leellen F. Solter,1 Organismic and Evolutionary Biology, University of Massachusetts, Amherst, MA, U.S.A.; 2Department of Microbiology, University of Massachusetts, Amherst, MA, U.S.A.; 3Department of Natural Resources and Environmental Sciences, University of Illinois, Champaign, IL, U.S.A.</td>
</tr>
<tr>
<td>11:45</td>
<td>107-STU How climate and host behaviour influence nucleopolyhedrovirus infection dynamics in the western tent caterpillar – Paul R. MacDonald, Judith H. Myers, Jenny S. Cory,1 Department of Biological Sciences, Simon Fraser University, Burnaby, Canada; 2Department of Zoology, University of British Columbia, Vancouver, Canada.</td>
</tr>
<tr>
<td>12:00</td>
<td>108-STU The specialist baculovirus SeMNPI induces light sensitive tree-top disease in Spodoptera exigua caterpillars facilitated by the viral egt gene – Yue Han,1 Stineke van Houte2, Monique M. van Oers,1 Vera I.D. Ros,1 Laboratory of Virology, Wageningen University, Droevedaalsesteeg 1, 6708 PB, Wageningen, the Netherlands; 2Centre for Ecology and Conservation, Biosciences, University of Exeter, Penryn, Cornwall, UK.</td>
</tr>
<tr>
<td>12:15</td>
<td>109 Baculovirus-induced tree-top disease revisited: The role of the egt gene – Vera I.D. Ros,1 Yue Han,1 Stineke van Houte,2 Monique M. van Oers1, Laboratory of Virology, Wageningen University, Droevedaalsesteeg 1, 6708 PB, Wageningen, the Netherlands; 2Centre for Ecology and Conservation, Biosciences, University of Exeter, Penryn, Cornwall, United Kingdom.</td>
</tr>
<tr>
<td>12:30</td>
<td>LUNCH (on your own)</td>
</tr>
<tr>
<td>13:00</td>
<td>110 Endophytic entomopathogenic fungus as “plant probiotics”: An important tool in protecting and promoting plant health? – Chad A. Keyser, Donald W. Roberts, Department of Biology, Utah State University, Logan Utah, USA.</td>
</tr>
<tr>
<td>14:00</td>
<td>111 Endophytic entomopathogenic fungus as endophytes: Interactions with host plants and herbivores – Stefan Vidal,1 Anant Patel2,1 Georg-August-University Goettingen, Department of Crop Sciences, Goettingen, Germany; 2University of Applied Sciences, Department of Engineering and Mathematics, Bielefeld, Germany.</td>
</tr>
<tr>
<td>15:00</td>
<td>112 Trading insect nitrogen for photosynthate: Carbon translocation from a plant to an insect pathogenic, endophytic fungus – Michael J. Bidochko, Scott W. Behie, Department of Biological Sciences, Brock University, St. Catharines, ON, Canada.</td>
</tr>
<tr>
<td>15:30</td>
<td>113 Metarhizium as a multifactorial plant growth promoter – Raymond J. St. Leger, Department of Entomology, University of Maryland, Maryland, USA.</td>
</tr>
</tbody>
</table>

### Workshop, with lunch

**Wednesday 12:30 – 14:00**

(Students only)

**Writing scientific articles: what reviewers, editors, and publishers are looking for**

Dale Seaton, Leelen Solter

**Symposium:** Fungus Endophytic Entomopathogenic Fungi: “Pro-biotic” Microbial Associates of Plants?

Moderators: Don Roberts and Ray St. Leger

**14:00** 110 Endophytic entomopathogenic fungus as “plant probiotics”: An important tool in protecting and promoting plant health? – Chad A. Keyser, Donald W. Roberts, Department of Biology, Utah State University, Logan Utah, USA.

**14:30** 111 Endophytic entomopathogenic fungus as endophytes: Interactions with host plants and herbivores – Stefan Vidal, Anant Patel, Georg-August-University Goettingen, Department of Crop Sciences, Goettingen, Germany; University of Applied Sciences, Department of Engineering and Mathematics, Bielefeld, Germany.

**15:00** 112 Trading insect nitrogen for photosynthate: Carbon translocation from a plant to an insect pathogenic, endophytic fungus – Michael J. Bidochko, Scott W. Behie, Department of Biological Sciences, Brock University, St. Catharines, ON, Canada.

**15:30** 113 Metarhizium as a multifactorial plant growth promoter – Raymond J. St. Leger, Department of Entomology, University of Maryland, Maryland, USA.

**Contributed Papers**

**Wednesday 14:00 – 16:00**

**Viruses 4**

Moderators: Elisabeth Herniou and Madoka Nakai

**14:00** 114 Population structure of Spodoptera litura multicapsid nucleopolyhedroviruses from Pakistan – Gulam Ali, Marleen Henkens, Elia Schijlen, Wopke van der Werff, Just M. Vlok, CABI Rawalpindi, Pakistan; Laboratory of Virology, Wageningen University, Wageningen, The Netherlands; Bioscience, Wageningen UR, Wageningen, The Netherlands; Centre for Crop Systems Analysis, Wageningen University, Wageningen, The Netherlands.

**14:15** 115 Genome sequence and environmental tolerance of a granulovirus mutant that produces abnormally large occlusion bodies – Madoka Nakai, Robert L. Harrison, Harushi Uchida, Yasuhisa Kunimi, Tokyo University of Agriculture and Technology, Saiwai, Fuchu, Tokyo 183-8509, Japan; Invasive Insect Biocontrol and Behavior Laboratory, USDA Agricultural Research Service (USDA-ARS), Beltsville Agricultural Research Center, 10300 Baltimore Avenue, Beltsville, MD 20705, USA.

**14:30** 116 The complete genome of Aedes sollicitans nucleopolyhedrovirus – Onaththage P. Perera, James L. Beclen, Southern Insect Management Research Unit, USDA-ARS, Stoneville, MS 38776; Mosquito and Fly Research Unit, CMAVE, USDA-ARS, Gainesville, FL, USA.
14:45  **117-STU** Lake Sinai Virus (LSV) diversity in Hymenoptera – *Diane Biao*¹, *Elisabeth A. Herniou*², *Nicolas Gallet*³, *Philippe Gayral*³, ¹Institut de Recherche sur la Biologie de l’Insecte, UMR 7261, CNRS, Université François-Rabelais, 37200 Tours, France; ²Institut des Sciences de l’Evolution de Montpellier, UMR 5554, CNRS, Université Montpellier 2, Place E. Bataillon, 34095 Montpellier, France.

15:00  **138 Genomic landscape of AcMNPV adaptation** – Aurélien Chatteigner, Cindy Pontlevé, Carole Labrousse, *Elisabeth A. Herniou*, Institut de Recherche sur la Biologie de l’Insecte, UMR CNRS 7261, Université François Rabelais de Tours, Faculté des Sciences et Techniques, Avenue Monge - Parc Grandmont, 37200 Tours, France.

15:15  **119 In search of the ancestor of banchine polydnaviruses** – Catherine Béliveau¹, Alejandro Cohen², Don Stewart¹, Georges Periquet¹, Abdelmadjid Djoudad¹, Lisa Kuhn¹, Don Stoltz², Brian Boyle², Anne-Nathalie Volkoff³, Elisabeth A. Herniou¹, Jean-Michel Drezen¹, Michel Cusson², ¹Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, Quebec City, Quebec, Canada; ²Proteomics Core Facility, Dalhousie University, Halifax, Nova Scotia, Canada; ³Institut de Recherche sur la Biologie de l’Insecte (IRBI), Université François-Rabelais et CNRS UMR 7261, Tours, France; 4Department of Microbiology and Immunology, Dalhousie University, Halifax, Nova Scotia, Canada; 5Institut de Biologie Intégrative et des Systèmes, Université Laval, Quebec City, Quebec, Canada; 6UMR 1333 INRA, Université Montpellier, "Diversité, Génomes, Interactions Microorganismes-Insectes" (DGIMI), Montpellier, France.

15:30  **120 Construction and rescue of a synthetic baculovirus, AcMNPV-WIV-Syn1.0, that retains the properties of the parental virus** – Yu Shang, Fei Deng, Gengfu Xiao, Dianhai Hou, Kai Pan, Manli Wang, Hualin Wang, Zhihong Hu, State Key laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, P.R. China.

15:45  **121 Generating a host ranges extended recombinant baculovirus** – Tronguyen Wu, Chao-Yi Tong, Mean-Shine Chen, Department of Bioscience Technology, Chung Yuan Christian University, Chung Li, Taiwan.

**Workshop Wednesday 14:00 – 15:00**

**Nematodes**

**Nematodes Workshop**

Moderators: David Shapiro-Ilan and Harry Kaya

14:00  **122 Entomopathogenic nematode species in insect pest suppression: Can their use be optimized by proper application approaches?** – Harry K. Kaya*¹, Selcuk Hazir², David Shapiro-Ilan³, ¹Department of Entomology and Nematology, University of California, Davis, CA 95616, USA; ²Department of Biology, Faculty of Arts and Sciences, Adnan Menderes University, Aydin, TURKEY; ³USDA-ARS, SE Fruit and Tree Nut Research Laboratory, Byron, GA 31008, USA.

14:15  **123 EPNs from lab to field against insect pests of fine turfgrass: Overcoming obstacles in research and implementation** – Albrecht M. Koppenhöfer¹, Olga S. Kostromytyska², ShaoHui Wu², Benjamin A. McGraw³, Lemma Ebbas⁴, ¹Department of Entomology, Rutgers University, New Brunswick, NJ 08901, USA; ²Department of Plant Science, Pennsylvania State University, University Park, PA, 16802, USA; ³Institute for Health, Health Care Policy and Aging Research, Rutgers University, New Brunswick, NJ 08901, USA.

14:30  **124 Plant scream, insect succumb: From concepts to applications** – J. Hiltpold, Hawkesbury Institute for the Environment, University of Western Sydney, Penrith, NSW, Australia.

14:45  **Discussion**

16:00 – 16:30  **BREAK**

**POSTERS**

**Bacteria**

**BA-1-STU** Novel mosquitocidal activity of strains LB1T 980 and LB1T-1217 of Bacillus thuringiensis – *Mariana Fernández-Navarro*¹, *Cristina Del Rincón-Castro*¹, *Jorge E. Ibarrá*², ¹Department of Biotechnology and Biochemistry, CINVESTAV-Irapuato, Gto. Mexico; ²Life Sciences Division, University of Guanajuato, Irapuato, Gto. Mexico.

**BA-2-STU** Inoculation and translocation of the spore-crystal complex from Bacillus thuringiensis in vascular tissue of bean plants – *Rosalina García-Suárez*², *Cristina Del Rincón-Castro*¹, *Jorge E. Ibarrá*², ¹Department of Biotechnology and Biochemistry, CINVESTAV-Irapuato, Gto. Mexico; ²Life Sciences Division, University of Guanajuato, Irapuato, Gto. Mexico.

**BA-3-STU** Diversity of Bacteria Composition of Spined Soldier Bug, Podisus maculiventris (Hemiptera: Pentatomidae) Digestive System – *E. M. Romagnoli*¹, *C. A. Dunlap*², *L. B. Flor-Weller*², *T. A. Coudron*³, *A. P. Rooney*², ¹“Luiz de Queiroz” College of Agriculture, University of Sao Paulo, Piracicaba, Sao Paulo, 13418900, Brazil; ²National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agricultural, Peoria, IL, 61604, USA; ³Biological Control of Insects Research Service, U.S. Department of Agricultural, Columbia, MO, USA.

**BA-4-STU** Use of NGS to assess the effect of antibiotics on the bacterial community of insects – *Diana Wilches*¹², *Kevin D. Floate*², *Paul Coghlin*³, ¹University of Lethbridge; ²Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB, Canada.

**BA-5** Status of resistance to Bt cotton in China: Cotton bollworm and Pink bollworm – *Yulin Gao*¹, *Chenxi Liu*¹, *Yidong Wu*¹, *Kongming Wu*¹, ¹State Key Laboratory for Biology of Plant Disease and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, PR China; ²Department of Entomology, College of Plant Protection, Nanjing Agricultural University, Nanjing 210095, PR China.

**BA-6** Evidence of field-evolved resistance of Spodoptera frugiperda to Bt corn expressing Cry1F in Brazil that is still sensitive to modified Bt toxin – *Anabela A. Lima*¹², *Rose Monnerat*³, *Erica Martins*³, ¹Institut de Recherche sur la Biologie des Systèmes, Université Laval, Faculté des Science de l’Insecte, UMR CNRS 7261, Université de Tours, Place 1.00.01, 37200 Tours, France; ²Institut de Recherche sur la Biologie de l’Insecte (IRBI), Université François-Rabelais et CNRS UMR 7261, Tours, France; ³University of Sao Paulo, Piracicaba, Sao Paulo, 13418900, Brazil; ⁴“Luiz de Queiroz” College of Agriculture, University of Sao Paulo, Piracicaba, Sao Paulo, 13418900, Brazil; ⁵National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agricultural, Peoria, IL, 61604, USA; ⁶Biological Control of Insects Research Service, U.S. Department of Agricultural, Columbia, MO, USA.
MACEDO1,2, PAULO QUEIROZ1, LIAN PRACÉ2, MARCELO C. SOARES1, HELIO MOREIRA1, ISABELLA GRISI1, JOSEANE SILVA1, MARIA SOBERON1, ALEJANDRA BRAVO1, EMBRAPA Recursos Genéticos e Biotecnologia, Brasília, Distrito Federal, Brazil; 1Instituto Matro-Grossense do Algodão, Cuiabá, Mato Grosso, Brasilia, Brasilia, Distrito Federal, Brazil; 2Departamento de Microbiologia, Universidade de Brasilia, Brasilia, Distrito Federal, Brazil; 3Instituto de Biotecnologia, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, Mexico; 4University Center of Brasilia, Distrito Federal, Brazil.

BA-7 Behavioural feeding responses of susceptible and resistant Trichoplusia ni larvae to Bacillus thuringiensis – Alida F. Jamnan1, Mandy Gelderman2, Martin Muermann3, Biology Department, University of the Fraser Valley, Abbotsford, BC, Canada.

BA-8 Discovering novel Bt toxins for better bio-pesticides and biotech crops – Jim X. J. Fang1,2, W. F. Zhang1,2, Y. Zhou1,2, P. T. Gong2, 1The HITAR Institute Canada Inc., Richmond, British Columbia, Canada; 2Hainan Institute of Tropical Agricultural Resources, Sanya, Hainan, China; 3College of Life Sciences, Hainan Normal University, Haikou, Hainan, China.

BA-9 Toxicity and interaction of Cry1 proteins from Bacillus thuringiensis in Helicoverpa armigera (Hübner) (Lepidoptera: Noctuidae) – Manoel Victor F. Lemos1, Isis Sebastião1, Camila S. Figueredo1, Ana Rita N. Lemes1, Ricardo A. Polanczyk2, Janete A. Desidério1, Faculdade de Ciências Agrárias e Veterinárias, UNESP – Univ. Estadual Paulista Júlio de Mesquita Filho; 1Departamento de Biologia Aplicada à Agropecuária; 2Departamento de Fitosanidade. Rod. Prof. Paulo Donato Castellane, km. 5, CEP14884-900, Jaboticabal, São Paulo, Brasil.

BA-10 Interaction of Vip3Aa42 and Cry1a10 proteins from Bacillus thuringiensis and toxicity to Anticarsia gemmatalis (Hübner, 1818) (Lepidoptera: Noctuidae) – Suzana C. Marucci1, Janete A. Desidério1, Manoel Victor F. Lemos1, Departamento de Biologia Aplicada à Agropecuária, Univ. Estadual Paulista Júlio de Mesquita Filho, UNESP/Campus de Jaboticabal, SP, CEP 14884-900, Brasil.

BA-11-STU Parallels between the Cry4Aa Parasporin and insecticidal Rt toxins – Barbara Domanska, Michelle West, Neil Crickmore, Department of Biochemistry, School of Life Sciences, University of Sussex, Falmer, Brighton, BN1 9QG, UK.

BA-12-STU Unusual pore formation by a new Bacillus thuringiensis toxin – Eva Partea Verdugo1, Vincent Lemieux2,3, Léna Potvin2, Timothy Hey1, Xiaoping Xu1, Samantha Griffin1, Vinmal Chokwana1, David McCaskill1, Ken Norval1, Vincent Vachon1, Jean-Louis Schwartz1,4, 1Département de physiologie moléculaire et intégrative et Groupe d’étude des protéines membranaires, Université de Montréal, Montréal, QC, Canada; 2Département de biologie, Université de Sherbrooke, Sherbrooke, QC, Canada; 3Dow Agrosciences LLC, Indianapolis (IN 46268), IN, USA; 4Centre SEVE de recherche en sciences du végétal, Université de Sherbrooke, Sherbrooke, QC, Canada.

BA-13-STU Construction & characterization of novel Bacillus thuringiensis Cry1-type genes with improved insecticidal activities – Jong Moon Kim1, Jo Young Chai1, Pang Ying1, Ho Kya Bok2, Seok Hee Lee3, Woo Jin Kim4, Yeon Ho Je2, 1Department of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea; 2Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.

BA-14-STU Development of a Cry toxin activity-improving method based on the directed evolution that targets ABCC2 – Kazuhiro Imamura1, Natsuko Nokajima1, Haruka Endo2,3, Ryoichi Satō2, 1Graduate School of Bio-Applications and Systems Engineering Tokyo University Of Agriculture and Technology, Koganei, Tokyo, Japan; 2Japan Society for the Promotion of Science Research Fellowship for Young Scientists.

BA-15 Carbohydrate binding domain of Vip3Aa is involved in receptor binding – Kun Jiang1, Yu Yuan1, Dong-hui Hua2, Tingting Wang, Yue-hua Chen1,2, Jun Cai1,2, 1Department of Microbiology, College of Life Sciences, Nankai University, Tianjin, China; 2Key Laboratory of Molecular Microbiology and Technology, Ministry of Education, Tianjin, China; 3Tianjin Key Laboratory of Microbial Functional Genomics, Tianjin, China.

BA-16 Insecticidal spectrum and mode of action of the Bacillus thuringiensis Vip3Aa insecticidal toxin – Joaquín Gomis-Cebollas1,2, Ólivo Ruiz de Escudero1,2, Maissa Chakroun1, Natalia Mara Vera-Velasco1, Patricia Hernández-Martínez1, Carmen Sara Hernández-Rodríguez1, Yolanda Bel1, Baltasar Escriche1, Primitivo Caballero2, Juan Ferré1,2, ERI of Biotechnología y Biomedicina (BIOTECMED), Universitat de València, Burjassot, Spain; 3Instituto de Agrobiotecnología, CSIC-UPNA, Gobierno de Navarra, Campus Arrosadia, Navarra, Spain; 4Laboratorio de Entomología Agrícola y Patología de Insectos, Universidad Pública de Navarra, Pamplona, Spain.

BA-17 Binding to brush border vesicles and midgut processing of Bacillus thuringiensis Vip3Aa toxin to Helicoverpa armigera susceptible and Vip3Aa-resistant insects – Maissa Chakroun1, Natalia Mara Vera-Velasco1, Patricia Hernández-Martínez1, Carmen Sara Hernández-Rodríguez1, Yolanda Bel1, Baltasar Escriche1, Primitivo Caballero2, Juan Ferré1,2, ERI of Biotechnología y Biomedicina (BIOTECMED), Universitat de València, Burjassot, Spain; 1Land and Water Flagship, CSIRO, Canberra ACT 2601; 2Agriculture Flagship, CSIRO, Narrabri NSW 2390.

BA-18 Proteolytic processing of Bacillus thuringiensis Cry3 proteins by gut proteases and binding to brush border membrane vesicles from Cylas punicicolis (Brentidae) – Natalia M. Vera-Velasco, Patricia Hernández-Martínez, Baltasar Escriche, Departamento de Genética, Facultad de CC, Biológicas, Universidad de Valencia, Burjassot, Spain; 2Land and Water Flagship, CSIRO, Canberra ACT 2601; 3Agriculture Flagship, CSIRO, Narrabri NSW 2390.

BA-19 Domain II of Bacillus thuringiensis Cry1e toxin contributes to its binding to peritrophic membrane of Asian corn borer – Dongmei Feng, Zhen Chen, Nan Zhang, Chunlu Zhang, Shuyuan Guo, School of Life Science, Beijing Institute of Technology, Beijing 100081, China.

BA-20-STU Loop regions of domain II of Cry1Aa have an important role for binding with BmABCC2 and its BmABCC2-dependent activity – Satoshi Adegawa1, Shih Tanaka2,3, Shingo Kikuta4, Ryoichi Satō2, 1Graduate School of Bio-Applications and Systems Engineering Tokyo University of Agriculture and Technology, Koganei, Tokyo, Japan; 2Japan Society for the Promotion of Science Research Fellowship for Young Scientists.
Diseases of Beneficial Invertebrates

DB-1-STU Chitin-degrading protein PICBP49 - a key virulence factor of Paenibacillus larvae – Henriette Knispel 1, Anne Fürnhaus 1, Eva García-Gonzalez 1, Lena Poppinga 1, Jennifer S M Loose 2, Gustav Vaoje Kolstad 1, Elke Genersch 1, Institute for Bee Research, Hohen Neuendorf, Division of Molecular Microbiology and Bee Pathology, Friedrich-Engels-Str 32, D-16540 Hohen Neuendorf, Germany; 2Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, P.O. Box 5003, N-1432 Ås, Norway.

DB-2-STU Characterization of virulence factors in the fatal honey bee disease American foulbrood caused by Paenibacillus larvae – Julia Ebeling 1, Lena Poppinga 1, Anne Fürnhaus 1, Elke Genersch 1, Institute for Bee Research, Hohen Neuendorf, Brandenburg, Germany.

DB-3 Decentralised molecular diagnostics and remote data reporting for management of disease in global aquaculture – Kelly S. Bateman 1, Michelle Pond 1, Peter Munday 2, Olga Gandelman 1, Grant D. Stentiford 1, European Union Reference Laboratory for Crustacean Disease, Centre for Environment, Fisheries and Aquaculture Science (Cefas), Barrack Road, The Nothe, Weymouth, Dorset DT4 8UB, UK; 2Epistem, Genedrive, Epistem Ltd., 48 Grafton Street, Manchester, M13 9XQ, UK.

DB-4 Virus prevalence in bee populations in apple orchards in New York, USA – John P. Burand 1, Shuning Zheng 1, Bryan N. Danforth 1, Department of Microbiology, 1Graduate Program in Molecular and Cellular Biology, University of Massachusetts - Amherst, Amherst, MA 01003, USA; 2Department of Entomology Cornell University, Ithaca, NY 14853 USA.

DB-5 Insect pathological challenges in insects produced for food and feed – Jürgen Ellenberg 1, Christina Nielsen-Lefkov 2, Silvia Cappellozza 2, Just M. Vlok 2, Annette B. Jensen 1, University of Copenhagen, Department of Plant and Environmental Sciences, Copenhagen, Denmark; 2INRA, UMR 1319 MicrobeAgroParisTech, France; 3Consiglio per la Ricerca in Agricoltura e l’Analisi dell’Economia Agraria, Honeybee and Silkworm Research Unit, Padova, Italy; 4 Wageningen University, Laboratory of Virology, Wageningen, the Netherlands.

FU-1 ITS region analysis of isolates of Beauveria bassiana, a pathogenic fungus to the silkworm, Bombyx mori L. – Liang Shui 1, Jie Jin 1, College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, P.R.China.

FU-2 Molecular characterization of Isaria fumosorosea from citrus and strawberry crops in Brazil – Celeste P. D’Alessandro 1, Ricardo Macedo do Nascimento 2, Gustavo Manuyama Mor 3, Maria I. Zucchi 1, Italo Delalibera Junior 1, 1Department of Entomology and Acralogy, “Luiz de Queiroz” College of Agriculture (ESALQ), University of São Paulo (USP), Piracicaba, São Paulo, Brazil; 2Center for Molecular Biology and Genetic Engineering, University of Campinas, Campinas, São Paulo, Brazil; 3São Paulo Agency for Agribusiness Technology, Piracicaba, São Paulo, Brazil.

FU-3-STU Comparative genomics of cold-adapted Metarhizium frigidum – Brian Lovett 1, Raymond St. Leger 2, 1University of Maryland, College Park, USA; 2Entomology Department, USDA-ARS, Stoneville, MS 38776, USA.

FU-4 Identification of Drosophila mutants affecting defense to an entomopathogenic fungus – Hisao-Ling Lu 1, Jonathan Wong 2, Markus Brown 2, Chris Ewerle 2, Raymond St. Leger 2, Entomology Department, University of Maryland, College Park, MD, USA.

FU-5-STU Persistence of two Brazilian isolates of Metarhizium in a strawberry cropping system using microsatellite markers – Thiago Rodrigues de Castro 1, Johanna Mayerhofer 1, Jürg Enkerli 2, Jürgen Ellenberg 1, Nicol
V. Meyling1, Italo Delalibera Jr.2, 1University of São Paulo (USP), Brazil; 2Department of Plant and Environmental Sciences, University of Copenhagen, Denmark; 3Institute for Sustainability Sciences, Agroscope, Switzerland.

FU-6 Susceptibility of biocontrol fungi in the genera Nomuraea, Isaria, Purpureocillium, Pochonia, and Trichoderma to imbibitional damage and its mitigation through increased conidial quality — Marcos Fariá, Irene Martins, Daniela A. Souza, Rogério B. Lopes, EMBRAPA Genetic Resources and Biotechnology, Brasilia, DF, Brazil.

FU-7 STU Light during mycelial growth induces increased tolerance of conidia to different types of stress in entomopathogenic fungi — Luciana P. Dias1, 2, Claudineia A. S. Araújo1, Paulo C. Ferreira1, Breno Pupin1, Drauzio E. N. Range2, 1Instituto de Pesquisa e Desenvolvimento, Universidade do Vale do Paraíba, São José dos Campos, SP 12244-000, Brazil; 2Escola de Engenharia de Lorena (EEL/USP)/Pós-Graduação em Biotecnologia Industrial, Estrada Municipal do Campinho, Lorena, SP, Brazil.

FU-8 The great soil-sampling survey: A Utah State University/USDA collaborative project to find new entomopathogenic fungi from western USA soil — Chad A. Keyser, Samuel P. Sherwood, Everett K. K. Fernandes, Carmina Moore, Patricia S. Golo, JoAnn Stark, Alejandra M. Fernandes, Rodrigo B. Ferreira, Scott Treat, Fabiana Alvarez, Janitha B. Nandolachana, Holly C. Suisse, Stefanie Selamet, Laurel Nicolson, Skyler Christensen, R. Nelson Foster*, Larry E. Jech*, Stefan T. Jaronski*, Donald W. Roberts, Department of Biology, Utah State University, Logan Utah, USA; 1USDA, APHIS, PPQ, CPHST.

FU-9 Comparison of the use of insect baiting methods versus selective media when determining the diversity of Metarhizium spp. in soil — Carmela Hernández-Dominguez1, Ariel W. Guzmán-Franco1, Postgrado en Fitosanidad-Entomología y Acarología, Colegio de Postgrados, Km. 36.5 Carretera México-Texcoco, Montecillo, Texcoco, Estado de México, 56230, Mexico.

FU-10 STU Antifungal activity of entomopathogenic fungi isolated in Korea and their geographical characteristics — Yang Oh Ah, Tae Young Shin, Sung Min Baek, Won Seok Gwak, Seung Hee Lee, Soo Dong Woo, Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea.

FU-11 Characterization and pathogenicity of a Beauveria pseudobaissiana stubbi2 isolate from a laboratory colony of Dendroctonus ponderosae (Coleoptera: Scolytidae) — George Kyei1, Johny Shajahan2, Roar S. Falster2, John F. Gaskin2, Maximiliano Castiglione3, 1Department of Biology, Utah State University, Logan Utah, USA; 2USDA-ARS Collection of Entomopathogenic Fungal Cultures, 1970 Research Center, Conrad MT 59425 USA; 3Agricultural Research Service, U.S. Department of Agriculture, Systematic Mycology Laboratory, Beltsville MD 20705 USA.

FU-12 Entomopathogenic fungi for six species of leaf-cutting ants from different sites of Argentina — Daniela Goffré, Jorge A. Marfetán, Patricia J. Folgarait, Laboratorio de Hormigas, Departamento de Ciencia y Tecnología, Universidad Nacional de Quilmes, Bernal, Buenos Aires, Argentina.

FU-13 First isolation of Beauveria and Metarhizium from a wheat stem borer, Cephus cinctus (Hymenoptera: Cephidae) in North America — Stefan T. Jaronski1, Gadi V. P. Reddy2, Shaohui Wu2, John F. Gaskin2, Stephen Rehner1, 1Agricultural Research Service, U.S. Department of Agriculture, Northern Plains Agricultural Research Laboratory, Sidney MT 50270 USA; 2Montana State University, Western Triangle Research Center, Conrad MT 59425 USA; 3Agricultural Research Service, U.S. Department of Agriculture, Systematic Mycology Laboratory, Beltsville MD 20705 USA.

FU-14 First report of a mosquito-pathogenic Leptoglossia sp. (Saprolegniales) in Brazil — Cristian Montalva1, Richard A. Humber2, Karine dos Santos3, Stefanie Buchter4, Karin Collier4, Luiz F. N. Rocha4, Everett K. K. Fernandes1, Christian Luz1, 1Laboratório de Patologia de Invertébrados, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brasil; 2USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA; 3Centro Universitário UNIRG, Gurupi, TO, Brasil; 4Instituto Federal de Educação, Ciência e Tecnologia de Goiás, Aparecida de Goiânia, GO, Brasil.

FU-15 The puzzle of identifying mosquito-pathogenic isolates of Leptoglossia — Richard A. Humber1, Cristian Montalva2, Christian Luz3, 1USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA; 2Laboratório de Patologia de Invertebrados, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brasil.

FU-16 A treasure among the trash: Pandora bulbata from a Brazilian garlic dump — Richard A. Humber1, Cristian Montalva2, Karin F. S. Collier5, Christian Luz3, 1USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA; 5Laboratório de Patologia de Invertebrados, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brasil; 3Centro Universitário UNIRG, PROPSQ, Gurupi, TO, Brasil.

FU-17 STU Effects of temperature on germination, growth, and sporulation of Culicinomycetes species — Jusselino Rodrigues1, 2, Richard A. Humber3, Everett K. K. Fernandes1, Christian Luz3, 1Laboratório de Patologia de Invertebrados, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brasil; 2USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA.

FU-18 STU Beauveria bassiana inhibits host seeking behavior of Anopheles stephensi — Minhae Jang1, Masanori Ishii1, Cristian Montalva2, Daigo Auchi2, 1The United Graduate School of Agricultural Sciences, Iwate University, Japan; 2Research Fellowship for Young Scientists, Japan Society for the Promotion of Science; 3Department of Agro-environmental Science, Obihiro University of Agriculture & Veterinary Medicine, Japan; 4Research Center for Global Agro-medicine, Obihiro University of Agriculture & Veterinary Medicine, Japan.

FU-19 Biological activity of entomopathogenic fungi over two species of sugarcane borer Diatraea spp. — (Lepidoptera: Pyralidae) — Gloria B. Barrera1, Emiliano Barredo2, Paula Sotelo2, Paola Cuartas4, Laura Villamizar5, 1Corporación Colombiana de Investigación Agropecuaria, Corpoica, Mosquera, Colombia; 2Centro de Bioinformática, Instituto de

FU-21  Effectiveness of *Metarhizium anisopliae* and *Beauveria bassiana* against eggs of tomato leafminer, *Tuta absoluta* Meyrick, 1917 (Gelichiidae: Lepidoptera) – **Laila A. M. Al-Shuroyam**, Nagdy F. Abdel-Baky, Department of Biology, College of Arts and Sciences in Buraydah, Qassim University, Saudi Arabia; Department of Plant Protection & Protection, College of Agriculture and Veterinary Medicine Qassim University, P.O. Box: 6622, Buraydah 51452, Saudi Arabia.

FU-22  *Metarhizium* F52 microsclerotia applied in hydromulch to control Asian longhorn beetle – **Tarryn Anne Goble**, **Ann Hjeik**, **Mark Jackson**, Sana Gardeschi, Department of Entomology, Cornell University, Ithaca, NY, 14853-2601; **USDA-ARS-NCAUR, Crop Bioprotection Research Unit, 1815 N University Street, Peoria, IL, 61604, USA.

FU-23-STU  Control of ticks (*Ixodes ricinus*) in sheep pastures in Norway with the fungal biocontrol agent BIPESCO 5 (*Metarhizium brunneum*) – **Hitoshi Ihwamick**, Lie Grova**, Hermann Strasser**, Annette Folkedal Schjødt, Maria Björkman**, Jürg Enkerli**, Nikolai V. Meyling**, Ingeborg Klingeler**, Department of Entomology and Acarology, ESAUQ, University of São Paulo, Brazil; **Norwegian Institute for Agricultural and Environmental Research (Bioforsk), Norway;** Institute of Microbiology, Leopold-Franzens Universität Innsbruck, Austria; Swiss Federal Research Station for Agroecology and Agriculture, Switzerland; Department of Ecology, Faculty of Life Sciences, University of Copenhagen.

FU-24-STU  Development of *Aphidius colemani* incapable of oviposition and the evaluation of control efficacy against cotton aphid by combined use of entomopathogenic fungus and parasitoid wasp – **Euka Okowa**, Minehiro Ishii**, Masanori Koike**, Daigo Aiuchi**, Department of Agro-environmental Science, Obihiro University of Agriculture and Veterinary Medicine, Japan; **The United Graduate School of Agricultural Sciences, Iwate University, Japan; Research Fellowship for Young Scientists, Japan Society for the Promotion of Science; **Research Center for Global Agro-medicine, Obihiro University of Agriculture and Veterinary Medicine, Japan.


FU-28  Physiochemical characteristics of entomopathogenic fungi-derived antifungal substances – **Tae Young Shin**, Sungh Min Bae, Won Seok Gwak, Seung Hee Lee, Yong Oh Ahr, Soo Dong Woo, Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea.

FU-29-STU  Entomopathogenic fungi “Infecting” young lives – **Alap Sahoo**, Sumanth S. R. Dará, Suchitra S. Dará, Sunrendra K. Dará, Massachusetts Institute of Technology, Cambridge, MA, USA; **Warren Junior High School, Bakersfield, CA, USA; University of California Cooperative Extension, San Luis Obispo, CA, USA.

**Microbial Control**


MC-3  Pathogens and nematodes of bark beetles (*Coleoptera: Scolytidae*) in Georgia coniferous forest – **Archil Supatavili**, Medea Burjanadze, Department of Forest Protection, Vasil Guilashvili Forest Institute, Agricultural University of Georgia, Tbilisi, Georgia.

MC-4-STU  PhopGV for control of *Tuta absoluta* in tomato and *Phthorimaea operculella* and *Tecia solanivora* in potato – **Andreas Larem**, Eva Fritsch, Karin Undorf-Spahn, Johannes A. Jehle, Julius Kühn-Institut (IKI), Federal Research Centre for Cultivated Plants, Institute for Biological Control, Heinrichstr. 243, 64287 Darmstadt, Germany.
MC-5-TU Sublethal effects of Cry1Ac on immune responses and baculovirus infection in Spodoptera frugiperda – Lucas N. Waisch, Jenny S. Cory, Daniel R. Sosa-Gómez, Pos-Graduation Program, State University of Ponta Grossa, Ponta Grossa, Paraná, Brazil; Dept. of Biologicl Sciences, Simon Fraser University, Burnaby, British Columbia, Canada; Entomology Research, Embrapa Soybean, Londrina, Paraná, Brazil.

MC-6-TU Virulence of a newly isolated Bacillus thuringiensis strain against lepidopteran larvae – Anna L. Moldovan, Natalia Munteanu, Molotievskiy, Svetlana G. Bacar, Ion K. Toderas, Faculty of Biology and Soil Science, Moldova State University, Chisinau, Republic of Moldova; Institute of Zoology, Academy of Sciences of Moldova, Chisinau, Republic of Moldova.

MC-7 Selection and characterization of formulation prototypes based of Beauveria bassiana for biological control of Ceratoma tingomariana – Erika Grijalba, Lorena García, Carlos Espinel, Judith Guevara, Hugo Fernando Rivera, Biological Control Laboratory; Entomological Laboratory, Colombian National Corporation for Agriculture Research, CORPOICA. Colombia.

MC-8 Sublethal effects of Cry1Ac Bacillus thuringiensis protein on Plutella xylostella (Lepidoptera: Plutellidae) Brazilian population: Life table study – Caroline P. De Bortoli, Ricardo A. Polanczyk, Neil Crickmore, Sergio A. De Bortoli, Alessandra M. Vacari, Department of Plant Protection, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil; Biochemistry, School of Life Sciences, University of Sussex, Falmer, Brighton, United Kingdom.

MC-9 Interaction between predator Podisus nigrispinus (Dallas) and the entomopathogenic bacterium Bacillus thuringiensis Berliner – Vanessa F. P. Carvalho, Sergio Antonio De Bortoli, Alessandra M. Vacari, Department of Plant Protection, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil.

MC-10 Reproduction and population parameters of predator Podisus nigrispinus (Dallas) providing Bacillus thuringiensis Berliner suspension as water source over generations – Vanessa F. P. Carvalho, Sergio Antonio De Bortoli, Alessandra M. Vacari, Department of Plant Protection, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil.

MC-11-TU Expression of recombinant ABC22 from Pectinophora gassypii and their influences on the cytotoxicity of activated Cry1Ac to H5 cells – Tufts Volpi, The State Key Laboratory of Plant Disease and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, West Yuanmingyuan Road, Beijing, 100193, China.

MC-12-TU Evaluation of commercial formulations of entomopathogenic fungi for managing the ambrosia beetles Xylotrechus crassiusculus and Xyleborus volvulus (Coleoptera: Curculionidae), vectors of the laurel wilt pathogen affecting avocado production in Florida – Pasco B. Avery, Verónica F. Bojorque, José M. Pérez-Martínez, Armando Monterroso, Ronald D. Cave, J. Daniel Carrillo, University of Florida, IFAS, Indian River Research and Education Center, Fort Pierce, FL, USA; PanAmerican School of Agricultural, El Zamorano, Honduras; Brooks Tropicals, LLC, Homestead, FL, USA; University of Florida, IFAS, Tropical Research and Education Center, Homestead, FL, USA.

MC-13 Efficacy of Metarhizium anisopliae ICPE 7 for the control of cattle tick – Paulin Nana, Sunday Ekesi, Mercy Mumbi, Nguya K. Maniania, International Centre of Insect Physiology and Ecology, Nairobi, Kenya; Faculty of Agriculture and Agricultural Sciences, University of Dschang, Cameroon; Department of Veterinary Pathology, Microbiology and Parasitology, University of Nairobi, Kenya.

MC-14 Morphological and physiognomic study of seven isolates of an entomopathogenic fungus – Cavallo E. C., Martefán J. A., Fulgorait P. J., Laboratorio de Hormigas, Departamento de Ciencia y Tecnologia, Universidad Nacional de Quilmes, Bernal, Buenos Aires, Argentina.

MC-15 Delivery of entomopathogenic fungi as a seed coating for control of soil-dwelling insect pests – Federico Rivas, Trevor Jackson, John Hampton, Per Wessman, Jayanthi Swaminathan, Michael Rostas, Travis R. Glare, Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand; AgResearch, Lincoln Research Centre, Lincoln, New Zealand; National Institute for Agricultural Research, Las Brujas, Uruguay.

MC-16 Fat pellet strategy applied to the boll weevil (Anthonomus grandis) under laboratory conditions – Marcos Faria, Lorena K. B. Bravo, Bruna M. Kraus, Rogério B. Lopes, EMBRAPA Genetic Resources and Biotechnology, Brasilia, DF, Brazil.

MC-17 Compatibility of fungicides with Beauveria bassiana – Sumanth S. R. Dara, Suchitra S. Dara, Alap Sahoo, Haripriya Bellam, Surendra K. Dar, Stockdale High School, Bakersfield, CA, USA; Warren Junior High School, Bakersfield, CA, USA; University of California Cooperative Extension, San Luis Obispo, CA, USA.


MC-19 Stress-induced changes in the dopamine levels of haemolymph of cabbage armyworm Mamestra brassicae and Colorado potato beetle Leptinotarsa decemlineata – Cherckova E. A., Yurolievseva O. N., Dubovsky I. M., Glavov V. V., Institute of Systematics and Ecology of Animals, Russian Academy of Sciences, Siberian Branch, Frunze str. 11, Novosibirsk 630091 Russia.

MC-20 Biosynthesis of silver nanoparticles using the fungus Trichoderma viride for the toxicity on Aedes aegypti mosquito and their antibacterial activity – Siva Komalakannee, Chandrakasan Gobinath, Kaidarkarai Murugan, Unit of Medical Entomology, Department of Zoology, Bharathiar University, Coimbatore-641046, India.
**Microsporidia**

**MI-1** Effects of the microsporidian pathogen, *Nosema adaliae* on the seven-spotted lady beetle, *Coccinella septempunctata* L. (Coleoptera: Coccinellidae) – *Entisar Elkahir, Susan Bjarnason*, Department of Biology, Saint Mary’s University, 923 Robie Street, Halifax, NS, B3H 3C3, Canada.

**NE-5** Roots exudates favor friends and hinder foes in the rhizospheric nematode community – *I. Hiltpold*, G. Jaffeur, T.C.J Turlings, *Hawkesbury Institute for the Environment, University of Western Sydney, Penrith, NSW, Australia; FARCE lab, University of Neuchâtel, Neuchâtel, Switzerland.

**MI-2** Online weather-based pest forecast model for *Nosema* spp. infections in Georgia honey bee apiaries and projected risk under climate change – *Arto Roja Dominic*, Sebastian Gisder, Elke Genersch, Andreas Linde, 1 Hochschule für nachhaltige Entwicklung Eberswalde, Dept. of Forest and Environment, Alfred-Möller-Str. 1, 16225, Eberswalde, Germany; 2 Länderinstitut für Bienenkunde Hohen Neuendorf e.V., Friedrich-Engels-Str. 32, 16540, Hohen Neuendorf, Germany.

**NE-6-STU** Host searching behavior of entomopathogenic nematode from the subarctic zone in Japan under low temperature – *Yohsuke Moguchi*, Toyoi Yoshiga, Daigo Auchi, Masanori Koike, 1 Department of Agro-environmental Science, Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Japan; 2 Laboratory of Nematology, Department of Applied Biological Sciences, Faculty of Agriculture, Saga University; 3 Research Center for Global Agro-medicine, Obihiro University of Agriculture and Veterinary Medicine, Japan.


**NE-7** Genomic determinants of the entomopathogenic lifestyle from independently arising nematodes – *Hillel Schwartz*, Adler Dillman, Paul Sternberg, 1 HHMI and Division of Biological Engineering, California Institute of Technology, Pasadena CA 91125, USA; 2 Department of Nematology, University of California Riverside, CA 92521, USA.

**Nematodes**

**NE-1** Improved survival time of infective juveniles of *Steinernema glaseri* collected on Paris plaster – *C. I. Cortés-Martínez*, J. Ruiz-Vega, E. E. Lewis, 1 Instituto Politécnico Nacional, CIIDIR-Oaxaca, Oaxaca, 71230. México; 2 Department of Nematology, University of California, Davis, CA 95616, USA.

**NE-2** Ecological characterization of *Steinernema siamkayai* (Rhabditida: Steinernematidae), a warm-adapted entomopathogenic nematode isolate from India – *Ramalingam Karthik Roja*, Aishwarya Dilipkumar, Sivaperumal Sivarmanrakrishnan, Seluck Hari, Pachiappan Perumal, 1 Department of Biotechnology, Periyar University, Salem, Tamil Nadu, India; 2 Faculty of Arts and Science, Department of Biology, Adnan Menderes University, 09010 Aydin, Turkey; 3 Department of Biotechnology and Genetic Engineering, Bharathidasan University, Tiruchirappalli, Tamil Nadu, India.

**NE-3** Evaluation of entomopathogenic nematodes *Steinernema feltiae* and *Heterorhabditis bacteriophora* against melon aphid (*Aphis gossypii* Glor, *Hemiptera, Aphididae*) – *Nona Mikaila*, Department of Natural Sciences and Health Care. Sokhumi State University. 9, Anna Politkovskaya Str. Tbilisi 0186, Georgia.

**NE-4-STU** A new way for number regulation of South American tomato moth, *Tuta absoluta* in Georgia – *Mariam Chubinishvili, Tsitsa Chkhubianishvili, Manana Kakhadze, Jataneze Malania, Rusudan Skhirtladze, Irine Rishadzade, Biological Control Laboratory, Kanchaveli Institute of Plant Protection, Agricultural University of Georgia.

**NE-5** Kluge viruses: A new mosaic virus in common house mosquitoes – *Diane Biot*. **VI-1-STU** Hunt for viral diversity on the evolution of pest resistance – *Leon Yu Zheng Li*, Jenny S. Cory, 1 Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada.

**VI-2** Constitutive and herbivore-induced defenses of soybean inhibits baculoviral disease in the fall armyworm, *Spodoptera frugiperda* – *Ikki Shikano, Kelli Hoover*, Department of Entomology, Pennsylvania State University, University Park, PA, USA.

**VI-3** Three baculoviruses infecting white satin moth (Lasenpy) drosif–tussucc moth (OpMNVP) and pale tussock moth (Dapunpy) cluster together on the phylogenetic tree – *Martyna Kremer*, Lukasz Rabalski, Iwona Skrzecz, Jadwiga Ziemnička, Boguslaw Szewczyk, 1 Intercollegiate Faculty of Biotechnology University of Gdansk and Medical University of Gdansk, Department of Recombinant Vaccines, Gdansk, Poland; 2 Forest Research Institute, Department of Forest Protection, Sekocin Stary, Poland; 3 Institute of Plant Protection, Department of Biological Control and Quarantine, Poznan, Poland.

**VI-4** Three baculoviruses infecting white satin moth (Lasenpy) drosif–tussucc moth (OpMNVP) and pale tussock moth (Dapunpy) cluster together on the phylogenetic tree – *Martyna Kremer*, Lukasz Rabalski, Iwona Skrzecz, Jadwiga Ziemnička, Boguslaw Szewczyk, 1 Intercollegiate Faculty of Biotechnology University of Gdansk and Medical University of Gdansk, Department of Recombinant Vaccines, Gdansk, Poland; 2 Forest Research Institute, Department of Forest Protection, Sekocin Stary, Poland; 3 Institute of Plant Protection, Department of Biological Control and Quarantine, Poznan, Poland.

**VI-5** Screening field collected Lepidoptera larvae for new virus isolates – *Michelle T. Franklin*, Amy Huang, Yan Han, Matilda Taber, Martin Erlandson, Stefan Richard, Deborah Henderson, 1 Institute for Sustainable Horticulture, Kwantlen Polytechnic University, Langley, BC, Canada; 2 Saskatoon Research Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, Canada; 3 Sylvan Technologies Inc., Fredericton, New Brunswick, Canada.
VI-6 Newly sequenced full genome of Nun moth (Lymatrina moancho) baculovirus shows its high similarity to gypsy moth (Lymatrina dispar) baculovirus – Lukasz Rabinski, Martyna Krejmer, Iwona Skrzeczy, Bartosz Wasag, Boguslaw Szweczyk.

VI-7 Comparison among betabaculoviruses isolated from Gelechiidae insect family – Gloria P. Barrera, Juliana A. Gómez, Mariano N. Belaich, Pablo D. Ghiringhelli, Laura Villamizar.

VI-8 Genome sequence analysis of a two alphabaculoviruses and a betabaculovirus from armyworms of genus Mythimna – Robert L. Harris, David A. Theilmann, Martin A. Erlandson, USDA Agricultural Research Service, Beltsville, MD, USA; Agriculture and Agri-Food Canada, Summerland, BC, Canada; Agriculture and Agri-Food Canada, Saskatoon, SK, Canada.

VI-9 Genome sequence of Trichoplusia ni granulovirus (TnGV), a novel sequenced betabaculovirus infecting the cabbage looper – Ma. de los Angeles Bivián, Jorge E. Olaya 464, Universidad de Guanajuato, Irapuato, GTO, México; Department of Biotechnology, University of Guanajuato, Irapuato, GTO, México.

VI-10-STU The gene p32 of Cydia pomonella granulovirus is essential for the production of budded viruses and the establishment of a systemic infection in codling moth – Jacqueline A. Frank, Manuela Gebhardt, Diana Schneider, Jörg T. Wernmann, Johannes A. Jehle.

VI-11-STU Membrane binding and fusion play no role in cross-resistance against a granulovirus in a strain of Adoxophyes honmai selected for resistance to a baculovirus – Kento Iwato, Maki N. Inoue, Yasuhisa Kunimi, Madoka Nakai, Tokyo University of Agriculture and Technology, Saiwai, Fuchu, Tokyo 183-8509, Japan.

VI-12 Enhancins and chitinases: Analysis of a granulovirus of Spodoptera frugiperda – Paola E. Cuartas, Emiliano Barreto, Gloria P. Barrera, Laura F. Villamizar.

VI-13 Heterologous recombination between Baculoviruses: Horizontal transfer genes analysis – Gloria P. Barrera, Mariano N. Belaich, Paola Cuartas, Laura Villamizar, Pablo D. Ghiringhelli, Corporación Colombiana de Investigación Agropecuaria, Corpoica, Bogotá, Colombia; Centro de Bioinformática, Instituto de Biotecnología IBUN, Universidad Nacional de Colombia, Bogotá, Colombia.

VI-14 Establishment of a winter moth, Operophthera brumata, cell line permissive for ObprNPV replication – John P. Burand, Robert L. Harrison, Matthew Boucher, Department of Microbiology, University of Massachusetts Amherst, MA, USA; USDA Agricultural Research Service, Beltsville, MD, USA.

VI-15 AcMNPV infection process in Trichoplusia ni midgut – Muhammad Afzal Javed, Stephanie Harris, David A. Theilmann, Martin A. Erlandson, Dwayne D. Hagedus, Saskatoon Research Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, S7N 0X2 Canada; Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, BC, V0H 1Z0 Canada.

VI-16-STU The effects of heterologous p10 expression in Autographa californica multipapisid nucleopolyhedrovirus replication in insect cells – Leo Graves, Sarah L. Irons, Robert D. Possee.

VI-17-STU Multiple amino acid residues of Autographa californica MNPV P143 are responsible for ribosomal RNA degradation in Bombyx mori cells – Rino Hamaichi, Michihiro Kobayashi, Motoko Ikeda, Graduate School of Biotechnology, Nagoya University, Chikusa, Nagoya 464-8603, Japan.

VI-18 Autographa californica multiple nucleopolyhedrovirus ORF11 and ORF78 are essential for budded virus production, occlusion-derived virus envelopment, and occlusion body formation – Yue Ying Tao, Woon Jin Kim, Joe Young Cho, Seok Ho Kim, Jong Hoon Kim, Panyi Ying, Ha Kyu Bok, Yeon Ho Je, State Key Laboratory of Food Science and Technology, Nanchang University, Nanchang, China; Jiangxi-OAI Joint Research Institute, Nanchang University, Nanchang, China; College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea; Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.

VI-19-STU Effects of lacking non-essential genes of BmNPV – Hitomi Takag, Chikako Ono, Masanao Sato, Shin-Ichiro Asano, Hisanori Bando, Graduate School of Agriculture, Hokkaido University, Sapporo, Japan; Institute for Advanced Biosciences, Keio University, Tsuruoka, Japan.
VI-20-STU  Relevance of BmSyndecan-1 for BmNPV proliferation  - Momoko Usui, Masanori Sato, Shinnichiro Asano, Hisanori Bandini, 1 Graduate School of Agriculture, Hokkaido University, Sapporo, Japan; 2 Institute for Advanced Biosciences Keio University, Yamagata, Japan.

VI-21-STU  Applications of DnaB mini-intein to baculovirus expression system – Won Seok Gwok, Sung Min Bae, Tae Young Shin, Seung Hee Lee, Yong Oh Ahn, Soo Dong Woo, Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea.

VI-22-STU  Production of porcine parvovirus virus-like particles using baculovirus in the silkworm larvae – Seung Hee Lee, Sung Min Bae, Tae Young Shin, Won Seok Gwok, Yong Oh Ahn, Soo Dong Woo, Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea.

VI-23  Transcriptional analysis of the putative glycansyl transferase gene (arnv248) of Amsacta moorei entomopoxivirus – Chan Inan, Hacer Muratoglu, Basli Ari, Zihni Demirkol, 1 Department of Biology, Karadeniz Technical University, Trabzon, Turkey; 2 Department of Molecular Biology and Genetics, Faculty of Sciences, Karadeniz Technical University, Trabzon, Turkey; 3 Laboratory for Molecular Virology, Great Lakes Forestry Centre, Sault Ste. Marie, Ontario, Canada.

VI-24-STU  GCV1 mimics host α-tubulin to sequester GAPDH, which plays a crucial role in cytoskeleton rearrangement – Sunil Kumar, Yonggyun Kim, Department of Bioresource Sciences, Andong National University, Andong 760-749, Republic of Korea.

VI-25  The use of zinc-based fixatives for high-fidelity histomorphology and molecular histochemical techniques on arthropod tissue – Damien M. Laudier, Laudier Histology, New York City, NY, USA.

SIP Division Business Meetings  Wednesday 20:00 – 22:00

Fungi  2311
Microsporidia (+Workshop)  2314
Viruses (+Workshop)  2301
Bacteria  2306
Nematode  2309

Workshop  Wednesday 20:00 – 22:00
Microsporidia  2314

War and Peace: The Comparative Impact of Morphology- and Sequence-based Phylogenies on Practical Taxonomy and Evolutionary History of Microsporidia  Organizer: Yuliya Sokolova

Workshop  Wednesday 20:00 – 22:00
Viruses  2301

Definition of Virus Species Concept  Organizers: Holly Popham and Robert Harrison

THURSDAY – August 13

7:30 – 12:00 Information & Registration  Outside Great Hall

Symposium  Thursday 8:00 – 10:00  2301

Recent Advances in Entomopathogenic Nematode Infection Behaviour: Inside and Outside

Moderators: David Shapiro-Ilan and Ed Lewis

8:00  125 Advances in entomopathogenic nematode dispersal and host-finding behavior – David Shapiro-Ilan, Edwin E. Lewis, USDA-ARS, SEFTNRL, Byron, GA, USA; 2 Department of Entomology and Nematology, University of California, Davis, USA.

8:30  126 Sex, age and following the leader drive infection dynamics of entomopathogenic nematodes – Ed Lewis, David Shapiro-Ilan, Yohandra Gonzales, Danica Maxwell, 1 Department of Entomology and Nematology, University of California – Davis, Davis, CA, USA; 2 USDA-ARS, SEFTNRL, Byron, GA, USA.

9:00  127 Impact of infection behaviour on lethal male fighting in Steinernema – Apostolos Kapranos, Abigail M. D. Maher, Annemie Zener, Kate O’Callaghan, Christine T. Griffin, Biology Department, Maynooth University, Maynooth, County Kildare, Ireland.

9:30  128 The stability of virulence in insect parasitic nematodes is determined by social interactions – Ben Raymond, David Shapiro-Ilan, Imperial College London, Silwood Park campus, Ascot, Berks, SLS 7PY, UK; 1 USDA-ARS, South Eastern Fruit and Nut Research, Byron, USA.

Contributed Papers  Thursday 8:00 – 10:00  2306/9

Fungi 2

Moderators: Stefan Jaronksi and Ann Hajek

8:00  129-STU Transcriptomic and physiological responses of Arabidopsis thaliana to endophytic Beauveria bassiana – Maya Rodd, Travis Glare, Michael Rostás, Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand.

8:15  130 Non-entomopathogenic role of entomopathogenic fungi in strawberry production – Surendra K. Dara, University of California Cooperative Extension, San Luis Obispo, CA, USA.

8:30  131-STU Phenotypic diversity among isolates of the entomopathogenic endophyte Beauveria bassiana affects plant-host interactions – Aimee McKinnon, Travis R. Glare, Hayley Ridgway, Andrew Holyoke, Artemio Mendoza Mendoza, 1 Bio-Protection Research Centre, Lincoln University, Christchurch, New Zealand; 2 Faculty of Agriculture and Life Sciences, Lincoln University, Christchurch, New Zealand.

8:45  132 Light affect sporulation patterns of the mite pathogenic fungus Nezygites floridana – Ingerborg Klingsi, Maren Pindse Holthe, Aruppillai Suthaparan, Karin Westrum, Torfinn Torp, Norwegian Institute for
Agricultural and Environmental Research (Bioforsk), Norway; 2Norwegian University of Life Sciences, Department of Plant Sciences, Norway.

9:00 **133** Environmental safety of Canadian *M. gemmatalis* SS4 for the northern crayfish, *Orconectes virilis*, and phantommid larva, *Chaoborus americanus* – Don Johnson1, Larry Kawchuk2, Stefan Jaronski2, Craig Wiebe1, Zhe Zhang1, 1Water and Environmental Science Building, University of Lethbridge, Lethbridge, Alberta, Canada T1K 3M4; 2Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada T1J 4B1; 3Pest Management Research Unit, Northern Plains Agricultural Research Laboratory, USDA Agricultural Research Service, Sidney, Montana, USA.

9:15 **134** Temporal density dependence of *Entomophaga maimaiga* – Ann E. Hajek, Department of Entomology, Cornell University, Ithaca, New York, USA.

9:30 **135** Importance of mecha-nocular for fungus removal in *Drosophila* grooming – Ayo Yanagawa1, Toshimitsu Hata2, Tsuyoshi Yoshimura2, Frederic Marion-Poll2, 1Kyoto University, Uji, Japan; 2CNRS, Laboratoire Evolution, GénoMS, Comportement et Ecologie, Gif-sur-Yvette, France; 3AgroParisTech, Département Sciences de la Vie et Santé, Paris, France.

9:45 **136-STU** Older beetles are stronger than young: Influence of mating and age on susceptibility to a fungal Pathogen – Joanna J. Fisher, Ann E. Hajek, Department of Entomology, Cornell University, Ithaca NY, USA.

---

**Contributed Papers**

Thursday 8:00 – 10:00

2311

**Microbial Control 3**

Moderator: Dietrich Stephan

8:00 **137-STU** Toxicity of *Bacillus thuringiensis* culture filtrate to *Meliodogyne incognita* – Jiehling QI1, Daigo Auchi2, Shin-Ichiro Asano1, Masanori Koke2, 1The United Graduate School of Agricultural Sciences, Iwate University, Iwate Japan; 2Department of Agriculture, Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Japan; 3Department of Applied Bioscience, Graduate School of Agriculture, Hokkaido University, Sapporo, Japan.

8:15 **138** Versoria entomophaga: A biopesticidal bacterium active against a wide range of insect pests – Mark Hurst1, Colin Ferguson1, Sarah Mansfield1, Richard Townsend1, Sean Marshall2, Sandra Jones3, Jayanthi Swaminathan4, David Wright1, Michael Wilson1, Derick Wilson1, Maureen O’Callaghan1, 1Innovative Farm systems, AgResearch, Lincoln Research Centre, New Zealand; 2Innovative Farm systems, AgResearch Invermay Agricultural Centre, New Zealand; 3Innovative Farm systems, AgResearch, Ruakura New Zealand.

8:30 **139** Toxicological and protein characterization of *Bacillus sphaericus* C3-41 strain from Karnataka – Basavraj S. Kalmath1, S. K. Kalurath2, A. Prabhuraj2, Katkar Gajanan3, R. S. Giradig4, B. V. Patil2, 1College of Agriculture Bhemarayanagu; 2College of Agriculture Raichur; 3Department of Biochemistry, Mysore University.

8:45 **140** A new invasive biotype of the coconut rhinoceros beetle (*Oryctes rhinoceros*) has escaped from biological control by *Oryctes rhinoceros* nivivorus – Sean D. G. Marshall1, Maclean Vaqalo1, Aubrey Moore1, Roland J. Quitugua2, Trevor A. Jackson3, 1Innovative Farming Systems, AgResearch, Lincoln Research Centre, Christchurch, New Zealand; 2Land Resources Division, Secretariat of the Pacific Community, Suva, Fiji Islands; 3College of Natural and Applied Sciences, University of Guam, GU, USA.

9:00 **141** Production of *Oryctes nudivorus* in DSIR-HA-1179 insect cell cultures in roller bottle systems – Gabriel Visnovsky1, Charlotte Pushparajan1, Juan D. Cibus1, 1Department of Chemical and Process Engineering, University of Canterbury, New Zealand; 2Lab. Virologia, Facultad de Bioquimica y Ciencias Biologicas, Universidad Nacional del Litoral, Santa Fe, Argentina.

9:15 **142** Control of *Chrysodeixis includens* (Walker) and *Anticarsia gemmatalis* Höhner with *Bacillus thuringiensis*, chlorantraniliprole, and a mixture of PaSNPV and AgMNPV – Daniel R. Sosa-Gómez1, Embrapa Soybean, Londrina, PR, Brazil.

9:30 **143** Fungal endophytes as first line of defense against the bean stem maggot *Ophiomyia phaseoli* (Tyron) on *Phaseolus vulgaris* (L.) – Beritha Mutowe2,3, Sunday Ekesi1, Salou Niassey1, Vivienne Matari1, Christine Bili1, 1University of AgroParisTech, Département Sciences de l’Environnement, Orléans, France; 2University of AgroParisTech, Département Sciences de l’Environnement, Orléans, France; 3University of AgroParisTech, Département Sciences de l’Environnement, Orléans, France.

9:45 **144** Performance of three Indian isolates of *Beauveria bassiana* (Balsamo) Vuillemin and three commercial mycoinsecticides against three developmental stages of *Bactrocer a dorsalis* (Hendel) (Diptera: Tephritidae) – Mohammed I. Elbashir1, P. Bishwajeet1, K. Shankarganesh1, P. Sharma1, 1Department of Biopesticides and Biofertilizers- Environment and Natural Resources and Desertification Research Institute, P.O. Box 6096, Khartoum, Sudan; 2Biological Control Laboratory Division of Entomology, Indian Agricultural Research Institute, New Delhi-110012; 3Division of Plant Pathology, Indian Agricultural Research Institute, New Delhi-110012.

10:00 – 10:30

**BREAK**

---

**Society for Invertebrate Pathology**

**Annual Business Meeting**

Presiding: Peter Kreil

12:30 – 14:00

**LUNCH** (on your own)

---

**Symposium**

Thursday 14:00 – 16:00

**Microbial Control 2301**

Moderator: Tobias Laengle

14:00 **145** Facilitating the registration and adoption of biological pest controls in Canada – Tobias Laengle, Pesticide Risk Reduction Program, AAFC, St. John’s, Newfoundland & Labrador, Canada.
14:45 146 The IR-4 biopesticide and organic support program – Michael Braverman, William Barney, Interregional Research Project Number 4 (IR-4), Rutgers University, Princeton, NJ, USA.

14:50 147 How does academia contribute to registration and adoption of biological control agents, a European perspective – Jørgen Ellenberg, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark.


15:40 Discussion

Contributed Papers Thursday 14:00 – 15:30

Viruses 5

Moderators: Adly Abd-Alla and Umut Toprak

14:00 149 Peritrophic matrix proteomics of the cotton leaf worm, Spodoptera littoralis (Lepidoptera: Noctuidae): Targets for pathogens infecting per or – Umut Toprak1, Dwayne Hegedus2, Esengül Ozdemir3, Doug Baldwin, Cathy Coutu4, Diney Bekkaoui1, Serife Bayram5, M. Oktas Gürkan6, Ankara University, Faculty of Agriculture, Dept. of Plant Protection, Ankara, Turkey; 2Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.

14:15 150 Analysis of occlusion derived virus infection in tissue culture using gene knock out viruses of the per os infectivity factors and GP64 – David A. Thelmann1, Leslie G. Willis2, Michael Weiss2, Com Danië1, Dwayne D. Hegedus2, Martin A. Erlandson3, Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, British Columbia, Canada; 4Southern Crop Protection and Food Research Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK, Canada.

14:30 151 Inhibition of Cotesia vanessae development in Trichoplusia ni larvae infected with alphabaculoviruses from Mamestra configurata – Martin A. Erlandson1,2, Stephanie Harris3, Edyta Sieminska4, Doug Baldwin2, Dwayne D. Hegedus2, David A. Thelmann1,5 Agriculture and Agri-Food Canada, Saskatoon Research Center, Saskatoon, SK, Canada; 2Department of Biology, University of Saskatchewan, Saskatoon, SK, Canada; 3Agriculture and Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, BC, Canada.

14:45 152 First successful elimination of an insect virus, Glossina pallidipes salivary gland hypertrophy virus, from insect factory: A model for managing insect viruses in insect factories for food and feed – Adly M. M. Abd-Allo1, Insect Pest Control Laboratory, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Vienna, Austria.

15:00 153 Impact of valacyclovir on the pathology of Hytrosavirus in Musca domestica – D. G. Boucias1, C. Geden2, A. M. M. Abd-Allo1, Entomology and Nematology Department, University of Florida, Gainesville, FL USA; 2Center for Medical, Agricultural and Veterinary USDA, ARS, Gainesville, FL 32608, USA; 3Insect Pest Control Laboratory, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Austria.

15:15 154 Pathogen-host interaction of deformed wing virus (DWV) and the honey bee (Apis mellifera) – Sebastian Guder, Elke Genersch, Institute for Bee Research, Molecular Microbiology and Bee Pathology, Hohen Neuendorf, Germany.

14:00 156 Cry1Aa-BiNA chimeric highly toxic to anopheine, aeidine, and culicine larvae including those tolerant or resistant to Lysinibacillus sphaericus – Dennis K. Bideshi3, Hyun-Woo Park4, Robert H. Hice1, Margaret C. Wirth1, Brian A. Federici1, 5 Department of Entomology, University of California, Riverside, California, USA; 6Department of Natural and Mathematical Sciences, California Baptist University, Riverside, California, USA; 7Institute for Integrative Genome Biology, University of California, Riverside, California, USA.

14:15 157 Effect of single versus multiple promoters and a high plasmid copy number on the synthesis and assembly of Cry1Aa crystals in Bacillus thuringiensis – Hyun-Woo Park4, Robert H. Hice1, Brian A. Federici5, Department of Entomology, University of California, Riverside, and Department of Natural and Mathematical Sciences, California Baptist University, Riverside, California, USA; 7Interdepartmental Graduate Programs in Microbiology and Cell, Molecular, and Developmental Biology, University of California, Riverside, Riverside, California, USA.

14:30 158 The island of mosquitocidal toxins in Bt strain 2160-1 identified by whole genome sequencing and proteogenomic analysis – Jim X. J. Fang1,2, Y. Zhou1, P. T. Gong1, Y. J. Wei1, Y. Zhang1, The HITAR Institute Canada Inc., Richmond, British Columbia, Canada; 2Hainan Institute of Tropical Agricultural Resources, Sanya, Hainan, China; 3Institute of Life Sciences, Jiaoyang College of Zhejiang A&F University, Zhuj, Zhejiang, China.

14:45 159 Engineering of Bacillus thuringiensis Cry proteins to improve the activity against western corn rootworm – Ruth Cong, Hana Ali, Michi Izumi Wilcoxen, Yi Zheng, Jingtong Hou, Mark Nelson1, Erica Bermudez, Mark McDonald, Takashi Yamamoto, Plant Protection, Ag Biotechnology, DuPont Pioneer, Hayward, CA and 4Wilmington, DE, USA.

15:00 160 Laboratory-selected western corn rootworm colony resistant to mCry3A – Jian-Zhou Zhao, Megan Ocone, Nina Richtman, Anaiza Alves, Stephen Thompson, DuPont Pioneer, Johnston, IA, U.S.A.

15:15 161 A new Cry1Ac toxin of Bacillus thuringiensis highly toxic to Manduca sexta and Trichoplusia ni – Yaritza Renosa-Pozo1, Cristina Del Rincon-Castro1, Jorge E. Ibarra2, Departament of Biotechnology and Biochemistry, CINVESTAV-Irapuato, Gto. Mexico; 2Life Sciences Division, University of Guanajuato, Irapuato, Gto. Mexico.

15:30 162 Rapid evolution and genetic basis of resistance to Cry1F in a lab-selected Asian corn borer and its cross-resistance to other Cry toxins – Yueqin Wang, Yidong Wang, Zhenying Wang, Janglai He, State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protect, Chinese Academy of Agricultural Sciences, Beijing 100193, China.
15:45 Evaluation of Bt corn with stacked genes for resistance to the Asian corn borer — Tiantao Zhang, Fan Jiang, Zhengying Wang, Kanglai He, State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China.
The abstracts included in this book should not be cited in print without the author’s permission

STU Indicates STUDENT presentation

000 Indicates number of ORAL presentation

BA - 00 Indicates abstract number for POSTER presentation
A large-scale mortality event affecting 20 species of sea star (Asteroidae) on the Pacific Coast of North America began in June of 2013. First detected in Ochre sea stars (Pisaster ochraceus) along the outer coast of Washington State, the event has been observed in at least 250 subtidal and intertidal locations extending from Southeastern Alaska to San Diego, California. Citizen science has been a key approach to monitoring the spread of the event affecting 20 species of sea star (Pycnopodia helianthoides) and a densovirus (Parvoviridae) community fingerprinting, and transcriptomics), culture, and genomic (metagenomics, epidemiology, technology, University of Maryland Baltimore County, Baltimore, MD, USA) approaches, including microscopic (histology and electron microscopy), culture, and experimental infection trials led to a diagnosis of a viral etiology and host response to sea star wasting disease. Pycnopodia helianthoides and Eusenastria are the most affected genera and mortality approaches 100% in select species at some locations. Both Pisaster and Pycnopodia are considered keystone species, and changes to community composition within ecosystems are possible. The progression of clinical signs includes: 1) loss of body turgor (deflation) and weakness; 2) curling of rays; 3) foci of epidermal pallor and tissue loss; 4) sloughing of multiple rays and/or rupture of the body wall with evisceration; 5) death. Evidence from multiple approaches, including microscopic (histology and electron microscopy), genomic (metagenomics, community finger-printing, and transcriptomics), culture, and experimental infection trials led to a diagnosis of a viral etiology and a densivirus (Parvoviridae) as a candidate causative agent. Pycnopodia helianthoides coelomocyte response measured by a transcriptomic analysis indicates both an immune and nervous system response to exposure.

Symbiont-mediated defense against parasitic nematodes in Drosophila

Steve J. Perlman
Department of Biology, University of Victoria, Victoria, BC, Canada
Correspondence: stevep@uvic.ca

Terrestrial arthropods commonly harbour bacterial endosymbionts that are transmitted primarily from mothers to their offspring, often in the egg cytoplasm. These inherited symbionts, of which Wolbachia is the best known and most widespread, are major players in the ecology and evolution of their hosts. One recent exciting development in the study of inherited symbionts is the discovery that many protect their hosts against diverse natural enemies, including pathogenic fungi, parasitoid wasps, and RNA viruses. In this talk, I will discuss one of the best examples of defensive symbiosis operating in the wild, whereby a Spiroplasma bacterial symbiont protects its host, the woodlouse fly Drosophila neodatoca, against a virulent generalist parasitic nematode, Howardula aoronymphium. The prevalence of infection is very high in the wild, ranging from ~25-40%, and in symbiont-free flies, nematode infection results in sterility. However, in flies that harbour Spiroplasma, fertility is fully restored. As a result, Spiroplasma-infected flies are at a selective advantage over their uninfected counterparts, and the infection is currently spreading across N. America. I will discuss the dynamics of Spiroplasma infection and spread, as well as its ecological and evolutionary consequences. I will also discuss our recent work attempting to understand how Spiroplasma provides protection, focusing on the characterization of a recently discovered Spiroplasma-encoded toxin.

The ecology of virulence in insect associated bacteria: Field experiments and experimental evolution

Ben Raymond
Imperial College London, Silwood Park campus, Ascot, Berks, SL5 7PY, UK
Correspondence: b.raymond@imperial.ac.uk

Bacillus thuringiensis invests a great deal of resources in producing diverse virulence factors during vegetative growth and at sporulation. However, for many decades B. thuringiensis had an uncertain reputation as a pathogen: the adaptive basis of investing in Cry toxins was questioned and it was suggested that B. thuringiensis might be a soil bacterium or a plant symbiont. Recent experiments have shown that reproduction of Bt is dependent on the death of its host. Moreover, presence of larval
Our view of the position of hosts can increase the population size of Bt in its soil reservoir in the field, from where Bt is able to colonize plant tissues. In general, evolution of virulence theory can explain the link between investment in virulence and pathogen fitness. For Bt, and other insect parasites, theories that include kin selection and cooperation have proved particularly powerful in explaining investment in Cry toxins, vegetative virulence factors and in symbiont growth rate. Kin selection theory shows that the conflict between investing in traits that are individually costly but beneficial to groups, can be resolved if individuals tend to cooperate with bacteria that share their genes (high relatedness), a pattern shown by these entomopathogens in natural contexts. Indirect transmission via a soil reservoir, and cooperative conflicts can explain some of the ecological mysteries of Bt, such as the rarity of cadavers and epizootics in the field. Moreover, interrogating the relationship between pathogen fitness and virulence with evolutionary theory can have relevance for understanding how to maintain or improve the virulence of biocontrol agents.

Microsporidia as Emerging Pathogens

**SYMPOSIUM CROSS-DIVISION Monday 14:00**

The complex relationship between microsporidia and fungi

**Patrick J. Keeling**
Department of Botany, University of British Columbia, Vancouver BC Canada V6T 1Z4
Correspondence: pkeeling@mail.ubc.ca

Our view of the position of microsporidia in the tree of eukaryotes has been substantially revised a number of times since they were first described many years ago. Identifying this position is not a trial task, because they lack many typically 'eukaryotic' characteristics often used to compare one cell to another, and they are equally problematic at the molecular level due to the accelerated rate of sequence change in their genomes. Together, these features make it hard to compare microsporidia to other eukaryotes, and accordingly hard to understand how they relate to other lineages. Because biologist often, even subconsciously, rely on a phylogenetic framework to make functional predictions and reconstruct the evolutionary history of organisms, reconciling microsporidia with eukaryotic diversity is an important challenge and worth the effort. I will review the long and winding road to our current view of where microsporidia fall in the tree of eukaryotes, highlighting new advances that stem from a greater appreciation for the diversity of fungal related lineages. There are good reasons to be optimistic that we are near to understanding exactly how microsporidia fit into the tree of eukaryotes, which affects our understanding of the origin of novel characteristics of the lineage.

**SYMPOSIUM CROSS-DIVISION Monday 14:20**

Fish microsporidians: Emerging pathogens or emerging knowledge?

**Mark A. Freeman**
Institute for Experimental Pathology at Keldur, University of Iceland, Reykjavik, Iceland
Correspondence: mf33bitw@gmail.com

Microsporidia are well-documented parasites of fish from both the marine and freshwater environments, with some genera causing the formation of large xenoparasitic complexes which are characterised by an extensive hypertrophic growth of host cells, referred to as xenomas. Such obvious and intriguing infections have meant that fish-infecting microsporidians have received substantial research attention over the last 100 years. In addition, the relatively recent intensification of fish farming practices have meant that microsporidians as pathogens of farmed fish have become increasingly important and we now consider them as problematic pathogens in the global aquaculture industry. There are also concerns about food safety and the zoonotic potential of these opportunistic obligate parasites.

Here we consider our current understanding of fish microsporidians and further examine important aspects about these organisms, including host specificity, host-parasites interactions, lifecycles and identify particular species of interest; especially those that have recently emerged as potentially problematic pathogens for the aquaculture industry.

**SYMPOSIUM CROSS-DIVISION Monday 14:40**

Understanding phylogenetic relationships among species in the Nosema/Vairimorpha clade: What does genetic similarity say about host switching in the microsporidia?

**Wei-Fone Huang**, **James Becnel**, **Leilien Salter**
1Illinois Natural History Survey, Prairie Research Institute at the University of Illinois at Urbana-Champaign, IL, USA; 2United States Department of Agriculture, Agricultural Research Service, Gainesville, FL, USA
Correspondence: wfhuang@illinois.edu

Microsporidian species with high genetic identity based on rDNA phylogenies have been isolated from different insect species and even higher level host taxa across the globe. Complicating the picture, for genera such as the lepidopteran Nosema and Vairimorpha, isolates from different hosts may be morphologically identical while some species complexes include isolates that differ significantly in morphology, tissue tropism, host range and pathogenicity. Morphological characters such as octospore formation in the Vairimorpha, once thought to be apomorphies, cannot be used to separate these two genera or possibly even species. Difficulties in distinguishing isolates in turn complicates research on microsporidia suspected of host-switching to new and economically or ecologically important hosts. We used a combination of rRNA, HSP70, and RP1B genes to evaluate and clarify the relationships among a large collection of species and isolates in the Nosema/Vairimorpha clade. Our data will be useful for classifying new isolates, describing species and evaluating the potential for microsporidia to invade new hosts.

**SYMPOSIUM CROSS-DIVISION Monday 15:10**

Emergent pathogens of invertebrates: Environmental sampling to identify novel parasite lineages

**Bryony A. P. Williams**, **Kristina Hamilton**, **David Bass**
1Biosciences, College of Life and Environmental Sciences, University of Exeter, Exeter, UK; 2Centre for Environment, Fisheries & Aquaculture Science, Weymouth, Dorset, UK
Correspondence: b.a.p.williams@exeter.ac.uk

Molecular surveys of environmental habitats using small subunit (SSU) ribosomal DNA environmental gene libraries now consistently uncover new microbial diversity and these new branches range in novelty from new subspecies to new branches in the tree of life equivalent to phyla. In some studies, parasitic cells make up a large proportion of this diversity, suggesting that protozoan parasites represent an important component of many ecosystems. However it can be challenging to fully sample
parasite diversity and distribution in the environment due to their changeable geographic and temporal distributions and the fact that they may be surrounded by a host that has to be sampled for the parasite DNA to be retrieved by the survey. In this piece of work, we sample invertebrates across a temporal and geographic gradient in the UK to retrieve DNA from hosts and their associated parasites. We use a broad eukaryotic primer set to amplify the V3 region of the SSU gene from hosts and pathogens. Additionally we used a specific primers set to target the V4 region of SSU in the microsporidia. We analysed sequences retrieved through 454 sequencing, uncover novel potentially parasitic lineages in the microsporidia and in other eukaryotic lineages, and look for association patterns between these and invertebrates that may represent their hosts. This work aims to uncover novel diversity of microsporidia and other important pathogens, with a view to understanding the reservoir within the environment with the potential to cause emergent infection in economically important hosts.

SYMPOSIUM CROSS-DIVISION Monday 15:30 9
Investigations into the composition of the microsporidian polar tube
Louis M. Weiss, Kaya Ghosh, Bing Han
Departments of Medicine and Pathology, Albert Einstein College of Medicine, Bronx, NY, 10461, USA
Correspondence: louis.weiss@einstein.yu.edu

Microsporidia are remarkable parasites that have been studied for more than 150 years. They are remarkable in their exploitation of all animals ranging from cryptic, benign infections to spectacular, massive infections that cause extensive damage and often death of the host. These organisms produce spores with a unique invasion mechanism that are one of the most complex single celled forms known in the biological world. In humans infection, in either immune competent and immune deficient hosts, can result in diarrhea, encephalitis, myositis or conjunctivitis. These enigmatic protists are classified as NIH category B priority pathogens and EPA pathogens of interest as they are transmitted by both food and water sources. Besides human disease burdens, infection with microsporidia has major economic impacts on agriculture (via effects on insects and sericulture), aquaculture and animals (food, domestic and wildlife). The invasion mechanism used by these organisms is unique involving a specialized organelle, the polar tube and its associated structures. Despite the polar tube being recognized for over 100 years, the composition, structural biology and mechanism of interaction of the polar tube with its host cell during invasion are still unknown. A long standing research program in my laboratory group is focused on understanding the mechanism of invasion and the structural biology and composition of the polar tube. We have developed techniques for the purification of this structure, identified polar tube proteins and their post translational modifications and how these proteins interact. Furthermore, our studies have begun to define the functional roles of these proteins in the structural biology of the polar tube and the process of invasion. In other microbes studies on invasion have provided key data for understanding pathogenesis and for new therapeutic approaches to the management of infections. To this end, we have demonstrated that both antibodies to polar tube proteins and glycans related to the o-glycosylation seen on polar tube protein 1 can block invasion. We have recently characterized polar tube protein 4 from *E. hellem* (EhPTP4) using both proteomic and microscopic approaches. Immunofluorescence using antibodies to PTP4 demonstrated that this protein localizes to the end of polar tube suggesting it may be involved in the process of invasion. This protein provides the first marker for the site of invasion of the host cell by the microsporidia. Binding assays confirmed EhPTP4 binding to RK13 and HFF cells. Analysis of the PTP4 demonstrates the presence of chitin binding, ricin and cellulose binding domains, and the presence of these various domains was confirmed by the ability of the rehPTP4 to bind chitin beads and inhibition of binding of rehPTP4 to host cells by various monosaccharides. Co-immunoprecipitation (Co-IP) coupled to proteomic analysis has identified a host cell surface membrane protein as a potential interacting protein for EhPTP4. Information gained by delineating, in detail, the function and components of the invasion organelle should lead to new and novel interventions that could limit or interdict the transmission of these emerging pathogens.

CONTRIBUTED PAPERS Monday 14:00 – 16:00

**Bacteria 1**

**CONTRIBUTED PAPER Monday 14:00 10**

Resistance to *Bacillus thuringiensis* Cry2Ab toxin in *Helicoverpa* spp. is conferred by mutations in a novel ABC transporter
Wee Tek Tay1, Rod J. Mahan1, Thomas K. Walsh2, Sharon Downes3, William J. James1, Siu Fai Lee4, Annette Reinike5, Adam K. Williams5, Karl J. H. Gordon1, David G. Heckel5
1CSIRO, Black Mountain Laboratories, Canberra, ACT, Australia; 2CSIRO, Australian Cotton Research Institute, Narrabri, NSW, Australia; 3Department of Genetics, University of Melbourne, Parkville, VIC, Australia; 4Institute for Phytomedicine, Geisenheim University, Geisenheim, Germany; 5Department of Entomology, Max Planck Institute for Chemical Ecology, Jena, Germany
Address for correspondence: heckel@ice.mpig.de

Transgenic crops expressing the insecticidal protein Cry2Ab from *Bacillus thuringiensis* (Bt) are used worldwide to suppress damage by lepidopteran pests, pyramided with Cry1Ac toxin to delay resistance evolution. Previous studies have shown that Cry2Ab binding-sites in the midgut are different from Cry1Ac-binding sites, but little additional information on Cry2Ab mode of action is available. Resistance to Cry1Ac can be caused by alterations in its binding targets, including a membrane-bound alkaline phosphatase, a 12-cadherin-domain protein, and the ABC transporter ABCC2, but resistance mechanisms to Cry2Ab have not been identified. In Australia, Cry2Ab-resistant strains of *Helicoverpa armigera* and *H. punctigera* have been isolated from the field using *F*1 and *F*2 screens, and these strains show no cross-resistance to Cry1Ac. Using a positional cloning approach, we identified mutations in a novel ABC protein in both species that truncate the protein and confer high levels of resistance to Cry2Ab. This resistance is genetically independent from Cry1Ac resistance caused by mutations or downregulation of a different ABC protein, ABCC2. We discuss the implications of this finding for Bt toxin modes of action and resistance management.

**CONTRIBUTED PAPER Monday 14:15 11-STU**

Functional range of insect ABC transporters as a Cry toxin receptor
Haruka Endo1,2, Shino Tanaka3, Ryoichi Sato1
1Graduate School of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology, Koganei, Tokyo, Japan; 2Research Fellow of Japan Society for the Promotion of Science
Correspondence: ryoichi@cc.tuat.ac.jp

Cry toxins produced by *Bacillus thuringiensis* have specific toxicity for target insects. Although the specificity for target insects seems
to largely depend on receptor interaction, it is still unclear which receptor(s) is/are involved in the specificity of each Cry toxin subfamily. ATP-binding cassette transporter C2 (ABCC2) in lepidopteran insects is a receptor of Cry1A toxins. Recently, ABCC3—a Paralog of lepidopteran ABCC2—was also reported to function as a receptor of Cry1 toxins, indicating the possibility that other ABCC transporters may function as Cry toxin receptors. In the present study, to clarify functional range of ABCC transporter as a receptor of Cry1A toxin, we analyzed cell swelling-inducing activity of insect ABCC transporters, which are close relative of ABCC2. Phylogenetic analysis among arthropods ABCC transporters tentatively showed that ABCC2 and ABCC3 are lepidopteran-specific and that non-target insects of Cry1A toxins such as dipteran and coleopteran insects have no members in these two clades. ABCC2 and ABCC3 in lepidopteran insects including Bombyx mori and Spodoptera exigua conferred Cry1A toxin-susceptibility to cultured cells. However, the most closely related ABCC transporters of ABCC2 in Tribolium castaneum and Aedes albopictus did not function as Cry1A receptors. These results suggested that the target specificity of Cry1A toxins for lepidopteran insects largely depends on the two ABCC transporters uniquely found in lepidopteran insects. We will report results from further analysis on receptor function of ABCC3 and discuss a role of ABCC transporters in determining specificity of Cry toxins.

**CONTRIBUTED PAPER Monday 14:30 12-STU**

**Cry1A toxins cause rapid cell lysis in a clonal stable non-lytic expression system, expressing ABC-C2 and cadherin**

Anne Karpinski, Yannick Pauchet, David Heckel
Department of Entomology, Max Planck Institute for Chemical Ecology, Jena, Germany

Correspondence: akarpinski@ice.mpg.de

Pest insect resistance to insecticidal crystal (Cry) proteins from *Bacillus thuringiensis* (Bt) is evolving due to their increasing usage in agriculture. Two genes (a 12-domain Cadherin protein and an ABC transporter) have been genetically linked to Cry toxin resistance in *Helicoverpa zea* and *H. virescens*. Even though the Cry1A toxin mode of action is quite well understood, the specific role of ABC-C2 and its importance for toxicity still need further investigation. Non-lytic stable sfn9 cell lines were created as follows: one cell line expressing only the Cadherin protein, one expressing only the ABC-C2 transporter, and one expressing both Cadherin and ABC-C2 from *H. virescens*. The absence of endogenous Cadherin, ABC-C2 and aminopeptidase N (APN) from the transcriptome of sfn9 cells was crucial for the success of our experiments. Toxicity of Cry1A proteins (Cry1Aa, Cry1Ab, Cry1Ac) can be observed in doubly transfected cells in which up to 86% of the cells died after 8 h treatment. Although cell swelling was observed in the cell line expressing only ABC-C2 and in the one expressing both Cadherin and ABC-C2, rapid lysis and death within 30 min after Cry1Ac treatment could only be observed for the doubly transfected cells. No such effect could be observed in control sfn9 cells or in cells only expressing the Cadherin. Our findings underline the central role played by ABC-C2 in the Cry1A toxin mode of action and resistance in *H. virescens*, but also emphasize that ABC-C2 and Cadherin interact to increase Cry1A toxicity.

**CONTRIBUTED PAPER Monday 14:45 13**

**Expressing a lepidopteran ABCC2 gene in transgenic *Drosophila* causes Bt Cry1Ac susceptibility without requiring a cadherin-like protein receptor**

Tristan Stevens, Simon W. Baxter
School of Biological Sciences, University of Adelaide, Australia

Correspondence: simon.baxter@adelaide.edu.au

The diamondback moth, *Plutella xylostella*, is a serious agricultural pest of *Brassica* crops worldwide and can be extremely difficult to control. Populations commonly evolve resistance to insecticides used against them, including Bt Crystal (Cry) toxins produced by the bacteria *Bacillus thuringiensis*. Hundreds of different Cry toxins have been described, and many are highly specific to targeted pests yet benign to non-target organisms. For example, Cry1Ac kills most lepidopteran moth pests but not flies, such as *Drosophila*.

The precise mode of action of Bt toxins remains controversial, as many midgut receptors and pathways to insect death have been identified. A lepidopteran cadherin-like protein is central to several models, as either a toxin receptor or protoxin activator. Mutations in the diamondback moth ABCC2 gene, rather than a cadherin-like protein, were previously associated with Cry1Ac resistance. As *Drosophila* is not susceptible to Cry1Ac and lacks a Cadherin-like protein orthologue, we used this insect model to investigate whether the diamondback moth ABC-C2 protein acts as a functional toxin receptor. The moth ABCC2 gene was fused with a GFP reporter gene, cloned into the pUAST vector and transgenic *Drosophila* lines generated. Using the GAL4/UAS system, we observed successful expression of the ABC-C2-GFP construct through GFP localization to cell membranes. When fed with artificial diet containing trypsin activated Cry1Ac toxin, or Cry1Ac protoxin, larvae expressing ABC-C2 in the midgut became highly susceptible. This data shows ABC-C2 acts as a Cry1Ac receptor, and toxin activation and mortality can be achieved without the Cadherin-like protein.

**CONTRIBUTED PAPER Monday 15:00 14**

**Differential toxicity of Cry1Ca and Cry1Ac to *Spodoptera exigua* (Lepidoptera: Noctuidae)**

Youngjin Park1, Salvador Herrero2, Yonggyun Kim2
1Department of Bioresources Science, Andong National University, Andong 760-749, Korea; 2Department of Genetics, Universitat de València, Dr Moliñer 50, 46100 Burjassot, Spain

Correspondence: happy2pyj@gmail.com

Cry toxins produced by an entomopathogenic bacterium, *Bacillus thuringiensis* (Bt), are pathogenic factors specific to insect species. A serious lepidopteran pest, *Spodoptera exigua*, is highly susceptible to Cry1Ca, but much less to Cry1Ac. This study investigated the differential toxicity with respect to their differential affinities to a Bt receptor, cadherin. RNA interference (RNAi) of a cadherin of *S. exigua* midgut significantly suppressed the Cry1Ca to the toxic level of Cry1Ac. Binding affinity of Cry1Ca to brush border membrane vesicle (BBMV) of *S. exigua* midgut was significantly lost after SeCad1 RNAi. Binding affinity of Cry1Ac to BBMV was much lower compared to that of Cry1Ca and less sensitive to SeCad1 RNAi. Direct binding assay of Cry toxins to SeCad1 was assessed using a recombinant cadherin repeat 10-11 (CR10-11) of SeCad1. The addition to CR10-11 to Cry1Ca significantly enhanced the toxicity under SeCad1 RNAI. However, the synergistic effect of CR10-11 on toxicity of Cry1Ac was not much significant. Binding assay of Cry toxins to CR10-11 explained the poor binding affinity of Cry1Ac compared to Cry1Ca. These results indicate that the differential toxicity of Cry toxins against *S.
Cry1Aa, Cry1Ab, and Cry1Ae receptors have been identified as the receptors of Bt Cry toxins. In this study, we aimed to identify the receptors of Bt Cry proteins. After homology modeling and a selective protein docking, two models describing the interactions of Cry1Ab to the M. sexta BT-R receptor were assessed using molecular dynamics simulations. Twelve binding regions were identified for each protein and their biophysical properties were further evaluated. To validate our models, we synthesized peptides corresponding to each region. Preliminary results for one model show that loop 3, notorious for receptor recognition, binds a region previously unidentified in Manduca sexta cadherin-like receptor. This new toxin binding region shows the same hydropathicity profile of an antibody epitope previously described to bind specifically to loop 3. Most interestingly, binding occurs with over 266-fold less peptide concentration in pH 9.0 than in pH 7.4. The physiological pH in the insect midgut is approximately 9.0, which corroborates that at least one of the models reproduces in vivo interaction. Ongoing work will show if both models are plausible to occur, or if one of them is preferable to the other. Overall, these models allowed the observation of the toxin’s behavior when binding to BT-R, and help explain many in vitro experiments concerning Cry1A and cadherin-like receptors.

CONTRIBUTED PAPER Monday 15:30 16
A high-throughput, in vitro assay for Bacillus thuringiensis Cry proteins
Michi Izumi Wilcoxon, Jaclyn Dennis, Sabina Lau, Weiping Xie, You You, Song Leng, Ryan Fong, Takashi Yamamoto
Plant Protection, Ag Biotechnology, DuPont Pioneer, Hayward, CA, USA
Correspondence: michi.izumi@pioneer.com

A high-throughput, in-vitro assay for Bacillus thuringiensis (Bt) Cry proteins was developed and evaluated for screening a large number of Cry protein variants produced by DNA shuffling. This automation-amenable assay exploits an insect cell line expressing a single receptor of Bt Cry proteins. Cell mortality caused by the activated Bt Cry toxin was determined by chemical cell viability assay in 96/384-well microtiter plates utilizing CellTiter 96® obtained from Promega. A widely-accepted mode-of-action theory of certain Bt Cry proteins suggests that the activated toxin binds to one or more receptors and forms a pore through the insect gut epithelial cell apical membrane. A number of insect proteins such as cadherin-like protein (Cad), aminopeptidase-N (APN), alkaline phosphatase (ALP) and ABC transporter (ABCC) have been identified as the receptors of Bt Cry toxins. In this study, Bt Cry toxin receptors, Ostrinia nubilalis (European corn borer) cadherin-like protein (On-Cad) and aminopeptidase-N 1 and 3 (On-APN1, On-APN3) and Spodoptera frugiperda (fall armyworm) cadherin-like protein (SF-Cad), were cloned in an insect cell line, Sf21, and a mammalian cell line, Expi293F. The sensitivity of the recombinant cells to the toxin was tested against a variant of Cry1Ab protein called IP1-88 which was tested previously by DNA shuffling.

CONTRIBUTED PAPER Monday 15:45 17
Transcriptome response of Aedes aegypti against Bacillus thuringiensis and the pathway for enhancing the mosquitocidal activity
Wu Songqing1,2, Liu Zhaoxiao1,2, Wang Yafang1,2, Xiong Yujing2, Mou Yan1,2, Zhu Xiaoli1, Zhang Feijiang2, Zou Shuangquan1, Zhang Lingling1, Guan Xiong2
1Collage of Forestry, Fujian Agriculture and Forestry University, Fuzhou, 350002, People’s Republic of China; 2Key Laboratory of Biopesticide and Chemical Biology, Ministry of Education, Fujian Agriculture and Forestry University, Fuzhou, 350002, People’s Republic of China
Correspondence: guanxfu@126.com, fpzhang1@163.com

It has been estimated that over one million people worldwide die from mosquito transmitted diseases every year. Bti is one of the few Bacillus thuringiensis strains that are highly pathogenic to mosquito larvae. But application of this insecticide is minor, because of the high cost and relative lower mosquitocidal activity, as compare with conventional pesticides. Therefore, how to enhance the mosquitocidal efficacy and reduce the cost of Bti insecticides has been a difficult issue which we are confronted. Understanding of Bti-mosquito interactions will help to develop new Bti toxins for mosquitoes and mosquito-borne disease management. To find some biotechnological applications for enhancing the activity of Bti toxins against mosquitoes, this study investigate mosquito-Bti interactions at both cellular and molecular levels. Ae. aegypti transcript responses to experimental challenge with mosquitocidal strain B. thuringiensis subsp. israelensis LLP29 has been analyzed with next generation sequencing. Three candidate genes, have been selected based on their differential expression as representatives of the different functional categories to perform gene silencing by RNA interference and analyze their functional role. Detoxification enzymes assay revealed that the exposure of Bti significantly affect the activities of amylase, cytochromes P450, Na+/K+-ATPase, acetylcholinesterase and Glutathione S-transferase. Cost-effective methods, by using spent mushroom substrate as raw material for Bti cultivation, have been established for the mass production of Bti toxins. Enhancement of mosquitocidal activity of B. thuringiensis by solid and liquid state fermentation. Results from this study will pave a scientific way for the future development of novel cost-effective anti-mosquito biological agents for mosquito pest management.

CONTRIBUTED PAPERS Monday 14:00 – 16:00
Microbial Control

CONTRIBUTED PAPER Monday 14:00 18
Autodissemination strategy for field suppression of Bactrocera dorsalis (Diptera: Tephritidae) using Metarhizium anisopliae-based biopesticide on mango
Sunday Ekesi, Nguya K. Mania
International Centre of Insect Physiology and Ecology (icipe), Nairobi, Kenya
Correspondence: sekesi@icipe.org
Bactrocera dorsalis is a major quarantine pest of horticulture in Africa and elsewhere attacking over 30 host plant species, although mango is the preferred host. Direct damage on mango has been reported to range from 30-80%. In a field experiment conducted over 2 seasons in Malindi, Kenya, we evaluated the use of autodissemination strategy with the entomopathogenic fungus, Metarhizium anisopliae ICIPE 69, for the suppression of B. dorsalis and the impact on fruit infestation and yield. Velvet-coated Lynfield traps were used as autoinoculators and laced with methyl eugenol on cotton-wick (as attractant) and 0.5 g of conidia of M. anisopliae. The autoinoculators were deployed at the rate of 30 traps ha$^{-1}$ in orchards assigned to biopesticide treatment. Control orchards were left untreated. In 2011, the biopesticide treatment reduced B. dorsalis catches relative to the control by 79.1% within 4 weeks and 94.6% within 8 weeks. Mean mortality of adult fruit flies mycotoxized as a result of M. anisopliae infection ranged from 54.2-76.5% in male flies and 32.2-61.8% in females. The fungus persisted for 3-4 weeks in the a uninoculator and declined significantly thereafter. At harvest, the proportion of fruit infested was significantly lower in treated orchards (6.4%) compared to control orchards (61.7%). Mango yield was significantly higher in orchards assigned to biopesticide (11,802 kg ha$^{-1}$) compared to control orchards (2,911 kg ha$^{-1}$). Similar results were obtained in 2012 season, indicating that autodissemination strategy using M. anisopliae-based biopesticide holds great promise for suppressing fruit flies and increasing yield in mango orchards.

CONTRIBUTED PAPER Monday 14:15 19
Development of granules based on the biomass of liquid fermented Metarhizium anisopliae, Isaria fumosorosea or Beauveria bassiana for control of soil dwelling pests

Dietrich Stephan¹, Medea Bueranazidé², Tanja Bernhardt³, Juliana Pels¹, Johannes Schäfer¹, Christopher Seib²

¹JKI-Institute for Biological Control, Heinrichstrasse 243, 64287 Darmstadt, Germany; ²Agricultural University of Georgia, 240, D.Amishenebelely Alley, Tbilisi 0159, Georgia

Correspondence: dietrich.stephan@jki.bund.de

Although entomopathogenic fungi can be grown on solid media the fermentation time in solid state fermenter is long and labor intensive. Therefore, we investigated the possibility of formulating granules based on liquid fermented biomass of the entomopathogenic fungi Metarhizium brunneum (strain JKI-BI-1339 = Ma43), Beauveria bassiana (strain Bza 007) and Isaria fumosorosea (strain JKI-BI-1496).

After fermentation the biomass was filtered to separate the filtrate, including submerged spores, from the rest of the biomass. After filtration submerged spores can be used for the development of sprayable formulations. The filtercake including mycelium and submerged spores was used for the production of granules using fluid bed drying. To analyze this, experiments on the thermal tolerance at temperatures of 25 °C, 50 °C and 70 °C were conducted firstly in a water bath and a compartment dryer. This was necessary to verify whether the fungi survive at a temperature of 50 °C when using fluid bed drying. Because the tested fungi survived these temperatures, granules were produced by coating millet with a strain specific biomass concentration. The sporulation on the granule was investigated and furthermore the influence of the soil moisture on the fungal growth. E.g. strain JKI-BI-1496 was able to grow out and sporulate at all tested residual moistures of the soil (3, 20, 30, 40 & 45 % rh). The highest sporulation was achieved for a residual moisture of 40 % rh. Further optimization steps and the practicability of biomass based formulations will be discussed.

CONTRIBUTED PAPER Monday 14:45 21
Less effort - more efficient: An attract and kill strategy for wireworm control in potato

Mario Schumann¹, Anant Patel², Stefan Vidal³

¹Georg-August-University Goettingen, Department of Crop Sciences, Goettingen, Germany; ²University of Applied Sciences, Department of Engineering and Mathematics, Bielefeld, Germany

Correspondence: vidual@gwdg.de

In recent years wireworms became the most important herbivorous pest species in potato production systems in many parts of Europe. The larvae feed on the roots of many root crops in North American and Europe. Using video tracking, we investigated how click beetle behaviour changed in the presence of pheromone. We then began to link how these behavioural changes can impact M. brunneum transmission through horizontal transmission and conidia pickup from the environment. Enhancement of pathogen epizootic potential could be a step in shifting microbial control practices from an inundative approach to one that is inoculative, where management of a pest is beyond the short term.
gradients significantly higher than the background CO₂ concentrations in the soil for at least several weeks. Lab experiments demonstrated that wireworms were attracted to and fed on these artificial CO₂-emitting capsules. In the field we combined these capsules with an isolate of an entomopathogenic fungus, acting as the kill component. Treatments were applied into the potato dams, either below or between the tubers at two different dates during the growing season. We used fields with a high incidence of wireworm damage in previous years. Application of the A&K capsules resulted in significantly lower tuber damage in most, but not all fields, depending on the treatment schedule. Late season application of the A&K capsules did not prevent damage by wireworms because mortality did not immediately occur following contact with the killing agent, thus feeding damage was still observed.

Necessary improvements of the A&K strategy for a standardized application routine in the field are currently tested in field experiments at several locations. The implementation roadmap for this strategy will be discussed.

**Contributed Paper Monday 15:00 22**

*Drosophila suzuki* fungal infections and transmissions: A potential field suppression strategy

*Joan Cossentine, Mairi Robertson*

Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, BC, Canada

Correspondence: joan.cossentine@agr.gc.ca

*Drosophila suzuki* adults were found to acquire lethal fungal infections in the laboratory through surface-treated contact with isolates of *Metarhizium brunneum*, *Beauveria bassiana*, *Isaria fumosorosea*, and *Lecanicillium lecanii*. In these trials, the *M. brunneum* F52 isolate had the greatest impact on the flies, followed by the *B. bassiana* GHA isolate. Scanning electron microscopy confirmed that conidia accumulated on *D. suzuki* pretarsi and labella after exposure to the treated surfaces and horizontal transmission of *M. brunneum* between flies was verified. Although *D. suzuki* longevity decreases with increasing temperatures, the flies generally survive for two to three weeks in the field and *M. brunneum*-induced mortality in the laboratory began 5 to 7 days post conidia exposure. Significantly lower F1 counts were recorded over 14 d from *D. suzuki* females exposed to *M. brunneum* in the laboratory; a decrease that was attributed to mortality over time. Based on these findings, it appears that field suppression of the new North American and European invasive pest may be possible through the incorporation of *Metarhizium* conidia into a bait or surface treatment.

**Contributed Paper Monday 15:15 23**

*Ant diseases: A neglected area in insect pathology?*

*Roberto M. Pereira*

Urban Entomology Lab., Entomology & Nematology Dept., University of Florida, Gainesville, FL, USA

Correspondence: rperreira@ufl.edu

Despite representing a considerable portion of the biomass on earth, their importance in many ecosystems, and role as pests in urban and agricultural systems, ants are relatively little studied for their pathology. With increasing number of ant species considered exotic pests in different parts of the globe, there is growing interest in the identification of ant pathogens that can be used in the microbial control of ant species. Indications from casual ant disease collections and more deliberate efforts point to a large number of diseases affecting Formicidae. However, relatively few ant pathogens have been studied sufficiently and/or exploited for control of ant pests. Fungal and protozoan pathogens have been identified from several ant species, while viruses are only known from Solenopsis spp. Bacteria associated with ants and their nests have been isolated but no effective bacterial pathogens have been identified for use in control efforts. Most pathogens described from Formicidae form obvious outgrowths or significant changes in behaviors normally associated with ants. However, other diseases seem to have little effect on ant behavior, and have been identified from foraging ants captured in pitfall traps or other capture methods favoring normal active ants. Several pathogens already identified from ants await further investigations on their effects on ant populations, complete description of their lifecycle, and other aspects that may lead to better understand of the pathogen-ant relationship and potential use in microbial control of ants.

**Contributed Paper Monday 15:30 24**

The importance of searching for appropriate strains for the control of leaf-cutting ants

*Patricia J. Folgarait, Daniela Goffré*

Laboratorio de Hormigas, Departamento de Ciencia y Tecnología, Universidad Nacional de Quilmes, Bernal, Buenos Aires, Argentina

Correspondence: patricia.folgarait@gmail.com

Leaf-cutting ants are important pests of pastures, plantations and several crops in Latin America. Nowadays there is a pressing need for replacing pesticides by alternative –environmentally safe– means of control. One of those within the biological type of control is the use of entomopathogens. It is very common to use collection strains or species found in the soil. Here, we compared the virulence of three different strains of *Purpureocillium lilacinum* when *Acromyrmex* colonies were infected. We also tested the concentration of conidia that remained in the ant’s body at increasing concentrations of inoculation. Finally, we tested the horizontal transmission from inoculated ants towards non-inoculated ones. Our results showed the importance of testing several strains, as they exhibited different degrees of virulence; the need for testing across many individuals from several nests, due to the innate dissimilarities found in colony responses; the relevance of knowing at which conidia concentration ants’ bodies’ saturated, as ants cannot carry and/or maintain the same concentrations as inoculated; that inoculated ants can transmit *P. lilacinum* conidia towards non-infected ants and produce their death; and finally, the relevance of testing the strains in more than one species if the pest is a species complex, as is the case with leaf-cutting ants. We advocate that the characteristics mentioned should be considered when choosing appropriate entomopathogenic strains for pest control.

**Symposium Cross-Division Monday 16:30 - 18:30**

**Fung/Microbial Control**

The (Underestimated) Value of Applied Research: Moving the Theoretical to the Practical

**Symposium Paper Monday 16:30 25**

Why biopesticides sometimes fail

*Roma L. Gwynn¹, Michael Brownbridge², Travis R. Glare³*

¹ Rationale, 1 Lintlaw Farm Cottages, Duns TD11 3QA, Scotland

² Vineyard Research and Innovation, 4890 Victoria Avenue North, Box 4000, Vineland Station ON, L0R 2E0, Canada

³ Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand

Correspondence: rgwynn@biorationale.co.uk
Biopesticides are increasingly used in crop protection for pest management in protected and field situations across a range of crops. They are used as stand-alone products, highly specific or as resistance management tools. However, micro-organism based biopesticides have a checkered history in terms of reproducible efficacy in the field. Some efficacy issues are more perception than reality, but the (apparent) lack of consistent effectiveness or ‘low’ efficacy can limit their uptake. What causes inconsistency after they have been properly delivered to the target in the crop? To what extent is the lack of consistency due to the innate nature of using living organisms and how much can be attributed to other factors? What roles do agro and microbial ecology play in the success of biopesticides after delivery? How do we measure this and then improve performance? This talk will place efficacy of applied biopesticides in an ecological context.

**SYMPOSIUM PAPER Monday 16:54 26**

Multiple roles so what should we measure? An ecological approach to promote the contribution of fungal entomopathogens in pest management within the agro-ecosystem

**Nicola V. Meyling**

Department of Plant and Environmental Sciences, University of Copenhagen, 1871 Frederiksberg C, Denmark

Correspondence: nvm@plen.ku.dk

Although often referred to as biopesticides, microbial products applied for pest control are living organisms and their function and effects in pest management systems should be considered from an ecological perspective rather than as the equivalent of chemical pesticides, i.e. spray-and-kill. Recent accumulated knowledge about the natural occurrence and distribution of fungal entomopathogens in agro-ecosystems, the factors governing the abundance of these fungi as well as new evidence for their ecological roles and functions will be valuable to promote the effects of these fungi when applied for pest control. Relevant examples will be presented and discussed in relation to application of fungal entomopathogens to elucidate how an ecological approach could promote the contribution of these fungi for pest management, how we could measure the effects, and what additional potential effects besides control of the target pest we could expect.

**SYMPOSIUM PAPER Monday 17:18 27**

Research and development of biological crop protection products – Bridging the gaps from discovery to field

**Reed N. Royalty, Denise C. Manker**

Bayer CropScience, Biologics. 890 Embarcadero Drive, West Sacramento, CA, USA 95605

Correspondence: reed.royalty@bayer.com

Basic agrichemical manufacturers are increasingly active participants in the biological crop protection space. A benefit of this participation is a substantial increase in R&D investment in biologics. This investment undoubtedly will result in the development and launch of more biologics products, but return-on-investment expectations means that these new products must deliver excellent and consistent in-field efficacy against major pests in major crops globally.

Bayer CropScience (BCS) approaches the challenge of developing profitable biologics that deliver excellent in-field performance at two levels. Prior to field testing, an R&D platform is being implemented that leverages three key components: 1) an understanding of the relationship between the crop, the pest, the biological, and the environment, 2) the development of enabling technologies that will improve greatly the performance, and 3) the R&D processes and benchmarks that BCS has used successfully to develop highly effective and safe synthetic crop protection products.

After biological development candidates move into large-scale field testing, BCS uses the attribute definition done in the lab and greenhouse to test the candidates in a manner that will define accurately their commercial potential. Integrated crop solutions are created globally and locally; these solutions capitalize on the strengths and minimize the deficiencies of the biologics. Appropriate field-trial design and the magnitude of BCS field research capabilities are leveraged to permit the robust testing necessary to validate these integrated solutions.

**SYMPOSIUM PAPER Monday 17:42 28**

Adapting field trials for microorganisms – in practice

**Edith Ladurner**, Massimo Benuzzi, Sergio Francescini

1CBC (Europe) S.r.l. – AREA TECNICA, via Calcinaro 2085 int. 7, 47521 Cesena (FC), Italy

2CBC (Europe) S.r.l. – BIOGARD Division, via XXV Aprile 44, 24050 Grassobbio (BG), Italy

Correspondence: eladurner@cbceurope.it

Micro-organisms are becoming increasingly important in integrated crop protection systems, because, in addition to being valuable pest control tools, they can help to reduce the risk of the development of pathogen resistance or as resistance management tools. Conventional plant protection products and of undesired residual levels in the final production. In order to be placed on the market as plant protection products, their efficacy against pests and diseases must be proven by following official guidelines, developed for conventional pesticides. However, by their nature, products based on micro-organisms may be highly specific in the pests or in the stage of the target pest they affect, and they may require specific conditions to reach acceptable efficacy. In many cases optimal efficacy can only be achieved when they are used as part of an integrated control strategy rather than as stand-alone products. This talk will provide examples on how field trials can be adapted for micro-organisms, and on how the experience of field trials can be transferred into practice for effective crop protection.

**SYMPOSIUM PAPER Monday 18:06 29**

How do we improve efficacy monitoring of biopesticides?

**Travis R. Glare**, Michael Brownbridge, Roma L. Gwynn

1Bio-Protection Research Centre, PO Box 85084, Lincoln University, Lincoln 7647, New Zealand

2Vineland Research and Innovation Centre, 4890 Victoria Avenue North, Box 4000, Vineland Station ON, L0R 2E0, Canada

3Rationale, 1 Lintlaw Farm Cottages, Duns TD11 3QA, Scotland

Correspondence: travis.glare@lincoln.ac.nz

To fulfil the predicted increasing use of biopesticides, these products must have demonstrated and reliable efficacy in the field. As will be discussed in the symposium, the perceived lack of reliable field efficacy has limited uptake of biopesticides. The actual efficacy of these products is likely to be much higher than the current methods of measurement suggest, given their multiple roles in the ecosystem. Our understanding of the complex interactions of biological agents after application suggest...
we underestimate efficacy by measuring only direct impacts. How can we better measure ‘efficacy’ of these micro-organisms, which may be lower than the chemicals they are compared to in terms of direct pest mortality, and how do we need to change perceptions and pest management programs to accommodate this? Is the way forward to consider efficacy in terms of population ecology? This talk will consider these questions in light of the information presented in the symposium and offer some suggestions for the future.

CONTRIBUTED PAPERS Monday 16:30 – 18:30

**Viruses**

CONTRIBUTED PAPER Monday 16:30 30

Overexpression of two microRNAs enhances the infectivity of Sindbis virus T5'2J strain in mosquitoes

Ning Huang1, Jessica Moffitt2, Kayvan Etebari1, Sassan Asgari2, Alexander W.E. Franz3, A. Lorena Passarelli1, Rolle J. Clem4
1 Division of Biology, Kansas State University, Manhattan, KS USA;
2 School of Biological Sciences, University of Queensland, St. Lucia, Queensland, Australia;
3 Department of Veterinary Pathology, University of Missouri, Columbia, MO USA

**Correspondence:** rclem@ksu.edu

The mosquito Aedes aegypti serves as a natural vector for chikungunya, dengue, and yellow fever viruses. In the laboratory, A. aegypti is also susceptible to infection by the model togavirus Sindbis virus (SINV). To be transmitted, these viruses must infect adult mosquitoes and the Aag2 cell line derived from the mosquito. In contrast, the majority of differentially expressed piRNAs showed significant up-regulation after exposure to the sub-lethal dose of a pyrethroid insecticide as a chemical stress inducer. Although insecticide exposure, arbovirus and Wolbachia infection possibly trigger different pathways in the host, we found 100 differentially expressed piRNAs common among the datasets from these three treatments. This suggested the piRNAs may play significant roles not only in TE silencing activity but also in host-pathogen interaction and stress responses.

CONTRIBUTED PAPER Monday 17:00 32-STU

A modified viral shuttle for exploring RNAi-related genes

David Neumann1, Heiko Vogel2, David G. Heckel3, Salvador Herrero4, Agata K. Jakubowska5
1 Entomology Department, Max Planck Institute for Chemical Ecology, Jena, Germany;
2 Department of Genetics, Universitat de València, Burjassot, Spain

**Correspondence:** dneunemann@ice.mpg.de

Gene silencing via dsRNA has become a powerful tool to explore functional genomics in a wide variety of eukaryotic organisms. However, RNA interference (RNAi) is still in the exploratory phase in non-model organisms. Especially in Lepidoptera, RNAi is not as straightforward and efficient as in other insects and it has been proven to be difficult to establish, exemplified by a larger number of studies done in the past years in different Lepidopteran species with sometimes questionable effects. We analyzed RNAi-related gene expression levels (miRNA-pathway and siRNA-pathway) in Helicoverpa armigera and Helicoverpa zea in third instar larvae in different tissues. We found that R2D2 is transcribed at very low levels in all tissues except testes, whereas Loquacious is transcribed at very high levels in all tissues. These results could suggest that, despite appropriate design, the dsRNA failed to enter the siRNA pathway and knock-down the gene of interest due to the observed very low levels of R2D2. As the siRNA pathway is also known as the “antiviral pathway” and defends the organism against RNA and DNA viruses, we analyzed RNAi related genes after infection of Helicoverpa armigera with an Autographa californica multiple nucleopolyhedrovirus (AcMNPV) and Helicoverpa armigera single nucleopolyhedrovirus (HaSNPV). After 48 h infection with AcMNPV we could observe an induction of R2D2. Based on these results we will now test the possibility of using a modified AcMNPV, which lacks an important transcription factor and carries a dsRNA construct, as a shuttle to deliver dsRNA into cells, potentially resulting in target gene knockdown.

CONTRIBUTED PAPER Monday 17:15 33-STU

Role of dsRNA-mediated mechanism in the establishment of “latent” Glossina hytrosavirus infections in the tsetse fly

Irene K. Meki1,2, Henry M. Karitihi1, Just M. Vlaš1, Adly M. M. Abd-Allo1, Monique M. van der Voet1
1 Laboratory of Virology, Wageningen University, The Netherlands;
2Insect Pest Control Laboratory, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Vienna, Austria;
Tsetse flies (Diptera; Glossinidae) are naturally infected by *Glossina* hytrosavirus (family *Hytrosaviridae*), a large dsDNA virus pathogenic specifically to the *Glossina* spp. The virus infections are largely asymptomatic. Whereas *G. pallidipes* is more susceptible to the virus infection, infection in *G. m. morsitans* is predominantly asymptomatic. In *G. pallidipes*, asymptomatic infection can convert to symptomatic infection that is characterized by salivary gland hypertrophy syndrome (SGH), leading to reproductive dysfunction of infected flies. It is hypothesized that the virus infection is maintained by dsRNA-mediated gene silencing, such that only a few of the viral genes are expressed during asymptomatic infections to avoid detection by the host’s immune system. To investigate whether host-mediated dsRNA mechanism(s) is involved in maintenance of asymptomatic virus infection, we performed a comparative analysis of expression levels of Dcr-2 and Ago-2 genes in *G. pallidipes* and *G. m. morsitans*. Whereas Ago-2 and Dcr-2 were significantly up- and down-regulated in symptomatic and asymptomatic *G. pallidipes*, respectively, the two genes were down- and up-regulated in infected and uninfected *G. m. morsitans*, respectively. Further, transcriptomic data indicated that miRNAs may be involved in the conversion of asymptomatic to the symptomatic infection states. These findings implicate dsRNA gene silencing (perhaps through miRNAs) is involved in controlling the virus infection in tsetse flies. These data provide avenues for further investigations into the roles of RNAi during latent hytrosavirus infections in *Glossina*.

**CONTRIBUTED PAPER Monday 17:30 34-STU**

**New target sites in pest control: Examining the role of REPAT proteins in defence against baculoviruses**

Esengül Ozdemir¹, Umut Toprak¹, Sibel Çavdar, Diana Bekkauer², Dwayne Hegedus²

¹Ankara University, Faculty of Agriculture, Dept. of Plant Protection, Ankara, Turkey; ²Agriculture and Agri-Food Canada, Saskatoon Research Centre, Saskatoon, SK Canada

Correspondence: utoprak@agri.ankara.edu.tr

Baculoviruses are invertebrate-specific pathogens with great potential for being developed as biopesticides; however, their slow speed of killing has been a barrier for widespread use. Development of more effective baculoviruses requires a detailed understanding of their infection mechanism. Baculoviruses initiate infection from midgut epithelial cells. This requires passage through a porous structure lining the midgut, the peritrophic matrix, which is composed of chitin and multiple proteins. One group of proteins associated with the PM are from the REPAT (Response to pathogen) protein family that have been shown to be involved in the defense against pathogens. The objective of this study was to identify the REPAT proteins in *Spodoptera littoralis* (Lepidoptera:Noctuidae), a major pest of cotton and vegetables in North Africa, Mediterranean region and the Middle-East. Scanning of a *S. littoralis* midgut-specific cDNA library revealed 11 REPAT (SpliREPAT1-11) proteins. Full length cDNAs were obtained by RACE analyses. Site-specific gene expression analyses by droplet digital PCR indicated that they were predominantly expressed in the midgut, while developmental gene expression analyses indicated that expression was specific to larval stages. Inoculation of 3rd instar larvae by a baculovirus revealed an upregulation in the expression of REPAT genes, suggesting they have a defense-related role. In conclusion, targeting defense-related midgut genes encoding proteins such as REPATs could help development of improved baculoviruses in pest control strategies.

**CONTRIBUTED PAPER Monday 17:45 35-STU**

**Wolbachia-mediated antiviral protection is life stage dependent**

Aleksij L. Stevanovic, Pieter A. Arnold, Karyn N. Johnson, School of Biological Sciences, The University of Queensland, Brisbane 4072, Australia

Correspondence: aleksij.stevanovic@uqconnect.edu.au

Viral infection and maintenance within insect populations is dependant on the pool of virus present within the system. The endosymbiotic bacterium *Wolbachia* has the ability to limit viral replication in adult *Drosophila* flies and mosquitoes, a feature that can be utilised to limit virus spread. To understand the effect of *Wolbachia* on insect populations, it is important to consider viral susceptibility throughout all developmental stages. We used *Wolbachia*-host combinations known to exhibit antiviral protection in adult flies, and investigated protection in larvae. *Drosophila* C virus was delivered to first instar larvae through oral feeding, and survival was scored to determine if antiviral protection was retained at larval stages. *Wolbachia* mediated protection was lost in all but one *Wolbachia*-host combination, wMelPop in W1118. Because *Wolbachia* density has been previously shown to be important in conferring antiviral protection in adult flies, we investigated *Wolbachia* density at the larval stages using RT-qPCR. The expression analysis showed that 5 out of 6 *Wolbachia* strains examined show reduced *Wolbachia* levels at larval compared to adult stages. Interestingly, the wMelPop strain, which retained high *Wolbachia* densities in larvae, was the only strain that provided protection at both the larval and adult stages, indicating that *Wolbachia* density is important for antiviral protection throughout all stages of development. Taken together these data show that *Wolbachia*-mediated antiviral protection can vary between life stages of an insect. We therefore suggest that consideration be given in selecting *Wolbachia* strains that confer protection at all stages of development when designing programs focused on minimizing the spread of insect vectored viruses.

**CONTRIBUTED PAPER Monday 18:00 36-STU**

**A viral histone H4 modulates host gene expression by down regulating chromatin remodeling machinery**

Sunil Kumar, Yonggyun Kim

Department of Bioresource Sciences, Andong National University, Andong 760-749, Republic of Korea

Correspondence: sunilkumar_micro@rediffmail.com

Histone H4 is a protein subunit of nucleosomes in eukaryotes and play crucial roles in DNA packaging, chromatin formation and in regulation of gene expression by covalent modification. A viral histone H4 is encoded in a polydnavirus called *Cotesia plutellae* bracovirus (*CpBV*). The viral H4 (*CpBV-H4*) is highly homologous with other H4 proteins except 38 extended residues in N terminus. Its expression alters insect gene expression and suppresses immune and development. In this study, *CpBV-H4* was expressed in a natural host, *Plutella xylostella*, and its suppressive activity on host gene expression was detected by suppressive subtractive hybridization (SSH) technique. SSH targets, of which expressions were down-regulated by *CpBV*-H4, were read by 454 pyrosequencing and annotated using the published *P. xylostella* whole genome. Resulting targets were assigned to most GO functional categories. Two chromatin remodeling factors were included in the SSH targets. Lysine demethylase (Px-KDM) of *P.
ABSTRACTS

Larvae of *P. xylostella* was highly expressed during entire larval period in all tested tissues. However, the suppression of Px-KDM expression by a specific RNA interference (RNAi) did not affect immune response, but significantly impaired the larval development. SWI/SNF of *P. xylostella* (Px-SWI/SNF) was expressed in all developmental stages. Its RNAi did not affect larval development, but led to significant alteration in adult metamorphosis. CpBV-H4 suppressed expressions of both Px-KDM and Px-SWI/SNF, but its truncated mutant lacking in the extended N-terminal tail did not. These results suggest that the biological alteration in *P. xylostella* parasitized by *C. plutellae* can be caused by an epigenetic control of CpBV-H4 against chromatin remodeling factors.

CONTRIBUTED PAPER Monday 18:15

Infection studies of an Agrotis segetum granulovirus isolate from Europe in cell cultures of AE1611T

Gianpietro Gueli Alletti1, Jörg T. Wemmmann2, Martina Eigenbrod2, D. Heiman3, Hiten D. Madhani3,4, 46
1Julius Kühn Institute, Heinrichstr. 243, D-64287 Darmstadt, Germany; 2Queen’s University, K7L 3N6 Kingston (ON), Canada
Correspondence: gianpietro.gueli.alletti@ki.bund.de

Larvae of *Agrotis segetum*, the common cutworm (*Denis & Schiffermüller*) and *A. ipidion*, the black or greasy cutworm (*Hufnagel*) are polyphagous lepidopteran pests, which cause severe damage on roots and stems of numerous cultivated plants and are of significant economic importance. Four baculoviruses, namely *Agrotis segetum* nucleopolyhedrovirus A (*AgseNPV-A*), *Agrotis segetum* nucleopolyhedrovirus B (*AgseNPV-B*), *Agrotis ipidion* nucleopolyhedrovirus (*AgipNPV*), and *Agrotis segetum* granulovirus (*AgseGV*), belonging to the genera *Betabaculovirus* and *Granulovirus*, respectively, are known to infect larvae of *A. segetum* and *A. ipidion*. Infections with these baculoviruses were characterized in dose-response bioassays and with molecular biological methods in neonate *A. segetum* larvae. Mixed infection of single *A. segetum* larvae with *AgseNPV* and *AgseGV* have been reported. As a further step to improve the understanding of the biology of *AgseNPV*-B and *AgseGV* in single and mixed infections, plaque purified virus stocks of these two viruses were prepared in the *A. ipidion* cell line AE1611T. Infected cell samples were characterized with light/electron microscopy and PCR assays. Genomic stability of *AgseNPV*-B and *AgseGV* were investigated in RFLP and sequence analysis. These analyses comprised genomic comparisons between two *AgseGV* isolates from China (*AgseGV*-Xi, *AgseGV*-L1) and the isolate in this study, *AgseGV*-JKI. These investigations revealed the ability of both *AgseNPV*-B and *AgseGV* to replicate in AE1611T.

CONTRIBUTED PAPER Monday 16:45

Ultrastructural analysis and SSU rRNA gene sequencing of Alfenia sp. and Agglomerata cladocera from Siberian microcrustaceans shed light on diversification within the “Aquatic Outgroup”

Yuliya V. Sokolova1,2, Yuri S. Tokarev1, Georgiy I. Rusakov1,2, Igor V. Sendersky1
1Institute of Cytology; 2Institute for Plant Protection, Russian Academy of Sciences, St.Petersburg, Russia; 3School of Veterinary Medicine, Louisiana State University, Baton Rouge LA, USA
Correspondence: sokolova@lsu.edu

Two microsporidia from freshwater crustaceans were discovered during the ongoing survey for microsporidia in the river Karasuk basin (Novosibirsk Region, Western Siberia). The first species, tentatively a new species of the genus Alfenia, parasitizes Cyclops sp. (*Maxillicopa, Copedopa*). The second one infects a cladoceran *Daphnia magna* (*Branchiopoda, Phyllopoda*), and basing on ultrastructure, was identified as *Agglomerata (Glugea) cladocera* (*Pfeifer, 1895*). Larson, Dieter, Vavra, 1996, comb. n. Siberian isolate of *A. cladocera* shares 99% SSU rRNA gene sequence similarity to *Binucleata daphniae* Refardt et al., 2008 from Belgium. No sequences belonging to representatives of genera *Alfenia* or *Agglomerata* have been available so far through public databases. New information sheds light on phylogenetic bonds within the Aquasporidia group of the Clade I (*Vossbrinck, Debrunner-Vossbrinck, 2005*). Both parasites fell in the “Aquatic outgroup” (AOG), a sister to the *Amblyosporida clade*. *Agglomerata cladocera* clusters with *Binucleata daphniae*, while *Alfenia sp.* – with *Trichouzetia guttata*. Interestingly, two major well supported branches can be identified within AOG: members of the first, the *Alfenia-Trichouzetia* lineage parasite predominantly copepods-cycloponds, and representatives of the second, the *Agglomerata-Gurleya-Larssonia-Berwaldia* lineage are mainly associated with cladocerans. AOG clade also includes a few taxa with dipeteran hosts suggesting that common ancestors of amblyosporids and AOG possessed polycystous life cycles that probably involved a copepod as an intermediate host, like some extant amblyosporids. Given morphological and sequence similarity of *Binucleata daphniae* to *Agglomerata* spp., the genus *Binucleata* may be amended to a junior synonym of *Agglomerata*. Supported by RFBR 13-04-00693 and RF President grant MD-4284.2015.4.

ABSTRACTS

Microsporidia

CONTRIBUTED PAPER Monday 16:30 – 17:30

Host-pathogen interactions and genome evolution in two host-specific and specialist microsporidian pathogens of mosquitoes

James J. Beem1, Christopher A. Desjardins2, Neil Sanscrainte2, Jonathan M. Goldberg2, Sarah Young1, Qianrong Zeng1, Hiten D. Madhani3,4, 46
1USDA, ARS, Center for Medical, Agricultural and Veterinary Entomology, 1600 SW 23rd Drive, Gainesville, Florida 32608, USA; 2Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA; 3Department of Biochemistry and Biophysics, University of California-San Francisco, San Francisco, California 94158, USA
Correspondence: James.Bee@ars.usda.gov

The adaptation of two distantly related microsporidia to their mosquito hosts was investigated. *Edhazirdia aedis* is a specialist pathogen that infects *Aedes aegypti*, the main vector of dengue and yellow fever arboviruses. *Vavraia culicis floridensis* is a generalist pathogen of several insects including *Anopheles* spp. that vector malaria. Genomic analysis and deep RNA-Seq across infection timecourses reveal fundamental differences between these two pathogens. *E. aedis* retains enhanced cell surface modification and signaling capacity, upregulating protein trafficking and secretion dynamically during infection. *V. culicis* is less dependent on its host for basic metabolites and retains a subset of spliceosomal components, with a transcriptome broadly focused on growth and replication. Transcripts of mosquito immune responses reveals that response to infection by *E. aedis* differs dramatically depending on the mode of infection, and that antimicrobial defenses may play a general role in mosquito defense against Microsporidia. This analysis illuminates fundamentally different evolutionary paths and host interplay of specialist and generalist pathogens of microsporidia.
Glycolysis is a metabolic process that breaks glucose into energy and is ubiquitous in eukaryotic cells. However, E. bieneusi, a human infecting microsporidian has been recently found to lack this pathway. Loss of this metabolic process in conjunction with the general absence of oxidative phosphorylation capabilities in the Microsporidia suggests that E. bieneusi solely relies on ATP import for its energy needs.

The placement of E. canceri, a crab infecting intranuclear microsporidia as the closest relative to E. bieneusi in phylogenetic studies sparked questions of whether this crab parasite also has lost glycolytic capabilities and how it attained energy from within its unusual intranuclear habitat. Comparative genomic analyses in this study have partly answered this question by confirming the absence of most glycolytic genes from not only the genome of E. canceri but from other members of the Enterocytozoon family as well.

However, hexokinase, the gene that codes for the first protein of the glycolytic pathway appears to be retained in the genome of all members of the Enterocytozoon family. Further comparative analysis has also revealed that the catalytic domains of this gene have undergone severe deletion mutations and in the case of E. canceri, an entire new domain is adjoined to the N-terminal of the predicted protein. Here, we are using kinetic and high-throughput phenotype assays to test the functionality and substrate specificity of these microsporidian hexokinases in order to better understand the role of these mutated proteins in microsporidian carbon metabolism and intranuclear living.

CONTRIBUTED PAPER Monday 17:15 41-STU
Characterization of the spliceosome and large introns in microsporidia
Thomas A. Whelan, Cameron J. Griddale, Naomi M. Fast
Department of Botany, University of British Columbia, Vancouver, BC, Canada
Correspondence: whelan.t@alumni.ubc.ca

Microsporidia are fungal intracellular parasites that have some of the most reduced and compacted genomes known. This reduction is particularly evident when looking at the spliceosome and spliceosomal introns. The genome of Encephalitozoon cuniculi is only 2.9 Mb, has lost the majority of its introns, and we predict its reduced spliceosome lacks the U1 snRNA, a component of the spliceosome that identifies introns early in the splicing process. Only 37 introns remain and they are predominantly shorter than 25 nt. To assess whether the dramatic reduction in intron length and spliceosomal size affects the splicing process, we carried out high-throughput transcriptome sequencing to determine splicing levels. Our analysis showed that the majority of introns in E. cuniculi were spliced at levels much lower than seen previously in other reduced fungi. One intron in the Poly-A ORF stood out not only because of its size (76 nt) but it was also spliced in 80% of the transcriptome reads. Of interest, two similarly large introns were independently found in Spraguea lophii: one in the Poly-A ORF (as in E. cuniculi) and one in the S23 ribosomal protein gene. We have now identified additional long introns with unusual levels of sequence conservation. We found that 14 of 20 microsporidian genomes possess a Poly-A intron and 6 have an S23 intron.

Assessing the distribution of these introns could provide us with insights into intron gain, a process rarely observed, and could also highlight a potential regulatory role for splicing in microsporidia.

TUESDAY – August 11th

SYMPOSIUM BACTERIA Tuesday 8:00 – 10:00
Mechanisms of Field Resistance to Bt Pesticides and Bt-Crops

SYMPOSIUM PAPER Tuesday 8:00 42
Bt resistance in Plutella – too many trees?
Neil Crickmore
School of Life Sciences, University of Sussex, Brighton, UK
Correspondence: n.crickmore@sussex.ac.uk

Plutella xylostella was the first pest insect in which field resistance to Bt was reported and consequently much work has been done in an attempt to understand the underlying mechanism. Most resistant populations conform to the so-called Mode 1 phenotype in which resistance to Cry1A toxins is observed but little cross-resistance to Cry1C exists. Resistance is recessive and characterized by the loss of binding of the Cry1A toxin(s). The similarity in these phenotypes, along with complementation data, suggested a commonality between the different resistant populations, yet detailed studies suggested a much more complex picture. Various reports for example have suggested that the following may all contribute to the resistance phenotype: multiple alleles, complex toxin binding scenarios, cross-resistance with pyrethroids, involvement of esterases, reduced proteolytic processing, altered membrane composition and the involvement of gut microbiota. More recent work has mapped the resistance allele to the ABC2C locus in at least two resistant populations and “omics” studies, combined with RNAi, have identified a number of genes that appear to contribute to the resistance phenotype. In this presentation I will consider to what extent the role of many of the above factors in resistance is justified by the experimental data and whether too much data can mask a more straightforward explanation. Finally I will consider whether there might be a unifying hypothesis, based on a single genetic lesion, that can explain the various results obtained. Although the presentation will use Plutella as an example the analysis could be applicable to other pest species.

SYMPOSIUM PAPER Tuesday 8:22 43
Multiple resistance mechanisms selected in cabbage looper populations resistant to DiPel
Ping Wang
Department of Entomology, Cornell University
New York State Agricultural Experiment Station, Geneva, NY 14456
Correspondence: pingwang@cornell.edu

The cabbage looper, Trichoplusia ni, is one of only two insect species that have developed resistance to Bt sprays in an
agricultural environment. The GLEN population of *T. ni* developed resistance to DiPel, a formulation of *Bacillus thuringiensis var. kurstaki* (Btk), in commercial greenhouses (Jannamatt and Myers, 2003. Proc. Biol. Sci., 270: 2263-2279). The DiPel-resistant GLEN strain, GLEN-DiPel, is highly resistant to Cry1Ac, a major Cry toxin in Btk. In the GLEN-DiPel population, resistance to Cry2Ab was also selected. Cry1Ac-resistance and Cry2Ab-resistance are conferred by two genetically independent mechanisms. The Cry1Ac resistance is associated with down-regulation of APN1 gene expression, and the resistance is controlled by a trans-acting resistance gene localized in the ABC transporter ABCC2 gene locus region. Cry2Ab resistance is conferred by a novel yet to be understood genetic mechanism. The presence of both Cry1Ac resistance and Cry2Ab resistance mechanisms in *T. ni* lead to resistance of *T. ni* larvae to the dual toxin Bt-cotton variety BollGard II.

**SYMPOSIUM PAPER Tuesday 8:44 44**

**Pink bollworm resistance to Bt cotton: Similar mechanism in the lab and field?**

Jeffrey A. Fabrick1, Jeyokumar Ponnuru2, Xianchun Li3, Yves Carrière4, Bruce E. Tabashnik5

1USDA-ARS, U.S. Arid Land Agricultural Research Center, Maricopa, Arizona, USA; 2National Institute of Plant Health Management, Rajendranagar, Hyderabad, Andhra Pradesh, India; 3Department of Entomology, University of Arizona, Tucson, Arizona, USA

Correspondence: jeff.fabrick@ars.usda.gov

Evolution of resistance by insect pests can reduce the benefits of insecticidal proteins from *Bacillus thuringiensis* (Bt) that are used extensively in sprays and transgenic crops. Despite considerable knowledge of the genes conferring insect resistance to Bt toxins in laboratory-selected strains and in field populations exposed to Bt sprays, understanding of the genetic basis of field-evolved resistance to Bt crops remains limited. We found that in pink bollworm (*Pectinophora gossypiella*), both laboratory-selected resistance to Cry1Ac and field-evolved resistance to Cry1Ac in Bt cotton are associated with mutations in a gene encoding a cadherin protein that binds Cry1Ac. Analysis of thousands of individuals from five laboratory-selected strains from the United States revealed four cadherin alleles that are genetically linked with resistance to Cry1AC. None of these four cadherin resistance alleles from the US strains were detected in screening DNA from 436 individuals collected from seven field populations in India. However, in only seven individuals collected from five field populations in India, we found eight novel, severely disrupted cadherin alleles associated with field-evolved resistance to Cry1Ac. For these eight alleles from India, analysis of complementary DNA (cDNA) revealed 19 transcript isoforms, each containing a premature stop codon, a deletion of at least 99 base pairs, or both. Seven of the eight disrupted alleles each produced two or more different transcript isoforms, which implicates alternative splicing of messenger RNA (mRNA). This represents the first example of alternative splicing associated with field-evolved resistance that reduced the efficacy of a Bt crop.

**SYMPOSIUM PAPER Tuesday 9:06 45**

**Mechanism of Spodoptera frugiperda resistance to Cry1Fa in Bt corn**

Juan Luis Jurat-Fuentes1, Siva R. K. Jakka2, Rahul Baneje3, James Hasler4, Fangneng Huang5, Robert Meagher6, Rodney Nagoshi7

1Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA; 2DOW AgroSciences, Indianapolis, IN, USA; 3Department of Entomology, Louisiana State University

AgCenter, Baton Rouge, LA, USA; 4USDA-ARS, Insect Behavior and Biocontrol Research Unit, Gainesville, FL, USA

Correspondence: jurat@utk.edu

Field-evolved resistance to transgenic corn producing the Cry1Fa insecticidal protein from *Bacillus thuringiensis* was detected and reported in populations of *Spodoptera frugiperda* (fall armyworm) from Puerto Rico in 2006. Resistance resulted in relevant field control failures, leading to voluntary withdrawal of the corn event from the local market. Using field-collected insects we have studied resistance genetics and fitness costs, as well as the mechanisms responsible for resistance. We have found that resistance to Bt corn in *S. frugiperda* is autosomally inherited and highly recessive, yet we failed to detect relevant fitness costs when compared to a susceptible colony. The Cry1Fa-resistant *S. frugiperda* were also cross-resistant to Cry1A insecticidal proteins, but not to the Cry1Ca protein. Comparison of Cry protein binding to brush border membrane vesicles prepared from susceptible and resistant *S. frugiperda* revealed a dramatic reduction of Cry1A and Cry1Fa toxin binding in resistant larvae. In contrast, Cry1Ca binding was not different among the compared strains, supporting an association between reduced binding and resistance and cross-resistance phenotypes. Considering this association, we examined alterations in putative Cry1 protein receptors in resistant *S. frugiperda*. Real time-PCR analyses detected a dramatic down-regulation of specific alkaline phosphatase isoforms in larval resistant to Cry1Fa corn. In this presentation we will share and discuss recent data towards the mechanistic description of resistance to Cry1Fa corn in *S. frugiperda*.

**SYMPOSIUM PAPER Tuesday 9:28 46**

**Characterization of Cry3Bb1 resistance in western corn rootworm (Diabrotica virgifera virgifera)**

Jeffrey A. Haas

Monsanto Company, 700 Chesterfield Parkway West, Chesterfield, MO 63017, USA

Correspondence: jeff.a.haas@monsanto.com

Western corn rootworm (WCR) is a significant pest of corn causing >$1B US in crop damage annually. Observations of WCR resistance to corn hybrids expressing the *Bacillus thuringiensis* 3-domain Cry protein (Bt; 3D-Cry), Cry3Bb1, have been documented, particularly in areas of repeated corn-on-corn production where hybrids expressing a single mode of action were grown (Gassmann, 2013). More recently, evidence for cross-resistance to both Cry3Bb1 and to mCry3Aa has been published (Gassmann, 2014). Previous biochemical studies of a WCR population derived from Hopkinson, IA, and reared under continuous MON88017 selection, did not reveal a clear association for Cry3Bb1 resistance. While in vitro binding and proteolytic processing appeared unchanged, RNASeq and proteomic analyses of whole larvae revealed changes in immune/pathogen response genes. However, involvement of these genes in Cry3Bb1 resistance could not be validated by RNAi feeding studies in WCR. Putative Cry1 receptor homologs (ex. ABC transporters, cadherin, alkaline phosphatase, aminopeptidase) were not detected in whole larval proteomics and RNA expression profiles were not significantly different when whole larvae of susceptible and resistant colonies were compared. Recently, detection of potential 3D-Cry receptor families has been observed by proteomic analysis of brush border membranes isolated from WCR larvae. Results from a comparative analysis of Cry3Bb1 susceptible and resistant WCR colonies will be discussed in the context of previous biochemical,
molecular, and genetic observations, and in relation to potential resistance mechanisms in WCR.

CONTRIBUTED PAPERS Tuesday 8:30 – 9:45

Diseases of Beneficial Invertebrates 1

CONTRIBUTED PAPER Tuesday 8:30 47
Pathogens on the horizon: Enhancing understanding of invasive alien entomopathogens and impacts on biodiversity
Helen Hesketh1, Jürgen Eilenberg2, Monique van Oers3, Helen Roy3, Alison Dunn4, Grant Stentiford4, Beth Purse5, Regina Kleespies6, Anja Amtoft-Wyns2
1Centre for Ecology & Hydrology (CEH), Wallingford, United Kingdom; 2University of Copenhagen, Denmark; 3 Wageningen University, Netherlands; 4University of Leeds, United Kingdom; 5Centre for Environment, Fisheries and Aquaculture Science (Cefas), United Kingdom; 6Julius Kühn-Institut, Federal Research Institute for Cultivated Plants, Germany
Correspondence: hhesketh@ceh.ac.uk

Horizon-scanning, the systematic examination of future potential threats and opportunities, leading to prioritisation of invasive alien species (IAS) threats is an essential component of IAS management. Consensus methods have been used to undertake IAS horizon scanning for Great Britain; 30 species considered a high risk with respect to arriving, establishing and posing a threat to native biodiversity were identified. Information on microbes is often lacking from alien species databases and so pathogens were excluded from this consensus approach. There is a significant gap in our knowledge in relation to risk posed to biodiversity by “alien” microorganisms. We organised a workshop of 40 experts with five subgroups (terrestrial invertebrates, aquatic, plants, wildlife diseases and vectors of disease) to specifically consider invasive alien pathogens that have the potential to impact on biodiversity in the EU. The aim was to undertake a cross-cutting review of pathogen life histories to enhance understanding of threats, methods and knowledge gaps within natural and seminatural systems, and to identify invasive alien pathogens that will impact on biodiversity in Europe. We identified key barriers to our understanding of the introduction, establishment and impact of invasive alien pathogens through two distinct phases; 1) preliminary consultation between experts prior to the workshop, and 2) consensus-building across the expert groups during the workshop. We highlight the results of this consensus approach by examining the top 10 barriers identified. We then detail specific examples from the terrestrial invertebrate and aquatic sub-groups that exemplify these barriers and indicate how this may inform pan-European policy.

CONTRIBUTED PAPER Tuesday 8:45 49
The prevalence of multi-host pathogens in Bombus pascuorum is influenced by honeybee domestication
Ivan Meeus1, Lauraan Parmentier1, Jafar Maharramov4, Niels Piot2, Dirk C. de Graaf2, Guy Smagghe1
1Department of Crop Protection, Gent University, Coupure links 653, B-9000 Gent, Belgium; 2Department of Biochemistry and microbiology, Gent University, Ghent, Belgium
Correspondence: ivan.meeus@UGent.be

Domesticated animals are known as potential sources of parasites and viruses spilling over toward sympatric wild life. Their relatedness with the wild species and overlap in habitat are two important parameters for pathogen spillover. We question whether the domesticated honeybee could act as a reservoir of parasites and viruses, facilitating the spillover toward wild bumblebees. As spillover of pathogens is one of the main drivers of emergent infectious diseases and could represent an important factor in the multi-fac torial problem of bumblebee decline. We followed parasite (n = 3) and virus (n = 4) prevalence in Bombus pascuorum (n = 100) in five location, each location having a study site rich with honeybees, being close to apiaries, paired with a study site with low honeybee counts. Study sites more distant from apiaries had decreased Apis mellifera bombi and virus infection, specifically sacbrood virus (SBV) and viruses from the AKI complex (acute bee paralysis virus, Kashmir bee virus and Israeli acute paralysis virus complex). We conclude that presence of domesticated honeybees can interfere with wild host-pathogen interactions. This disturbance can occur because the honeybees are infected by the pathogens and/or because they are the most abundant pollinator in our study area. In order to further detect the effect of external vectoring. We discuss possible mitigation actions for the beekeeping sector, basically advising the reduction of 1) the pathogen load of bee hives, 2) the sector’s mobility and 3) bee hive abundance, especially in vulnerable ecosystems.

CONTRIBUTED PAPER Tuesday 9:00 50-STU
From the mosquito model to the bumblebee: A different perspective: Vago mediated cross-talk between the small interfering RNA and Jak/stat pathways upon virus infection
Jinshi Niu, Ivan Meeus, Guy Smagghe
Department of Crop Protection, Faculty of Bioscience Engineering, Ghent University, Coupure links 653, B-9000 Gent, Belgium
Correspondence: jinshi.niu@ugent.be

Both small interfering RNA (siRNA) and Jak/stat pathways are recognized as important host defense mechanisms against virus infection. In mosquito, they are not only activated during virus infection, but also present a cross-talk through Vago in a Dicer-2 dependent manner. Upon virus infection, the upregulation of Dicer-2 leads to the activation of Vago transcription, which increases the level of secreted Vago. Subsequently, Vago influences Jak/stat signaling. In our study, we comparatively analyzed the bumblebee siRNA response to systemic infection of virulent-Israeli acute paralysis virus (IAPV) and avirulent -slow bee paralysis virus. Both virus infections can induce the expression of Dicer-2, which was also confirmed by production of virus derived siRNAs during IAPV infection. A “RNAi of RNAi” strategy was used to pre-silencing Dicer-2. In our study, we comparatively analyzed the bumblebee siRNA response to systemic infection of virulent -Israeli acute paralysis virus (IAPV) and avirulent -slow bee paralysis virus. Both virus infections can induce the expression of Dicer-2, which was also confirmed by production of virus derived siRNAs during IAPV infection. A “RNAi of RNAi” strategy was used to pre-silencing Dicer-2. In our study, we comparatively analyzed the bumblebee siRNA response to systemic infection of virulent -Israeli acute paralysis virus (IAPV) and avirulent -slow bee paralysis virus. Both virus infections can induce the expression of Dicer-2, which was also confirmed by production of virus derived siRNAs during IAPV infection.
The edible crab (Cancer pagurus) is a major commercial species within Europe, total fishery production of edible crabs from European waters in 2013 was 49,763 metric tonnes, and 58% of this was landed in UK (www.fao.org/figis). Despite their commercial value relatively little is known about their susceptibility to disease and the effects that these diseases may have upon populations. It is known from previous research that the disease prevalence present in juvenile (un-fished) and adult (fished) populations differs, for example juvenile edible crabs have been shown to display different pathogen profiles when compared to adults of the same species from the same population (Bateman et al. 2011). We carried out a disease survey on juvenile crabs sampled from three distinct sites around the United Kingdom. Using histology, molecular biology and electron microscopy we surveyed 60 animals per month over a 12-month period. We show that the disease profiles varied between the three sites, pathogens prevalent at one site and absent in others, prevalence of others varying considerably between sites and month sampled. This study has highlighted the potential role of disease in leading to un-monitored (silent) mortalities in the un-fished juvenile stocks, data will be incorporated into fisheries models to predict true risk of disease. This presentation will describe the pathologies and prevalence of these diseases during the 12 month study.

**CONTRIBUTED PAPER Tuesday 9:30**

**Apicomplexan parasites cause regular mass mortalities in commercial scallop populations**

**Mark A. Freeman**, 1, **Susan Inglis**, 1, **Arni Kristmundsson** 2

1Institute for Experimental Pathology at Keldur, University of Iceland, Reykjavik, Iceland; 2Institute of Ocean and Earth Sciences, University of Malaya, Kuala Lumpur, Malaysia

**Correspondence:** mf33bitw@gmail.com

Scallops with reduced, discoloured and loosely bound adductor muscles have also been reported from scallops from the Gulf of Alaska (Patinopecten caurinus) and the Barents Sea (C. islandica). Based on the clinical signs reported and the broad distribution of this apicomplexan, it seems probable that it is also the causative agent.

**CONTRIBUTED PAPERS Tuesday 8:00 – 10:00**

**Viruses 2**

**CONTRIBUTED PAPER Tuesday 8:00**

**53-STU**

AcMNVP encoded RING domain protein AC141 (Exon0) is associated with the GP64 and ME53 budding complex at the plasma membrane

**Siddhartha Biswas**, 1 **Yong Liu**, 1 **Peter I. Kreil**, 1 **David A. Theilmann** 1, 2

1Plant Science, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada V6T 1Z4; 2Department of Molecular and Cellular Biology, University of Guelph, Guelph, Ontario, Canada N1G 2W1; 3Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, British Columbia, Canada V0H 1Z0

**Correspondence:** siddharthabiswasw@gmail.com

During AcMNVP infection, nucleocapsids egress from the nucleus, traverse the cytoplasm and bud from the plasma membrane (PM) to form budded virus (BV). GP64 is an integral membrane protein that forms foci at the PM which are believed to be budding sites of nucleocapsids. ME53 is also required for efficient BV production and is found associated with GP64 foci and appears to form a budding complex. AC141 is a unique RING domain protein encoded by AcMNVP and deletion of this gene reduces the BV titer by 99%. Here we hypothesize that AC141 associates with the budding complex to facilitate the budding of nucleocapsids. Association of AC141 with ME53 and GP64 was analyzed by co-immunoprecipitation (Co-IP) and confocal microscopy in two different hosts, SF9 and Tn581 cells, at 24 hpi. Cells were infected with a virus expressing ME53 tagged at the C-terminus with the HA epitope (ME53-HA). For confocal microscopy analysis a virus containing ME53 fused at the C-terminal to EGFP (ME53-GFP) virus was used. Co-IP was performed with anti-HA agarose beads with a virus expressing ME53 tagged at the C-terminus with the HA epitope (ME53-HA). For confocal microscopy analysis a virus containing ME53 fused at the C-terminal to EGFP (ME53-GFP) virus was used. Co-IP was performed with anti-HA agarose beads and eluent showed specific association with ME53, GP64 and VP39. Reciprocal co-IP with AC141 polyclonal antisera also showed specific association with ME53, GP64 and VP39. These results suggested that AC141 was part of the budding complex. Further analysis using confocal microscopy examined co-localization of AC141, ME53-GFP and GP64. Distinct patterns of localization with GP64 foci were observed. Both AC141 and ME53 have nuclear and cytoplasmic localizations. AC141 localized adjacent to where ME53/GFP and GP64 co-localized at the budding complex.

**CONTRIBUTED PAPER Tuesday 8:15**

**54**

AcMNVP LEF-3 plays a critical role in both viral DNA replication and late gene expression

**Mustapha El-Ayoubi**, 1 **Eric B. Carstens**

Department of Biomedical and Molecular Sciences, Queen’s University, Kingston, Ontario, Canada

**Correspondence:** carstens@queensu.ca

Baculoviruses tightly coordinate different stages of viral gene expression with the initiation of viral DNA replication as a key process separating early and late phases. Early genes are transcribed by the host RNA polymerase. Late genes are...
transcribed by a baculovirus-encoded RNA polymerase, composed of four subunits: LEF-4, LEF-8, LEF-9 and P47. We have determined the interactions of these subunits using fluorescent protein complementation assays. Each of the four subunits form homo-oligomers, when expressed on their own, and remain in the cytoplasm. All of the subunits form hetero-oligomers, except LEF-4 and LEF-8, which do not interact with each other. When tagged proteins were expressed in recombinant viruses, all the subunits interacted and localized to the nucleus. We also studied the interaction of these proteins with viral DNA replication genes including P143 and LEF-3. We previously showed that LEF-3 is responsible for transporting P143 into the nucleus. We have now discovered that the LEF-3 is also required for transporting the viral RNA polymerase subunits to the nucleus, and in the case of LEF-9, is essential for stabilizing the expressed protein. Additionally, we investigated the effect of temperature sensitive mutations in P47 and LEF-4 on their protein-protein interactions. The preliminary results demonstrated that single amino changes dramatically affected these interactions, and that LEF-3 was not able to overcome the defects. In summary, we will present data showing that the correct interaction of all the RNA polymerase subunits and their transport to the nucleus by LEF-3 are required for late viral gene expression.

CONTRIBUTED PAPER Tuesday 8:30 55
The ODV-e66 of Helicoverpa armigera nucleopolyhedrovirus is involved in viral oral infection but is not essential for BV synthesis
Dianhai Hou, Sijiani Luo, Fengqiao Zhou, Ranran Wang, Yanfeng Zhang, Manli Wang, HuaLin Wang, Zhihong Hu, Fei Deng
State Key laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, P.R. China
Correspondence: dff@wh.iov.cn

Baculoviral ODV-e66 is a structural protein of the occlusion-derived virus (ODV) that has been revealed to be a novel viral chondroitinase. In this study, the function of Helicoverpa armigera nucleopolyhedrovirus (HearNPV) ODV-e66 was explored. Odv-e66 is a late gene, transcribed beginning at 18 h post infection until the very late stage of infection. odv-e66 deleted- and repaired recombinant HearNPV viruses were subsequently generated and the one-step growth curve showed that deletion of odv-e66 did not affect HearNPV BV replication in vitro. Electron microscopy showed that odv-e66 deletion didn’t cause an obvious change in ODVs/OBs morphology in comparison with the repaired virus. Bioassay results suggested that ODV-e66 facilitates the oral infection of HearNPV in H. armigera larvae. The LC50 value of odv-e66-deleted virus against 3rd instar larvae increased ~3-fold, while this value increased ~30-fold for 4th instar larvae, compared with the repaired virus. It was previously postulated that the chondroitinase activity of ODV-e66 could partially digest the peritrophic membrane (PM) thus enhances per os infectivity. We proposed that the odv-e66 deleted virus might be less capable to establish oral infection in elder-instar larvae because of the development of PM. Further in-depth investigations will be focused on the effect of odv-e66 deletion on oral infectivity in larvae of different instars and the integrity of PM of larvae.

CONTRIBUTED PAPER Tuesday 8:45 56
Phosphorylation induces structural changes in the Autographa californica nucleopolyhedrovirus P10 protein
Linda A. King, Farheen Raza, Leo Graves, Sarah Irons, Robert D. Possee
Department of Biological and Medical Sciences, Oxford Brookes University, Oxford OX3 0BP UK
Correspondence: jaking@brookes.ac.uk

The baculovirus P10 protein is non-essential for virus replication in insect cells but has several roles very late in infection. It forms fibrillar structures in virus-infected cells that co-align with the polyhedron envelope to occlusion bodies and also in nuclear lysis and release of polyhedra from virus-infected cells. Viruses lacking p10 do not lyse insects as efficiently as the wild type but otherwise replicate normally. Phosphorylation of proteins can affect their structure and biological functions. The Autographa californica nucleopolyhedrovirus (AcMNPV) P10 has three potential phosphorylation sites at serine residues 84, 92 and 93. Using mutational analysis and MALDI-TOF mass spectrometry, we showed that P10 from AcMNPV-infected Trichoplusia ni TN368 cells at 72 hours post infection (hpi) was most likely phosphorylated at ser93. P10 phosphorylation mutants were expressed in TN368 cells and examined using confocal microscopy. This showed that mutation of ser93 caused conformational differences in P10 filament structures with delayed detachment from the nucleus very late in infection. The ser93 mutant appeared to cause normal nuclear lysis and release of occlusion bodies in TN368 cells. Interestingly, we noted that Spodoptera frugiperda (SF21 and S9P) did not undergo extensive nuclear lysis after infection with wild type AcMNPV as reported in previous studies, suggesting a degree of host specificity for P10 function. Further studies showed that AcMNPV P10 appears to act in concert with viral cathepsin but not chitinase to cause cellular and nuclear lysis.

CONTRIBUTED PAPER Tuesday 9:00 57-STU
Bombyx mori nucleopolyhedrovirus ARIF-1 enhances systemic infection in B. mori larvae
Ryuhei Kokusho, Toru Shimada, Susumu Katsuma
Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, the University of Tokyo, Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-8657, Japan
Correspondence: katsuma@ss.ab.a.u-tokyo.ac.jp

Infection of lepidopteran-specific nucleopolyhedroviruses (NPVs) spreads systemically via hemolymph and tracheal systems. In each tissue, lepidopteran NPVs demonstrate a distinct tropism that results in diverse levels of viral propagation and gene expression according to the types of tissues. Although tissue tropism and the efficiency of systemic infection directly affect the final yield of progeny virus, the related factors and their detailed function are limtedly investigated. In this study, we identified a baculovirus gene, actin rearrangement inducing factor-1 (arif-1), as a novel factor involved in systemic infection. arif-1 was previously shown to be the inducer of filamentous actin concentration on the plasma membrane during the early stage of Autographa californica NPV infection in cultured cells. Our research revealed that Bombyx mori larvae infected with arif-1-deficient B. mori NPVs (BmNPVs) did not show locomotor hyperactivity that was normally observed in BmNPV-infected larvae. arif-1-deficient BmNPVs also showed reduced pathogenicity and total viral propagation in B. mori larvae, whereas viral propagation of arif-1-deficient viruses was comparable to control viruses in B. mori cultured cells. To monitor the spread of infection in tissues of B. mori larvae, an arif-1-defective BmNPV expressing green fluorescent protein (gfp) was injected into B. mori larvae. GFP expression and quantitative reverse transcription-polymerase chain reaction analyses revealed that the infection by the arif-1-disrupted virus was significantly delayed in trachea, fat body,
suboesophageal ganglion, and brain, but not in hemocytes. These results indicate that BmNPV ARF-1 enhances systemic infection in B. mori larvae in a tissue-specific manner.

CONTRIBUTED PAPER Tuesday 9:15 58
Effect of me53 in baculovirus transcriptional regulation
Yang Liu1, Eva Nagy1, Peter J. Kreil1
1Department of Molecular and Cellular Biology; 2Department of Pathobiology, University of Guelph, Guelph, ON, Canada
Correspondence: pkrell@uoguelph.ca

The conserved lepidopteran baculovirus protein ME53, is expressed both early and late during infection. The deletion of me53 results in a significant decrease in virus production but no change in viral DNA synthesis. ME53 localizes to both the plasma membrane and nucleus of virus-infected cells. As a nuclear protein with a conserved C4 zinc finger domain at its C-terminus which is usually considered to be related to transcriptional regulation, me53 is consequently assumed to regulate transcription of viral genes. In order to determine if me53 has an effect on transcriptional regulation, the transcript levels of 30 selected viral early and late genes were quantified by qRT-PCR in both wildtype bacmid transfected cells and me53 knockout bacmid transfected cells. The presence of me53 increases the transcription of some viral immediate early genes, genes encoding the viral RNA polymerase subunits, and some genes necessary for virus production. Moreover, the most highly up-regulated genes are the ones required for viral nucleocapsid assembly and egress. This suggests that me53 might function as a transcription factor in the nucleus that regulates the expression of both viral early and late genes, in particular the late genes involved in virus production.

CONTRIBUTED PAPER Tuesday 9:30 59
Termination of invertebrate iridescent virus mRNA transcripts: The role of a CATTATA-containing hairpin
Ilkay Agah Ince1,2, Monique M. van Oers1,3, Gorben P. Pijlman4, Just M. Vlak2
1Laboratory of Virology, Wageningen University, Droevenaaiesteeeg 1, 6708 PB Wageningen, The Netherlands; 2Medical Microbiology Dept., Acıbadem University Medical School, Istanbul, Turkey; 3School of Life Sciences, Northeast Agricultural University, Harbin, P. R. China; 4School of Life Sciences, University of Sussex, Falmer, Brighton, UK
Correspondence: monique.vanoers@wur.nl, ogah.ince@acibadem.edu.tr

Invertebrate iridescent virus mRNAs are not polyadenylated, in line with the absence of canonical polyA transcription termination motifs downstream of the open reading frames. Iridoviruses may apply a different termination mechanism than most viral and host transcripts. Recently, we developed a method to determine the 3’ ends of these non-polyadenylated mRNAs by adding a linker sequence to the 3’ end using RNA-ligase. This linker can then be used to anneal to a specific primer to carry out RT-PCR. Using this method, we analyzed the transcripts of Chlo iridescent virus (CIV) or invertebrate iridescent virus 6 (IIV-6) upon infection of Drosophila Schneider 2 (S2) cells. The sequence of the 3’ untranslated region (UTR) of the cDNAs obtained was examined. Most transcripts terminated at or after a CATTATA (AUAAU in RNA) sequence or a close variant thereof. The complementary motifs CATTA and TAATG were strongly enriched in the 100 basepairs downstream of CIV ORFs compared to their occurrence in the whole CIV genome. In the viral genome these motifs are present in larger inverted repeat sequences with the ability to form hairpin (stem-loop) structures varying in length between 22 and 56 nt. The in silico and in vivo analyses suggest that hairpin-based transcription termination is a conserved characteristic in the genus Iridovirus (at least for IIV-6 and IIV-9), which may represent a novel transcript termination mechanism. The iridovirus situation may be comparable to the termination of metazoan histone transcripts, where a stem-loop structure controls mRNA termination.

CONTRIBUTED PAPER Tuesday 9:45 60
Post-translational modifications of the baculovirus protamine-like protein P6.9 and regulation of its hyperphosphorylation
Ao Li1, Haizhou Zhao1, Qingying Lai2, Zhihong Huang1, Mejin Yuan1, Kai Yang1
1State Key Laboratory of Biocontrol, Sun Yat-sen University, Guangzhou 510275, China
2University Medical School, Istanbul, Turkey
Correspondence: yangkai@mail.sysu.edu.cn

Diverse PTMs of histones and protamines constitute a code that creates highly selective binding platforms for the association of specific transcription regulatory proteins that determine the transcriptional state of genes. Many viral pathogens also utilize host- or virus-induced chromatin machinery to promote efficient infections. All of the insect-specific pathogen baculoviruses encode the protamine-like protein P6.9, which is required for versatile viral physiological processes. Currently, P6.9’s post-translational modification sites and its regulating factors remain poorly understood. In the present study, we found that the P6.9 species could be categorized as unphosphorylated, hypophosphorylated, and hyperphosphorylated and that a virally encoded serine/threonine kinase, protein kinase 1 (PK1), was essential for hyperphosphorylation. Abundant post-translational modification sites on P6.9 were identified by MS, among which 7 Ser/Thr and 5 Arg phosphorylated sites were PK1-dependent. Mutation of these Ser/Thr sites dramatically reduced the transcription of the very late viral genes and viral infectivity, indicating that the PK1-mediated phosphorylation of P6.9 contributes to viral proliferation. Our data suggest that a potential “code” might exist in the sophisticated post-translational modification of the viral protamine-like protein and that this code is involved in viral gene transcription and infection.

Contributed Papers Tuesday 10:30 – 11:30

Bacteria 2

CONTRIBUTED PAPER Tuesday 10:30 61
Screening Bacillus thuringiensis strains with unapparent crystals Changlong Shu1, Xuewen Zhang2, Neil Crickmore3, Fuping Song1, Jie Zhang1
1State Key Laboratory of Biology for Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, P. R. China; 2School of Life Science, Northeast Agricultural University, Harbin, P. R. China; 3School of Life Sciences, University of Sussex, Falmer, Brighton, UK
Correspondence: jzhang@ippcaas.cn

The Bacillus thuringiensis (Bt) is an entomology pathogen, during the sporulation process, the Cry proteins accumulated in Bt mother cells can form parasporal crystalline inclusions and contribute to Bt insecticidal activities. Currently, during strain isolation process, the recognizant of Bt still based on microscopic morphology observe of crystals. As several Cry proteins been reported lacks of crystal forming domain as well as some of cry gene were silencing, the current method may missing these crystal unapparent Bt isolates. Therefore, new methods to recognize these crystal unapparent Bt strain is needed. Here we illustrated a method using cry gene conserved primers PCR test
instead of microscopic morphology observation to recognize Bt strains. By this method, 79 Bt isolates including 43 with no or unapparent crystals were screened out. The 43 isolates with no or unapparent crystals will miss in the microscopic morphology observation method. 9 of the 43 isolate shown toxicity to Lepidoptera insects. One of the Lepidoptera insects’ toxic isolate was sequenced by 454 Genome Sequencer FLX™ System, and a cry1Ac mutation gene was found. This cry1Ac mutation gene can express but cannot form apparent crystals in BT. This mutation not only affects its toxicity, however, it increase the BT spore formation rate, with may benefit’s BT environmental adaptability. And, that may be the reason why there was such a high ratio unapparent crystal Bt isolate.

CONTRIBUTED PAPER Tuesday 10:45 62-STU
In search for novel bioactive molecules: Genome mining of the entomopathogenic bacterium Photorhabdus luminescens sonorensis (Gamma-Proteobacteria: Enterobacteriaceae)
Rousel A. Orozco, S. Patricia Stock
Department of Entomology, University of Arizona.
Tucson, AZ, USA
Correspondence: rouselo@email.arizona.edu

Microbial genome mining has become a worldwide approach for the discovery of novel compounds with biological activity. In this respect, insect pathogenic bacteria in the genus Photorhabdus are viewed as a rich source of diverse classes of small molecules with antimicrobial activity among other properties. One of our research focus is on Photorhabdus luminescens sonorensis (PLS), the bacterial symbiont of the nematode Heterorhabditis sonorensis. In particular, we are interested in investigating secondary metabolites which are natural products with great promise for application in agriculture. We have recently completed the sequencing of PLS and are currently annotating its genome and conducting an in depth bioinformatic analysis to identify and characterize biosynthetic gene clusters. Initial analyses have revealed the presence of more than 20 biosynthetic clusters. Some of these clusters are a apparently exclusive to this bacterium and many have not been reported in other Photorhabdus species such as P. luminescens (TT01 strain), P. temperata, and P. asymbiotica. In this presentation, we will discuss functional predictions, substrate specificities, and structure of biosynthetic enzymes encoded in PLS gene clusters. Levels of synteny conservation and phylogenetic relatedness of enzymes encoded will be also be discussed.

CONTRIBUTED PAPER Tuesday 11:00 63
Structural mutants of the anti-feeding prophage
Mark Hurst1, Dario Rybakovic2, Alok Mitra2
1Innovative Farm systems, AgResearch, Lincoln Research Centre, New Zealand; 2Institute of Environmental Biotechnology, Graz University of Technology, Austria; 3School of Biological Sciences, University of Auckland, Auckland, New Zealand
Correspondence: mark.hurst@agresearch.co.nz

Some strains of Serratia entomophila and S. proteamaculans (Enterobacteriaceae) cause amber disease of the New Zealand grass grub Costelytra zealandica (Coleoptera: Scarabaeidae). Larvae cease feeding within 2-3 days of ingestion of pathogenic strains of either S. entomophila or S. proteamaculans. The cessation of feeding virulence determinant termed Afp for anti-feeding prophage is encoded on a large 153,404-bp conjugative plasmid termed pADAP. The Afp is encoded by a cluster of 18 genes, with products of these genes combining to form a virus-like particle that is a bullet-shaped toxin-delivery apparatus similar in appearance to the R-pycins of Pseudomonas aeruginosa. Morphologically it resembles the sheathed tail of bacteriophages such as T4, including a baseplate at one end. It also shares features with the type VI secretion systems. A 3 day LD50 of approximately 500 cell free Afp particles per larva is required to cause cessation of feeding in C. zealandica. Genes (afp1-18) encoding components of Afp were expressed and their products purified allowing morphological assessment of the products by transmission electron microscopy (TEM). Several constructs and mutants have been shown to produce aberrant sheathless structures and Afp-like assemblies that are of shorter lengths, allowing us define the function of Afp16 and Afp14 as a sheath maturation protein and a length determining protein, respectively. This information, combined with bioinformatics data and TEM observations has allowed us to propose a model on the maturation of the Afp assembly.

CONTRIBUTED PAPER Tuesday 11:15 64
Loops replacements in domain II of Cry1Ab toxin with gut binding peptides alter insecticidal activity against the rice brown planthopper, Nilaparvata lugens (Stål)
Shao Ensi1, Liu Sijun2, Lin Li1, Guan Xiong1
1Key Laboratory of Biopesticide and Chemical Biology, Ministry of Education, Fujian Agriculture and Forestry University, 350002 Fuzhou, Fujian, PR China; 2Department of Entomology, Iowa State University, Ames, IA 50011, USA
Correspondence: guanxfafu@126.com

Cry toxins derive from Bacillus thuringiensis (Bt) have been widely used in the management of lepidopteran, coleopteran, dipteran pests and nematode. Alone with the widely planting of Bt transgenic crops, target pests will be effectively controlled. However, insecticidal spectrum of Cry toxins is limited. Seldom reports concerned to the toxicity from Cry toxins against hemipteran pests such as aphids, planthoppers and leaffoppers. As a result, after the expansion of Bt transgenic crops, hemipteran pests will only be managed by the use of traditional chemical pesticides and the deterioration of these Bt nontarget pests will increase. In our research, we screened a N. lugens gut binding peptide P2S and brush border membrane vesicles (BBMV) binding peptide P1Z. Then three receptor-binding loops in Cry1Ab domain II were replaced by P2S or P1Z respectively. After screening, one novel Cry toxin Cry1Ab-2S with loop 2 be replaced by P2S was selected. Cry1Ab-2S was the most stable novel toxin after the treatment by N. lugens gut proteases and had the strongest binding activity with N. lugens BBMV. Bioassay results showed that toxicity of Cry1Ab-2S against N. lugens nymphs were ~13 folds higher than Cry1Ab toxin (LC50=17.47μg/mL). Observation of N. lugens gut ultrastructure showed that gut microvilli of N. lugens fed by Cry1Ab-2S was obviously damaged. This research provides a new method for molecular modification of Cry toxins target on specific pests. Furthermore, result of this research will help the understanding of mechanism of Cry toxins in hemipteran insects.

CONTRIBUTED PAPERS Tuesday 10:30 – 11:30
Diseases of Beneficial Invertebrates 2
**White Spot Syndrome Virus (WSSV)** is the viral pathogen that causes White Spot Disease (WSD) in a wide range of crustacean hosts. In Panaeid shrimp, mortality rates cause $5$ billions in annual losses to the shrimp aquaculture industry. Currently there is no treatment for WSD. Previous studies have shown that the shore crab (*Carcinus maenas*) is relatively resistant to WSD. In a novel approach, we are investigating molecular mechanisms of resistance in this species to inform on new opportunities for treatment in susceptible species. Our approach requires that we generate genomic resources for this work. We have therefore sequenced RNA samples from $12$ individual *C. maenas* tissue types on an Illumina HiSeq platform and assembled a transcriptome encompassing approximately $212,000$ transcripts; representing $62,000$ unique annotated genes. The transcriptome was mined to identify genes from innate immune system pathways including melanization, JAK-STAT and Toll signalling and documented their expression profiles across individual tissues. Additionally we assembled a draft genome scaffold for *C. maenas*, approximately $1$ Gb in size. This genome assembly is used to characterize regulatory elements for expressed transcripts, repeat structures and miRNAs. Currently we are investigating the temporal transcriptomic and miRNA dynamics of *C. maenas* exposed to WSSV over a period of $28$ days post-infection. Preliminary analysis has identified a number of differentially regulated miRNAs that target Rab7, an important player in WSSV infection. Together, these data will allow us to elucidate how WSSV and host pathways interact, and their relationship to resistance. This information opens up new opportunities to the development of WSD treatments.

**Using genomics to identify host-pathogen interactions following white spot syndrome virus infection**

Lisa K. Bickley, Bas Verbruggen, Kelly S. Bateman, Grant D. Stentiford, Eduardo M. Santos, Ronny van Aarle

Exeter University, College of Life and Environmental Sciences, Exeter, UK

Correspondence: bv213@exeter.ac.uk

White Spot Syndrome Virus (WSSV) has emerged as one of the most prevalent and widespread viruses in the marine environment and is highly virulent in panaeid shrimp, a globally important aquaculture species. Recent studies demonstrated that European decapods show widely differential susceptibility to WSSV. Experimental infections of the shore crab (*Carcinus maenas*) with WSSV have found limited disease or mortality. This suggests *C. maenas* may be naturally resistant to WSSV, potentially offering an opportunity to study how this resistance is mediated.

In this project, we infected *C. maenas* with WSSV to investigate temporal changes in both the transcriptomic and miRNA responses up to $28$ days post-infection. We generated the necessary genomic resources, including a reference transcriptome and a draft genome scaffold (discussed in the abstract submitted by Verbruggen et al). Bioinformatics analyses identified relevant immune-response pathways and suggest the endocytic pathway as an important regulator of the response to WSSV in this species. In particular, a number of differentially expressed miRNAs were identified that may target Rab7; a regulator of intracellular vesicle trafficking that has previously been shown to bind to WSSV envelope protein. Differential expression of Rab7 following virus infection has been confirmed via qPCR, further supporting its role in the response to WSSV in this species. Further analysis of generated RNA-Seq data is revealing other pathways that may be important in the response of *C. maenas* to WSSV infection. We will discuss how this is bringing further understanding to host-pathogen interactions and how we envisage this to inform on new opportunities for treatment in susceptible species.

**Effect of temperature on the immune, clinical and tissue response of American lobster (Homarus americanus) experimentally infected with white spot syndrome virus**

Louise-Marie D. Roux, Philip J. Byrne, K. Fraser Clark, Spencer J. Greenwood, Glenda M. Wright, Dorota Wadowska

1Department of Biomedical Sciences, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada; 2Gulf Biodiversity Unit, Department of Fisheries and Oceans Canada, Charlottetown, PE, Canada; 3AFC Lobster Science Centre, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada; 4Department of Pathology and Microbiology, Atlantic Veterinary College, University of Prince Edward Island, PE, Canada; 5Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada; 6Electron Microscopy, Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada

Correspondence: roux@upei.ca

Water temperature influences basic life history traits of the American lobster (*Homarus americanus*) such as growth, reproduction and migration. Yet, relatively little is known about the effects of water temperature on the immune response of *Homarus americanus*. At $20\,^\circ\text{C}$, the American lobster produces a targeted immune response to intramuscular injection of White Spot Syndrome Virus (WSSV). However, under natural pathways (consumption trials at $10\,^\circ\text{C}$) no infection or disease occurs. This study will investigate the constraints imposed by a range of temperatures on the immune response of American lobster to experimental WSSV injection. A combination of light and electron microscopy will be used to examine tissue response to WSSV, as well as for evidence of viral replication. In addition, health assessments including haemocytone concentration and qPCR of haemolymph will be used to monitor the host response over time and to determine presence of viral infection, respectively. Gene expression analysis will use a lobster specific microarray and RT-qPCR to identify differentially expressed immune and temperature related genes in the host. Initial results from this study involving changes in haemocytone concentration (as an indicator of health) corroborate previous work in which experimental establishment of infection and disease only occurs at higher temperatures. The use of a range of experimental temperatures may help to explain why post-infection occurs at higher temperature. Results from the study will broaden our understanding of how temperature influences immune response and provide insight into host pathogen interactions in the American lobster.

**Paramyxes: Emergence of an enigmatic class of invertebrate parasites**

David Bass, Georgia Ward, Rose Kerr, Martyn Bennett, Rosaline Hulse, Grant D. Stentiford

Atlantic Veterinary College, University of Prince Edward Island, Charlottetown PE, Canada

Correspondence: bvas@upei.ca

Many marine invertebrates have evolved complex symbiotic relationships with viruses and the Paramyxes are an enigmatic group of viruses that causes morphological changes in crustaceans. In this exploratory study, we will sequence and characterise Paramyxes from a series of sponges and crustaceans. We will also employ electron microscopy to visualise viral structural proteins and determine the Paramyxes genome size and organisation. In addition, we will determine whether Paramyxes can cause symptoms similar to those seen in crustaceans. This will lead to the development of new treatments for Paramyxes infections in marine invertebrates.
Baculoviruses are most probably the largest group of insect-pathogenic dsDNA viruses worldwide. They co-evolved with their insect hosts in the orders Lepidoptera, Diptera, and Hymenoptera. They are classified in four genera, the Alpha-, Beta-, Gamma-, and Delta baculoviruses. Phylogenetically, baculoviruses are related to nudiviruses, bracoviruses, hytrosaviruses and most probably whispoviruses. All these viruses share a number of highly conserved structural proteins involved in the infection process, transcription, and DNA replication. Nearly 60 baculovirus genomes have been completely sequenced, so far. All sequenced baculovirus genomes share 37 conserved gene homologues, called “core genes”. It is assumed that these core genes are ancient and represent the footprint of a common ancestor of all recent baculoviruses. In an evolutionary process, the genomes of baculoviruses have been further shaped by gene insertion through lateral gene transfer from other viruses, microorganisms and hosts, genome rearrangements such as inversions, translocations of single genes or gene blocks, as well as deletions and duplications of single genes. On nucleotide level, heterogeneity is caused by nucleotide transitions, transversions, and indel mutations. Based on the arrangement of 37 baculovirus core genes in fully sequenced baculoviruses, we try to retrace major trends in genome evolution of baculoviruses and related dsDNA viruses, providing some hints about the possible genome arrangement of the common baculovirus ancestor. Using the examples of the Agrotis-specific nucleopolyhedroviruses as well as single isolates of Cydia pomonella granulovirus, micro-evolutionary trends can be delineated and correlated with alignment based phylogenies on species and isolate level of baculoviruses.
to recognize polydnaviruses. I then will discuss the more recent literature, founded on genomics and experimental data, and what these results reveal about polydnavirus evolution and function.

SYMPOSIUM PAPER Wednesday 9:12 72

Dicistrovirus - hijacking the host translational machinery

Eric Jan
Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC Canada
Correspondence: ej@mail.ubc.ca

Dicistroviruses are monopartite, plus strand RNA viruses that primarily infect arthropods of agricultural and economic significance including honey bees, fire ants and shrimp. Members of this family include Cricket paralysis virus, Taura syndrome virus and Israeli acute paralysis virus. Dicistrovirus infection results in a shutoff of host protein synthesis concomitant with preferential translation of viral proteins. The dicistrovirus utilizes a cis-acting RNA element called an internal ribosome entry site (IRES), which adopts a unique structure that directly recruits the host ribosome without the need of any translation factors and initiates translation from a non-AUG codon. Structural and biochemical analyses have revealed that the IRES partially mimics a tRNA to occupy the conserved ribosomal core in order to manipulate the ribosome for viral protein synthesis. Recent work demonstrate that a subset of dicistroviruses (honey bee and fire ant viruses) contain an IRES that can direct translation in two different reading frames thus leading to expression of a hidden +1 overlapping open reading frame. Our work suggests that distinct structural conformations of the IRES affect translational reading frame selection. These studies have revealed a novel viral strategy that uses an unprecedented RNA element that mimics a natural tRNA to directly hijack the host ribosome and initiate translation in alternative reading frames in order to increase the coding capacity of the viral genome.

SYMPOSIUM PAPER Wednesday 9:36 73

Insect metagenomics-based discovery of novel, small RNA viral genomes

Sijun Liu, Yuting Chen, Bryony C. Bonning
Department of Entomology, Iowa State University, Ames, IA 50011
Correspondence: sijun@iastate.edu

In recent years, sequences derived from more than a hundred novel RNA viruses have been found from insects and insect cell lines in the absence of disease symptoms. The vast majority of these virus genome sequences were identified on assembly and analysis of Next Generation Sequencing (NGS) data. Caution is required for interpretation of such sequence discoveries on the bases that 1) the presence of virus-derived sequences does not necessarily mean that a virus is present, and 2) viruses associated with a given insect do not necessarily infect that insect. It is therefore inappropriate to ascribe virus sequences discovered through the metagenomics approach to viruses of a particular host without experimental confirmation. Evidence for replication in the putative host is required before the virus can be assigned to that host. By analyzing Illumina transcriptome sequence data, we identified several novel small RNA viruses from the soybean aphid (Aphis glycines), Western corn rootworm (WCR) (Diabrotica virgifera virgifera) and various stink bug species. We used multiple approaches to verify these viruses, including RT-PCR and Sanger sequencing to confirm assembled viral sequences, 5'- and 3'-RACE for acquisition of the complete viral genome sequence, isolation of virions for visualization by TEM, characterization of viral proteins, examination of tissue tropism, assessment of virus transmission routes, susceptibility of cell lines to infection, and small RNA sequencing to assess the role of RNA interference in degradation of viral RNA. A combination of NGS technology, bioinformatics analysis and conventional virological methods are required for the discovery and confirmation of insect viruses.

CONTRIBUTED PAPERS Wednesday 8:00 – 9:45

Microbial Control 2

CONTRIBUTED PAPER Wednesday 8:00 74

Potential of Aprehend™ (Beauveria bassiana) as a bed bug control agent

Alexis M. Barbarin1, Nina E. Jenkins2, Giovanni Bellicanta2, Matthew B. Thomas1,2, Coby Schol1

1Department of Entomology, North Carolina State University, 100 Derieux Pl. Campus Box 7613, Raleigh, NC, 27695, USA; 2Department of Entomology, Penn State University, Merkle Lab University Park, PA 16802, USA; 3Center for Infectious Disease Dynamics, Penn State University, Merkle Lab, University Park, PA 16802, USA
Correspondence: alexis.barbarin@ncsu.edu

Pyrethroids have been a mainstay chemistry in bed bug control, yet resistance to pyrethroid insecticides is prevalent and high in field populations of bed bugs. A series of bioassays was conducted on the human bed bug Cimex lectularius, to evaluate the efficacy of Aprehend™, a Beauveria bassiana based residual insecticide, against a pyrethroid-susceptible and three field-collected strains of bed bugs. Aprehend™ was applied to box spring batting at a rate of 3 x 10³ conidia/cm² (draft label rate) using a modified sprayer. Suspend® SC (Al detsamethrin) was applied to box spring batting at both the low (maintenance, 0.03% active ingredient) and high (cleanout, 0.06% active ingredient) labeled rates, using a Potter Tower. All four strains were exposed to sprayed substrates for 15 minutes, then transferred to an unsprayed environment and monitored for mortality over a period of 14 days. Assays revealed that the three field-collected strains were resistant to Suspend® SC, whereas the laboratory strain was susceptible to Suspend® SC. A 15 min exposure to Aprehend™ caused rapid infection and mortality in bed bugs from all four strains. These results demonstrate that relatively short exposure to Aprehend™ results in mortality of pyrethroid-resistant bed bugs, highlighting the potential utility of Beauveria bassiana as an effective tool within an integrated bed bug management toolkit.

CONTRIBUTED PAPER Wednesday 8:15 75

Beauveria bassiana for the control of stored grain pests

Aoife B. Dillon1, Clare G. Storm2, Freya C. L. Scoates3, Adam J. Nunn1, Sue E. Harris2, Maureen F. Wakefield2, Belinda Luke1

1Exosect Ltd, Leylands Business Park, Colden Common, Winchester, Hampshire, SO21 1TH, UK; 2The Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, UK; 3CABI Europe-UK, Bakeham Lane, Egham, Surrey, TW20 9TY, UK; 4agrains, 18 route de Mauvérières, ZI Tivoli, Loches, France
Correspondence: Aoife.Dillon@exosect.com

Concerns over resistance development, residues and environmental impacts together with changes in EU legislation have led to a decline in available pesticides to protect stored food. Alternative products for pest control are required to maintain levels of food production and anticipate future demand. Exosect
 Selection and characterization of Colombian entomopathogenic fungi against Cerotoma tingomariana

Erika Grijalba, Carlos Espinel, Adriana Santos, Cindy Mejia, Carolina Ruiz

Biological Control Laboratory, Colombian Corporation for Agriculture Research, CORPOICA. Mosquera, Colombia
Correspondence: egrijalba@corpoica.org.co

Cerotoma tingomariana (Coleoptera: Chrysomelidae) is the most limiting pest among the Chrysomelids of soybean in Colombia, due to its high frequency and distribution. This insect can affect seeds, nodules, leaves and roots, reducing the yield crop and is controlled with insecticides that some of them are forbid in USA or Europe. The aim of this work was to select and characterize an efficient entomopathogenic fungus on C. tingomariana. Seven isolates of Beauveria bassiana (Bv) and six isolates of Metarhizium anisopliae (M1) were biological testing on laboratory. M1 isolates showed efficiency under 50%. Isolates Bv060 and Bv003 showed an efficiency of 100%. These isolates were tested on different temperatures (5°C, 15°C, 25°C, 30°C, 35°C), pH values (3, 5, 7, 9) and tolerance to UVB radiation (302 nm) by measuring germination, radial growth and Colony Formate Unit (CFU). In the UVB radiation test, Bv060 reduced the conidia viability between 75% and 80%, and Bv003 between 65% and 66%. At 5 and 9 pH value, the two isolates showed germination higher than 90% and the faster rate of radial growth. Bv003 showed the best growth at 15°C and 25°C and Bv060 at 25°C and 30°C. Lethal concentration 90 of Bv060 and Bv003 were determined in 5,8x10^-7 conidia/ml and 1,3x10^-7 conidia/ml, respectively. A compatibility test with excipients was performed by measuring germination (%) and (CFU). The isolated Bv060 was compatible with six excipients and Bv003 with seven excipients, which will be used to develop a granulated and an emulsifiable concentrate.

Obstacles and opportunities for the use of biopesticides in conventional agriculture

Surendra K. Dara
University of California Cooperative Extension, San Luis Obispo, CA, USA
Correspondence: skdara@ucdavis.edu

In 2012, poinsettia cuttings shipped into Ontario from offshore production facilities carried large numbers of Bemisia whitefly eggs and nymphs. Although releases of parasitoids (Encarsia formosa, Eretmocerus mundus) proceeded as normal, they failed to regulate whitefly populations due to pesticide residues and higher-than-usual starting populations of whiteflies. Endemic whitefly resistance meant that growers had limited (insecticide) options available to them to mitigate the pest; new early season tools are required that can be applied to cuttings to prevent pest populations developing beyond the ‘capacity’ of the parasitoids used, and to ensure that effective biological control systems can be maintained through the production cycle. Previous research showed that immersion of infested cuttings in a combination of BotaniGard® (Beauveria bassiana) and insecticidal soap prior to sticking can efficiently suppress early season infestations, mitigating larger pest problems later in the season. To ensure compatibility with subsequent releases of biocontrol agents, and improved overall efficacy, trials were undertaken to assess different strategies where the ‘Clean Start’ approach was taken, and to validate the utility of this technique on a commercial scale. Results from these trials will be presented.

CONTRIBUTED PAPER Wednesday 9:00 78

A clean start strategy for seasonal poinsettia cuttings

Michael Brownbridge1, Rose Buitenhuys2, Graeme Murphy2, Tara Saito, Angela Brommit2

1Vineyard Research and Innovation Centre, 4890 Victoria Avenue North, Box 4000, Vineland Station, Ontario LOR ZEO, Canada; 2BioLogical Control Solutions, Welland, Ontario L3C 3G9, Canada
Correspondence: michael.brownbridge@vinelandresearch.com

In 2012, poinsettia cuttings shipped into Ontario from offshore production facilities carried large numbers of Bemisia whitefly eggs and nymphs. Although releases of parasitoids (Encarsia formosa, Eretmocerus mundus) proceed as normal, they failed to regulate whitefly populations due to pesticide residues and higher-than-usual starting populations of whiteflies. Endemic whitefly resistance meant that growers had limited (insecticide) options available to them to mitigate the pest; new early season tools are required that can be applied to cuttings to prevent pest populations developing beyond the ‘capacity’ of the parasitoids used, and to ensure that effective biological control systems can be maintained through the production cycle. Previous research showed that immersion of infested cuttings in a combination of BotaniGard® (Beauveria bassiana) and insecticidal soap prior to sticking can efficiently suppress early season infestations, mitigating larger pest problems later in the season. To ensure compatibility with subsequent releases of biocontrol agents, and improved overall efficacy, trials were undertaken to assess different strategies where the ‘Clean Start’ approach was taken, and to validate the utility of this technique on a commercial scale. Results from these trials will be presented.
Biopesticide industry has been showing a consistent growth for the past few years and is projected to reach $6 billion by 2020. In spite of many major chemical companies investing in biopesticide production, their use in conventional agriculture is very limited in many cropping systems in California. Biopesticides can play an important role in integrated pest management. Understanding their modes of action, influence of various agronomic practices, impact of environmental conditions, and interaction with various pest management options will help growers and researchers to explore their full potential. Various challenges and opportunities in using biopesticides in conventional agriculture will be discussed.

CONTRIBUTED PAPER Wednesday 9:30 80-STU
Evaluation of the entomopathogenic fungi Isaria sp. as a biocontrol agent against pest insects in greenhouses
Katharina Saar1, Jasmin Phillipi2, Edgar Schliephake2, Andreas Leclerque2, Manuel Werner1, Johannes A. Jehle1, Dietrich Stephan1
1Institute for Biological Control, Julius Kühn Institute, Darmstadt, Germany; 2Institute for Resistance Research and Stress Tolerance; Julius Kühn Institute, Quedlinburg, Germany; 1Institute for Microbiology and Biochemistry, Geisenheim University, Geisenheim, Germany
Correspondence: katharina.saar@jki.bund.de

The use of the entomopathogenic fungus Isaria sp. in an integrated pest management strategy offers a promising approach for pest insect control in greenhouses. One necessary prerequisite is to find highly virulent and effective strains. Virulence of ten strains of Isaria sp., obtained from different geographical origins and hosts were compared and discriminated by their metabolic profiles and virulence against various pest insects which are up to now mainly controlled by synthetic insecticides. Using different methods, the efficacy and LC50 of different Isaria strains against Spodoptera exigua (Lepidoptera) and Bemisia tabaci (Hemiptera) were studied. The mortality rate differed depending on the isolate from 30 % to 76 %. Additionally to this mortality effects, the feeding (sucking) behaviour of Isaria-infected, by application of 1x105 conidia/ml, and non-infected adult whiteflies B. tabaci was studied, using the electrical penetration graph method (EPG). The feeding of whiteflies not only causes direct plant damages but it is also important for plant virus transmission. First results of the comparisons concerning differences in the penetration frequencies and changes within the waveform, monitored by EPG, durations will be shown.

Currently, different molecular methods, such as RFLP and others, are used for the characterisation of virulence factors of Isaria sp. and its influence on different activity patterns of B. tabaci as mentioned above.

CONTRIBUTED PAPERS Wednesday 8:00 – 9:45
Nematodes 1

CONTRIBUTED PAPER Wednesday 8:00 81
Selection of lipid and protein sources for liquid fermentation of entomopathogenic nematodes
Luis G. Leite2, David I. Shapiro-Ilan2, Selcuk Haziz2, Mark A. Jackson1
1Instituto Biologico, APTA, CP 70, Campinas, SP 13001-970, Brazil; 2USDA-ARS, SEFTNRL, Byron, GA 31008, USA; 1Adnan Menderes University, Faculty of Arts and Sciences, Department of Biology, Aydin-Turkey; 1USDA-ARS, NCAUR, Peoria, IL, 61604, USA
Correspondence: lgleite@biologico.sp.gov.br

Despite great progress in the past couple of decades, entomopathogenic nematodes production in liquid fermentation still requires improvements to maximize efficiency, yield and nematode quality. Thus, this study was aimed at developing more suitable liquid media for mass production of S. feltiae. In this phase of the project, we focused on selection of lipid and protein sources, which are critical requirements for nematode growth. Two experiments were conducted. In the first experiment, seven lipid sources (corn oil, palm oil, fish oil, peanut oil, sun oil, canola oil and pork lard) were tested at a concentration of 4%; media contents included also yeast extract (2.3%), NaCl (0.5%) and egg yolk (1.23%). In the second experiment, six protein sources (egg yolk, yeast extract, egg white, soy extract, beef extract and fish collagen) were tested at a concentration of 1.25%; media contents also included yeast extract (2.3%) and NaCl(0.5%). Also, for the second experiment, one group of treatments was run with corn oil and one group with peanut oil (both at 4%). For each treatment, 3 replications were included. Each replication, consisting of a 250 ml Erlenmeyer flask containing 50 ml of liquid media, was kept in a shaker for 28 days. Both experiments were repeated in time. For the lipid experiment, pork lard provided the lowest nematode yield, while peanut oil provided the highest. For the protein experiment, the yeast extract provided the lowest nematode yield, whereas egg yolk and egg white provided the highest.

CONTRIBUTED PAPER Wednesday 8:15 82
An unsolvable root maze: Elevated atmospheric CO2 increases root architectural complexity and reduces entomopathogenic nematode infectiousness
A. Sri Kumar, L. Demarta, S.N. Johnson, J. Hiltjold
Hawkesbury Institute for the Environment, University of Western Sydney, Penrith, NSW, Australia

Atmospheric CO2 concentration is now higher than it has ever been over the last 400,000 years. Because CO2 concentration is typically 10-fold higher in soil, direct effect of elevated CO2 [eCO2] on rhizospheric trophic cascades is supposed to be limited. However, eCO2 impacts root architectural complexity. Little is known about the physical role of root on entomopathogenic nematode (EPN) foraging behavior; yet, increasing root architecture complexity weakens the infectiousness of the EPN Heterorhabditis megidis. To evaluate the impact of atmospheric CO2 concentration on EPN infectiousness, maize plants were grown in either ambient or eCO2 environments before insect baits were placed at the bottom of each pot. The number of adult of the EPN Heterorhabditis bacteriophora present in baits was recorded 36h after their injection. Atmospheric eCO2 favored EPN infectiousness in pots with soil only. However, the dramatic increase in root architecture of plants grown at atmospheric eCO2 significantly reduced EPNs infectiousness; less EPN adults were recovered from these baits than from baits at the bottom of plants grown at ambient atmospheric CO2. These results add to the scarce data on the impact of root complexity on EPN infectiousness. Even though it is often thought that atmospheric eCO2 has minimal impact on soil communities, especially in agricultural systems, the increase in atmospheric CO2 concentration negatively affected the present belowground trophic cascade, possibly leading to the reduction of specific soil ecological services in soil-dwelling insect pest management.

CONTRIBUTED PAPER Wednesday 8:30 83-STU
Investigating Deladenus siricidicola Kamona (Tylenchida: Neotylenchidae) to control Sirex noctilio (Hymenoptera: Siricidae) In North America
Interactions between co-infesting nematodes and bacteria in host flies shows marked variation in susceptibility to infection. These nematodes infect fly hosts by piercing a hole in the larval cuticle with a harpoon-like stylet, after which they devolve within host haemocoel. This method of entry leaves the larval flies vulnerable to pathogenic bacteria that gain direct access to host haemolymph through this hole. As *Howardula* require their fly hosts to complete development for transmission, this raises intriguing questions regarding the fly’s response to these unwelcome guests. To assess the effects of interactions amongst co-infesting natural enemies, we investigated the responses of Testacea group flies to nematodes and bacteria in larvae and adults. We orally infected Testacea group flies with a *Serratia* bacterium we isolated from *Drosophila*; *Serratia* is a common soil bacterium and model of intestinal infection in *Drosophila*. We later co-infected larval and adult flies with *Howardula aoronymphium* and *Serratia*, and determined their effects on host fitness. We found interesting variation in Testacea group responses to *Serratia* infection, and describe the effects of co-infection with nematodes and bacteria on host fitness.

CONTRIBUTED PAPER Wednesday 8:45  84-STU

**Interactions between parasitic nematodes and bacteria in *Drosophila***

M. A. Hanson, S. J. Perlman

Biology Department, University of Victoria, Victoria BC, Canada

Correspondence: markhans@uvic.ca

The filarial nematode *Brugia malayi* is one of the causative agents of lymphatic filariasis, a neglected tropical that affects millions of people worldwide. Due to the limited effectiveness of the drugs available and the absence of a vaccine, understanding the basic biology of *B. malayi* and its symbiotic association with Wolbachia endobacteria is a priority. At present, little is known about the mechanisms underlying *Brugia*’s immune system. This overlooked area of research is of high interest, as it can help to advance our understanding on the interaction between *Brugia* and *Wolbachia*. It has been suggested that in order to reside within the nematode’s tissue, *Wolbachia* may evade the host immune system. Therefore, understanding what mechanisms are involved in *Brugia* immunity can help in identifying targets for the development of new drugs and vaccines. In order to characterize the main genetic pathways involved in *B. malayi* immunity, we performed a transcriptome analysis of adult female worms exposed to different immune elicitors, including bacterial lysetes, short dsRNA, and dsDNA. Small RNA and differential gene expression analysis of untreated and immune challenged worms were used to characterize gene expression patterns associated to each type of immune insult and allowed to identify selected candidate immune genes.

CONTRIBUTED PAPER Wednesday 9:15  86-STU

**One ring to bind them all: Is heme biosynthesis an influencing factor in *Wolbachia*-filarial nematode endosymbiosis?***

Ashley N. Luck, Jeremy M. Foster, Barton E. Slatko

Genome Biology Division, New England Biolabs, 240 County Road, Ipswich, MA 01938

Correspondence: Slatko@neb.com

Genomic sequencing has revealed that many human filarial nematodes, such as *Wuchereria bancrofti, Brugia malayi* and *B. timori*, (causative agents of lymphatic filariasis (LF) and Onchocerca volvulus (causative agent of onchocerciasis (river blindness)) contain the obligate endosymbiont, *Wolbachia*. Laboratory and human trials show that depletion of *Wolbachia* by antibiotics (e.g. doxycycline), can lead to blocking of embryogenesis, elimination of microfilariae (mf) output and adult worm killing. While the factors which are key to this obligate inter-relationship are not fully understood, genome sequencing identified a number of critical processes implicated in the host-endosymbiont interaction, one of which was heme biosynthesis. By serving as a co-factor in a number of enzymatic and biochemical processes, heme and heme regulation is essential to organism survival. Although *B. malayi* contains a functional ferrochelatase gene (the final step in the heme biosynthetic pathway and a product of lateral gene transfer), as with other nematodes they are incapable of synthesizing heme. However, the *Wolbachia* genome contains a complete and functional heme biosynthesis pathway, suggesting that *Wolbachia* may supply the host nematode with heme. Exploiting "NextGen" transcriptome and DNA sequencing, we have investigated differential expression patterns of the host and symbiont responses to heme in filarial nematodes. Numerous heme response genes (hrgs) from both organisms are differentially expressed in the presence of heme. Several show homology hrgs found in the free living nematode, *C. elegans*, that does not contain *Wolbachia*. RNAi and inhibitor
Uncontrolled growth of bacterial T6SS will further increase our understanding of the bacteria outcompete the attenuated strains. Examining the role of this bacterium’s virulence. Our results suggest that virulent the T6SS is involved in intra-bacterial competition. Preliminary results indicate a type VI secretion system in its genome of this bacterium revealed a type VI secretion system and four attenuated strains were identified. Analysis of the pan-genome of this bacterium, revealed a type VI secretion system (T6SS) present only in virulent strains. Recent studies have shown that PirB toxin can be coupled to Cry2A toxin and have insecticidal activity when delivered per os to Spodoptera exigua. However, the combined activity of this toxin chimera is apparently host-specific. Additionally, it has been suggested that PirB can be insecticidal without PirA as long as similar structural domains, putatively for membrane recognition, are adequately replaced. Recently, the shrimp pathogen Vibrio parahemolyticus, which causes acute hepato-pancreatic necrosis disease in farmed shrimp populations, has been investigated for its toxins and its pathogenic properties. Bioassays have confirmed the pathogenic activity of PirAB-like toxins in shrimp, but until now no insect pathogenic effect has been assessed. We hypothesized that Vibrio PirAB-like toxins in combination with Bt Cry toxins may have effects similar to other Pir/Cry combinations. In this respect, we have further investigated interactions between Cry1AC/2Ab toxins with Pir toxins from two Photorhabdus spp.: P. luminescens, P. asymbiotica, and from V. parahaemolyticus. Using selected insect species, we have investigated cellular components of host gut- tissue, protein and lipids, involved in the interaction with Cry and Pir toxins. We have further characterized the toxicity of PirAB with Cry1AC/2Ab by analyzing toxin response pathways upon ingestion. Finally, we have investigated binding/receptor recognition, insecticidal motifs, structure, and homology of Vibrio PirAB sequence, considering a bioinformatics approach. Results of these studies will be presented and further discussed.

**Insecticidal action, cellular interactions and response of combinations of Photorhabdus-Insect-Related (Pir) and Bacillus thuringiensis Crystal (Cry) Toxins**

*Anaïs Castagnola*¹, *Rousel Orozco*², *Kathy Teng-Nelson*¹, *Don Lightner*³, *Patricia Stock*²

¹Center for Insect Science, University of Arizona, Tucson; ²Entomology Department, University of Arizona, Tucson; ³School of Animal and Comparative Biomedical Sciences, University of Arizona, Tucson

Correspondence: anais@email.arizona.edu

*Response to Cry1Ac intoxication in midgut cells of Heliothis virescens larvae*  
*Cris Oppert*¹, *Omaathache P. Perera*¹, *Thomas Lane*², *Margaret Staton*¹, *Heba M. Abdelgaffar*³, *Juan Luis Jurat-Fuentes*³

¹Department of Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA; ²USDA-ARS, Southern Insect Management Research Unit, Stoneville, MS, USA

Correspondence: jurat@utk.edu

The Cry1 insecticidal proteins from the bacterium Bacillus thuringiensis (Bt) target insect midgut cells. While still under discussion, the specific mechanism of entomocyte killing is associated with binding of the Cry1 proteins to receptors followed by insertion and formation of toxin-lined pores on the cell membrane. Alternative proposed models suggest the possibility of intracellular cell death pathways activated by binding of the toxin to receptors as being responsible for entocyte death. To elucidate the importance of intracellular pathways in entocyte death and the identification of defensive responses to the bacteria, we performed transcriptome profiling by RNAseq using midguts of Heliothis virescens larvae exposed to Cry1Ac or a Bt-based pesticide. Moreover, we included in the comparison H. virescens strains with high levels of resistance to the Cry1Ac protein due to highly reduced Cry1Ac protein binding. Gene expression comparisons between controls (untreated) or unaffected (resistant) and susceptible larvae identify intracellular pathways involved in entocyte death as well as putative defensive mechanisms. In this presentation we will report findings from this analysis and discuss their relevance to current models of Cry1 intoxication in Lepidoptera.

**Syringe-like injection mechanism of bacterial ABC toxins revealed in molecular detail**

*Christos Gatsogiannis*¹, *Dominic Meusch*¹, *Alexander E Lang*², *Klaus Aktories*², *Stefan Rauwerd*²

¹Department of Structural Biochemistry, Max Planck Institute of Molecular Physiology, Dortmund, Germany; ²Institut für
ABSTRACTS

Tc toxin complexes are dominant virulence factors of many pathogenic bacteria such as the Far East scarlet-like fever pathogen Yersinia pseudo tuberculosis, the plague pathogen Yersinia pestis and the insect pathogenic Photorhabdus luminescens. They are typically composed of TcA, TcB and TcC subunits that are only biologically active as tripartite complexes. TcB and TcC together form a closed cage, that encapsulates and sequesters the cytotoxic, C-terminal region of TcA. The largest class of bacterial pore-forming toxins (PFTs), produced by a variety of human pathogens. The cell biology of these toxins (PFTs), produced by a variety of human pathogens. The cell biology of these toxins (PFTs), produced by a variety of human pathogens.

Here we show that TcA in Photorhabdus luminescens (TcdA1) forms a transmembrane pore and is required for survival of the nematode host. The cell biology of these toxins (PFTs), produced by a variety of human pathogens.

The cell biology of these toxins (PFTs), produced by a variety of human pathogens. Filarial nematodes maintain a mutualistic relationship with the bacterial endosymbiont Wolbachia, however the molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear.

Our results allow us for the first time to understand key steps of infections involving ABC toxins at molecular level and shed new light on the interaction of the bacterial pathogens with their hosts.

The cell biology of Wolbachia-filarial nematode interactions and the dark side of symbiosis

Filarial nematodes maintain a mutualistic relationship with the bacterial endosymbiont Wolbachia, however the molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear. In embryos derived from B. mayali, the causative agent of lymphatic filariasis, we find the normal molecular and cellular basis of this relationship remains unclear.
the mechanism and evolutionary implications of this. Finally, to put our analyses into context we have performed whole genome sequencing of a range of P. asymbiotica isolates from different continents to derive a whole genome phylogeny of these human pathogenic strains.

CONTRIBUTED PAPERS Wednesday 10:30 – 12:30
Fungi 1

RNA-seq analysis reveals the potential antioxidant pathways regulated by multiprotein bridging factor 1 (BbMBF1) in the fungal entomopathogen Beauveria bassiana

Xin-Ling Chu, Ming-Guang Feng, Sheng-Hua Yang
College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, China
Correspondence: yingsh@zju.edu.cn

Oxidation resistance is crucial to environmental fitness and potency of the fungal entomopathogen Beauveria bassiana. Multiprotein bridging factor 1, an evolutionarily conserved transcriptional cofactor, plays an important role in development and stress tolerance of eukaryotic organisms. It has been established that the B. bassiana homolog (BbMBF1) contributes to the fungal response to menadione stress under lower nutritional conditions. Present study indicated that rich nutrient reduces the fungal sensitivity to menadione stress, but further confirmed that the BbMBF1 is also required for the fungal tolerance to oxidation under rich nutritional conditions. To explore the down-stream targets regulated by BbMBF1 under menadione stress, a comparative transcriptome was performed on the wild type and the ΔBbMBF1 mutant strains. Transcriptomic analysis showed that the oxidation-response genes regulated by BbMBF1 were significantly enriched in the functional catalogs of metabolism, cell rescue, and transportation. Moreover, bioinformatic analysis predicted a putative motif which distributed mainly over the promoters of genes associated with metabolism and detoxification. Conclusively, these results indicate that BbMBF1 contributes to B. bassiana response to oxidative stress by mediating the potential transcription factors regulating pathway of metabolism and detoxification. These findings highlight the potential antioxidant strategies in the fungal entomopathogens, and provide the new clues/targets for improving potency of entomopathogenic fungi by molecular manipulation.

CONTRIBUTED PAPER Wednesday 10:45
Unveiling a link of the Fus3 pathway to the biological control potential of Beauveria bassiana

Zhi-Dong Wang, Ming-Guang Feng
Institute of Microbiology, College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, China
Correspondence: mgfeng@zju.edu.cn

The Fus3 pathway comprises the cascaded protein kinases Fus3 (MAPK), Ste7 (MAPKK) and Ste11 (MAPKKK) in filamentous fungi and has not been fully explored in fungal insect pathogens. In this study, we characterized the cascaded proteins and upstream Ste50 in Beauveria bassiana. Single-deletion mutants of four genes coding the proteins grew slower and conidiated less than wild-type, and lost whole virulence due to an incapability their penetrating through insect cuticle. Cell cycle analysis of their unicellular blastospores revealed significantly longer G2/M transition, which was evident with weakened phosphorylation signal of cyclin-dependent kinase 1 (Cdc1) required for normal cell cycle. In addition, the four deletion mutants showed different degrees of increased sensitivities to nutritional, fungicidal, thermal, and UV-B radiative stresses. The results highlight a link of the Fus3 pathway to the biological control potential of B. bassiana.

CONTRIBUTED PAPER Wednesday 11:00
Contributions of monothiol glutaredoxin and glutathione reductase to antioxidant capability and biological control potential of Beauveria bassiana

Long-Bin Zhang, Li Yang, Ming-Guang Feng
Institute of Microbiology, College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, China
Correspondence: mgfeng@zju.edu.cn

Glutaredoxins (Grx) involved in cellular thiol-disulfide redox system function in conjunction with thioredoxins but are poorly understood in fungal filamentous insect pathogens. Beauveria bassiana harvests five Grx homologs (Grx1-5) and one glutathione reductase (Glr), which are classified to the distinct clades dithiol Grx, monothiol Grx and Grx-like protein respectively. Deletion of a grx homolog of glr resulted in transcriptional compensation of other partners despite undeletable grx3. Deletion of grx3 or glr reduced significantly the activities of the antioxidant enzymes superoxide dismutases (SODs), glutathione-peroxidase and oxidized/reduced glutathione. Consequently, the Δglr and Δgrx3 mutants became significantly more sensitive to two oxidants (H2O2 and menadione) and two thiol oxidizing agents than wild-type during conidial germination and colony growth. The two mutants showed remarkable defects in conidiation, conidial germination, conidial thermostolerance, conidial UV-B resistance and virulence. In addition, intracellular iron homeostasis was biased in the Δglr and four Δgrx mutants. Among the characterized proteins, Grx3 and Glr were proven to play much more important roles in regulating cellular redox homeostasis and antioxidant responses than other Grx homologs except Grx4, thereby contributing significantly to the biological control potential of B. bassiana.

CONTRIBUTED PAPER Wednesday 11:15
The Pal pathway regulates growth, conidiation, acidification, osmotic stress and virulence in Beauveria bassiana

Jing Zhu, Ming-Guang Feng
Institute of Microbiology, College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, China
Correspondence: mgfeng@zju.edu.cn

Adaption to environmental pH is critical for fungal survival and host infection and regulated by the Pal pathway in filamentous fungi. The Pal pathway of Beauveria bassiana comprises PacC and PalA/B/C/F/H/I homologs. Alkaline and stressful conditions upregulated much more transcriptional expression of pacC than the pal genes in wild-type. Single-deletion mutants of these genes except ΔpolI showed growth defects in an alkaline medium (pH 9.0) but grew as well as wild-type in an acidic medium (pH 3.0). For all the deletion mutants, conidiation level was increased under acidic and neutral conditions but slightly decreased under alkaline conditions except for an increase in ΔpolI, followed by increased size and density of their conidia. Extra- and intracellular production of organic acids, such as lactic acid, oxalic acid and citric acid, was up- or down-regulated by different degrees and hence resulted in much delayed acidification in their liquid cultures, accompanied with transcriptional up-regulation of

ABSTRACTS
ABSTRACTS

CONTRIBUTED PAPER Wednesday 11:30 98-STU
Regulative role of a novel Ras GTPase (Ras3) in conidiation, stress responses and virulence and its involvement in the HOG pathway of Beauveria bassiana
Yi Guan, Ding-Yi Wang, Ming-Guang Feng
Institute of Microbiology, College of Life Sciences, Zhejiang University, Hangzhou, Zhejiang, 310058, China
Correspondence: mfgfeng@zju.edu.cn

Two Ras GTPases (Ras1 and Ras2) are well known to regulate antagonistically or cooperatively various cellular events in many fungi, contrasting to a novel Ras homolog (Ras3) not characterized in filamentous fungi. Ras3 in Beauveria bassiana has five domains and two GTP/GDP switches typical for the Ras family and was proven to localize in plasma membrane in this study. Deletion of ras3 altered greatly temporal transcription patterns of ras1 instead of ras2. Compared with wild-type, Δras3 grew significantly faster in a rich medium but slower in some minimal media, and produced far fewer conidia with impaired quality, which was evident with slower germination, altered tolerance, reduced thermotolerance and decreased UV-B resistance. Moreover, Δras3 was much more sensitive to the oxidative stress of menadione than of H2O2 and to the stress of high osmolarity than of cell wall perturbation during growth. All the phenotypic changes were restored by ras3 complementation. The high sensitivity of Δras3 to manadione was concurrent with depressed gene transcripts and reduced total activity of superoxide dismutases. Intriguingly, the high osmosensitivity was concurrent not only with drastically depressed transcripts of a critical transcription factor (Msn2) and most signaling proteins in the Hog1 pathway but with largely weakened phosphorylation signal of Hog1 hallmarking the transcription factor (Msn2) and most signaling proteins in the Hog1 pathway. Overall, Ras3 is involved in the Hog1 pathway required for cellular osmoregulation and hence can mediate positively conidiation, germination, multi-stress tolerance and virulence linked to the biological control potential of B. bassiana.

CONTRIBUTED PAPER Wednesday 11:45 99-STU
A genome wide association study of resistance to Metarhizium anisopliae
Jonathan B. Wang, Hisao-Ling Lu, Raymond J. St. Leger
Entomology Department, University of Maryland, College Park, MD, USA
Correspondence: jowang@umd.edu

In a sister study to this one we screened more than 2,500 mutations for their effects on disease resistance. A complementary approach to mutagenesis is to identify loci at which alleles with more subtle effects segregate in natural populations. Single nucleotide polymorphisms (SNPs), insertions, and deletions in a natural population of flies are mutations that have survived the filter of natural selection and can be tested via genome-wide association (GWA) for effects on genetic variation in resistance. Here we used 203 fly lines from the Drosophila Genetic reference Panel (DGRP) to identify SNPs associated with natural variation to disease resistance. Using topical infections with Metarhizium anisopliae (MaS49), we calculated LT50’s, fungal loads, latent period (interval between infection and sporulation), and sporulation capacity. All parameters were genetically variable among the DGRP lines and LT50s were sexually dimorphic. We identified many SNPs in novel loci that are potentially associated with natural variation in disease resistance, as well as SNPs within genes previously known to affect resistance. Many of these loci are known to interact physically and/or genetically, enabling us to place them in candidate genetic networks. Several of the candidate genes have human homologues that were identified in studies of human disease, suggesting that genes affecting variation in susceptibility are conserved across species.

CONTRIBUTED PAPER Wednesday 12:00 100-STU
GeoChip analysis of the soil microbial community in turf and winter wheat treated with genetically modified Metarhizium anisopliae
Brian Lovett, Raymond St. Leger
University of Maryland, College Park
Correspondence: lovettbr@umd.edu

The availability of genome sequences and robust technologies have allowed production of genetically manipulated Metharizium strains that could represent a major new arsenal for combating pest insects and enhancing plant growth. However, for these tools to be used safely, we need thorough understanding of the impact they would have in a new environment. This research examines how intensive deployment of transgenic M. robertsi impacts microbial communities in the soil root interface (a preferred habitat of Metarhizium) in natural (turf) and agricultural (winter wheat) field sites. In our investigation, we employed a high-throughput metagenomic tool (GeoChip 4.6) that is able to assess all functionally known geochemical, ecological, and environmental processes including N, C, S, and P cycling, metal reduction and resistance, and organic xenobiotic degradation. Our study provides a comprehensive analysis into how and to what extent applied Metharizium robertsi can alter community structure and key functional roles. As well, this study provides a unique opportunity to use a global-scale methodology to compare the activity of the microbial communities of agricultural versus natural soil systems and of bulk soil versus the rhizosphere.

CONTRIBUTED PAPER Wednesday 12:15 101
Diversity and distribution of Metarhizium flavoviride in agroecosystems: An overlooked entomopathogenic fungus?
Chad A. Keyser, Henrik H. De Fine Licht, Bernhardt M. Steinwender, Nicolai V. Meyling
Department of Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, 1871 Frederiksberg, Denmark
Correspondence: nvm@plen.ku.dk

Knowledge of the natural occurrence and community structure of entomopathogenic fungi is important to understand their ecological role. Within the genus Metarhizium, the species M. flavoviride has received little attention and intra-specific diversity among isolate collections has never been assessed. We found M. flavoviride to be abundant among Metarhizium spp. isolates obtained from roots and root-associated soil of winter wheat, winter oilseed rape, and neighboring uncultivated pastures at three geographically separated agricultural fields in Denmark, and we evaluated the molecular diversity to resolve the potential population structure of M. flavoviride. Of the 132 Metarhizium isolates obtained, morphological data and DNA sequencing revealed that 118 belonged to M. flavoviride, 13 to M. brunneum and one to M. majus. Further characterization of intraspecific variability within M. flavoviride was achieved by using amplified fragment length polymorphism (AFLP) to evaluate diversity and potential crop and/or area associations. A high level of diversity among the M. flavoviride isolates was observed. However, no
population structure in the form of significant haplotype groupings or habitat associations could be determined among the 118 analyzed M. flavoviride isolates. The ecological significance and natural distribution of M. flavoviride will be discussed by including earlier observations in Denmark.

CONTRIBUTED PAPERS Wednesday 10:30-12:30

Viruses 3

CONTRIBUTED PAPER Wednesday 10:30 102

Insecticidal parameters for the baculovirus infecting Agrotis ipsilon neonates

Robert W. Behle
USDA-ARS-NCAUR, Crop Bioprotection Research Unit, Peoria, Illinois, USA

Correspondence: robert.behle@ars.usda.gov

The recently discovered multi-nuclear polyhedrosis virus capable of infecting larvae of the Agrotis ipsilon (Hufnagel) (black cutworm) has the potential to be developed as a biological insecticide for controlling this polyphagous pest of crops. High toxicity and short lethal time are necessary characteristics for the virus to provide effective control and prevent plant damage, but are not interchangeable as assessments for treatment evaluations. Toxicity (LC50) and lethal time (LT50) were determined using a droplet-feeding laboratory assay with neonates. Prob analysis calculated the LC50 to be 1.2 x 10^3 occlusion bodies (OB) ml^-1. Lethal times were determined for larvae killed by virus after exposure to one of four virus dosages representing the estimated LC50, LC50, LC50, and LC50 concentrations (0.51 x 10^3, 1.2 x 10^3, 3.0 x 10^3, and 10.7 x 10^3 OB ml^-1), with LT50 values of 67.1, 65.3, 64.4, and 61.5 hours, respectively. Thus, LT50 values for larvae exposed as neonates decreased significantly, although only slightly with increasing virus concentration. Altering experimental conditions such as the type of experiment (laboratory versus field), type of exposure (acute versus chronic), and larval size at the time of exposure will likely impact values for toxicity and lethal time. The low LC50 and short LT50 reported here demonstrate the suitability of this agent for further consideration as a biopesticide for control of A. ipsilon, although additional studies are necessary to select appropriate parameters to measure for future research to support product development.

CONTRIBUTED PAPER Wednesday 10:45 103

Haemocytes from Crassostrea gigas and OsHV-1: A promising in vitro model to study host/virus interactions

Benjamin Morga1, Nicole Foury1, Tristan Renault1

1Ifremer (Institut Français de Recherche pour l’Exploitation de la Mer) Laboratoire de Génétique et Pathologie des Mollusques Marins, La Tremblade, France; 2Ifremer Département Ressources Biologiques et Environnement, Nantes, France

Correspondence: benjamin.morga@ifremer.fr

Since 2008, mass mortality outbreaks associated with OsHV-1 detection are reported in Crassostrea gigas spat and juveniles in several countries. Some recent studies reported information on viral replication during an experimental infection. Viral RNA detection was noticed in spat mantle 4h post virus suspension injection. Moreover, an in situ hybridization approach showed that OsHV-1 mRNAs were mainly present in the connective tissue of gills, mantle, adductor muscle, digestive gland and gonads following the injection of the virus suspension in the muscle. Consequently, one hypothesis putted forward is that the virus could be transported by the haemolymph. In oyster haemolymph contains immune cells, the haemocytes. In this context, is the virus transported in the haemolymph or is it able to initiate a replication in haemocytes? No marine mollusc cell lines are available. In the present study, we have thus collected haemocytes from the adductor muscle of C. gigas spat and put them in vitro in contact with a viral suspension. Results showed that viral RNA were detectable one hour after contact and the number of virus transcripts increased across the time of contact in association with an increase of viral DNA detection. These results suggested that the virus is able to initiate replication rapidly inside haemocytes maintained in vitro. These in vitro trials were also used to carry out a dual transcriptomic study. We analysed concomitantly the expression of some host immune genes and the expression of viral genes. Results showed an up regulation of oyster genes currently studied in this model during an OsHV-1 infection. All the results suggest that the in vitro model based on the use of haemocytes can be a valuable model opening new perspectives host – pathogen interactions.

CONTRIBUTED PAPER Wednesday 11:00 104-STU

Comparison of viral growth characteristic of two nucleopolyhedroviruses isolated from the genus Adoxophyes Yasumasa Saito1, Yasushiro Kurniimit2, Maki N. Inoue1, Madoka Nakao2

1Laboratory of Biological Control, United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology, 3-5-8 Saiwi-cho, Fuchu, Tokyo 183-8509, Japan; 2Japan Society for the Promotion of Science

Presenting: saitoysasu@gmail.com

Correspondence: madoka@cc.tuat.ac.jp

The smaller tea tortrix, Adoxophyes honmairai (Lepidoptera: Tortricidae), is susceptible to two nucleopolyhedroviruses (NPVs), A. honmairai NPV (AdhoNPV) and A. orana NPV (AdorNPV), which are genetically closely related but differ in killing speed. AdhoNPV is slow-killing and the infected host is always killed in the final instar regardless of the infection timing, whereas AdorNPV is fast-killing and it kills the host in the first or second instar. In this study, we investigated whether killing speed of both viruses are related to viral growth speed. Second and 4th instars of A. honmairai were orally inoculated with >LC50 of AdhoNPV or AdorNPV. Then, each inoculated host was collected every 24h and larval weight and viral DNA were quantified. Viral DNA was measured by qPCR and the growth curve was fit to "modified Gompertz model" which consists of three parameters as maximum concentration of viral DNA (A), maximum rate of viral increase (µr) and time lag. Mean lethal time of 2rd and 4th instar infection was 15 and 7 days, and 10 and 8 days for AdhONPV- and AdorNPV-inoculated host, respectively. For 2nd instar inoculation, “A” of AdhoNPV-infected was significantly higher than those of AdorNPV-infected, whereas “µr” of AdorNPV-infected was significantly higher than that of AdhoNPV-infected. On the other hand, there was no significant difference of both parameters between AdhoNPV and AdorNPV at 4th instar inoculation. In conclusion, the higher viral growth speed (µr) can be attributed to faster killing speed of AdorNPV as compared to AdhoNPV at 2nd instar inoculation.

CONTRIBUTED PAPER Wednesday 11:15 105-STU

A novel type of resistance of the codling moth against Cydia pomonella granulovirus shows two different resistance mechanisms

Annette J. Sauer, Manuela M. Gebhardt, Eva Fritsch, Karin Undorf-Spahn, Johannes A. Jehle
Control of codling moth (CM, *Cydia pomonella*) in pome fruit production is successfully achieved by applying *Cydia pomonella* granulovirus (CpGV, *Baculoviridae*). Since 2005, CM populations resistant to the widely used isolate CpGV-M have been found in about 40 orchards in different European countries. The resistance allele of most of these populations is assumed to be dominant and located on the sex-chromosome Z. Most populations can be controlled by resistance-breaking isolates, such as CpGV-S. However, one population in Germany showed resistance to both CpGV-M and the resistance-breaking isolate CpGV-S. In order to elucidate this unusual type of resistance, successive mass crossings of this population were carried out under virus pressure to establish a genetically homogeneous resistant CM strain, called CpRSM. Subsequent reciprocal crossing experiments with CpRSM and a susceptible laboratory CM strain (Cps) followed by bioassays revealed a dominant but autosomal inheritance. Whereas CpRSM was also resistant to mixed infections with CpGV-M and CpGV-S, CpRSM was fully susceptible to a recombinant CpGV-M carrying the pe38 of CpGV-S. These results suggest that two independent resistance mechanisms, one directed against pe38 of CpGV-M and a second one directed against an unknown factor of CpGV-S but not present in CpGV-M are involved in this type of resistance. Because a recombinant genome of CpGV-M and CpGV-S but not a mixture of CpGV-M and CpGV-S can overcome this novel type of resistance, it is further concluded that resistance to CpGV-S is most likely directed to an extracellular receptor, whereas resistance to CpGV-M is systemically directed via pe38.

**CONTRIBUTED PAPER Wednesday 11:30 106-STU**

**Nucleopolyhedrovirus and microsporidia in winter moth (Operophtera brumata) and bruce spanworm (O. bruceata) populations in the northeastern U.S.**

Hannah J. Bradley¹, Joseph S. Ellikton¹, John P. Burand², Matt L. Zink¹, Leenlen F. Solter²

¹Organismic and Evolutionary Biology, University of Massachusetts, Amherst, MA, U.S.A.; ²Department of Microbiology, University of Massachusetts, Amherst, MA, U.S.A.; ³Department of Natural Resources and Environmental Sciences, University of Illinois, Champaign, IL, USA

Correspondence: hbroadley@cns.umass.edu

Winter moth (WM, *Operophtera brumata*), a polyphagous geometrid, was accidently introduced to the northeastern United States from Europe in the 1990s. Since its introduction, WM has exhibited population outbreaks. However, its native congener, Bruce spanworm (BSW, *O. bruceata*), rarely outbreaks. We propose that this difference in population dynamics exists because BSW experiences different pathogens, which may exist at higher prevalence or be more virulent. Field collected WM and BSW larvae were reared in the lab and percent mortality was noted for 2013 and 2014. Cadavers were examined microscopically for evidence of nucleopolyhedrovirus (NPV) and microsporidia (possibly *Nosema sp.* infections). For both species, we amplified the polyhedron and p74 gene from NPV isolates and compared them using phylogenetic analysis. To test for cross infection, WM eggs were surface sterilized, induced to hatch, and fed diet infected with BSW NPV. Moribund larvae were analyzed for NPV. Across years, BSW larvae suffered higher mortality (~26%) than did WM (~3.2%). BSW had higher rates of microsporidian infection (23x higher), while WM experienced higher rates of NPV (3.3x higher). The BSW polyhedron gene sequence was only 82% identical to WM, while the p74 sequence was most closely related to, but distinct from, WM. This indicates that NPV infecting these species are different but only recently diverged. In cross-infection trials, BSW NPV did not infect WM larvae. In conclusion, WM and BSW experience different pathogens at different rates. Understanding the activity of epizootics in these species may provide insight into biological control agents for WM.

**CONTRIBUTED PAPER Wednesday 11:45 107-STU**

How climate and host behaviour influence nucleopolyhedrovirus infection dynamics in the western tent caterpillar

Paul R. MacDonald¹, Judith H. Myers², Jenny S. Cory²

¹Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada; ²Department of Zoology, University of British Columbia, Vancouver, BC, Canada

Correspondence: pmacdonal@sfu.ca

Western tent caterpillar (WTC) populations display cyclical dynamics with 8-11 year periodicity in southwestern B.C. Long-term population data show that nucleopolyhedrovirus (NPV) is an integral component of these dynamics, with high incidence of viral mortality coinciding with substantial population decline. Our research involves two areas of NPV transmission that remain unclear. Firstly, how climate influences NPV transmission and secondly, how host behaviour contributes to transmission and the eventual formation of an epizootic. Using historical population and weather data we have shown a correlation between warm springtime temperatures and heightened levels of NPV infection. We conducted a series of laboratory and field-based experiments that suggest possible mechanisms for this observation. Additionally, we have conducted experiments that reveal whether infected hosts differ from uninfected hosts in their behaviour and discuss how these differences could facilitate NPV transmission at the population scale. We conclude by discussing how empirical evidence and theoretical modelling may be used to predict how WTC population dynamics behave under various climate and behavioural scenarios.

**CONTRIBUTED PAPER Wednesday 12:00 108-STU**

The specialist baculovirus SeMNPV induces light-dependent tree-top disease in *Spodoptera exigua* caterpillars facilitated by the viral egt gene

Yue Han¹, Stineke van Houte¹, Monique M. van Oers², Vera J. D. Ros²

¹Laboratory of Virology, Wageningen University, Droevendaalsesteeg 1, 6708 PB, Wageningen, the Netherlands; ²Centre for Ecology and Conservation, Biosciences, University of Exeter, Penryn, Cornwall, United Kingdom

Correspondence: yue.han@wur.nl

Many parasites enhance their transmission by manipulating host behaviour. One example concerns baculoviruses that induce hyperactivity and tree-top disease (i.e. climbing to elevated positions prior to death) in their caterpillar hosts. Little is known about the underlying mechanisms of such parasite-induced behavioural changes. Here, we studied tree-top disease in *Spodoptera exigua* caterpillars induced by the specialist baculovirus *S. exigua* multiple nucleopolyhedrovirus (SeMNPV). We found that SeMNPV induced positive phototactic climbing behaviour prior to death in *S. exigua* larvae. In addition, we showed that larvae infected with a mutant virus lacking the edysteroid UDP-glucosyltransferase (egt) gene showed a shorter time to death and died before the onset of phototaxis.
deletion of either the open reading frame or the ATG start codon of the egt gene prevented tree-top disease, indicating that the EGT protein is required for tree-top disease. We hypothesize that EGT facilitates the phototactic climbing behaviour via prolonging the larval time to death.

CONTRIBUTED PAPER Wednesday 12:15 109 Baculovirus-induced tree-top disease revisited: The role of the egt gene
Vera I. D. Ros¹, Yue Han¹, Stíneke van Houte²,³, Monique M. van Oers
¹Laboratory of Virology, Wageningen University, Droevendaalsesteeg 1, 6708 PB, Wageningen, the Netherlands; ²Centre for Ecology and Conservation, Biosciences, University of Exeter, Penryn, Cornwall, United Kingdom
Correspondence: vera.ros@wur.nl

Baculoviruses-infected caterpillars climb to elevated positions prior to death, a phenomenon known as ‘tree-top disease’. The past years, several studies have focused on the underlying mechanism, considering a range of baculovirus-host systems. Particularly, the role of the viral ec dys teroid UDP-glucosyltransferase (egt) gene has received attention. In some virus-host interactions egt seems to induce tree-top disease, while in other systems egt has no apparent role in tree-top disease or has an indirect role, through affecting the time to death and/or moulting-related climbing behaviour. Here, we review the current knowledge on the mechanism of tree-top disease, including an overview on the role of the egt gene.

SYMPOSIUM Wednesday 14:00 – 16:00
Endophytic Entomopathogenic Fungi: “Pro-biotic” Microbial Associates of Plants?

SYMPOSIUM PAPER Wednesday 14:00 110
Endophytic entomopathogenic fungi as “plant probiotics”: An important tool in protecting and promoting plant health?
Chad A. Keyser, Donald W. Roberts
Department of Biology, Utah State University, Logan Utah, USA
Correspondence: chadaltonkeyser@gmail.com

Élie Metchnikoff is well-known among many Society for Invertebrate Pathology members as the discoverer of the first isolate of the entomopathogenic fungal genus Metarhizium. He is also credited, however, with being the first to propose ingesting certain microorganisms to improve health in humans – a phenomenon now known as “probiotics”. Probiotics are defined as: live micro-organisms which, when administered in adequate amounts, confer a health benefit on the host. Currently the term “probiotics” is only used to refer to interaction between beneficial microbes and human/animal hosts; however, in a biological control context, some rhizosphere-competent and -endophytic microbes behave “probiotic-like” in that they promote plant heath. The primary modes of action for probiotics in mammals include: competition for nutrients, competition for adhesion sites, direct antagonism, and immune stimulation. Research findings within the past decade indicate that these same modes of action are often seen following application of microbes on plants to control plant pests or pathogens. As will be discussed in this symposium, it is abundantly clear that entomopathogenic fungi are both endophytic and interact beneficially with plants. Viewing entomopathogenic organisms as potentially playing a “probiotics-like” role for a host plant emphasizes their importance in both plant protection and plant-health promotion.

SYMPOSIUM PAPER Wednesday 14:30 111
Entomopathogenic fungi as endophytes: Interactions with host plants and herbivores
Stefan Vidal¹, Anant Paté²
¹Georg-August-University Göttingen, Department of Crop Sciences, Göttingen, Germany; ²University of Applied Sciences, Department of Engineering and Mathematics, Bielefeld, Germany
Correspondence: vidal@gwdg.de

There is growing evidence that most, if not all, entomopathogenic fungi are able to colonize plant tissues as fungal endophytes in most, if not all plant species. Depending on the specific organisms involved these interactions may be beneficial to both the plant and the fungus, neutral or even antagonistic. Data so far published in this regard mainly refer to Beauveria bassiana, but Metarhizium anisopliae and Lecanicillium lecanii have also been shown to endophytically colonize plant tissues. Given the prevailing problems in using entomopathogenic fungi as biocontrol agents under field conditions it sounds like a good idea to use these fungi as endophytes, which would allow protecting the crop plants from the seedling stage to harvest. However, several open questions and constrains need to be addressed before these organisms can be fully implemented as plant protection agents. Data will be presented addressing the following issues:
- Do plants respond to the inoculation by entomopathogenic endophytes with changes in physical or physiological parameters?
- Are data available corroborating that re-growing plant parts are systemically colonized following an inoculation via the seeds or the roots?
- Is there sufficient evidence that an inoculation of a plant results in higher mortality of herbivores feeding on these plants?
- Are plants colonized by these endophytes less attractive for herbivores and do volatile pattern contribute to plant-herbivore interactions?
- Are there technical strategies available to increase the efficacy of entomopathogens as endophytic biocontrol agents?

Results addressing these questions are discussed in the context of improving herbivore pest control options.

SYMPOSIUM PAPER Wednesday 15:00 112
Trading insect nitrogen for photosynthate: Carbon translocation from a plant to an insect pathogenic, endophytic fungus
Michael J. Bidochka, Scott W. Behie
Department of Biological Sciences, Brock University, St. Catharines, ON Canada
Correspondence: bidochka@brocku.ca

Many vascular plants are able to form close symbiotic associations with endophytic fungi. Metarhizium is a common soil fungus that is both a plant endophyte and an insect pathogen. Previously we have shown that the endophytic capability and insect pathogenicity of Metarhizium are coupled to provide an active method of nitrogen transfer to a host plant via fungal mycelia. We speculated that in a reciprocal exchange for insect-derived nitrogen, the plant provided photosynthate to the fungus. We used $^{15}$CO$_2$ in airtight plant growth chambers to track the incorporation of $^{15}$C into plant (haricot bean; Phaseolus vulgaris) carbohydrates and the subsequent translocation of $^{15}$C.
into fungal-specific carbohydrates (trehalose and chitin) in the root/endophytic fungal complex. The amount of 13C present in root-associated fungal biomass was determined over a 21 day period by sequentially extracting trehalose and N-acetylglucosamine (GlcNAc) from roots and analyzing for 13C-trehalose and 13C-GlcNAc using nuclear magnetic resonance (NMR) spectroscopy. The translocation of photosynthate to endophytic *Metarhizium* occurred in the absence of a host insect (as a nitrogen source) in the soil; however, in the presence of an insect host we observed a significant increase in plant-derived photosynthate in fungal-specific carbohydrates. These findings are evidence that the host plant is trading photosynthate for insect-derived nitrogen in this tripartite symbiotic interaction that involves a plant, an endophytic insect pathogenic fungus and soil insects.

**SYMPOSIUM PAPER Wednesday 15:30 113**

_Metarhizium_ as a multifactorial plant growth promoter

Raymond J. St Leger

Department of Entomology, University of Maryland, Maryland, USA, 20742

Correspondence: stlger@umd.edu

_Metarhizium_ spp are amongst the most abundant fungi isolated from soils worldwide, under various environmental conditions, with sparse nutrients and in the presence of compounds lethal to other fungi. Several labs have shown that the _Metarhizium_ fungal species used for biocontrol of insect pests are capable of interacting with plant roots directly, behaving as symbiotic microorganisms. Many narrow host range _Metarhizium_ strains germinate poorly on plant roots and have no impact on root or shoot growth, whereas strains that grow well on roots without increasing plant growth usually have plant growth promoting relations. Root colonizing _Metarhizium_ strains promote plant growth by mechanisms that include killing insects, making nutrients available, increasing stress resistance and producing growth promoting metabolites. I will discuss how a combination of mass spectrometry, mutant analysis, easily identified marker genes and genomic tools for identifying genetic changes has provided knowledge of how _Metarhizium_ persists on plant roots and its modes of promoting plant growth. Field trials have confirmed that the ability to adhere to root surfaces plays an important part in maintaining _Metarhizium_ population size, irrespective of the presence of insects, and that some strains are multifactorial plant growth promoters.

**CONTRIBUTED PAPER Wednesday 14:15 115**

Genome sequence and environmental tolerance of a granulovirus mutant that produces abnormally large occlusion bodies

Madoka Nakai1, Robert L. Harrison2, Haruaki Uchida3, Yasuhsa Kunim1

1Tokyo University of Agriculture and Technology, Saiwai, Fuchu, Tokyo 183-8509, Japan; 2Invasive Insect Biocontrol and Behavior Laboratory, USDA Agricultural Research Service (USDA-ARS), Beltsville Agricultural Research Center, 10300 Baltimore Avenue, Beltsville, MD 20705, USA

Correspondence: madoka@ctu.tuat.ac.jp

Occlusion bodies (OBs), a diagnostic feature of family Betabaculoviridae, are comprised of a viral matrix protein that occludes virions in a paracrystalline array. OBs protect virions from environmental degradation and are the basis for baculovirus biopesticides. We isolated a novel Betabaculovirus isolate, *Adoxophyes orana* granulovirus isolate M (AdorGV-M) from Miyazaki, Japan, that produces abnormal OBs. AdorGV-M OBs are cuboidal in shape and reach a maximum diameter of 2.0 µm, whereas the reference isolate of AdorGV from UK (AdorGV-E) produces ellipsoid, 0.5 µm-long OBs typically observed for granuloviruses. AdorGV-M OBs were also found to be more resistant to inactivation by UV light and heat and to persist longer in the field than AdorGV-E OBs. To identify specific gene sequences that correlate with the abnormal OB morphology and greater environmental stability of AdorGV-M, the full genome sequence of AdorGV-M (99,507 bp) was compared to AdorGV-E and several AdorGV isolates from other regions in Japan. AdorGV-M exhibited 99.7% sequence identity with AdorGV-E, and 66 of 121 shared putative ORFs exhibited 100% predicted amino acid sequence identity between the two AdorGV genomes. No difference was observed in the granulin matrix protein gene, but other candidate OB morphology genes, including _pep-p10_, differed in sequence between AdorGV-M and other AdorGV isolates. These genes constitute a starting point in further studies on the molecular basis of the properties of AdorGV-M OBs.
Non-model animal species are a potential source of unknown viruses. This is especially important in the context of viral emergence. To describe the evolutionary origins of new RNA insect viruses, our study used Next Generation Sequencing technologies (NGS) for virus discovery. Thirty harvester ants (six species of the Messor genus) were sampled in the fields and these new viruses. Seven complete viral genomes close to Lake Sinai Virus (LSV) diversity in Hymenoptera Diane Bigot1, Elisabeth A. Herniou1, Nicolas Galter1, Philippe Gayral1
1 Institut de Recherche sur la Biologie de l’Insecte, UMR 7261, CNRS, Université François-Rabelais, 37200 Tours, France; 2 Institut des Sciences de l’Évolution de Montpellier, UMR 5554, CNRS, Université Montpellier 2, Place E. Bataillon, 34095 Montpellier, France
Correspondence: diane.bigot@etu.univ-tours.fr

The complete genome of Aedes sollicitans Deltabaculovirus (AesoNPV) was assembled using short sequence reads obtained with Illumina HiSeq2000 platform. The genome was 84,974 bp and contained 75 open reading frames (ORFs), of which 45 ORFs were highly similar to Culex nigriceps NPV (CuniNPV). The remaining 30 ORFs did not have any similarity to sequences available in the public databases. Genes conserved between AesoNPV and CuniNPV included all six per as infectivity genes, vp1055, all late expression factor except lef-5, the occlusion body protein, and most envelope proteins. Lack of a DNA polymerase gene (similar to AcMNPV ORF65 and CuniNPV ORF 91) was a notable exception in the AesoNPV genome. Compared to CuniNPV, AesoNPV genome is smaller in size and has substantial differences in gene organization.

Omaththage P. Perera, Catherine Beliveau1, Alejandro Cohen2, Don Stewart2, Georges Periquet1, Abdelmadjid Djoumad3, Lisa Kuhn1, Don Stoltz2, Brian Boyle1, Anne-Nathalie Volkoff2, Elisabeth A. Herniou1, Jean-Michel Drezen1, Michel Coissac1
1 Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, Quebec City, Quebec, Canada; 2 Proteomics Core Facility, Dalhousie University, Halifax, Nova Scotia, Canada; 3 Institut de Recherche sur la Biologie de l’Insecte (IRBI), Université François-Rabelais et CNRS UMR 7261, Tours, France; 4 Department of Microbiology and Immunology, Dalhousie University, Halifax, Nova Scotia, Canada; 5 Institut de Biologie Intégrative des Systèmes, Université Laval, Quebec City, Quebec, Canada; 6 UMR 1333 INRA, Université Montpellier, “Diversité, Génomes, Interactions Microorganismes-Insectes” (DGIMI), Montpellier, France
Correspondence: michael.cusson@nrcan.gc.ca

Genetic variation underpins the evolutionary process of adaptation. As populations become adapted to different environments, they diverge from one another. Baculoviruses infecting different host species thus usually belong to different species. Yet some viruses, such as Autographa californica multiple Nucleopolyhedrovirus (AcMNPV), have retained the capacity of infecting many host species. To understand how AcMNPV could draw on standing genetic variation to adapt to different host species we undertook an experimental evolution protocol. A highly polymorphic AcMNPV population was passaged 10 times through 4 different host species of various susceptibilities. We then characterised the genetic make up of the original and evolved baculovirus populations by ultra-deep Illumina sequencing. Using a population genomics approach, we then estimated the genetic diversity of each of the evolved populations and their divergence from one another. We found that the lines that evolved on the same host species were more similar to one another than to other lines, showing that the experimental evolution did led to specific adaptation. Furthermore, we found a general diminution of genetic diversity compared to the ancestral population. However, none of the evolved populations became clonal. Lastly the viral lines that could adapt to more resistant host retained higher genomic diversity than those that did not. This suggests that indeed standing genetic variation is an important component of baculovirus adaptation.

Aurélien Chateigner, Cindy Pontelevé, Carole Labrousse, Elisabeth A.
Genomic landscape of AcMNPV adaptation

CONTRIBUTED PAPER Wednesday 14:30 116
The complete genome of Aedes sollicitans nucleopolyhedrovirus Omaththage P. Perera1, James I. Beccal1
1 Southern Insect Management Research Unit, USDA-ARS, Stoneville, MS 38776; 2 Mosquito and Fly Research Unit, CMAVE, USDA-ARS, Gainesville, FL 32606
Correspondence: op.perera@ars.usda.gov

CONTRIBUTED PAPER Wednesday 14:45 117-5TU
Lake Sinai Virus (LSV) diversity in Hymenoptera

CONTRIBUTED PAPER Wednesday 15:00 118
Genomic landscape of AcMNPV adaptation

CONTRIBUTED PAPER Wednesday 15:15 119
In search of the ancestor of banchine polydnaviruses

CONTRIBUTED PAPER Wednesday 15:45 120
Polynavirus form a group of unconventional dsDNA viruses transmitted by endoparasitic wasps during egg laying into caterpillar hosts, where viral gene expression is essential to immature wasp survival. A copy of the viral genome is present in wasp chromosomes, thus ensuring vertical transmission. Recent work indicates that the two recognized polynavirus taxa, braconivirus and ichnovirus, are derived from distinct viruses whose genomes integrated into the genomes of ancestral wasps. However, the identity of the ichnovirus ancestor is unknown and questions remain regarding the possibility that the two described ichnovirus subgroups, banchine and campoplegine ichnoviruses, have distinct origins. To address the latter question, we used genomic, proteomic and transcriptomic analyses to characterize particle proteins of the banchine Glypta fumiferanae ichnovirus
and the genes encoding them. Our study provides unequivocal evidence that the two ichnovirus types are derived from related viral progenitors. This suggests that morphological and genomic differences observed between them, including features unique to banchine ichnovirus genome segments, result from evolutionary divergence either before or after their endogenization. Strikingly, analysis of selected wasp genomic regions revealed genes presumed to be part of the replicative machinery of the progenitor virus, shedding new light on the likely identity of this virus. Homology searches pointed to nuclear- and cytoplasmic large DNA viruses as the likely source of these genes, which could well play a role in ichnovirus replication as they were overexpressed in the viroenic tissue.

CONTRIBUTED PAPER Wednesday 15:30 120
Construction and rescue of a synthetic baculovirus, AcMNPV-WIV-Syn1.0, that retains the properties of the parental virus
Yu Shang, Fei Deng, Gengfu Xiao, Dianhai Hou, Kai Pan, Manli Wang, Hualin Wang, Zhihong Hu
State Key laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, P.R. China
Correspondence: hzh@wh.iov.cn

Baculoviruses contain a large circular DNA genome ranging from 80-180 kb and have been widely used as bio-control agents and protein expression vectors. To date, recombinant baculoviruses have been constructed based on homologous recombination in either insect cells or in E. coli. Here we report the first synthesis of AcMNPV, the prototype baculovirus, via transformation-associated recombination (TAR) in Saccharomyces cerevisiae. First, 45 overlapping fragments each of ~3 kb covering the entire genome of AcMNPV were amplified by PCR. Then three rounds of TAR were performed step by step in S. cerevisiae to assemble the fragments into nine constructs each containing ~15 kb of the viral genome, then into three constructs each containing ~45 kb viral DNA and finally into one having the entire AcMNPV genome. The final construct with the correct sequence was used to transfect Sf9 cells and the recovered virus was designated AcMNPV-WIV-syn1.0. The synthetic genome is 145,258 bp in size containing the complete genome sequences of AcMNPV except hr40, which was replaced by an 11.5 kb cassette of bacterial and yeast artificial chromosomal elements. The results of one-step growth curve, electron microscopy and oral infectivity showed that AcMNPV-WIV-syn1.0 had similar biological properties to the parental virus. The study proved the concept that a baculovirus can be synthesized de novo from parental sequences. In comparison to traditional recombination, the new method allows manipulating the baculoviral genome at multiple loci at one time and may likely be extended to other large DNA viruses such as poxviruses and herpesviruses. Currently, we are deleting/replacing multiple genes from the genome, which can be further used to study host range, identifying a baculovirus minigenome, as well as improving it as an expression vector.

CONTRIBUTED PAPER Wednesday 15:45 121
Generating a host ranges extended recombinant baculovirus
Tsongyuan Wu, Chao-Yi Teng, Mean-Shine Chen
Department of Bioscience Technology, Chung Yuan Christian University, Chung Li, Taiwan
Correspondence: tywu@cycu.edu.tw

Baculovirus expression system (BEVS) has been one of the versatile platforms for the production of recombinant proteins. Combination of multiple promoters or IRES elements were improved methods for expressing multiple genes from a single baculovirus vector, and made it possible to express multiple proteins simultaneously in a single recombinant virus. However, most baculoviruses have restricted, narrower host ranges, which is one of the important limitations for its applications in using insect larvae as a bioreactor. We previously co-infected the AcMNPV and MaviMNPV into Sf21 cells and isolated the hybrid virus (Ac-Mv-bac), which could infect both host cells of AcMNPV and MaviMNPV. To further extend the host range, we have successfully isolated the “ABM” virus, which can replicate in Sf21, Mv532 and BmN cells, by using the same approach. Here, we utilized the ABM-Bac baculovirus expression system to express H5N1 avian flu virus like particle (VLP) comprises HA, NA, and M1 proteins in the three hosts. Besides, we also provided an alternative approach to produce multiple proteins from the separated locus within the viral DNA. We had constructed six transfer vectors with different recombination loci and various fluorescence markers to establish a multiple locus-based polycistronic baculovirus expression vector, named as poly-Bac. In order to optimize the production of secreted or membrane bounded proteins, incorporation of the translation initiation factor-eIF4E and molecular chaperones Calreticulin and β-synuclein into poly-Bac system were also established.

NEMATODE WORKSHOP Wednesday 14:00 – 15:00
Nematodes Workshop

WORKSHOP PAPER Wednesday 14:00 122
Entomopathogenic nematode species in insect pest suppression: Can their use be optimized by proper application approaches?
Harry K. Kaya1, Sekuc Hazir2, David Shapiro-Ilan3
1Department of Entomology and Nematology, University of California, Davis, CA 95616, USA; 2Department of Biology, Faculty of Arts and Sciences, Adnan Menderes University, Aydin, TURKEY; 3USDA-ARS, SE Fruit and Tree Nut Research Laboratory, Byron, GA 31008, USA
Correspondence: hhkaya@ucdavis.edu

Successful application of entomopathogenic nematodes (EPNs) for insect suppression requires an understanding of nematode behavior, insect biology, and environmental conditions. One of the basic principles in EPN application is matching the right species with the target insect. Suitability to a target pest depends on the nematode’s innate virulence as well as other factors (such as foraging strategy). The concept of mixing two EPN species or the application of EPNs with a stressor such as a low concentration of an insecticide has enhanced insect control. Optimization of environmental conditions and proper timing of EPN applications (such as avoiding harmful UV radiation or desiccation) is critical for biocontrol success. Besides these basic procedures, genetic improvement of EPNs to desiccate or heat tolerance, the addition of adjuvants, and improved nematode formulations can enhance insect control. EPN persistence and efficacy can be improved by the use of insect cadavers containing EPNs. More recently, the use of live insects infected with EPNs was found to enhance insect control. Before dying, the live infected insects move to an area where the target pest resides. Then the EPNs in the dead insects produce infective juveniles that infect target insects in the vicinity. This concept has been referred to as “living insect bombs” and is particularly useful against insect pest species that occur in cryptic habitats. Finally, we have found that insect cadavers with nematodes are protected from being consumed by insect scavengers and this protection enhances nematode reproduction.
Implementation of entomopathogenic nematode (EPN) use against insect pests on golf courses in the USA is challenging due to high turf quality standards. We will discuss how to streamline the development of meaningful data through lab and greenhouse management option. Black cutworm, Agrotis ipsilon (Lepidoptera: Noctuidae), larvae damage golf course tees and putting greens. Because they can easily be reared we conducted extensive laboratory screening. In 30-ml plastic Heterorhabditis megidis was the most virulent species. But in 500-ml cups with bentgrass growing on soil, S. carpocapsae tended to be most effective species. Field experiments, in 0.1 m²-enclosures to prevent BCW escape and bird predation, confirmed S. carpocapsae as the most effective species due to a combination of control rates, speed of control, and consistency. Twice daily light irrigation and split applications further improved EPN efficacy to excellent levels. Nonetheless, EPN will likely continue to be limited wherever cheaper and easier-to-use highly effective synthetic insecticides can be used. Annual bluegrass weevil (ABW), Listronotus maculicollis, larvae damage all short mown areas on golf courses. Screening for effective EPN for this pest was challenging since it cannot be easily reared. Ultimately, S. carpocapsae was the most promising EPN species but excellent field efficacy could only be achieved through combination with imidacloprid (used at the same time for white grub control) and split applications. Widespread issues with broad insecticide resistance will likely make EPN a viable options for ABW management.

**WORKSHOP PAPER Wednesday 14:30 124**

**Plant scream, insect succumb: From concepts to applications**

I. Hiltpold

Hawkesbury Institute for the Environment, University of Western Sydney, Penrith, NSW, Australia

Insect herbivory induces synthesis and release of specific volatile compounds in plants. These volatiles have been shown to be highly attractive to natural enemies of the herbivores, such as predators, parasitic wasps or entomopathogenic nematodes. In maize, the volatiles emitted upon feeding by leaf- or root-feeding arthropods have been particularly well studied. Among several, some key compounds mediating these so-called tritrophic interactions have been identified. Moreover, several genes and biochemical pathways responsible for the production of the emitted volatiles have been elucidated. These advances in understanding the volatile emission and its ecological signaling open novel ways to modify and/or exploit plant volatile blends in order to enhance their attractiveness to natural enemies. Beside this plant manipulation, different other approaches are explored in order to better control belowground herbivory exploiting belowground volatile signaling. For instance, entomopathogenic nematodes have been selected for a better responsiveness to belowground cues or technics to lure the foraging insect herbivore are currently developed. Most of these manipulations could be simultaneously used for the benefit of agriculture.

**POSTER Wednesday 16:30 BA-1-STU**

**Novel mosquitocidal activity of strains LBIT-980 and LBIT-1217 of Bacillus thuringiensis**

Maríana Fernández-Navarro¹, Cristina Del Rincón-Castro², Jorge E. Ibarra²

¹Department of Biotechnology and Biochemistry, CINVESTAV-Irapuato, Gto. Mexico; ²Life Sciences Division, University of Guanajuato, Irapuato, Gto. Mexico

Correspondence: jibarra@ira.cinvestav.mx

**Bacillus thuringiensis svar. israelensis and Lysinibacillus sphaericus** are successfully used to control mosquito populations. However, the possibility of finding novel mosquitocidal activities is still interesting and feasible. In this work, two strains of B. thuringiensis were selected by preliminary bioassays, showing activity against Aedes aegypti larvae: LBIT-980 (serovar kim) isolated from soil; and LBIT-1217 (not serotyped), isolated from vermicompost. LBIT-980 showed a collapsed-balloon shaped crystals which contains the Cry59Aa1 protein; while LBIT-1217 strain showed a typical bipyramidal crystal morphology. Identification of Cry protein(s) is underway. Quantitative bioassays were performed following the standard procedure, using early fourth instar larvae of A. aegypti, to determine the toxicity levels. The LC₅₀ of spore-crystal complexes were 6.53 μg/mL and 13.42 μg/mL for LBIT-980 and LBIT-1217 strains, respectively; whereas using pure crystals LC₅₀ of 2.85 μg/ml and 3.99 μg/ml were estimated. Although these toxicity level are far lower than those shown by Bti, they are comparable to those shown by the BT toxin components tested separately. None of both strains showed the presence of Cyt toxins, neither in the gene content nor in the protein content. That is why bioassays using mixtures of LBIT-980/Cyt and LBIT-1217/Cyt are underway. As part of the characterization, plasmids patterns from the LBIT-980/Cyt and LBIT-1217/Cyt are underway. Studies in cotto, soybean, corn, sugar cane, cabbage, etc., have reported that Bacillus thuringiensis (Bt) has been successful in endophytic colonization. The efficient colonization of Bt in seedling roots suggests that this could be the main route to gain entry into the plant and, subsequently, migrate through the xylem.
to aerial tissues. In this paper, Bt subsp. *kurstaki* HD-73 was transformed with the green fluorescent protein reporter gene in order to obtain fluorescent vegetative cells and spores. The spore-crystal complex was inoculated in bean plants via two mechanisms: in the rhizosphere of plants grown in conventional substrate and in a hydroponic salt solution. Fluorescent spores were observed in the sap of plants inoculated with the spore-crystal complex, which were absent in the sap of non-inoculated plants. Interestingly, mortality was observed when *Trichoplusia ni* neonate larvae were fed with leaves of Bt-inoculated plants. To determine the possible lethal effect of recombinant strain carrying the Cry1Ac toxin, dead larvae were homogenized and cultured, recovering the fluorescent strain. As above, larvae fed on non-inoculated plants showed absence of Bt. Moreover fluorescent spores were observed within the aerial tissue of inoculated plants. These results suggest that the spore-crystal complex of the bean plants is able to penetrate and translocate through the vascular system to aerial parts of the plant, without losing its toxicity. The translocation mechanism is still unknown but its study and improvement may innovate the way Bt is used in the field.

**POSTER Wednesday 16:30 BA-3-STU**

**Diversity of bacteria composition of spined soldier bug, *Podisus maculiventris* (Hemiptera: Pentatomidae) digestive system**

E. M. Romagnoli\(^1\), C. A. Dunlop\(^2\), L. B. Flor-Weiler\(^3\), T. A. Coudron\(^4\), A. P. Rooney\(^5\)

\(^1\)Luiz de Queiroz College of Agriculture, University of Sao Paulo, Piracicaba, Sao Paulo, 13418900, Brazil; \(^2\)National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL, 61604, USA; \(^3\)Biological Control of Insects Research Service, U.S. Department of Agriculture, Columbia, MO, 65203

Correspondence: emilianaromagnoli@gmail.com

Spined soldier bug is an important biological control agent that preys on eggs and larvae of important forest and agricultural pests. Attempts at mass production of the insect have not been successful, due to limited success of artificial diets used for long-term colony rearing. One possible solution is to incorporate probiotic microorganisms into artificial diets. Unfortunately, virtually nothing is known concerning which microorganisms are effective probiotic agents in insects. As a first step in answering this question for the spined soldier bug, we analyzed the gut microbial community of wild and laboratory populations using next-generation sequencing of 16S ribosomal RNA (rRNA) gene amplicons. Bacteria was found in both populations were dominated by Proteobacteria, followed by Firmicutes, Bacteroidetes, and Actinobacteria, although differences were apparent. Laboratory populations had a higher composition of Proteobacteria (96%) than those collected from the wild (74%). On the other hand, wild populations showed higher levels of of *Firmicutes* (6% vs 3%) as well as *Bacteroidetes* (6% vs 0.2%), as well as the proportion of unclassified species (9% vs 1%). Interestingly, the community composition differences concerning the minor community components (i.e., Firmicutes, Bacteroidetes and unclassified bacteria) could represent potential probiotic species on the basis of comparison to studies in other organisms. The implications of these findings for designing an improved artificial diet are discussed.

**POSTER Wednesday 16:30 BA-4-STU**

**Use of NGS to assess the effect of antibiotics on the bacterial community of insects**

Diana Wilches\(^1,2\), Kevin D. Floate\(^1\), Paul Coghlin\(^2\)

\(^1\)University of Lethbridge; \(^2\)Agriculture and Agri-Food Canada, Research Centre, Lethbridge, AB

Correspondence: Diana.Wilches@agr.gc.ca

Symbiotic bacteria are common in insects and can influence the biology, reproduction and survival of their host. *Wolbachia* are among the most common of these symbionts that are often studied by applying antibiotic treatments to the host to eliminate the infection and, assessing the effects on host fitness. Antibiotic treatments may also affect other bacteria associated with the host, but this issue is rarely assessed. We used next-generation sequencing (NGS) methods to characterize the effect of antibiotic treatments on *Wolbachia* and non-*Wolbachia* bacteria associated with *Drosophila suzukii*. Efforts to distinguish the effects of *Wolbachia* and non-*Wolbachia* bacteria on host biology may lead to improved methods of insect pest control.

**POSTER Wednesday 16:30 BA-5**

**Status of resistance to Bt cotton in China: Cotton bollworm and pink bollworm**

Yulin Gao\(^1\), Chenxi Liu\(^1\), Yidong Wu\(^2\), Kongming Wu\(^3\)

\(^1\)State Key Laboratory for Biology of Plant Disease and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, PR China; \(^2\)Department of Entomology, College of Plant Protection, Nanjing Agricultural University, Nanjing 210095, PR China

Correspondence: gaoyulin@caas.cn

Transgenic cotton that expresses a gene derived from the bacterium *Bacillus thuringiensis* (Bt) has been deployed for combating *Helicoverpa armigera* and *Pectinophora gossypiella* since 1997 in China. The pest management tactics associated with Bt cotton have resulted in a drastic reduction in insecticide use. However, evolution of resistance by the pests threatens the continued success of Bt cotton. The development of resistance to Bt is of great concern, and there is a vast body of research in this area aimed at ensuring the continued success of Bt cotton. Here, we review studies on the evolution of Bt resistance in these two bollworms, focusing on commercial release of Bt cotton varieties in China, the biochemical and molecular basis of Bt resistance. We also discuss resistance management strategies, and monitoring programs implemented in China and other countries.

**POSTER Wednesday 16:30 BA-6**

**Evidence of field-evolved resistance of *Spodoptera frugiperda* to Bt corn expressing Cry1F in Brazil that is still sensitive to modified Bt toxin**

Lima A. Anabele\(^1,2\), Monnerat Rose\(^1\), Martins Eric\(^1\), Macedo Cristiano\(^1\), Queiroz Paulo\(^2\), Praça Lilian\(^1\), Soares C. Marcelo\(^2\), Moreira Helio\(^1\), Grisi Isabella\(^1\), Silva Joseane\(^1\), Soberon Mario\(^1\), Bravo Alejandra\(^3\)

\(^1\)Embrapa Recursos Genéticos e Biotecnologia, Brasilia, Distrito Federal, Brazil; \(^2\)Instituto Mato-Grossense do Algodão, Cuiabá, Mato Grosso, Brazil; \(^3\)Departamento de Microbiologia, Universidade de Brasília, Brasília, Distrito Federal, Brazil; \(^4\)Instituto de Biotecnologia, Universidad Nacional Autonoma de México, Cuernavaca, Morelos, Mexico; \(^5\)University Center of Brasilia, Distrito Federal, Brazil

Correspondence: anabelebio@gmail.com, anabele.lima@uniceub.br

Brazil ranked second only to the United States in hectares planted to genetically modified crops in 2013. Recently corn producers in the Cerrado region reported that the control of Spodoptera
frugiperda with Bt corn expressing Cry1Fa has decreased, forcing them to use chemicals to reduce the damage caused by this insect pest. A colony of S. frugiperda was established from individuals collected in 2013 from Cry1Fa corn plants (SBt) in Brazil and shown to have at least more than ten fold higher resistance levels compared with a susceptible colony (SFlab). Laboratory assays on corn leaves showed that in contrast to SFlab population, the SBT larvae were able to survive by feeding on Cry1Fa corn leaves. The SBT population was maintained without selection for eight generations and shown to maintain high levels of resistance to Cry1Fa toxin. SBT showed higher cross-resistance to Cry1La than to Cry1Lab or Cry1Ac toxins. As previously reported, Cry1A toxins competed the binding of Cry1Fa to brush border membrane vesicles (BBMV) from SFlab insects, explaining cross-resistance to Cry1A toxins. In contrast, Cry2A toxins did not compete Cry1Fa binding to BBMV and no cross-resistance to Cry2A was observed, although Cry2A toxins show low toxicity to S. frugiperda. Bioassays with Cry1LabMod and Cry1AcMod show that they are highly active against both the SFlab and the SBT populations. The bioassay data reported here show that insects collected from Cry1Fa corn in the Cerrado region were resistant to Cry1Fa suggesting that resistance contributed to field failures of Cry1Fa corn to control S. frugiperda. Bioassays with Cry1AbMod and Cry1AcMod show that effects of pre-exposure to sublethal Bt concentrations on larval feeding behaviour of resistant and susceptible T. ni. Tolerance to Bt is induced in susceptible larvae and resistant larvae exhibit increased growth in response to sublethal Bt doses. These effects may modify the feeding behaviour of T. ni larvae and alter subsequent Bt exposure. The effects of pre-exposure on sublethal Bt concentrations on larval feeding behaviour of resistant and susceptible Trichoplusia ni larvae were examined through diet choice tests. Both control and pre-exposed susceptible larvae avoided diet treated with Bt, despite the reduction in mortality experienced by the pre-exposed larvae. Resistant larvae experienced an increase in weight gain when exposed to Bt, and exhibited an increase in avoidance of diet with Bt when given a choice of diets. Feeding observations suggest that both susceptible and resistant T. ni larvae modify the impact of Bt exposure through behavioural avoidance and compensatory feeding.

**POSTER Wednesday 16:30 BA-7**

**Behavioural feeding responses of susceptible and resistant Trichoplusia ni larvae to Bacillus thuringiensis**

Alida F. Janmaat, Mandy Gelderman, Martin Muermann

Biology Department, University of the Fraser Valley, Abbotsford, BC, Canada

Correspondence: alida.janmaat@ufv.ca

Exposure of Trichoplusia ni larvae to sublethal levels of Bt have differential effects on Bacillus thuringiensis resistant and susceptible T. ni. Tolerance to Bt is induced in susceptible larvae and resistant larvae exhibit increased growth in response to sublethal Bt doses. These effects may modify the feeding behaviour of T. ni larvae and alter subsequent Bt exposure. The effects of pre-exposure on sublethal Bt concentrations on larval feeding behaviour of resistant and susceptible Trichoplusia ni larvae were examined through diet choice tests. Both control and pre-exposed susceptible larvae avoided diet treated with Bt, despite the reduction in mortality experienced by the pre-exposed larvae. Resistant larvae experienced an increase in weight gain when exposed to Bt, and exhibited an increase in avoidance of diet with Bt when given a choice of diets. Feeding observations suggest that both susceptible and resistant T. ni larvae modify the impact of Bt exposure through behavioural avoidance and compensatory feeding.

**POSTER Wednesday 16:30 BA-8**

**Discovering novel Bt toxins for better bio-pesticides and biotech crops**

Jim X. J. Fang¹,², W. F. Zhang¹, Y. Zhou², P. T. Gong³

¹The HITAR Institute Canada Inc., Richmond, British Columbia, Canada; ²Hainan Institute of Tropical Agricultural Resources, Sanya, Hainan, China; ³College of Life Sciences, Hainan Normal University, Haikou, Hainan, China

Correspondence: jim.x.j.fang@hitar.org

Bacillus thuringiensis, B.t., is one of the most famous bacterium that generates many virulence factors including phospholipases, hemolysins, enterotoxins, exotoxins and endotoxins. Since discovered in 1901, humans have always benefited from this soil saprophyte. The project titled China National Bt Collection Initiative (BtSRI) was initiated by HITAR in 2005, which aimed to sample the soils across mainland of China for isolating the Bacillus and identifying the strains of Bacillus thuringiensis. So far, 27250 Bacillus isolates were collected in stock at HITAR and 2137 isolates were identified as B.t. strains. More than 150 strains were characterized in crystal shape, SDS-PAGE, plasmid profiles and cry genotypes, Bioassay etc., of which 30 strains being working strains in HITAR are applying to whole genome sequencing to characterize the genome and discover novel Bt. toxins. Five strains, S2160-1, S2480-1, S2096-2, S3299-1, W015-1 and 2012-2, were proposed to be new model strains. B.t. strains, W015-1, S1478-1and S3299-1 having new high toxic to Lepidoptera, were proposed to be alternative to Btk, while S2160-1, a new high mosquitocidal isolate being alternative to Bti. S2096-2 being significantly highly toxic to the hookworm (Necator americanus) might be applied to produce bioicides. S3012-2 has significant toxicity against corn rootworm. The Genomes of the selected 36 isolates including above mentioned S2160-1, S2096-2, S2480-1, S3299-1 and S3012-2 were sequenced to characterize the strains and to discover new toxins, which show the potentials for commercial application both in engineering bacteria and genetically modified crops.

The cotton bollworm Helicoverpa armigera is the major pest in countries like that India, China and Australia. It causes many damages in several crops of the world. After its introduction in Brazil showed this pest affected soybean, cotton, tomato and bean crops. Bacillus thuringiensis (Bt) toxins can be used to control this pest through its biopesticides proteins or under transgenic Bt crops protection. Reports about Bt use to control H. armigera are scarce in Brazil and the aim of this research was evaluate the toxicity and interaction of the B. thuringiensis proteins, Cry1Aa, Cry1Ab, Cry1Ac and Cry1Ea. To estimate the LC50 there were performed bioassays with H. armigera neonate larvae. The interaction was evaluated in vitro using competitive binding assays with the activated and biotinylated proteins and "brush border membrane vesicles" BBMV from the midgut larvae. The toxicity resulted in Cry1Ac protein was the most toxic followed by Cry1Ab and Cry1Aa proteins. The Cry1La showed no toxicity. Heterologous competitive binding assays revealed that Cry1Aa, Cry1Ab, Cry1Ac compete for a common receptor from the midgut larvae.

**POSTER Wednesday 16:30 BA-9**

**Toxicity and interaction of Cry1 proteins from Bacillus thuringiensis in Helicoverpa armigera (Hübner) (Lepidoptera: Noctuidae)**

Manuel Víctor F. Lemos¹, Isis Sebastião², Camilla S. Figueiredo², Ana Rita N Lemes², Ricardo A Polanczyk³, Janete A Desidério¹

¹ Faculdade de Ciências Agrárias e Viticulturárias, UNESP – Univ. Estadual Paulista Júlio de Mesquita Filho; ² Departamento de Biologia Aplicada à Agropecuária; ³ Departamento de Fitossanidade, Rod. Prof. Paulo Donato Castellane, km. 5, CEP14884-900, Jaboticabal, São Paulo, Brasil

Correspondence: mvctor@fcav.unesp.br

The cotton bollworm Helicoverpa armigera is the major pest in countries like that India, China and Australia. It causes many damages in several crops of the world. After its introduction in Brazil showed this pest affected soybean, cotton, tomato and bean crops. Bacillus thuringiensis (Bt) toxins can be used to control this pest through its biopesticides proteins or under transgenic Bt crops protection. Reports about Bt use to control H. armigera are scarce in Brazil and the aim of this research was evaluate the toxicity and interaction of the B. thuringiensis proteins, Cry1Aa, Cry1Ab, Cry1Ac and Cry1Ea. To estimate the LC50 there were performed bioassays with H. armigera neonate larvae. The interaction was evaluated in vitro using competitive binding assays with the activated and biotinylated proteins and “brush border membrane vesicles” BBMV from the midgut larvae. The toxicity resulted in Cry1Ac protein was the most toxic followed by Cry1Ab and Cry1Aa proteins. The Cry1La showed no toxicity. Heterologous competitive binding assays revealed that Cry1Aa, Cry1Ab, Cry1Ac compete for a common receptor from the midgut larvae.
Anticarsia gemmatalis (Hubner, 1818) (Lepidoptera: Noctuidae) is a soybean pest and is considered a risk to the Brazilian crop production. The insect’s larval instars, feed on the young leaves causing extensive damage to crops ranging from defoliation to the complete plant destruction. For the control of this pest, the use of Vip3Aa and Cry1Aa proteins becomes an excellent alternative, since they can be used on pest resistance management strategies. Therefore, this study aimed to the cloning and expression of Vip3Aa and Cry1Aa proteins from Bacillus thuringiensis (Bt) in Escherichia coli, in order to analyze the correlation between the binding to receptors through competition assays between the different toxins and the toxicity to A. gemmatalis larvae. Therefore, vip3Aa and cry1Aa genes were cloned into the pET SUMO vector, expressed in E. coli and the proteins toxicity were tested based on bioassays with neonate A. gemmatalis larvae. The BBMV were prepared from the larva mesenteries and competition assays were performed. The Vip3Aa and Cry1Aa proteins showed LC50 of 239.2 ng/cm2 and 246.2 ng/cm2, respectively. Binding assays to BBMVs demonstrated that Vip3Aa and Cry1Aa proteins binding effectively to receptors present in the larvae midgut and, therefore, there was a correlation between the toxicity and the binding to receptors for the population of A. gemmatalis. Thus, the combination of Vip3Aa and Cry1Aa proteins is indicated for the production of biological insecticidal, as well as for the transgenic plants construction to overcome the resistance emergence by A. gemmatalis population to Bt toxins.

POSTER Wednesday 16:30 BA-11-STU
Parallels between the Cry41Aa parasporin and insecticidal Bt toxins
Barbara Domanska, Michelle West, Neil Crickmore
Department of Biochemistry, School of Life Sciences, University of Sussex, Falmer, Brighton, BN1 9QG
Correspondence: bd73@sussex.ac.uk

In this study the cytotoxic activity associated with the Cry41Aa human cancer cell-acute toxin of Bacillus thuringiensis (Bt), also known as Parasporin-3, was characterized. Our initial data were consistent with Cry41Aa being a pore-forming toxin in rapid membrane damage was observed in susceptible cells and microscopic observation revealed cellular and nuclear swelling. The activation of apoptosis effectors Caspase 3/7 was not observed, although phosphorylation of p38 MAP kinase was. Interestingly, the extracellular depletion of divalent cations by different chelators prevented toxicity. This loss of toxicity could be rescued by the addition of metal ions such as calcium or zinc but not others such as magnesium or iron. Divalent cations have previously been implicated in the mode of action of both insecticidal Bt toxins and other parasporins where mechanisms other than pore formation were proposed to lead to cell death. We will discuss models designed to explain our results. In these models the divalent cations have several potential functions including a direct role in toxin binding, maintaining the structural integrity of the cell membrane and as a component of a cell signalling pathway that could lead to either cell death or cell repair. Although these models are based on our Parasporin / human cell assays they may be applicable to other Bt Cry toxin systems.

POSTER Wednesday 16:30 BA-12-STU
Unusual pore formation by a new Bacillus thuringiensis toxin
Eva Fortea Verdejo1, Vincent Lemieux2, Léna Potvin1, Timothy Hey3, Xiaoping Xu4, Samantha Griffin4, Vinhthai Chikwan4, David McCaskill5, Ken Narva5, Vincent Vachon5, Jean-Louis Schwartz2,4
1Département de physiologie moléculaire et intégrative and Groupe d’étude des protéines membranaires, Université de Montréal, Montréal, QC, Canada; 2Département de biologie, Université de Sherbrooke, Sherbrooke, QC, Canada; 3Dow AgroSciences LLC, Indianapolis (IN 46268), IN, USA; 4Centre SÈVE de recherche en sciences du végétal, Université de Sherbrooke, Sherbrooke, QC, Canada
Correspondence: jean-louis.schwartz@umontreal.ca

Typical three-domain Bacillus thuringiensis (Bt) insecticidal and nematocidal proteins, and Bt parasporins permeabilise receptor-free planar lipid bilayers (PLBs) by forming pores at doses in the 1-50 µg/ml range. At lower doses, pore formation may only take place when PLBs are enriched with purified target organism receptors or midgut brush border material. Under symmetrical 150 mM KCl conditions, the conductance of the pores is comprised between 10 and 500 pS and the pores are mildly selective for cations. Activation of the purified and solubilized proteins obtained from Bt inclusion bodies by trypsin, target organism gut proteases or gut juice is a necessary step for PLB permeabilisation. DS1 is a new Bt toxin which displays insecticidal activity in vivo. Contrary to other Bt toxins tested so far in PLBs, DS1 forms pores in receptor-free bilayers without the need of protease or target insect gut juice pretreatment, and at doses that are 2 to 3 orders of magnitude lower than those required for other Bt toxins under similar conditions. Pore formation by DS1 is highly pH-dependent; the conductance of the pores ranges between 100 and 450 pS under symmetrical 150 mM KCl conditions; they are cation-selective and display a complex kinetic behaviour. The molecular determinants of the mode of action of this new pore-forming Bt toxin appear therefore to differ from those reported before for other Bt toxins, which may imply a radically different structural organisation of the protein.

POSTER Wednesday 16:30 BA-13-STU
Construction & characterization of novel Bacillus thuringiensis Cry1-type genes with improved insecticidal activities
Jong Hoon Kim1, Jae Young Choi1, Pang Ying2, Ha Kyu Baik2, Seok Ree Lee3, Woon Jin Kim3, Yeon Ho Je4
1Department of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea; 2Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea
Correspondence: KH1018@sunu.ac.kr

Crystals of proteinaceous insecticidal proteins, Cry proteins, produced by Bacillus thuringiensis (Bt) have been generally used to control insect pests. In this study, through the 3D structure prediction and accompanying mutagenesis study for the Mod-Cry1Ac, 7 and 16 amino acid residues from domain I and II, respectively, responsible for its insecticidal activity against larvae of Plutella xylostella, Spodoptera exigua and Ostrinia furnacalis were identified. To construct novel cry genes with enhanced insecticidal activity, we randomly mutated these 24 amino acid sequences by in vitro multi site-directed mutagenesis, resulting in a total of 34 mutant cry genes. For further characterization, these mutant cry genes were expressed as a fusion protein with polyhedrin using baculovirus expression system. SDS-PAGE analysis of the recombinant polyhedra revealed that expressed Cry proteins were occluded into polyhedra and activated to yield 65 kDa by trypsin. When the insecticidal activities of these mutant Cry proteins against larvae of P. xylostella, S. exigua, and O. furnacalis were assayed, they showed higher or similar insecticidal activity compared to those of Cry1Ac and Cry1C. Especially, among these 34 mutant cry genes, Mutant-N16 showed the
highest insecticidal activity against *P. xylostella*, *S. exigua* and *Ostrinia furnacalis* larvae. Therefore, Mutant-N16 is estimated to have the potential for the efficacious bioagent.

**POSTER Wednesday 16:30 BA-14-STU**

**Development of a Cry toxin activity-improving method based on the directed evolution that targets ABC2**

Kazuhiro Imamura, Natsuko Nakajima, Haruka Endo, Ryoichi Sato

1Graduate School of Bio-Applications and Systems Engineering, Tokyo University of Agriculture and Technology, Koganei, Tokyo, Japan; 2Japan Society for the Promotion of Science Research Fellowship for Young Scientists

Correspondence: ryoichi@cc.tuat.ac.jp

ABC transporter C2 (ABC2) is a functional receptor of Cry1A in lepidopteran insects, and thought to play an important role in the mechanism of action of Cry toxins. Since the interaction to the receptors are necessary to exert insecticidal activity for Cry toxin, the improvement of binding affinity to ABC2 is expected to lead the insecticidal activity enhancement. Directed evolution is a method that can screen proteins that display higher binding affinity to a target protein. This research aims to assess the possibility of enhancement of the Cry toxins insecticidal activity by applying directed evolution that targets ABC2. Cry1Ca has low affinity to the B. mori ABC2 (BmABC2). Domain II loop regions of Cry toxins have been indicated to bind to receptors and effect to the insecticidal activity. Hence, at first, random mutations were introduced in successive 4 amino acid residues on Cry1Ca loop 3, and these mutants were displayed on T7 phage surfaces. Subsequently, a basic selection method to screen mutants that exhibit higher binding affinity to BmABC2 from the phage library were attempted to construct. Native phages containing few Cry1la-expressing phages which should bind to BmABC2 were subjected to the selection. After the selection, the percentage of Cry1la-expressing phages has increased 6-fold. This suggested that phages which possess mutant Cry toxins with improved binding ability to BmABC2 can be obtained through repeat of this selection. Selection of the phage library with Cry1Ca mutant has been started.

**POSTER Wednesday 16:30 BA-15**

**Carbohydrate binding domain of Vip3Aa is involved in receptor binding**

Kun Jiang, Yu Yuan, Dong-hui Hua, Tingting Wang, Yue-hua Chen, Jun Cai

1Department of Microbiology, College of Life Sciences, Nankai University, Tianjin, China; 2Key Laboratory of Molecular Microbiology and Technology, Ministry of Education, Tianjin, China; 3Tianjin Key Laboratory of Microbial Functional Genomics, Tianjin, China

Correspondence: caijun@nankai.edu.cn

Vip3Aa, a soluble insecticidal protein produced during vegetative growth phase by Bacillus thuringiensis, possesses insecticidal activity against a wide spectrum of lepidopteran insects. In contrast to the situation with δ-endotoxins, little is known about insecticidal action mechanism of Vip3A. In our previous work, we found that a carbohydrate binding domain (CBD) exists on the C-termini 536 to 667 residues of Vip3Aa. In this study, in order to investigate the function of CBD, we create several truncated Vip3Aa proteins and Vip3Aa CBD-site-directed mutants. Binding assays experiments showed that all the truncated proteins which contain the whole CBD, as well as CBD itself, still maintain binding activity to sf9 cells and brush border membrane vesicles of Spodoptera exigua, while the truncated protein with incomplete CBD loses the binding activity. Moreover, bioassay results showed that the CBD site-directed mutants of Vip3Aa lost their toxicity. Furthermore, SDS-PAGE and western blotting analysis suggested that CBD mutant proteins were degraded in E. coli. These results demonstrate that CBD of Vip3Aa conceivably participates in toxin-receptor recognition and it is critical for maintaining the activity.

**POSTER Wednesday 16:30 BA-16**

**Insecticidal spectrum and mode of action of the Bacillus thuringiensis Vip3Ca insecticidal protein**

Joaquín Gomis-Cebolla, Ilígo Ruiz de Escudero, Maissa Chakroun, Natalia Maro Vera-Velasco, Patricia Hernández-Martínez, Carmen Sara Hernández-Rodríguez, Yolanda Be, Baltasar Escriche, Primitivo Caballero, Ruy Ferré

1ERI of Biotecnología y Biomedicina (BIOTECMED), Unversitat de València, Burjassot, Spain; 2Instituto de Agrobiotecnología, CSIC-UPNA, Gobierno de Navarra, Campus Arrosadía, Navarra, Spain; 3Laboratorio de Entomología Agrícola y Patología de Insectos, Universidad Pública de Navarra, Pamplona, Spain

Correspondence: juan.ferre@uv.es

The Vip3Ca protein, discovered in a screening of Spanish collections of *Bacillus thuringiensis*, was shown to be toxic to *Chrysodeixis chalcites*, *Mamestra brassicae* and *Trichoplusia ni* (Palma et al., 2012, Appl. Environ. Microbiol. 78:7163-5). In the present study, we have tested additional species and found three more lepidopteran species relatively susceptible to this protein: *Cydia pomonella*, *Grapholitha molesta* and *Ephestia kuehniella*. Vip3Ca (a ca. 90 kDa protein) is processed to a ca. 60 kDa protein when incubated with midgut juice of larvae, no matter if they are susceptible (*M. brassicae*) or tolerant (*Agritis ipsilon*) or non-susceptible (*Ostrinia nubilalis*) to this protein. This result suggests that the activation step is not critical in determining the susceptibility of an insect species. In vivo binding of Vip3Ca was performed by feeding *M. brassicae* larvae with Vip3Ca followed by detection with an anti-Vip3 protoxin polyclonal antibody. Histopathological inspection showed swelling of the epithelial cells with further disruption, which suggests that the mode of action of Vip3Ca is similar to that described for Vip3Aa. Comparative analysis of Vip3Ca binding to BBMV from tolerant and susceptible insects was performed.

**POSTER Wednesday 16:30 BA-17**

**Binding to brush border vesicles and midgut processing of Bacillus thuringiensis Vip3Aa toxin to Helicoverpa armigera susceptible and Vip3Aa-resistant insects**

Maissa Chakroun, Nuria Banyuls, Tom Walsh, Sharon Downes, Rod Mahon, Bill James, Juan Ferré

1ERI of Biotecnología y Biomedicina (BIOTECMED), Universitat de València, Burjassot, Spain; 2Land and Water Flagship, CSIRO, Canberra ACT 2601; 3Agriculture Flagship, CSIRO, Narrabri NSW 2390

Correspondence: juan.ferre@uv.es

Two *H. armigera* colonies, one susceptible to the Vip3Aa toxin from *Bacillus thuringiensis* and the other selected for resistance, have been tested for two steps in the mode of action: binding to midgut receptors and activation by midgut juice. Competition-binding experiments were performed with brush border membrane vesicles prepared from larval midguts and sensitive and resistant Vip3Aa. Specific binding was found with vesicles of insects from both colonies, with similar binding parameters in both. Nevertheless, differences were found at the level of Vip3Aa
proteases and binding to brush border membrane vesicles from Cylas puncticollis (Brentidae)

Natalia M. Vera-Velasco, Patricia Hernández-Martínez, Baltasar Escriche
Departamento de Genética, Facultad de CC. Biológicas, Universitat de València, Spain
Correspondence: baltasar.escriche@uv.es

Bacillus thuringiensis Cry3Aa and Cry3Ca proteins have been reported to be toxic against the African sweet potato pest Cylas puncticollis. However, relatively little is known about the processing and binding interactions of these two Cry proteins. Proteolytic processing of Cry3Aa and Cry3Ca by the larval gut fluid of C. puncticollis was studied to characterize the proteases involved in the proteolytic processing. Moreover, we determined whether Cry3Aa and Cry3Ca proteins have shared binding sites in C. puncticollis brush border vesicles (BBMV). Processing of the Cry3Aa or Cry3Ca toxins using either the gut fluid from C. puncticollis or commercial trypsin or chymotrypsin rendered similar fragments of about 55 kDa and 53 kDa, respectively. A serine-like protease from C. puncticollis gut fluid was found to be involved in the proteolytic processing of both Cry3 proteins. Homologous binding assays showed specific binding for the two Cry3 proteins on BBMV from C. puncticollis larvae. Heterologous competition assays showed that Cry3Aa and Cry3Ca partially competed for the same binding sites, suggesting that these proteins may have two different binding sites and only one of them is shared. Hence, our results suggest that pest resistance mediated by alteration of the shared Cry-receptor binding site might not render both Cry proteins ineffective.

POSTER Wednesday 16:30 BA-19
Domain III of Bacillus thuringiensis Cry1le toxin contributes to its binding to peritrophic membrane of Asian corn borer
Dongmei Feng, Zhen Chen, Nan Zhang, Chunlu Zhang, Shuyuan Guo
School of Life Science, Beijing Institute of Technology, Beijing 100081, China
Correspondence: guosy@bit.edu.cn

The insecticidal IE648 toxin is a truncated Cry1le protein with increased toxicity against Asian corn borer (ACB). Cry toxins form pores in the apical membrane of midgut cells. However, the peritrophic membrane (PM) is an important barrier that Cry toxins must cross before binding to midgut cells. PM is a semipermeable matrix composed of chitin fibrils and protein-glycojugates that protect the insect gut epithelial cells from injury and infection. Previously it was shown that Cry toxins are able to bind and to accumulate in the PM of various lepidopteran insects. In this work we analyzed the binding interaction of IE648 to the PM of ACB, which showed to be specific by homologous competition binding assay. Heterologous competition binding assays performed with different fragments of domain I, domain II and domain III allowed us to identify that not domain I, but domain III of IE648 contributes to the interaction with PM, situation of domain II remains unclear. Furthermore, ligand blot assays indicated that IE648 and its domain III interact with chitin and with similar PM proteins. These data provide a primary direction to understand the mechanism of interaction between PM and 3D-Cry toxin.
Using gfp and lacZ as report genes, we showed that BMBsr1 acts the RBS site of cry5Ba. Then we mapped the key action sites of BMBsr1 and showed the +5, +7, +13 sites are required for BMBsr1 mediated cry5B0 silencing. Finally, we found Cry5B0 does express in vivo after YBT-1518 was ingested by nematode C. elegans, and YBT-1518 benefits from cry5B0 silencing in colonization in vivo. This phenotype may help B. thuringiensis to cheat nematode host to feed its spores and crystals, and then express the toxin in vivo to kill the host. This work provides a special expression and regulation model for pathogen interaction with its host.

**Diseases of Beneficial Invertebrates**

**POSTER Wednesday 16:30 DB-1-STU**

**Chitin-degrading protein PICBP49 - a key virulence factor of Paenibacillus larvae**

Henriette Knispel1, Anne Fünfhaus1, Eva García-Gonzalez1, Lena Poppinga1, Jennifer S M Loo1, Gustav Vosse-Kolstad1, Elke Genersch1

1Institute for Bee Research, Hohen Neuendorf, Division of Molecular Microbiology and Bee Pathology
Friedrich-Engels-Str. 32, D-16540 Hohen Neuendorf, Germany;
2Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, P.O. Box 5003, N-1432 As, Norway

Correspondence: elke.genersch@rrz.hu-berlin.de

American Foulbrood (AFB) of honey bees is a globally occurring epizootic, caused by the gram-positive bacterium Paenibacillus larvae. Although AFB has been known for over hundred years, cellular and molecular details of pathogen-host interactions during pathogenesis of AFB remain poorly understood. However, the chitinolytic protein PICBP49 was recently identified as a key virulence factor during P. larvae infections. PICBP49 is responsible for degradation of the chitin-rich peritrophic matrix, a protective barrier in the larval gut. In silico analyses revealed a module belonging to the auxiliary activity 10 (AA 10) family of lytic polysaccharide monoxygenases (LPMOs), predicting PICBP49 to putatively degrade chitin via a special mechanism.

**POSTER Wednesday 16:30 DB-2-STU**

**Characterization of virulence factors in the fatal honey bee disease American foulbrood caused by Paenibacillus larvae**

Julia Ebeling, Lena Poppinga, Anne Fünfhaus, Elke Genersch

Institute for Bee Research, Hohen Neuendorf, Brandenburg, Germany

Correspondence: elke.genersch@rrz.hu-berlin.de

American foulbrood is a very contagious, worldwide occurring honey bee brood disease caused by the gram-positive, spore-forming bacterium Paenibacillus larvae. The larvae ingest the bacterial spores together with their regular food. The spores germinate in the larval midgut, where the vegetative cells proliferate until the midgut is massively filled. Thereafter, it comes to the breaching of the peritrophic matrix and the midgut epithelium. Thereupon, the bacteria are free to invade the host’s hemocoel followed by larval death. Interestingly, four P. larvae genotypes exist which are classified by enterobacterial repetitive intergenic consensus polymerase chain reaction, and accordingly named ERIC I-IV. The most relevant genotypes being isolated from current American foulbrood outbreaks are ERIC I and II. The genotypes also differ phenotypically, and most importantly have developed different infection strategies. Recently, two binary AB toxins, Phx1 and Phx2, have been identified as virulence factors in the genotype ERIC I. Contrarily in ERIC II, the S-layer protein SpIA is involved in pathogenesis. Previous studies predict these proteins to play a role in the breakthrough of the epithelial cell barriers in the larval midgut.
ABSTRACTS

Disease is widely acknowledged as the prominent bottle-neck to achieving global food security and poverty alleviation targets relating to aquaculture with annual losses exceeding US $6bn. High profile disease in $15bn shrimp industry include those relating to aquaculture with annual losses exceeding US $6bn.

Disease is widely acknowledged as the prominent bottle-neck to achieving global food security and poverty alleviation targets relating to aquaculture with annual losses exceeding US $6bn. High profile disease in $15bn shrimp industry include those relating to aquaculture with annual losses exceeding US $6bn.

POSTER Wednesday 16:30  DB-3

Decentralised molecular diagnostics and remote data reporting for management of disease in global aquaculture

Kelly S. Bateman1, Michelle Pond2, Peter Munday3, Olga Gandelman4, Grant D. Stentiford5

1European Union Reference Laboratory for Crustacean Diseases, Centre for Environment, Fisheries and Aquaculture Science (Cefas), Barrack Road, The Nothe, Weymouth, Dorset DT4 8UB, UK; 2Epistem, Genedrive, Epistem Ltd., 48 Grafton Street, Manchester, M13 9XX, UK

Correspondence: kelly.bateman@cefas.co.uk

Disease is widely acknowledged as the prominent bottle-neck to achieving global food security and poverty alleviation targets relating to aquaculture with annual losses exceeding US $6bn. High profile disease in $15bn shrimp industry include those caused by White Spot Syndrome Virus (WSSV), the bacterial pathogen implicated in Acute Hepatopancreatic Necrosis Disease (AHPND) and emergent pathogens such as Enteroctozoon hepatopneumaei, implicated in Early Mortality Syndrome (EMS); these pathogens implicated in annual losses of $3bn per annum. Genedrive® is a small footprint molecular diagnostics platform capable of rapid, sensitive and specific detection of pathogens within an hour. It combines proprietary ‘hybrid’ thermal engine technology with bespoke smartphone applications designed for detection of the pathogen/s of interest. An ultra-simple, ‘single-button’ operation allows for the operation of the equipment by un-skilled operatives, with minimal training. Developed for use in human pathogen diagnostics (currently tuberculosis testing in Africa), the technology has high potential for accurate detection of pathogens in other settings where rapid detection is required and where centralised laboratory infrastructure is poor. We are currently working to test and validate Genedrive® against gold standard diagnostics for WSSV and AHPND applied to penaeid shrimps. In addition, we are developing a bespoke smartphone app to interface with Genedrive® and to transmit field data to a centralised data repository for subsequent analysis. The formation of an accurate, low-cost diagnostic and integration with user-friendly reporting of data has the potential to revolutionise disease management in global aquaculture and will contribute directly to poverty alleviation and global food security associated with aquaculture.

POSTER Wednesday 16:30  DB-4

Virus prevalence in bee populations in apple orchards in New York, USA

John P. Burand1, Shuning Zheng2, Bryan N. Donforth3

1Department of Microbiology, 2Graduate Program in Molecular and Cellular Biology, University of Massachusetts - Amherst, Amherst, MA 01003, USA; 3Department of Entomology Cornell University, Ithaca, NY 14853 USA

Correspondence: jburand@microbio.umass.edu

We examined the prevalence of Black Queen Cell Virus (BQCV), and Deformed Wing Virus (DWV) and Sacbrood Virus (SBV) in Apis (Apidae) and Andrena (Andrenidae) bee pollinators found foraging on apple in five orchards in Central New York State. While Apis is a social bee found primarily in managed hives, Andrena are solitary, ground-nesting bees. Bees were collected in mid-May and included approximately 24 bees of each group when available. BQCV was the most prevalent of the three viruses with 71% of the Apis and 49% of the Andrena testing positive for this virus. DWV was found in 38% of Apis and 29% of the Andrena collected from these sites. The prevalence of SBV was 29% and 6% in Apis and Andrena respectively. For all orchards virus levels were higher in Apis than Andrena except at two sample sites were BQCV was more prevalent in Andrena. We are currently examining BQCV gene sequences to determine the relationship between the viruses amplified from bees of these two different families. This is the first reported survey of honey bee viruses in native, solitary andrenid bees.

POSTER Wednesday 16:30  DB-5

Insect pathological challenges in insects produced for food and feed

Jørgen Eilenberg1, Christina Nielsen-LeRoux2, Silvia Cappellozzo3, Just M Vilk4, Annette B Jensen5

1University of Copenhagen, Department of Plant and Environmental Sciences, Copenhagen, Denmark; 2INRA, UMR 1319 Micails-AgroParisTech, France; 3Consiglio per la Ricerca in Agricoltura e l’Analisi dell’Economia Agraria, Honeybee and Silkworm Research Unit, Padova, Italy; 4Wageningen University, Laboratory of Virology, Wageningen, the Netherlands

Corresponding author: jei@plen.ku.dk

Over the latest years, there has been a significant increase in the production of insects for food and feed. Increased production of insects at large scale will lead to many novel challenges, including problems with diseases, similar to what is seen in any other large scale production system. In addition, it is to be expected that new and hitherto neglected or even unknown diseases will emerge in insect production systems. Honeybee and silkworm are mostly produced for other reasons than as human food, yet we can use them as examples to learn about emergence over time of new diseases in production insects. Insect pathologist are needed for disease diagnostics and to develop guidelines for disease control. Contact and collaboration with commercial producers is essential. We provide an overview of insect diseases in the most commonly produced insect species for food and feed, based on a 2014 questionnaire send to commercial producers.

POSTER Wednesday 16:30  DB-6-STU

The influences of insect-mediated mental healthcare program to children with mental disease

Seung Hee Lee1, Sung Min Bae2, Tae Young Shin2, Young Oh Ahn2, Jong Hee Lee3, Won Seok Gwak4, Soo Dong Woo4

1Department of Agricultural Biology, College of Agriculture, Life & Environmental Science, Chungbuk National University, Cheongju 361-763, Korea; 2Department of Neuropsychiatry, Konkuk University Chungju Hospital, Chungju 380-704, Korea

Correspondence: sddwoc@cbnu.ac.kr

Insects are among the most diverse groups of animals on the planet, representing more than half of all known living organisms. These insects are found in nearly every environment. Although humans regard certain insects as pests and attempt to control them using insecticides, most insects perform complex ecological functions, and provide either direct or indirect economic benefits to humans. Recently, the importance of insects used as food sources or as pets has increased in many countries, including Korea. In addition, several insects have a strong influence on people’s emotion. Insect-mediated mental healthcare program is...
Adolescence is a critical period of rapid growth physically, emotionally, mentally and for the development of personality. These students are the real workhorses of the society, and they have the added stress of struggling to get noticed so they can move up in the society one day. Therefore, the goal of our study was to develop of healthcare program using rearing of insects and making of handicraft relation insects, these are limelight in the world. In addition, we attended to develop our own insect-mediated program to middle students and evaluate their psychological healing effects after program. The insect-mediated program was performed once a week for 2 months. The each session did not over 50 min and psychological healing effects were investigated by psychological test paper. As results, the participated students at insect-mediated program increased their mental health including a self-worth to rearing of insects and making of handicraft relation insects. These results may be helpful to develop insect-mediated mental healthcare programs.

Mental health is a great concern to people in modern times. Mental health includes subjective well-being, perceived self-efficacy, autonomy, competence, intergenerational dependence, and self-actualization of one’s intellectual and emotional potential. Maintaining good mental health is crucial to living a long and healthy life; this has become increasingly clear in recent years. Various therapies have been developed to prevent mental health problems, including music therapy, art therapy, play therapy, drama therapy, horticultural therapy, and animal-assisted therapy. Recently, the importance of insects used as food sources or as pets has increased in many countries, including Korea. In addition, several insects have a strong influence on people’s emotion. In this study, we developed the insect-mediated mental healthcare program for the public and evaluated its efficacy. This program was divided into beginning, middle and final parts that were subdivided into six sections, one section per week, 60 minutes per section, followed by pre-test and post-test. They increased to self-esteem, subjective quality of life and quality of life after the completion of the program. Further research on the basis of this study is expected to help public with emotional therapy in other areas.

Molecular characterization of *Isaria fumosorosea* from citrus and strawberry crops in Brazil

Cleomel P. D’Alessandro, Ricardo Macedo do Nascimento, Gustavo Maruyama Morii, Maria I. Zucchi, Paulo Delalibera Junior

Department of Entomology and Acarology, “Luiz de Queiroz” College of Agriculture (ESALQ), University of São Paulo (USP), Piracicaba, São Paulo, Brazil; Center for Molecular Biology and Genetic Engineering, University of Campinas, Campinas, São Paulo, Brazil; São Paulo Agency for Agribusiness Technology, Piracicaba, São Paulo, Brazil

Correspondence: cele1881@gmail.com

The entomopathogenic fungus *Isaria fumosorosea* (Ascomycota: Hypocreales: Cordycipitaceae) is a natural soil inhabitant and infects several species of arthropods. This fungus has been used for the design of insect-mediated mental healthcare programs. The objective of this study was to perform insect-mediated mental healthcare program to adolescents for 8 weeks. The program was conducted once a week for 2 months. The students were divided into experimental and control groups. The experimental group that was provided with an insect-mediated mental healthcare program over a total of 8 sections, one section per week, 60 minutes per section, followed by pre-test and post-test. They responded to therapeutic effect after the completion of the program. Further research on the basis of this study is expected to help children with emotional therapy in other areas.

POSTER Wednesday 16:30 **DB-7**

Development and efficacy of insect-mediated mental healthcare program for the public

Sung Min Bae, Young Soon Jun, Won Seok Gwak, Yong Oh Ahn, Seung Hee Lee, Soo Dong Woo

1 Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea; 2 Department of Neuropsychiatry, Konkuk University Chungju Hospital, Chungju 380-704, Korea

Correspondence: sdmoo@cbnu.ac.kr

Mental health is a great concern to people in modern times. Mental health includes subjective well-being, perceived self-efficacy, autonomy, competence, intergenerational dependence, and self-actualization of one’s intellectual and emotional potential. Maintaining good mental health is crucial to living a long and healthy life; this has become increasingly clear in recent years. Various therapies have been developed to prevent mental health problems, including music therapy, art therapy, play therapy, drama therapy, horticultural therapy, and animal-assisted therapy. Recently, the importance of insects used as food sources or as pets has increased in many countries, including Korea. In addition, several insects have a strong influence on people’s emotion. In this study, we developed the insect-mediated mental healthcare program for the public and evaluated its efficacy. This program was divided into beginning, middle and final parts that were subdivided into six sections, one section per week, 60 minutes per section, followed by pre-test and post-test. They increased to self-esteem, subjective quality of life and quality of life after the completion of the program. Further research on the basis of this study is expected to help public with emotional therapy in other areas.

POSTER Wednesday 16:30 **DB-8-STU**

Efficacy of insect-mediated mental healthcare program to an adolescent

Won Seok Gwak, Tae Young Shin, Young Soon Jun, Sung Min Bae, Yong Oh Ahn, Seung Hee Lee, Soo Dong Woo

1 Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea; 2 Department of Neuropsychiatry, Konkuk University Chungju Hospital, Chungju 380-704, Korea

Correspondence: sdmoo@cbnu.ac.kr

ITS1-5.8S rDNA-ITS2 region of 21 isolates of *Beauveria bassiana*, a pathogenic fungus to the silkworm, *Bombyx mori* L.

Liangen Shu, Jie Jin

College of Animal Sciences, Zhejiang University, Hangzhou, Zhejiang, P.R.China

Correspondence: slgsilk@zju.edu.cn

ITS1-5.8S rDNA-ITS2 region of 21 isolates of *Beauveria bassiana*, a pathogenic fungus to the silkworm, *Bombyx mori* L. were amplified and sequenced. The analysis of all aligned sequences by Mega 3.0 produced a most parsimonious phylogenetic tree. The ITS region of the *Beauveria bassiana* isolates from Nanning (Bb03), Zunyi (Bb06) and Mengzi (Bb07) are significant differences with other isolates, but were 100% homology to the sequence of *Cordyceps bassiana*, teleomorph of *Beauveria bassiana* by submitted to GenBank in National Center for Biotechnology Information (NCBI) through accession number AB027382. There are many sites of mutation in the *Beauveria bassiana* isolates from Yongji (Bb20) and Yantai (Bb21), but were deletion or mutation of base pair of only a few points in other isolates. ITS region was relatively conservative within species level, was no significant differences among isolates. So, ITS region analysis was very reliable to classification and identification between species of *Beauveria bassiana*, a pathogenic fungus to the silkworm, *Bombyx mori* L.

POSTER Wednesday 16:30 **FU-1**

Molecular characterization of *Isaria fumosorosea* from citrus and strawberry crops in Brazil

Celeste P. D’Alessandro, Ricardo Macedo do Nascimento, Gustavo Maruyama Morii, Maria I. Zucchi, Paolo Delalibera Junior

Department of Entomology and Acarology, “Luiz de Queiroz” College of Agriculture (ESALQ), University of São Paulo (USP), Piracicaba, São Paulo, Brazil; Center for Molecular Biology and Genetic Engineering, University of Campinas, Campinas, São Paulo, Brazil; São Paulo Agency for Agribusiness Technology, Piracicaba, São Paulo, Brazil

Correspondence: cele1881@gmail.com

The entomopathogenic fungus *Isaria fumosorosea* (Ascomycota: Hypocreales: Cordycipitaceae) is a natural soil inhabitant and infects several species of arthropods. This fungus has been used for the...
biological control of several important agricultural pest insects and the genetic diversity knowledge would substantially add for its rational use as a biological control agent. The aim of this study was to characterize the genetic diversity of I. fumosorosea strains from soil, rhizosphere and insects found on citrus and strawberry crops and from native vegetation in Brazil. We evaluated 44 isolates and their genetic variability was investigated using eight microsatellite loci and amplified fragment length polymorphism (AFLP). For microsatellite markers, we observed a substantially low genetic diversity by means of Nei’s gene diversity, allelic richness or Shannon-Weiner diversity index. Regarding the AFLP marker, we performed 14 combinations of selective primers and 200 polymorphic fragments ranging from 50 to 350pb were yielded. Nei’s gene diversity was also relatively low (0.25), but we did not detect clones considering 3% of genotyping errors. Using the Bayesian clustering method implemented in the Structure software, the genetic variation of the 44 isolates was clustered in two main groups. Furthermore, the analysis of molecular variance (AMOVA) showed that the grouping that retained the maximum variation corresponded to the grouping based on the fungi source (soil or insect), not on crops nor on geographic origin. These results, besides being scientifically interesting from a microevolutionary perspective, will be useful for properly managing I. fumosorosea as a biological control agent.

POSTER Wednesday 16:30 FU-3-STU
Comparative genomics of cold-adapted Metarhizium frigidum
Brian Lovett, Raymond St. Leger
University of Maryland, College Park
Correspondence: lovettbr@umd.edu

The genomes of entomopathogenic fungi are being sequenced at an impressive rate. Thus far, these include over seven high-quality genomes of Metarhizium spp. that illuminate the unique biology of these fungi, and the enigmatic behavior behind their divergence as specialist or generalist insect pathogens that are also multifactorial plant growth promoters. Here, I present the finished sequence for Metarhizium frigidum, a cold-adapted member of the Metarhizium genus. Using a whole genome approach, we report the full annotation of the genome with analysis of protein family enrichment and other notable genomic features of this unique Metarhizium species. Apart from bolstering the ranks of sequenced Metarhizium fungi, this fungus represents an opportunity to examine cold adaptation in fungi, and in particular, M. frigidum’s ability to maintain pathogenicity at sub-zero temperatures. This in turn can be applied to efforts to use entomopathogenic fungi as biofertilizers and in biocontrol. Since Metarhizium fungi have emerged as model organisms for studying host specificity and plant associations, the results will include characterization of genetic information associated with these lifestyles.

POSTER Wednesday 16:30 FU-4-STU
Identification of Drosophila mutants affecting defense to an entomopathogenic fungus
Hsiao-Ling Lu, Jonathan Wang, Markus Brown, Chris Euerle, Raymond St. Leger
Entomology Department, University of Maryland, College Park, MD, USA
Correspondence: jlwang@umd.edu

Fungi cause the majority of insect disease. However, to date attempts to model host-fungal interactions with Drosophila have focused on opportunistic human pathogens. Here, we performed a screen of 2,613 mutant Drosophila lines to identify host genes affecting susceptibility to the natural insect pathogen Metarhizium anisopliae (Ma549). Overall, 241 (9.22%) mutant lines had altered resistance to Ma549. Life spans ranged from 3.0 to 6.2 days, with mutations increasing susceptibility being 1.6-fold commoner than mutations increasing resistance, and females being more susceptible than males in all lines. Speed of kill correlated with within-host growth and onset of sporulation, but slow kill did not reduce total spore production indicating that this measure of fitness is decoupled from host genotypes. Results showed that mutations affected the ability of Drosophila to restrain rather than tolerate infections and suggested trade-offs between antifungal and antibacterial genes affecting cuticle and gut structural barriers. Approximately, 13% of mutations where in genes previously associated with host pathogen interactions. These encoded fast-acting immune responses including coagulation, phagocytosis, encapsulation and melanization but not the slow-response induction of anti-fungal peptides. The non-immune genes impact a wide variety of biological functions, including behavioral traits; over 62% of mutations have pleiotropic interactions with starvation stress. Many have human orthologs already implicated in human disorders; while others were mutations in protein and non-protein coding genes for which disease resistance was the first biological annotation.

POSTER Wednesday 16:30 FU-5-STU
Persistence of two Brazilian isolates of Metarhizium in a strawberry cropping system using microsatellite markers
Thiago Rodrigues de Castro,1,2, Johanna Mayerhofer,3 Jürg Enkerli4, Jürgen Ellenberg*5, Nicolai V. Meyling*, Italo Delalibera Jr.*
¹University of São Paulo (ESALQ), Brazil; ²Department of Plant and Environmental Sciences, University of Copenhagen, Denmark; ³Institute for Sustainability Sciences, Agroscope, Switzerland
Correspondence: castrotr@gmail.com

The aim of this study was to evaluate the persistence of two Brazilian isolates of Metarhizium (M. anisopliae-ESALQ1037- and M. robertsi-ESALQ1426) that were applied in an strawberry crop in Minas Gerais state in Brazil. The application was made as a randomized block set (10 blocks with 3 treatments), applying 4x10⁶ conidia/ha of the isolates on the surface of the soil near the root of the plants in each plot. The control plot was treated with water only. Soil samples were collected once before the application (September 2012) and 3 times after (January, April and August 2013), and one root sample was being performed in August 2013. Two methods, i.e., insect baiting and plating soil suspensions on a selective medium, were used to isolate Metarhizium spp. To determine the different genotypes, fifteen simple sequence repeat (SSR or microsatellite) markers were PCR amplified from each of the 138 isolates. The EF1-α and MzFGS43igs of one representative isolate per genotype was sequenced to determine species affiliation. Twenty six percent and 22% of the obtained isolates were identified as M. robertsi-ESALQ1426 and M. anisopliae-ESALQ1037. Of the remaining 52% of the isolates, 42% belonged to two indigenous M. robertsii clades, 8% to M. anisopliae and 1 % each to M. pingshaense and M. brunneum. Results have shown that the two applied isolates persisted in the soil for at least one year after application. Furthermore, results indicated that, M. robertsii is better adapted to the experimental field than other Metarhizium spp., since a) it was found to occur naturally, and b) the applied M. robertsii strain was re-isolated at a higher (2,24 times) rate than the applied M. anisopliae isolate.

*IMBICONT “Improved biological control for IPM in fruits and berries” (Brazil/FAPESP:2011/51556-3 and Denmark/FP7-ENV-2011-ECO-INNOVATION:282767-2)
Susceptibility of biocontrol fungi in the genera Nomuraea, Isaria, Purpureocillium, Pochonia, and Trichoderma to imbibitional damage and its mitigation through increased conidial quality

Marcos Faria, Irene Martins, Daniela A. Souza, Rogério B. Lopes
EMBRAPA Genetic Resources and Biotechnology, Brasilia, DF, Brazil
Correspondence: marcos.faria@embrapa.br

When dried conidia are plunged into cold water, rapid imbibition may cause cell death. We assessed the susceptibility to imbibitional damage (ID) of two or three isolates for each of the seven species or varieties of biocontrol fungi considered in this study. A commercial Metarhizium anisopliae isolate, known to be sensitive to ID, was also included. All Isaria farinosa isolates showed significant viability losses (19.1-93.0%) due to drying of conidia with a desiccant, prior to immersion in water. For other isolates, losses in this step were in the 0-12.7% range. Dried M. anisopliae conidia were the most sensitive to ID, with a 41% germination drop following immersion in cold water (15 °C) when compared to immersion in warm water (37 °C). For some I. farinosa, I. fumosorosea and Trichodermaasperellum isolates, and all isolates belonging to Purpureocillium lilacinum and Pochonia chlamydosporia (varieties catenulata e chlarnydospora), losses varied from 15.3 to 38.5%. Germination losses for germinating conidia (including two Nomuraea rileyi isolates produced on agar medium) were in the 0.5-2.6% range. Complementary studies with dehydrated M. anisopliae conidia produced on different substrates revealed that low sensitivity to ID is directly correlated with elevated conidial vigour following dehydration. Low mortalities (0-7%) of dehydrated conidia plunged into cold water were seen when post-drying vigor was ≥ 95% (i.e., 95% of conidia plated on PDA were capable of germinating within 22 h following incubation at 25 °C), regardless of agar medium or cooked cereal used for production of propagules.

Light during mycelial growth induce increased tolerance of conidia to different types of stress in entomopathogenic fungi

Luciana P. Dias1, Claudia J. A. S. Araujo1, Paulo C. Ferreira2
1Instituto de Pesquisa e Desenvolvimento, Universidade do Vale do Paraíba, São José dos Campos, SP 12244-000, Brazil; 2Escola de Engenharia de Lorena (EEL/USP), Pós-Graduação em Biotecnologia Industrial, Estrada Municipal do Campinho, Lorena, SP, Brazil
Correspondence: lucianapereiradias@live.com

The effect of visible-light exposure during mycelial growth was investigated on the conidial tolerance of ten insect-pathogenic fungi to: UV radiation (A), osmotic stress caused by potassium chloride (B), and genotoxic stress caused by 4-nitroquinoline1-oxide (C). Conidia of ten species were produced: 1) on potato dextrose agar medium (PDA) in the dark (control), 2) on PDA under continuous visible light, and 3) under nutritional stress (= Czapek medium without sucrose - MM) in the dark. Conidia of Metarhizium robertsii (ARSEF 2575) and Isaria fumosorosea (ARSEF 3889) produced under visible light had higher tolerance to (A). Five species (Beauveria bassiana (ARSEF 252), M. brunneum (ARSEF 1187), M. robertsii (ARSEF 2575), Tolypocladium cylindrosporum (ARSEF 3392), and Aschersonia aleyrodis (ARSEF 10276)) were more tolerant to (B). Three species (M. brunneum (ARSEF 1187), M. anisopliae (ARSEF 5749), and A. aleyrodis (ARSEF 10276)) become more tolerant to (C). The mycelial growth under MM significantly induced increased conidial tolerance to all three stress conditions for the species B. bassiana (ARSEF 252), and T. inflatum (ARSEF 4877). MM induced higher tolerance of M. brunneum (ARSEF 1187), M. robertsii (ARSEF 2575), and M. anisopliae (ARSEF 5749) to (A) and (B), but not to (C). T. cylindrosporum (ARSEF 3392) grown on MM was more tolerant to (A) only. The only species that did not respond either to light or nutritional stress were Lecanicillium applanocadali (ARSEF 6433) and Simplicillium lanosoniveum (ARSEF 6651). Visible light is, therefore, an important factor that induces stress tolerance in some insectpathogenic fungi.

Comparison of the use of insect baiting methods versus selective media when determining the diversity of Metarhizium spp. in soil

Carmela Hernández-Domínguez, Ariel W. Guzmán-Franco
Postgrado en Fitosanidad-Entomología y Acarología, Colegio de Postgrados, Km. 36.5 Carretera México-Texcoco, Montecillo, Texcoco, Estado de México, 56230, Mexico
Correspondence: gargel@colpos.mx

When developing a fungal-based biocontrol agent, it is important to assess the regional diversity of native entomopathogenic fungi.
prior to release. The two methods commonly used for the detection of entomopathogenic fungi such as Metarhizium spp. in soil are (i) the use of Galleria mellonella larvae as a bait, and (ii) selective media. When used simultaneously these methods can provide different results and, therefore, their use is currently under discussion. We compared the accuracy of baiting with G. mellonella versus the use of two selective media (CTC and DOD) for the recovery of M. anisopliae, M. robertsi, M. brunneum and M. pingshaense. For this, we artificially inoculated soil with conidia from the four species to produce two concentrations (2 x 10^5 and 2 x 10^6 conidia g^-1). Using selective media it was possible to identify significant differences amongst the four Metarhizium species, with M. robertsi producing most colony forming units (CFU) recovered followed by M. anisopliae, M. pingshaense and M. brunneum. More CFU’s of M. anisopliae, M. robertsi were recovered using CTC media compared to DOD regardless of the conidia concentration whilst DOD was the optimal media for M. brunneum and M. pingshaense. More CFU were recovered at the higher concentration (2 x 10^6 conidia g^-1). The results of baiting with G. mellonella showed a greater recovery of M. anisopliae followed by M. brunneum, M. Pingshaense and M. robertsi, regardless of the conidia concentration. The possibility of combining both methods to obtain more accurate results are discussed.

POSTER Wednesday 16:30 **FU-10-STU**

**Antifungal activity of entomopathogenic fungi isolated in Korea and their geographical characteristics**

Yong Oh Ahn, Tae Young Shin, Sung Min Bae, Won Seok Gwak, Seung Hee Lee, Soo Dong Woo

Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea

Correspondence: sdwoo@cbnu.ac.kr

Entomopathogenic fungi are natural enemies of insects and contribute to the regulation of their host populations. Their mode of action against insects involves the attachment of conidia to the insect cuticle, followed by germination, cuticle penetration, and internal dissemination throughout the insect. During this process, secreted enzymes, protein toxins, and secondary metabolites can be used by the fungus to overcome the host immune system, modify host behavior, and defend host resources against competing pathogens and saprophytes. Additionally, these metabolites exhibit variety bioactivities, and they have been suggested as potential candidates for the development of new bioactive agents. In this regard, recently, most of studies searching for antifungal substances from fungi were performed in worldwide. However, the distribution and characterization of entomopathogenic fungi having antifungal activity is not reported yet to our knowledge. At present, 28 species and 20 genera of 342 entomopathogenic fungi from diverse natural habitats of South Korea soils have been isolated and identified in our laboratory. From our preliminary experiments, we have identified of fungi especially entomopathogenic fungi that have antibacterial, antioxidant and anticancer activities. The goal of our study was to establish a pool of entomopathogenic fungi having antifungal activity regard to habitat type. This study can be a little guide for future entomopathogenic fungal source programs and the selected fungal isolates having antifungal activity in this study may be useful as the source of antifungal substances.

**FU-11**

**Characterization and pathogenicity of a Beauveria pseudobassiana strain that collapsed a laboratory colony of Dendroctonus ponderosae (Coleoptera: Scolytidae)**

George Kyei-Poku, Debbie Gauchier, Fernando Mantouvane, Johny Shajahan

1Natural Resources Canada, Canadian Forest Service, Great Lakes Forestry Centre Sault Ste. Marie, Ontario, Canada; 2Amco Farms Inc., Leamington, ON, Canada

Correspondence: gkyeipok@nrcan.gc.ca

The mountain pine beetle (MPB), Dendroctonus ponderosae Hopkins is a well-entrenched insect pest to western Canada and the United States and causes severe disturbance regime by the ever range expansion in lodgepole and other pine forests. Control strategies which have been applied so far are still insufficient to prevent its damage and eastward spread. Entomopathogenic fungi which have shown potential to regulate other beetle pests as biological control agents could play a relevant role in the management of MPB. The Beauveria isolate (MPB-UBK) that caused the collapse of our lab MPB colony had been identified as a new member of the species B. pseudobassiana based on the partial EF1-alpha, intergenic Bloc and ITS sequences homology and concurrent phylogenetic analysis. Virulence of B. pseudobassiana - MPB-UBK isolate was compared with commercial agents Beauveria bassiana (Botanigard ES; Bb); Metarhizium brunneum (Met F52 ES; Mb); Isaria fumosorosea (PFR 97 20% WDG™; Ifr); nine highly pathogenic strains including Beauveria bassiana (2), Beauveria pseudobassiana (2), Metarhizium robertsi (2), and Isaria fumosorosea (1) on MPB adults under laboratory conditions. All the Beauveria spp. isolates were found to be highly infectious and virulent against MPB. The B. pseudobassiana - MPB-UBK isolate caused approximately 90.0% mortality of MPB adults 6 days post inoculation in the concentration of 1 x 10^5 conidia/mL. Consequently, B. pseudobassiana - MPB-UBK appears to be a promising microbial control agent to exploit in the management of for biocntrol of Dendroctonus ponderosae.

**FU-12**

**Entomopathogenic fungi for six species of leaf-cutting ants from different sites of Argentina**

Daniela Gaffre, Jorge A. Marfetan, Patricia J. Folgarait

Laboratorio de Hormigas, Departamento de Ciencia y Tecnología, Universidad Nacional de Quilmes, Bernal, Buenos Aires, Argentina

Correspondence: patricia.folgarat@gmail.com

We investigated the entomopathogenic fungi associated with workers from 6 species of leaf-cutting ants (Acromyrmex lundii, A. crassipinus, A. heyeri, A. lobiconis, A. aspersus and A. striatus), in 8 sites located in 5 Phytogeographical Provinces (Pampeana, Espinal, Monte, Yungas and Patagónica) in Argentina. We hypothesized that, at least, the sampling site could explain similarities among entomopathogenic’s communities, mainly because of opportunistic horizontal transmission. From 3748 ants, we recorded 31.2% of ants infected with entomopathogenic fungi. Fusarium oxysporum and F. solani were the most widely distributed, followed by Purpureocillium lilacinum. Río Negro (Patagónica Province) exhibited the greatest richness with 13 species, followed by the site from Monte Province with 10 species. We advanced the hypothesis that Penicillium sp.1 and C. equinula var. verticillata could be considered indicator species of Río Negro and Salta (Yungas), respectively, as they were registered in most nests only from these sites. We found that A. aspersus located in Tucumán (Yungas) had more
entomopathogens (median: 59%) than other ant species and sites, followed by A. lobicornis (41%) from La Pampa (Monte). We run several cluster analyses with presence-absence of entomopathogens at different levels: nests, sites, phytogeographical provinces, and ant species. We found that only sites exhibited similarities among the entomopathogen’s communities in agreement with our hypothesis. However, there were great differences among nests within sites probably due to the dissimilar health status or capacity to avoid infections.

POSTER Wednesday 16:30 FU-13

First isolation of Beauveria and Metarhizium from a wheat stem borer, Cephus cinctus (Hymenoptera: Cephidae) in North America

Stefan T. Jaronski1, Gadi V. P. Reddy2, Shaohui Wu2, John F. Gaskin2, Stephen Rehner2
1Agricultural Research Service, U.S. Department of Agriculture, Northern Plains Agricultural Research Laboratory, Sidney MT 50270 USA; 2Montana State University, Western Triangle Research Center, Conrad MT 59425 USA; 1Agricultural Research Service, U.S. Department of Agriculture, Systematic Mycology Laboratory, Beltsville MD 20705 USA

Correspondence: Stefan.Jaronski@ars.usda.gov

The wheat stem sawfly, Cephus cinctus, a grass-mining cephid attacking wild grasses and small grains, is the most important pest of wheat in the Plains region of the U.S. and southern Canada. Yield losses occur due to larval tunneling and stem lodging and annual losses are estimated at more than $100 million just in MT. Except for the adult stage, entire development of C. cinctus takes place inside the plant. We unexpectedly encountered Beauveria bassiana s.l. infections in live, diapausing larvae in spring 2013. Subsequent surveys in autumn 2013 and 2014 yielded 61 additional Beauveria isolates, plus three isolates of Metarhizium flavoviride s.l. Analysis with Bloc gene sequence revealed the isolates fall into either Rehner’s B. bassiana Clade A4, or B. pseudobassiana. Only a few of 50+ wheat fields sampled had Beauveria infections among the larvae from a site, but prevalence in positive fields was very high, reaching 100% in some fields. Overall prevalence was 1.1%. While there was strong clustering of genotypes within a wheat field, there was great overall diversity. Given the biology of the insect, totally isolated within the wheat pith, it is highly likely that these infections arose from endophytic Beauveria and Metarhizium. Several of the original isolates were found to be highly pathogenic to wheat stem sawfly larvae and work is underway to determine endophytic potential of several strains. Research reported here is being funded by multiple grants from the Montana Wheat and Barley Committee.

POSTER Wednesday 16:30 FU-14

First report of a mosquito-pathogenic Leptolegnia sp. (Saprolegniales) in Brazil

Cristian Montalva1, Richard A. Humber2, Karine dos Santos2, Stefanie Buchter3, Karin F.S. Collier4, Luiz F.N. Rocha1, Éverton K.K. Fernandes1, Christian Luz2
1Laboratório de Patologia de Invertebrados, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brasil; 2USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA; 3Centro Universitário UNIRG, Gurupi, TO, Brasil; 4Instituto Federal de Educação, Ciência e Tecnologia de Goiás, Aparecida de Goiânia, GO, Brasil

Correspondence: montalva.cristian@gmail.com

A Leptolegnia chapmani-like oomycete is reported in Brazil for the first time. These aquatic oomycetes were bailed with Aedes aegypti sentinel larvae in stagnant, transitory breeding sites in secondary tropical gallery forests from September 2014 to February 2015 (spring–summer) in the State of Goiás, Central Brazil. The measurements of major characters of this fungus (given as lower and higher means of two separate series of 25 measurements) are as follows: hyphae 7–7.5 µm wide, zoosporangia 814.1–1297.8 × 11.1–12.2 µm with zoospores formed in a single file, primary zoospore cysts 10.9–11.3 µm in diameter, oogonia 31–32.6 µm in diameter decorated by finger-like projections, and oospores (11.3 µm in diameter, n=25). Overall morphology made it clear that this isolate is closely related to Leptolegnia chapmani. The pathogenicity of 15 isolates was tested under laboratory conditions against A. aegypti larvae (L2/L3). Rapid development of disease was observed for five isolates resulting to a complete mortality of tested larvae at a 36 h exposure to the oomycete. The larvicidal activity of the other isolates was lower, resulting in fewer dead larvae in the same period (< 50%). The findings of this study contribute to a better vision about the geographical distribution of this important entomopathogen and suggest that its function and prevalence as a natural control agent of mosquitoes in South America so far has been probably underestimated.

POSTER Wednesday 16:30 FU-15

The puzzle of identifying mosquito-pathogenic isolates of Leptolegnia

Richard A. Humber1, Cristian Montalva2, Christian Luz2
1USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA; 2Laboratório de Patologia de Invertebrados, Instituto de Patologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brasil

Correspondence: richard.humber@ars.usda.gov

The first Brazilian collections of a Leptolegnia species (Peronosporomycetes: Saprolegniales) pathogenic for mosquitoes illustrate how difficult it can be to identify some taxa, even in this age of phylogenetic systematics. Apparently, the only existing living cultures of Leptolegnia chapmani Seymour, the sole mosquito-pathogenic species of its genus, in major culture collections were isolated from several sites in the United States and one in Argentina. All of these cultures were isolated after L. chapmani was described. No living authentic or ex-type material of L. chapmani seems to be available for taxonomic comparisons, and the exact location of the holotype specimen of L. chapmani is uncertain. This poster illustrates how the vital information inherent to the descriptions and typification of species names needs to be applied in a real-world setting to a significant biological problem that affects the way in which biodiversity information for Brazil and, indeed, for the entire continent of South America needs to be recorded. And the answer regarding how the Brazilian isolates of Leptolegnia should best be identified will also profoundly impact how the scientific world should regard the distribution and comparative frequency of incidences of a taxon such as Leptolegnia chapmani.

POSTER Wednesday 16:30 FU-16

A treasure among the trash: Pandora bullata from a Brazilian garbage dump

Richard A. Humber1, Cristian Montalva2, Karin F.S. Collier4, Christian Luz2
1USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA;
Species of *Fungi* are where one finds them, and if one seeks fungal pathogens affecting flies, then a garbage dump may be an ideal place to find persistent and abundant fly populations and their fungal pathogens. An obvious fungal epizootic affecting large populations of a muscid fly (possibly *Musca domestica*) was found in the local garbage dump outside of the city of Cavaclante, northern Goiás. The outbreak was observed over three consecutive days in mid-February 2015. This site harbored very large populations of a muscid fly (possibly *Musca domestica*) as well as of *C. megacephala* but only the calliphorids were found to be heavily mycotized by a fungus that can now be unequivocally identified as the first Brazilian (and South American) findings of *Pandora bullata* (Entomophthorales: Entomophthoraceae). Very few infected individuals of *Chrysomya* were found at this site in early April, but those cadavers included small numbers of the characteristically bullate resting spores of *P. bullata*. We do not know whether such abiotic factors as altitude (13° 48’40” 53” S), day length, or even precipitation patterns in this mid-tropical, montane site might somehow diminish the capacity of this fungus to produce the much more abundant resting spores characteristically seen for entomopathoraceous entomopathogens in more temperate latitudes. During the course of this epizootic 261 individuals were collected in February; of these, 187 (71.6% of the population) were females, 74 (28.4%) were males, but the overall sex ratio within the healthy fly population on this site was not determined.

**POSTER Wednesday 16:30**

**FU-17-STU**

**Effects of temperature on germination, growth, and sporation of *Cucilominyses* species**


1Laboratório de Patologia de Invertebrados, Instituto de Pathologia Tropical e Saúde Pública, Universidade Federal de Goiás, Goiânia, GO, Brazil; 2USDA-ARS Collection of Entomopathogenic Fungal Cultures, RW Holley Center for Agriculture and Health, Ithaca, NY, USA

Species of *Cucilominyses* (Hyponoctae) facultatively infect the aquatic larval stages of a range of mosquitoes and blackflies through the digestive tract after conidia ingestion. While *C. clavisporus* was most studied in the 1980s, little is yet known about how temperature affects the development and sporulation of various isolates. Conidia of ten *C. clavisporus* isolates (ARSEF 372, 582, 644, 706, 964, 1260, 2471, 2478, 2479, 2480) and one *C. bisporalis* (ARSEF 1479) were inoculated on SDAY/4 and incubated at 15, 20, 25, 30 or 35°C. Conidial germination was assessed after 24 and 48 h of incubation. Colony sizes were measured daily for 15 days, and conidial production was quantified after 15 days. The best conidial germination rates (>95%) after 48 h of incubation were obtained at 25 and 20°C; the poorest germination (<12%) was at 35°C. The best temperature for radial growth was 25°C (>11.8mm) followed by 20°C for all isolates; ARSEF 706, 582 and 372 showed the most vegetative growth (>20mm). There was little growth at 30°C (<2.5mm), and none at 35°C. The maximal conidial production occurred at 25°C for all isolates (21.42×10^3 conidia/plate), and the isolates ARSEF 964, 2479, and 644 produced the largest numbers of conidia (24×10^3 conidia/plate). After testing these basic growth properties, the isolates producing the most conidia on the medium surface (964) or on submerged mycelium (644, 2479) were passed three times through *Aedes aegypti* larvae before re-testing the isolates’ conidial production and to assess their comparative virulence.

**POSTER Wednesday 16:30**

**FU-18-STU**

**Beauveria bassiana inhibits host seeking behavior of *Anopheles stephensi***

Minehiro Ishii1,2, Masanori Koike3, Daigo Aiuchi4

1The United Graduate School of Agricultural Sciences, Iwate University, Japan; 2Research Fellowship for Young Scientists, Japan Society for the Promotion of Science; 3Department of Agro-environmental Science, Obihiro University of Agriculture & Veterinary Medicine, Japan; 4Research Center for Global Agromedicine, Obihiro University of Agriculture & Veterinary Medicine, Japan

In our previous study, various entomopathogenic fungi were isolated from wild adult mosquitoes. Among them, *Beauveria bassiana sensu lato* 60-2 showed highest virulence against *Anopheles stephensi*. We also found new pathway of fungal infection via mosquito proboscis, and fungal development was observed from their head compared with other parts. Female mosquitoes search target hosts using multiple sensory inputs, including CO₂ and non-olfactory stimuli such as heat and visual cues. They have such sensory organs in their head. So the present study was focused on the alteration of the host searching behaviors by entomopathogenic fungus infection. The adult female mosquitoes were inoculated with *B. bassiana* s.l. 60-2, and host searching behavior to heat (40°C) and color (black) were evaluated by using automated-recording device, and host searching behavior to odor (CO₂) was evaluated by using Y-tube olfactometer. Consequently, attractiveness to the heat was drastically decreased from 3 days post inoculation (dpi), and attractiveness to the color had a tendency to decrease from 6 dpi. Furthermore, attractiveness to the odor was decreased from 2 dpi. Our results showed that the mosquitoes could not recognize the heat, visual and odor cues. In other words, they might not be able to recognize hosts by entomopathogenic fungus infection. Conventional vector control method was evaluated only the death of vector. If such kind of behaviors will be inhibited, it also could prevent the disease transmission. So our further study will focus on not only the death of organisms but also “the death as vectors” by entomopathogenic fungi.

**POSTER Wednesday 16:30**

**FU-19**

**Biological activity of entomopathogenic fungi over two species of sugarcane borer *Diatraea spp.* (Lepidoptera: Pyralidae)**

Gloria P. Barrera1, Emiliano Barreto2, Paula Sotelo1, Paola Cuartas3, Laura Villamizar1

1Corporación Colombiana de Investigación Agropecuaria, Corpoica, Mosquera, Colombia; 2Centro de Bioinformática, Instituto de Biotecnología, Universidad Nacional de Colombia, Bogotá, Colombia

Manufacture of the main food product obtained from the sugarcane in Colombia depends of sucrose content, which is seriously affected by the stem borers complex including *Diatraea saccharalis* and *Diatraea indiginella*. Due to the disadvantages of chemical control of these pests, the biological control with entomopathogenic microorganisms is an excellent alternative. In this work, five geographical entomopathogenic fungi were taxonomically classified and biochemically evaluated as alternative
for biological control of *D. saccharalis* and *D. indiginella* larvae. The fungi proceeded from different insect species. *Metarhizium* sp. (M3015) from *Premnotrypes vorax* (Coleoptera: Curculionidae), *Isaria* sp. (P013) from *Bemisia tabaci* (Homoptera: Aleyrodidae), *Nomuraea* sp. (Nn006) from *Spodoptera frugiperda* (Lepidoptera: Noctuidae) and *Beauveria* sp. from *P. vorax* (Bb025) and *Diatraea* sp. (Bv062). Molecular identification of fungi was performed using PCR and sequencing of two genomics regions of ribosomal RNA, ITS and 18S genes and elongation factor-1 alpha (EF1-a). The biological characterization was performed using a bioassay by inoculating of second instar larvae of each species with specific suspensions (10⁷ conidia/ml). The fungi were classified as *Metarhizium robertsi*, *Isaria javanica*, *Nomuraea rileyi* and the two isolates of *Beauveria* sp. as *B. bassiana*. The efficacies over *D. saccharalis* larvae were 73.3% (Bv062), 63.3% (M3015), 56.6% (Nn006) and 26.6% (Bb025). The efficacies over *D. indiginella* larvae were 83.3% (Bv062), 80% (Bb025), 66.6% (M3015) and 26.6% (P013). The highest larvae mortalities for these two species of sugarcane borers were obtained with the *B. bassiana* isolated from *Diatraea* spp. (Bv062), showing the adaptation of entomopathogenic fungi to the host from which were isolated.

**POSTER/ Wednesday 16:30 FU-20**

**Entomopathogenic fungi for the control of Thaumastocoris peregrinus Carpenter and Dellappé (Heteroptera: Thaumastocoridae)**

*Sofia Simeto¹*, Ana B. Corallo¹, Sandra Lupo¹, Lina Bettucci²


Correspondence: ssimeto@itb.inia.org.uy

The bronze bug, *Thaumastocoris peregrinus* (Heteroptera: Thaumastocoridae) is one of the most important pests of *Eucalyptus* plantations worldwide. Its lacerate- and flush feeding habit produces foliage blight and defoliation, thus reducing photosynthesis and leading to the death of mature trees when severe infestation occurs. Chemical control is seldom used in commercial forestry because of environmental and economical disadvantages; therefore biological control is seen as the only feasible option. In this work, entomopathogenic fungi were isolated from dead and mycosed bronze bug from *Eucalyptus* plantations in Uruguay. Fungi identification was based on spore morphology and biochemical characterization was performed using a bioassay by inoculating second instar larvae of each species with specific suspensions (10⁷ conidia/ml). The fungi were classified as *Metarhizium robertsi*, *Isaria javanica*, *Nomuraea rileyi* and the two isolates of *Beauveria* sp. as *B. bassiana*. The efficacies over *D. saccharalis* larvae were 73.3% (Bv062), 63.3% (M3015), 56.6% (Nn006) and 26.6% (Bb025). The efficacies over *D. indiginella* larvae were 83.3% (Bv062), 80% (Bb025), 66.6% (M3015) and 26.6% (P013). The highest larvae mortalities for these two species of sugarcane borers were obtained with the *B. bassiana* isolated from *Diatraea* spp. (Bv062), showing the adaptation of entomopathogenic fungi to the host from which were isolated.

**POSTER Wednesday 16:30 FU-21**

**Effectiveness of Metarhizium anisopliae and Beauveria bassiana against eggs of tomato leafminer, Tuta absoluta Meyrick, 1917 (Gelichiidae: Lepidoptera)**

Laila A. M. Al-Shuraym¹, Nagdy F. Abdel-Baky²

¹Department of Biology, College of Arts and Sciences in Buraydhah, Qassim University, Saudi Arabia; ²Department of Plant Production & Protection, College of Agriculture and Veterinary Medicine, Qassim University, P.O. Box: 6622, Buraydah 51452, Saudi Arabia.

Correspondence: nafabel2005@yahoo.com

The tomato leaf-miner, *Tuta absoluta* Meyrick is a very serious and dangerous leaf mining, stalk borers and fruits pest of *Solanaceae* plants (eggplants, potatoes, sweet peppers, other various cultivated plants and certain weeds of *Solanaceae* family), but tomatoes are considered their principal host plant. This insect pest has an ability to cause great reduction in tomato fruits ranged from 50-100% of the yield and so, the insect presence may leads to limit the tomato exports among countries and to several destinations. So, this study was carried out to assay the effectiveness of two entomopathogenic fungi *Metarhizium anisopliae* and *Beauveria bassiana* against *T. absoluta* eggs under lab conditions. As well as, the planning use of these entomopathogenic fungi as bio-insecticides to reduce the insecticide use within IPM programs was discussed. In this paper, the ability of *M. anisopliae* and *B. bassiana* in reducing the vitality of *T. absoluta* eggs was assessed. Eggs of *T. absoluta* were treated with different conidal concentrations of the two entomopathogenic fungi under laboratory conditions. The obtained results suggest that the moderate (8x10⁴) and the higher (10x10⁴) spore concentration/ml of *M. anisopliae* and *B. bassiana* were the effective conidial concentrations against *T. absoluta* eggs and could be developed into bio-control agents against *T. absoluta* eggs in IPM programs with another safety control tools.

**POSTER Wednesday 16:30 FU-22**

**Metarhizium F52 microsclerotia applied in hydromulch to control Asian longhorn beetle**

Tarynn Anne Goble¹, Ann Hajeck², Mark Jackson³, Sana Gardescu³

¹Department of Entomology, Cornell University, Ithaca, NY, 14853-2601; ²USDA-ARS-NCAUR, Crop Bioprotection Research Unit, 1815 N University Street, Peoria, IL, 61604.

Correspondence: tagoble@gmail.com

Metarhizium brunnurn F52 (Hyphocreales: Clavicipitaceae) produces environmentally persistent microsclerotia, which can be mixed with a carrier (clay, carboxymethyl-cellulose, or diatomaceous earth) to produce granules. These are incorporated into hydromulch (water, wheat straw mulch and pyllium tackifier), which holds moisture and allows microsclerotia to produce many conidia. The formulation represents a novel mycoinsecticide to spray onto trunks and branches of trees. No significant differences were observed in conidia production or viability between granule types, for five water activities (αw), averaging 1.74x10⁴ conidia/g at the highest αw (0.983) compared to 3.45 x10⁴ conidia/g at the lowest αw (0.929). F52-hydromulch reduces Asian longhorned beetle, *Anoplophora glabripennis* fecundity. Breeding pairs exposed to logs sprayed with F52-hydromulch had only 3.9 viable offspring per female, versus 18.3 for controls. When beetles were exposed by walking 80 cm on a log sprayed with microsclerotia in hydromulch, median time survived was 18-22 days, but 23-26 days using logs sprayed with
microsclerotia only, which produced fewer conidia. Conidial production and field persistence were evaluated using substrates sprayed with hydromulch and exposed on forest tree trunks. Conidial densities increased over time, reaching 5.5 × 10⁶ conidia/cm² by 20-30 d periods of higher temperature, humidity and rainfall. Increased conidial densities resulted in significantly decreased survival of A. glabripennis, especially females, in laboratory bioassays using field-collected sprayed substrate. Females exposed 2 d to high conidial densities had median survival times of 16-22 d. The results suggest reapplication might only need to occur after 6-8 weeks.

**POSTER Wednesday 16:30** **FU-23-STU**

Control of ticks (*Ixodes ricinus*) in sheep pastures in Norway with the fungal biocontrol agent BIPESCO 5 (*Metarhizium brunneum*)

Natascha Iwanicki¹, Lise Greva², Hermann Strasser³, Annette Folkedal Schjælfi⁴, Maria Björkman⁵, Karin Westrum⁶, Jürg Enkerli⁷, Nicolai V. Meyling⁸, Ingeborg Klingenberg⁹

¹Department of Entomology and Acarology, ESAOL, University of São Paulo, Brazil; ²Norwegian Institute for Agricultural and Environmental Research (Bioforsk), Norway; ³Institute of Microbiology, Leopold-Franzens University of Innsbruck, Austria; ⁴Swiss Federal Research Station for Agroecology and Agriculture, Switzerland; ⁵Department of Ecology, Faculty of Life Sciences, University of Copenhagen

Correspondence: ingeborg.klingen@bioforsk.no

Tick-borne fever, vectored by the tick *Ixodes ricinus*, is a major challenge in Norwegian sheep farming during the grazing season. Field trials were carried out to evaluate the efficacy of the entomopathogenic fungus *Metarhizium brunneum*, BIPESCO 5, in controlling natural tick populations in two sheep pastures. In 2013, plots were treated with BIPESCO 5 at: no fungus (control), fungus application in May or fungus application in May and June in 2014. Another pasture was treated either with no fungus (control), fungus application in May and June, or fungus application in May, June and September. Tick populations were monitored by flagging and incubated for fungal infection. The application of *M. brunneum* BIPESCO5 reduced the tick population in fungus treated plots but <15% of ticks with *M. brunneum* spp. were observed. Baiting of soil samples prior to fungus application with wax moth larvae *Galleria mellonella* showed very low natural occurrence of *Metarhizium* spp. at the first field site. The retrieved fungal isolates from ticks are being molecularly characterized by microsatellite markers to verify if infections were caused by BIPESCO 5 or naturally occurring fungi.

**POSTER Wednesday 16:30** **FU-24-STU**

Development of *Aphidius colemani* incapable of oviposition and the evaluation of control efficacy against cotton aphid by combined use of entomopathogenic fungus and parasitoid wasp

Fuka Oikawa¹, Minehiro Ishii¹, Masanori Koike², Daigo Auchi³

¹Department of Agro-environmental Science, Obihiro University of Agriculture and Veterinary Medicine, Japan; ²The United Graduate School of Agricultural Sciences, Iwate University, Japan; ³Research Fellowship for Young Scientists, Japan Society for the Promotion of Science; ⁴Research Center for Global Agro-medicine, Obihiro University of Agriculture and Veterinary Medicine, Japan

Address for Correspondence: aigo@obihiro.ac.jp

In our previous study, entomovectoring ability of *Aphidius colemani* to carry *Leconicillum muscarium* was reported. However, it was not possible to evaluate the single control efficacy of insect-vectored fungus against cotton aphid, so we could not judge whether this efficacy is synergistic or additive. The present study aimed to develop *A. colemani* incapable of oviposition, and evaluation of control efficacy against cotton aphid by combined use of entomopathogenic fungus and parasitoid wasp were conducted. The tip of the ovipositor of parasitoid was closed by adhesive, and then the abilities of *A. colemani* to host searching and/or oviposition behavior were evaluated. Consequently, there were no significant difference between parasitoid incapable of oviposition and parasitoid capable of oviposition on the number of host searching and ovipositional behavior. This result suggests that both parasitoids were equivalently contact with the aphid host and carrying entomopathogenic fungus to aphid population equally. So this parasitoid was applied for bioassay as vector of *L. muscarium* without oviposition, namely fungus single inoculation plot. The evaluation of control efficacy against cotton aphid by combined use of parasitoid and entomopathogenic fungi was resulted in no significant difference between *L. muscarium* single inoculation plot and combined use plot on the number of fungus infected aphid. Moreover, there were no significant difference between *A. colemani* released plot and combined use plot on the number of mummy. From the above results, it was revealed that the cotton aphid control by combined use of *A. colemani* and *L. muscarium* will operate 2‘additional’ effect.

**POSTER Wednesday 16:30** **FU-25**

Latent infection of wireworms and its relation to ambient *Metarhizium* levels in soil

Todd Kabaluk, Erica Li-Leger

Agriculture and Agri-Food Canada, Agassiz, BC, Canada

Correspondence: Todd.Kabaluk@agr.gc.ca

Wireworms (*Coleoptera: Elateridae*) are serious agricultural pests, with soil-dwelling larvae attacking roots and tubers of crop plants, and fruit in contact with the soil surface. Researchers collect wireworms for laboratory experiments to study of their behaviour and test pest control agents but frequently lose them to Metarhizium Petch (Ascomycota: Hypocreales: Clavicipitaceae) infection in the absence of an inundative application. We found Metarhizium infection in 13-100% of live wireworms acquired directly from field collections, and in wireworms collected in the field and maintained indoors. *Metarhizium* DNA in living wireworms maintained indoors sometimes exceeded 250 pg/ug total DNA (0.025% of wireworm mass). Expressed as copies of *Metarhizium* DNA/µg, soil levels of *Metarhizium* ranged from 4,037 in agricultural field soil to 721,538 (soil harbouring a wireworm collection indoors). The quantity of soil *Metarhizium* was related to the incidence of infection of live specimens as % infected wireworms = 34.03 log[copies Met DNA/µg soil] – 99.90; R² = 0.98. These findings have implications for *Metarhizium* as a regulator of wireworm populations in nature, as a biological control agent for wireworms, storage of specimens, and raise questions about wireworm immune response.

**POSTER Wednesday 16:30** **FU-26**

Smell the danger! Odor-perception of fungal infection risk in a below-ground parasitoid

Belén Cotes¹, Linda-Marie Ränström², Maria Björkman³, Hans R Norlid⁴, Nicolai V. Meyling⁵, Birgitta Råmart⁶, Peter Anderson⁷

¹Department of Plant Protection Biology, Division of Integrated Plant Protection, Swedish University of Agricultural Sciences, Växjöskylsvägen 3, P.O. Box 102, SE-230 53 Alnarp, Sweden; ²Bioforsk. Plant Health and Plant Protection Division, Høgskoleveien 7, 1430, Ås, Norway; ³Department of Plant and Environmental Sciences, University of Copenhagen, Thorvaldsensvej 40, DK-1871 Frederiksberg C, Denmark

Correspondence: nvm@plen.ku.dk
To locate and evaluate host patches before oviposition, parasitoids of herbivorous insects utilize plant volatiles and host-derived cues, but also evaluate predator-derived infochemicals to reduce predation risks. When foraging in host habitats infested with entomopathogenic fungi, parasitoids may reduce the risk of fungal infection by avoiding such patches. In this study, we examined whether the presence of the entomopathogenic fungi Metarhizium brunneum and Beauveria bassiana in soil habitats of a root herbivore, Delia radicum, affects the behavior of Trybliographe rapae, a parasitoid of D. radicum. Olfactometer bioassays revealed that T. rapae avoided fungal infested host habitats and that this was dependent on fungal species and density. In particular, the parasitoid avoided habitats with high densities of the more virulent fungus, M. brunneum. In contrast, host density was found to be important for attraction of T. rapae. Volatiles collected from host habitats revealed different compound profiles depending on fungal presence and density, which could explain the behavior of T. rapae. We conclude that T. rapae females may use volatile compounds to locate high densities of prey, but also compounds related to fungal presence to reduce fungal infection risk towards themselves and their offspring.

**POSTER Wednesday 16:30 FU-27-STU**

**Maize endophytes offer potential protection against insects and disease**

Jenny J. Brookes, Travis R. Glare, Michael Rostás

Bio Protection Research Centre, Lincoln University, New Zealand

Correspondence: jenny.brookes@lincoln.ac.nz

Endophytes of plants are increasingly seen as including species beneficial to the growth of plants. In some cases the presence of endophytes results in increased tolerance to insect pests or plant diseases. In this study, endophytes have been isolated from maize plants over two seasons and identified, to determine the full complement of fungi associated with maize in New Zealand. Endophytic ability is being confirmed by re-establishment in maize plants. Bioassays using several insect species and a disease of maize are being used to identify beneficial endophytes. It is hoped that this work will expand the range of species known to improve maize growth.

**POSTER Wednesday 16:30 FU-28**

**Physiochemical characteristics of entomopathogenic fungi-derived antifungal substances**

Tae Young Shin, Sung Min Bae, Won Seok Gwak, Seung Hee Lee, Yong Oh Ahn, Soo Dong Woo

Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongiu 361-763, Korea

Correspondence: sdwoo@cbru.ac.kr

The bioactive substances from entomopathogenic fungi have been suggested as potential candidates for the development of new bioactive agents. Our previous study suggested that a lot of entomopathogenic fungi have antifungal activity against plant pathogenic fungus Botrytis cinerea on solid medium. Additionally, their culture filtrates suppressed the growth of B. cinerea, indicating that the suppression was due to the presence of antifungal substances in the fungal culture filtrates. In this study, therefore, the physiochemical characteristics, such as thermal stability, polarity, proteases susceptibility and molecular weight, of the antifungal substances from fungal culture filtrates were investigated to evaluate their usefulness. As the results, the antifungal substances from various fungi had various features according to the isolated fungus. Most of all antifungal substances were hydrophilic and stable at high temperature (100°C, 15 min). They were also resistant to degradation by protease and had various range of molecular weights. These antifungal substances may be a good candidates to be used in the development of a new biocontrol method.

**POSTER Wednesday 16:30 FU-29-STU**

**Entomopathogenic fungi “infecting” young lives**

Alap Sahoo1, Sumanth S. R. Dara2, Suchitra S. Dara2, Surenadra K. Dara2

1Massachusetts Institute of Technology, Cambridge, MA, USA;
2Warren Junior High School, Bakersfield, CA, USA; 3University of California Cooperative Extension, San Luis Obispo, CA, USA.

Correspondence: skdara@ucdavis.edu

Working with entomopathogenic fungi has changed our lives and academic careers. We went from people who were reluctant to even look at insects, let alone handle them, to people who could carry out major scientific research projects. Engaging in real life research at a young age helped us know about the specialized area of entomopathology and develop research skills that are very important in life. Among other skills, we learned how to plan and execute scientific studies, prepare for challenges, adapt to changing situations, learn to be patient, engage in the meticulous process of data collection, do proper data analysis, and write and present results. After all of this work, it is truly rewarding because we were able to contribute to science and provide practical solutions. Various laboratory experiments we conducted with Beauveria bassiana led to field studies against major arthropod pests such as Lygus hesperus, B. hilaris, Tetranychus urticae in strawberries and vegetables.

**Microbial Control**

**POSTER Wednesday 16:30 MC-1**

**Next generation biopesticides for New Zealand’s key insect pests and plant diseases**

Maureen O’Callaghan1, Travis Glare2, Mark Hurst3, Sean Marshall4, Tracey Nelson5, Michael Wilson5, Sarah Mansfield5, Sue Ydenbos5

1Innovative Farm systems, AgResearch, Lincoln Research Centre, New Zealand; 2Bio-Protection Research Centre, Lincoln University New Zealand; 3Innovative Farm systems, AgResearch, Ruakura New Zealand

Correspondence: maureen.ocallaghan@agresearch.co.nz

New Zealand’s agricultural and horticultural producers are seeking to reduce their environmental footprint but are vulnerable to major production losses caused by insect pests and diseases. Research is underway to provide farmers and growers with New Zealand-appropriate, cost effective biopesticides for control of intractable indigenous insect species emerging as pests as a result of land use change, farming intensification, and climate change. Targets include key pests complexes such as foliar-feeding pests of brassicas and subterranean turf pests. Biopesticides are also being developed for control of incursions of exotic cosmopolitan pests and diseases such as diamondback moth, African black beetle. To minimise regulatory hurdles, microorganisms under development as biopesticides include new species/strains isolated from productive ecosystems within New Zealand, such as the broad host range insecticidal bacterium
Yersinia entomophaga, Brevibacillus sp.; and fungal species (Metarhizium and Beauveria) are being developed for independent and dual use (synergy) for the control of insect pests. A range of formulations and delivery systems (e.g. baits, sprays, granules, seed treatments) are being developed. Prototype biopesticides are being trialled in field tests, in conjunction with industry partners. For biopesticides to succeed in mainstream agriculture and horticulture in New Zealand, new biopesticide products will need to have levels of efficacy comparable to currently available controls, and be able to be used by farmers with minimal change of practice.

POSTER Wednesday 16:30 MC-2
Appearance of pathogens within outbreak populations of native porina caterpillar (Wisenea spp.) populations in New Zealand
Sean D. G. Marshall\(^1\), Richard J. Townsend\(^2\), Colin M. Ferguson\(^3\), Sarah Mansfield\(^4\)
\(^1\)Innovative Farming Systems, AgResearch, Lincoln Research Centre, Christchurch, New Zealand; \(^2\)Innovative Farming Systems, AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand
Correspondence: sean.marshall@agresearch.co.nz

The Gondwanaland remnant of Aotearoa-New Zealand developed a unique flora and fauna over >60 million years. When settlers introduced European grasses and clovers they initially grew spectacularly in the absence of their usual pest complex. However, some native herbaceous insects were capable of adapting to the new environment and reached unprecedented numbers destroying the pastures until the associations between native herbivorous insects and population regulating systems could be re-established. Today, an uneasy balance of nature has been reached across many New Zealand grasslands, except where major new land conversions have caused fresh pest outbreaks. The new large scale pasture development that is happening on the New Zealand West Coast (‘flipping’ of swamps to create new pastures), central North Island Volcanic Plateau (conversion of pine forest to dairy pasture), and in Otago (development of largely undisturbed soil) has reset the conditions to total environmental disruption. After initial vigorous pasture growth, the endemic porina caterpillar (Wisenea spp.), normally only present at >20/m\(^2\), reaches numbers exceeding 800/m\(^2\) causing extensive damage within 1-3 years of land development. The enemy release hypothesis states that invasive species thrive in new environments due to the lack of natural enemies present in their home range. While this hypothesis has generally been investigated for exotic invasions around the world, invading organisms can also be indigenous, moving into new or disrupted ecosystems. Research has indicated a growing awareness of the importance of pathogens in population regulation. We have discovered disease is beginning to infect porina caterpillar populations found in recently modified New Zealand lands and will discuss our current findings.

POSTER Wednesday 16:30 MC-3
Pathogens and nematodes of bark beetles (Coleoptera: Scolytidae) in Georgia coniferous forest
Archil Supatashvili, Medea Burjanadze
Department of Forest Protection, Vasil Gulisashvili Forest Institute, Agricultural University of Georgia, Tbilisi, Georgia
Correspondence: m.burjanadze@agruni.edu.ge

Georgia is distinguished by its biodiversity, with endemic and relict species of plants in Caucasus. Picea orientalis, Pinus sosnowskyi and Pinus Eldaric, are widespread and present in Georgian coniferous forest. Principal species of bark beetles: Spruce bark beetle - Ips typographus L, Great spruce bark beetle - Dendroctonus micans (Kugelann), Six-toothed bark beetle - Ips sexdentatus (Börner), Pine shoot beetle–Tomocerus piniperda L. are causing tree mortality throughout the coniferous forest. 50-70-ies of the last century had emerged in forests of Borjomi gorge an extremely harmful insect pest D.micans, which caused the death of millions of spruce trees. From 2000, I. typographus became a major outbreak in the last decade. Human activity, changing climate, changing physiological conditions of host plants, influence on insect activity, increase its responsibility and risk for new colonization, not only in Georgia, but in Caucasian and Black sea region.

During 2013-2014, our research focused on the control of bark beetles using mechanical methods and pheromone traps. Also we investigated natural enemies: predators and pathogens (microorganisms and parasitic nematodes) which are responsible to make balance density of bark species. Various pathogen species and nematodes were observed in the populations of bark beetles. Gregaria typographi, was found in I. typographus (40.5-45.5%) and I. sexdentatus (15.3%). Chytridiopsis typographi was found in I. typographus and T.piniiperda (6.3% -12%) and I. sexdentatus, (4.5%). Fungus Beauveria bassiana (3.5%) was found in I.typographus. Nematodes (42.7-65.0%) Contortylenchus diplogaster were observed in I. typographus. Contortylenchus sp. was found in I.sexdentatus. 26.1% nematodes were associated with D.micans.

POSTER Wednesday 16:30 MC-4-STU
PhopGV for control of Tuta absoluta in tomato and Phthorimaea operculella and Tecta solanivora in potato
Andreas Larem, Eva Fritsch, Karin Undorf-Spahn, Johannes A. Jehle
Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Biological Control, Heinrichstr. 243, 64287 Darmstadt, Germany
Correspondence: andreas.larem@jki.bund.de

Due to increasing standards in food production alternatives are needed to reduce the usage of chemical plant protection agents. A promising method to protect plants against insect pests is the usage of baculoviruses. Previous studies have shown that there may be the opportunity to use a single baculovirus isolate to control three different but close related insect species i.e. Phthorimaea operculella (potato tuber moth), Tecta solanivora (Guatemalan potato moth) and Tuta absoluta (tomato leaf miner). Isolates of Phthorimaea operculella granulovirus (PhopGV) were found to infect all of these three pests. To find a highly virulent isolate to control these three pests different PhopGV isolates are characterized by biological and molecular means. To distinguish between different isolates variable regions like ORF 129 which is coding for egt (ecdysteroid UDP-glucosyltransferase) can be a useful tool in combination with restriction fragment length polymorphism (RFLP) analysis. Bioassays give a hint of the host interaction and virulence of the several isolates. As an outcome of this research the development of a combined control of different pests by highly selective baculoviruses is aimed.

POSTER Wednesday 16:30 MC-5-STU
Sublethal effects of Cry1Ac on immune responses and baculovirus infection in Spodoptera frugiperda
Lucas N. Wisch\(^5\), Jenny S. Cory\(^\dagger\), Daniel R. Sosa-Gómez\(^5\)
\(^5\)Pos-Graduation Program, State University of Ponta Grossa, Paraná, Brazil; \(^\dagger\)Dept. of Biological Sciences, Simon Fraser University, Burnaby, , Canada; \(^\dagger\)Entomology Research, Embrapa Soybean, Londrina, Paraná, Brazil; \(^5\)Supported by Capes
Correspondence: wisch02@hotmail.com
**POSTER Wednesday 16:30 MC-6-STU**

**Virulence of a newly isolated Bacillus thuringiensis strain against lepidopteran larvae**

Anna I. Moldovan\(^1\), Natalia Munteanu Molotievskiy\(^2\), Svetlana G. Baco\(^1\), Ion J. Toderas\(^3\)

\(^1\)Faculty of Biology and Soil Science, Moldova State University, Chisinau, Republic of Moldova;  
\(^2\)Institute of Zoology, Academy of Sciences of Moldova, Chisinau, Republic of Moldova

Correspondence: anna.moldovan@yahoo.com

A large number of fruit trees, including apples, pears and quinces are cultivated in temperate climates. A rich diversity of insects attacks the fruit trees, among them, lepidopterans being considered the most dangerous pests in many countries in Europe including Moldova, causing substantial yield losses.

We evaluated the virulence of a newly isolated Bacillus thuringiensis strain CNMM B8-04 to three lepidopteran species: Cydia pomonella (L. 1758), Archips rosana L. 1758 and Lymantria dispar L. 1758, larvae. In bioassay test, apple leaves were used as diet. Leaves of approximately the same size were treated with prepared bacterial suspension, dried at 20°C and placed into petri dishes. Sterile 0.9% NaCl solution was used as control. At least 10 larvae and 2-5 treated leaves were used per repetition. Three repetitions were made for each lepidopteran species. Insect mortality was recorded after 3 days of incubation at 21°C and photoperiod of 24 h and all dead insects were removed from petri dishes. In assays with treated apple leaves, at a concentration of 9 x 10⁷ spores/ml, larval mortality of Archips rosana, Cydia pomonella and Lymantria dispar was 90.0, 93.33 and 96.67% respectively. The virulence of the strain was expressed in LC₅₀ values calculated according to Kerber’s formula, the highest value 1.392 x 10⁹ spores/ml being recorded for Lymantria dispar. These results show that Bacillus thuringiensis strain CNMM B8-04 is virulent to all tested lepidopteran species and has potential as a biological control agent in fruit trees pest management programs.

**POSTER Wednesday 16:30 MC-7**

Selection and characterization of formulation prototypes based of Beauveria bassiana for biological control of Cerotoma tingomariana

Erika Grijalba\(^1\), Lorena Garcia\(^1\), Carlos Espino\(^1\), Judith Guevara\(^2\), Hugo Fernando Rivero\(^3\)

\(^1\)Biological Control Laboratory; \(^2\)Entomological Laboratory, Colombian Corporation for Agriculture Research, CORPOICA, Colombia

Correspondence: egrijalba@corpoica.org.co

A microbial formulation is composed of an active ingredient with biological activity and excipients that are raw materials inerts that protect and release the active ingredient. The formulation should ensure stability during production, processing and storage; facilitate application, provide protection against ultraviolet radiation and the temperature. In the biological control laboratory we development nine formulation prototypes corresponding to a granulated and nine formulation corresponding to an emulsifiable concentrate based of Beauveria bassiana (Bv060), isolation previously selected for its efficacy against Cerotoma tingomariana, pest of soybean crop that reduces the nitrogen fixation and the yield crop. The aim of this work was to select two formulation prototypes based of B. bassiana against C. tingomariana. Inoculum, the selection of four prototypes was doing from of test of resistance to temperature and to ultraviolet radiation. The prototypes were exposed to a storage temperature of 25°C and 35°C and the germination and Colony Formate Unit (CFU) were evaluated in the zero time and after of 1, 2 and 3 months. Later, the prototypes were reconstituted in Tween 80 0,1% and were exposed to ultraviolet radiation type B (UVB) for different times. Again, was evaluated the germination and Colony Formate Unit (CFU). From these results were selected four prototypes. The prototypes selected were biological testing on laboratory and were determined the lethal concentration 90 (LC90). With the value LC90 be evaluated the efficacy of the prototypes in greenhouse.

**POSTER Wednesday 16:30 MC-8**

Sublethal effects of Cry1Ac Bacillus thuringiensis protein on Plutella xylostella (Lepidoptera: Plutellidae) Brazilian population: Life table study

Caroline P. De Bortoli\(^1\), Ricardo A. Polanczyk\(^2\), Neil Crickmore\(^2\), Sergio A. De Bortoli\(^1\), Alessandra M. Vaccari\(^1\)

\(^1\)Department of Plant Protection, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil; \(^2\)Department of Biochemistry, School of Life Sciences, University of Sussex, Falmer, Brighton, United Kingdom

Correspondence: carubortoli@yahoo.com.br

The sublethal effects of Cry1Ac Bacillus thuringiensis protein were investigated on life table parameters of the Plutella xylostella (L.) Brazilian population. After dip-leaf bioassay with kale leaves, the sublethal concentrations 0.5, 0.25, and 0.1 µg/mL were determined. The control group was water and Tween 0.05%. Third instar P. xylostella larvae were placed on kale leaves after dry and the evaluations were performed in 3 days. The results showed that the mean values of the life table parameters were significantly affected by treatment. The net reproductive rate (R₀), intrinsic rate of increase (rₒ), and finite rate of increase (A) decrease with the increase of concentrations of Cry1Ac protein. The values of R₀ were 64.6 females/female to control, 28.8 females/female to 0.1 µg/mL, 21.1 females/female to 0.25 µg/mL, and 20.8 females/female to 0.5 µg/mL. The values of rₒ were 0.303 females/female*day to control, 0.218 females/female*day to 0.1 µg/mL, 0.183 females/female*day to 0.25 µg/mL, and 0.157 females/female*day to 0.5 µg/mL.
to 0.1 µg/mL, 0.206 females/female*day to 0.25 µg/mL, and 0.195 females/female*day to 0.5 µg/mL. The mean generation time (T) and doubling time (Dt) increase with the increase of concentrations of Cry1Ac. The values of T were 15.6 days to 0.5 µg/mL, 14.9 days to 0.25 µg/mL, and 13.7 days to control. The values of Dt were 3.5 days to 0.5 µg/mL, 3.2 days to 0.5 µg/mL, and 2.3 days to control. The sublethal concentrations of Cry1Ac protein may reduce the population of P. xylostella by decreasing its survival and reproduction, and by delaying its development.

The use of the insecticide the basis of Bacillus thuringiensis Berliner in combination with other management tactics can be a good strategy for overcoming the resistance. The aim of this research was to verify the effect of B. thuringiensis on the predator Podisus nigrispinus (Dallas), providing suspension of the bacteria HD1 strain or commercial product as water source. The predators fed regularly with Diatraea saccharalis (F.) larvae as prey. Three treatments were performed: B. thuringiensis kurstaki HD1 strain (3 x 10^9 spores/mL), commercial product suspension (B. thuringiensis aizawai - Agree®), and water (control). The commercial product was used in the concentration recommended by the manufacturer. We evaluated the survival, number of eggs per female and sex ratio of the offspring. This information was used to estimate the fertility life table parameters. The survival to adulthood was 60.0% for the control treatment, 44.0% for HD1 strain, and 40.0% for the Agree® product. The female fecundity was 200.8 eggs/female for the control treatment, 112.0 eggs/female for the HD1 strain, and 106.9 eggs/female for the Agree® product. The population parameters of fertility life table R_0, r_0, T, and DT were 62.9 females/female, 0.142 females/female*day, 29.2 days, and 4.9 days for the control treatment; 36.9 females/female, 0.137 females/female*day, 26.4 days, and 5.0 days for the strain HD1; 31.5 females/female, 0.135 females/female*day, 25.5 days, and 5.1 days for the Agree®, respectively. The HD1 strain and the Agree® product affected the biological characteristics and population parameters of P. nigrispinus when the predators ingest suspension.

The predators fed regularly with Diatraea saccharalis (F.) larvae as prey. Three treatments were performed: B. thuringiensis kurstaki HD1 strain (3 x 10^9 spores/mL), commercial product suspension (B. thuringiensis aizawai - Agree®), and water (control). The commercial product was used in the concentration recommended by the manufacturer. The third generation of predators submitted to treatments was evaluated. We evaluated the survival, number of eggs per female and sex ratio of the offspring. This information was used to estimate the fertility life table parameters as net reproduction rate (\(R_0\)), intrinsic rate of increase (\(r_0\)), average generation time (\(T\)), and doubling time (\(DT\)). The population parameters of fertility life table \(R_0\), \(r_0\), \(T\), and \(DT\) were 88.8 females/female, 0.168 females/female*day, 26.7 days, and 4.1 days for the control treatment; 30.4 females/female, 0.121 females/female*day, 28.2 days, and 5.7 days for the strain HD1; 90.4 females/female, 0.177 females/female*day, 25.6 days, and 3.9 days for the Agree®, respectively. Only HD1 strain affected the population parameters of P. nigrispinus when the predators ingest suspension over the generations by reducing the number of females produced per female.

*ABSTRACTS*

**Interaction between predator Podisus nigrispinus (Dallas) and the entomopathogenic bacterium Bacillus thuringiensis Berliner**

Vanessa F. P. Carvalho, Sergio Antonio De Bortoli, Alessandra M. Vacari

Department of Plant Protection, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil

Correspondence: bortoli@fcav.unesp.br

The use of the insecticide the basis of Bacillus thuringiensis Berliner in combination with other management tactics can be a good strategy for overcoming the resistance. The aim of this research was to verify the effect of B. thuringiensis on the predator Podisus nigrispinus (Dallas), providing suspension of the bacteria HD1 strain or commercial product as water source. The predators fed regularly with Diatraea saccharalis (F.) larvae as prey. Three treatments were performed: B. thuringiensis kurstaki HD1 strain (3 x 10^9 spores/mL), commercial product suspension (B. thuringiensis aizawai - Agree®), and water (control). The commercial product was used in the concentration recommended by the manufacturer. We evaluated the survival, number of eggs per female and sex ratio of the offspring. This information was used to estimate the fertility life table parameters. The survival to adulthood was 60.0% for the control treatment, 44.0% for HD1 strain, and 40.0% for the Agree® product. The female fecundity was 200.8 eggs/female for the control treatment, 112.0 eggs/female for the HD1 strain, and 106.9 eggs/female for the Agree® product. The population parameters of fertility life table \(R_0\), \(r_0\), \(T\), and \(DT\) were 62.9 females/female, 0.142 females/female*day, 29.2 days, and 4.9 days for the control treatment; 36.9 females/female, 0.137 females/female*day, 26.4 days, and 5.0 days for the strain HD1; 31.5 females/female, 0.135 females/female*day, 25.5 days, and 5.1 days for the Agree®, respectively. The HD1 strain and the Agree® product affected the biological characteristics and population parameters of P. nigrispinus when the predators ingest suspension.

**Reproduction and population parameters of predator Podisus nigrispinus (Dallas) providing Bacillus thuringiensis Berliner suspension as water source over generations**

Vanessa F. P. Carvalho, Sergio Antonio De Bortoli, Alessandra M. Vacari

Department of Plant Protection, Sao Paulo State University, Jaboticabal, Sao Paulo, Brazil

Correspondence: amvacari@gmail.com

A better control strategy could be to use a combination of Bacillus thuringiensis-based insecticide along with other management tactics, such as the use of other natural enemies, to try to maintain the balance in the agroecosystem. The aim of this research was to verify the effect of B. thuringiensis on the predator Podisus nigrispinus (Dallas), providing suspension of HD1 strain or commercial product as water source over generations.
The ambrosia beetles *Xylosandrus crassiusculus* (Xc) and *Xyleborus volvulus* (Xv) (Coleoptera: Curculionidae: Scolytinae) vector the fungal pathogen *Raffesio lauriciola*, which causes laurel wilt, a lethal disease of avocado. The objectives of these studies were to determine the beetles' susceptibility to infection and subsequent death rate by exposure to three commercial strains of entomopathogenic fungi over time. Two different sets of bioassays (dipping beetles and dipping paper disks) were conducted to determine the time that each formulation of entomopathogenic fungi, *Beauveria bassiana* (BotaniGard® ES), *Isaria fumosorosea* (PFR 97%+ 20% WDG), and *Metarhizium brunneum* (MFS2 ES), takes to cause mortality of the ambrosia beetle species. The spore density of the fungal solutions in all bioassays was 2.4 x 10^5 spores/ml. The median survival time (ST50) sequences for beetles dipped in the fungal suspensions were *Beauveria < Metarhizium < Isaria* for Xc and *Beauveria = Metarhizium = Isaria* for Xv. The ST50 value sequence for both beetle species consuming treated filter paper disks was *Beauveria = Metarhizium = Isaria*. Results from field persistence of the fungal suspensions sprayed on avocado bolts demonstrated that conidia of *Beauveria* and *Metarhizium* persisted up to 21 days after treatment (DAT); more *Isaria* colony-forming units (CFUs) appeared 21 DAT than at 1 DAT. At 21 DAT, CFUs of *Isaria* were also found in plates of the *Beauveria* and control treatments. Field persistence trials after application of *Beauveria* or *Isaria* on avocado trees are ongoing; findings will be reported as available.

**POSTER Wednesday 16:30 MC-13**

**Efficacy of *Metarhizium anisopliae* ICPE 7 for the control of cattle tick**

Paulin Nana1,2, Sunday Ekezie, Mercy Mumbi1, Nguy 1Centre of Insect Physiology and Ecology, Nairobi, Kenya; 2Faculty of Agriculture and Agricultural Sciences, University of Dschang, Cameroon; 3Department of Veterinary Pathology, Microbiology and Parasitology, University of Nairobi, Kenya

Correspondence: pnana@icipe.org

Ticks and tick-borne diseases cause serious economic losses to cattle industry. Current control strategies for these vectors rely on extensive use of chemical acaricides against which they have developed resistance. Entomopathogenic fungi are perceived as a promising alternative to acaricides. The present study evaluates the efficacy of *Metarhizium anisopliae* ICPE 7 in controlling on-host ticks under field conditions. Twenty cows with an average of 437 ticks/animal were separated into four groups representing the following treatments: (1) Control; (2) Emulsifiable formulation of conidia (1 x 10^4 conidia ml^-1); (3) Amitraz and (4) Combination of Amitraz and fungus (1 x 10^4 conidia ml^-1 + 0.1% Amitraz). Each cow was sprayed once a week with two litres of the corresponding treatment in a crush. Tick load was recorded once per week. The persistence of conidia was also determined by sampling different parts of the skin of cattle using a cotton swab. Average number of ticks on cattle treated with fungus (133.4 ± 27.0) was significantly lower (P < 0.05) than the one in the controls (318.0 ± 60.4), representing 58.2% reduction. Treatment with Amitraz resulted in 79.5% reduction while 63.9% tick reduction was recorded in combination of fungus with Amitraz. Mortality of the ticks sampled from cows after spray applications ranged between 94-98% in fungus treatments against 3% in the controls. Viability of conidia varied according to animal body parts and ranged between 62.6 and 72.4% 7 days post-spray. These results indicate that *M. anisopliae* ICPE 7 has potential for on-host tick control.

**POSTER Wednesday 16:30 MC-15**

**Delivery of entomopathogenic fungi as a seed coating for control of soil-dwelling insect pests**

Federico Rivas1,3, Trevor Jackson2, John Hampton1, Per Wessman1, Jayanthi Swaminathan1, Michael Rostas2, Travis R. Glare2

1Bio-Protection Research Centre, Lincoln University, Lincoln, New Zealand; 2AgResearch, Lincoln Research Centre, Lincoln, New Zealand; 3National Institute for Agricultural Research, Las Brujas, Uruguay

Correspondence: Federico.RivasFranco@lincolnuni.ac.nz

Recently, it has been shown that *Metarhizium* spp. can act as both insect pathogens and plant-growth-promoting agents. This bifunctional lifestyle of *Metarhizium* is illustrated by the expression of genes involved in the adhesion to insect (*mad1*) or plant surfaces (*mad2*). In addition, a plant carbon transporter, *Metarhizium* raffinosae transporter (*mrt*), was reported as required for successful root colonization. The development of fungal entomopathogens as biocontrol agents requires an understanding of the interactions between fungi, insect pests and plants. Our present work is focused on the selection of entomopathogenic fungi to both colonize the plant rhizosphere and have biocontrol activity against insect pests when delivered through seed coating. In order to determine root competence, growth response of *Metarhizium* spp. isolates to maize root exudates was determined using microplate assays. Additionally, the presence of *mad1*, *mad2* and *mrt* was determined by PCR. Finally, the effects of *Metarhizium* spp. on maize plant growth and plant resistance...
against larvae of the scarab beetle Costelytra zealandica was determined. The selection of root-competent strains is advisable for improve establishment and persistence of entomopathogenic fungi delivered as seed coating.

**POSTER Wednesday 16:30 MC-16**

**Fat pellet strategy applied to the boll weevil (Anthonomus grandis) under laboratory conditions**

Marcos Faria, Lorena K. B. Bravo, Bruna M. Kraus, Rogério B. Lopes
EMBRAPA Genetic Resources and Biotechnology, Brasilia, DF, Brazil
Correspondence: marcos.faria@embrapa.br

An attract-and-kill approach based on fat pellets blended with an aggregation pheromone and conidia of entomopathogenic fungi was tested against adults of the boll weevil, Anthonomus grandis (Coleoptera: Curculionidae). In a preliminary screening assay, A. grandis from a rearing facility was immersed for 20 sec in 2-mL suspensions containing 6x10⁶ viable conidia/mL of either Beauveria bassiana or Metarhizium anisopliae. Average confirmed mortality rates were ≤ 35.8% for B. bassiana isolates and 61.7% for isolate CG46 of M. anisopliae. In another set of experiments, weevils were forced to contact fat pellets (without pheromone) impregnated with CG46 conidia, for either 30 min or 4 h at two incubation temperatures (26 or 30°C). The higher the exposure time and temperature, the higher the mycosis-confirmed mortality, reaching an average of 85.2% for the most favorable combination. Olfactometer assays revealed that fat pellets impregnated with both conidia and pheromone were highly attractive to weevils. Attraction was improved when other semiochemicals were added to pellets. Greenhouse experiments will be performed in 2015. The aim of this project is to develop an alternative strategy that could be tested under field conditions in the management of boll weevil populations.

**POSTER Wednesday 16:30 MC-17-STU**

**Compatibility of fungicides with Beauveria bassiana**

Sumanth S. R. Daru¹, Suchitra S. Darar, Alap Sahoo, Haripriya Bellam², Surendra K. Darra³
¹Stockdale High School, Bakersfield, CA, USA; ²Warren Junior High School, Bakersfield, CA, USA; ³University of California Cooperative Extension, San Luis Obispo, CA, USA
Correspondence: skdara@ucdavis.edu

Field studies in California demonstrated the potential of Beauveria bassiana in managing strawberry pests. Growers, however, are concerned about its compatibility with fungicides that are frequently applied to manage foliar diseases. To address this issue, pathogenicity of B. bassiana to Tenebrio molitor in the presence of eight fungicides from different mode of action groups that are commonly used for disease management in strawberries. Captan, Merivon, Microthiol Disperss, Pristine, Rally, Roval, Switch, and Thiram were applied from 0 to 6 day interval prior to the application of B. bassiana and the mortality of T. molitor larvae were measured for six days. Captan and Thiram caused a significant reduction in the efficacy of B. bassiana. Remaining six fungicides did not affect B. bassiana. Time interval did not have any influence on any of the tested fungicides. Results address a major concern of grower by demonstrating that several fungicides are compatible with B. bassiana and support sustainable pest management practices.

**POSTER Wednesday 16:30 MC-18**

**Characterization of Tolypocladium cylindrosporum (Hypocreales: Ophiocordycipitaceae) and its effectiveness in infecting Aedes aegypti eggs (Diptera: Culicidae)**

Lina B. Flor-Weiler¹, Alejandro P. Rooney², Robert W. Behle², Daniel A. Strickman²
¹Crop Bioprotection Unit, Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL 61604; ²(Retired), Office of National Programs, Agricultural Research Service, U.S. Department of Agriculture, Beltsville, MD 20705
Correspondence: lina.weiler@ars.usda.gov or alejandro.rooney@ars.usda.gov

Availability of an effective egg-targeting system would allow for the control of a much greater portion of mosquito populations, because after emergence adults disperse away from egg-laying sites. Consequently, eggs form a reservoir of individuals highly susceptible to control measures. The purpose of this study was to evaluate the potential of the fungus Tolypocladium cylindrosporum as a control agent for the mosquito Aedes aegypti. Morphological characterization of T. cylindrosporum IBT 41712 was conducted and pathogenic activity of the fungus against A. aegypti eggs was evaluated. Fungal growth at different temperatures, conidia germination and sporulation on solid media was observed using light microscopy and scanning electron microscopy. The fungus formed white colonies turning creamy white when mature, and sporulation occurred after 8-10 days of incubation. The mycelia bore flask-shaped or swollen conidiophores producing smooth-walled, single-celled conidia that are oblong and cylindrical in shape when mature. Conidia had 96-98% germination after 10 days incubation and appeared to vary in size, ranging from 1µm to 2.5µm long. The optimum temperature for growth was 28°C, with a maximum mean radial growth rate of 1.1 ± 0.02 mm/day. There was no fungal growth observed at 33, 37 or 40°C. However, growth was observed at 4, and 12°C, albeit much more slowly than at room temperature or optimal levels. Significant reduction in larval hatch was observed for fungus treated eggs with significantly fewer larvae surviving (20%) at 14 days post treatment compared with those surviving in the control (93%).

**POSTER Wednesday 16:30 MC-19**

**Stress-induced changes in the dopamine levels of haemolymph of cabbage armyworm Mamestra brassicae and Colorado potato beetle Leptinotarsa decemlineata**

E. A. Chertkova, O. N. Yaroslavtseva, I. M. Dubovskiy, V. V. Glupov
Institute of Systematics and Ecology of Animals, Russian Academy of Sciences, Siberian Branch, Frunze str. 11, Novosibirsk 630091, Russia
Correspondence: chertkaterina@yandex.ru

We've studied effect of several stress factors on dopamine levels in haemolymph of cabbage armyworm Mamestra brassicae and Colorado potato beetle Leptinotarsa decemlineata. It was detected the increase of dopamine concentration in haemolymph of M. brassicae in 7 times against to control under high temperature (50°C) treatment. The mechanical injury (burn) leded to increase of dopamine concentration in haemolymph of M. brassicae in 5.5 times against to control. We’ve found that Beauveria bassiana fungal infection resulted to 4 times rising of dopamine concentration in haemolymph of M. brassicae. Toxigenic strain of Metarhizium robertsi induced the enhancing dopamine level in haemolymph of Leptinotarsa decemlineata in 70 times compared with control and in 2.5 times against to biotrophic strain M. robertsi. Present data show that dopamine
is one of the key stress molecule and its level can be important in immune defence against entomopathogenic fungi.

**POSTER Wednesday 16:30 MC-20**

**Biosynthesis of silver nanoparticles using the fungus* Trichoderma viride* for the toxicity on* Aedes aegypti* mosquito and their antibacterial activity**

*Siva Kamalakathnang, Chandrakesan Gobinath, Kadarkarai Murugan*

Unit of Medical Entomology, Department of Zoology, Bharathiar University, Coimbatore-641046, India

Correspondence: kamal410@yahoo.com

Silver nanoparticles are explored in recent years as an alternative approach to effectively kill mosquito vector and drug resistant pathogenic microorganisms. In the present study, an eco-friendly process for the synthesis of nanoparticle, using a fungus (*Trichoderma viride*) has been attempted. The fungus biomass supernatant was used for the biosynthesis of Ag-NPs. The aqueous silver ions (Ag+) were reduced to silver metal nanoparticles (Ag m-NPs), when treated with the fungal supernatant. After 24h of treatment, silver nanoparticles (Ag-NPs) were obtained. These Ag-NPs were characterized by UV-Vis, Scanning Electron Microscopy (SEM) with Energy Dispersive Spectroscopy (EDS) and X-ray Diffraction (XRD) were used to identify these NPs. The nanoparticles exhibited maximum absorbance peak at 420 nm in UV-Vis spectroscopy. The NPs surface morphology revealed from SEM images shows formation of well-dispersed Ag-NPs of 50 nm, and the presence of silver was confirmed by EDX and Fourier transform infrared spectroscopy (FTIR) analysis. The efficacy of mycosynthesized AgNPs tested concentrations of 5, 10, 15, 20 and 25 ppm against L1 to L4 instar larvae and pupae of *Aedes aegypti*; LC50 (LC90) values are 13.15(24.55); 12.08(29.45); 10.47(36.65); 9.85 (41.31) and 9.72 (42.24) in larvae and LC50 (LC90) values was 5.09 (15.53) in pupae, respectively. The mortality rates were positively correlated with the concentration of AgNPs. The microbes selected for the present study for the antibacterial activity were *E. coli*, *P. aeruginosa*, *B. cereus*, *Enterococi*, *E. aerogens*. We conclude that the nanoparticle synthesized from the fungus has great potential mosquito larvicidal agents as well as antimicrobial compound against pathogenic microorganisms.

**Microsporidia**

**POSTER Wednesday 16:30 MI-1**

**Effects of the microsporidian pathogen, *Nosema adaliae* on the seven-spotted lady beetle, *Coccinella septempunctata* L.**

(Coleoptera: Coccinellidae)

*Elkabir Entisar, Bjørnson Susan*

Department of Biology, Saint Mary’s University, 923 Robie Street, Halifax, NS B3H 3C3 Canada

Correspondence: Susan.Bjornson@smu.ca

There has been a noticeable decline in lady beetles in North America over the past few decades. Because lady beetles play an important role in the regulation of aphids and other soft-bodied insect populations in nature, lady beetle population decline has become a significant cause for concern in agriculture systems. Decreased populations are attributed to several causes, including competition from more aggressive lady beetle species (such as the multi-coloured Asian lady beetle, *Harmonia axyridis* Pallas) and the potential impact of insect pathogens. Microsporidia are fungal pathogens that commonly infect lady beetles. Recent studies have focused on the prevalence and potential impact of microsporidia in lady beetles, including the effects of microsporidian pathogens on host development and host specificity. The objective of the study is to gain knowledge about the effect of the microsporidian pathogen *Nosema adaliae* from the two-spotted lady beetle *Adalia bipunctata* L. on the development of the seven-spotted lady beetle, *Coccinella septempunctata* L. An examination of the effects on development and the impact of the pathogen on second-generation beetle larvae could provide insight to the population dynamics of *C. septempunctata*. The results from this study will provide more information to understand the effects of pathogen on host development, fecundity, and vertical transmission.

**POSTER Wednesday 16:30 MI-2**

**Online weather-based risk forecast model for *Nosema* spp. infections in German honey bee apiaries and projected risk under climate change**

*Anto Roja Dominic*, *Sebastian Gisler*, *Elke Genersch*, *Andreas Linde*

1Hochschule für nachhaltige Entwicklung Eberswalde, Dept. of Forest and Environment, Alfred-Möller-Str. 1, 16225, Eberswalde, Germany; 2Länderinstitut für Bienenkunde Hohen Neuendorf e.V., Friedrich-Engels-Str. 32, 16540, Hohen Neuendorf, Germany

Correspondence: Anto.rojadominic@online.de

Amidst wide-spread concerns of the loss of honeybee colonies around the world in the last decades, the increasing spread of the microsporidian *Nosema ceranae* was cause for alarm. The consequences of *N. ceranae* infections in colonies concerning honeybee health are discussed controversially. However, it has been shown that *N. ceranae*, originally a pathogen of the Asian honeybee, has already replaced *N. apis*, a native pathogen of the European honeybee, in many parts of the world. Laboratory studies have conclusively shown that *N. ceranae* is better adapted to warmer weather and is sensitive to close to freezing temperatures.

With this background, we analyzed the relationship between local weather conditions and *Nosema* spp. prevalence in the apiaries of Northeastern Germany. The prevalence data come from a cohort study of 44 apiaries in autumn and early spring over a period of 10 years from 2005-2014. The weather variables that best described the relationship were tested and found reliable for their predictive performance on (pseudo) new data.

We used the selected variables to forecast risk of *Nosema* spp. infections for 6 of the federal States of Northeastern Germany. This risk map is available as an online tool to help the beekeepers to monitor their colonies and take precautionary measures to prevent disease outbreak and further spread of the infection. Due to strong correlation between prevalence and temperature, we also project future prevalence of *Nosema* spp. under different climate change scenarios for the next 60 years.

**POSTER Wednesday 16:30 MI-3**

**rRNA organization in a new light: A microsporidium infecting mountain pine beetle, *Dendroctonus ponderosae* (Coleoptera: Scolytidae)**

*George Kyei-Poku, Debbie Gauthier*

Natural Resources Canada, Canadian Forest Service, Great Lakes Forestry Centre, 1219 Queen Street East, Sault Ste. Marie, Ontario, Canada PE5 1E5

Correspondence: gkyeipoku@nrcan.gc.ca
There is enormous interest in the evolution of microsporidian genomes and understandings gained from such studies may help decipher the plausibility of various scenarios and shed light on the evolutionary origin of reorganized RNA in microsporidia. The rRNA cistron of microsporidia is traditionally arranged in the order of small subunit-internal transcribed spacer-large subunit, which conforms to the typical arrangement of these gene units in almost all organisms. We found a rearrangement of the cluster in a microsporidium infecting mountain pine beetle (MPB) where the large subunit precedes the small subunit (reverse organization of the rRNA subunits; LSU/ITS2-SSU-rRNA-IGS-5S) as has previously been reported for several species in the microsporidian genus Nosema and a species, Glugoides intestinais. We provide evidence that the arrangement reported in the microsporidium infecting MPB is a third, independent event occurring in the microsporidia species with reverse organization of the rRNA subunits and may have taxonomic implications for members of the genus Nosema.

POSTER Wednesday 16:30 MI-4
Light and electron microscopic observations of Annecalia sp. (Microsporidia: Tubulinosematidae) from Dikerogamarus villusos (Amphipoda: Gammaridae)
Yuri S. Tokarev1, Tuluya Y. Sokolova1, Irina V. Issi2
1Institute for Protection; 2Institute of Cytology, Russian Academy of Sciences, St. Petersburg, Russia; School of Veterinary Medicine, Louisiana State University, Baton Rouge LA, USA
Correspondence: sokolova@lsu.edu

Among 100 specimens of Killer Shrimp Dikerogamarus villusos captured in 2013 at the intertidal zone of the Azov sea, five were infected with a microsporidium producing masses of elongate binucleate spores within hypertrophied inner tissues. Ultrastructural analysis showed disporoblastic sporogony and diplokaryotic organization of the nucleus in all developmental stages. The additional surface layer of the sporogonial developmental stages was composed of tubular extensions, translucent vesicles and electron-dense granules. The spores possessed a two-layered exosporium and thick endosporium. The polaroplast was bipartite, its anterior and posterior parts were made of rare lamellae and thick tubular structures, respectively. The diplokaryon was surrounded by 2-4 layers of endoplasmatic reticulum, encrusted with abundant ribosomes. The polar tube was slightly anisofilar, possessing between 13 and 18 coils arranged in one layer with 1-3 distal coils of lesser diameter. The ultrastructural characters corresponded to those of the genus Annecalia and molecular phylogenetic study supports this diagnosis. This is a first case of a natural infection of crustaceans with an Annecalia species, though experimental infection via injection was demonstrated in Decapoda for Annecalia algerae (Undeen, Maddox, 1973, J. Invertebr. Pathol., 22:258–265).

Nematodes

POSTER Wednesday 16:30 NE-1
Improved survival time of infective juveniles of Steinernema glaseri collected on Paris plaster
C. I. Cortés-Martínez1, J. Ruiz-Vega2, E. E. Lewis2
1Instituto Politécnico Nacional, CIDIR-Oaxaca, Oaxaca, 71230, México; 2Department of Nematology, University of California, Davis, Davis, CA 95616, USA
Correspondence: solemia7@hotmail.com

To evaluate the survival time and infectivity of Steinernema glaseri Infective Juveniles (IJ’s) mechanically pelletized in Celltei® 209 brand diatomaceous earth (DE), IJ’s of Steinernema glaseri (strain NI-43) were reproduced in larvae of Galleria mellonella and subjected to two collect treatments, namely: White traps (WT) and plaster of Paris (PP). The IJ were collected 3 days after the onset of the emergency and a prototype machine was used to produce the pellets. IJ’s in bi-distilled water suspension (AS) was the control. The formulations were stored at temperature of 24 ± 5 °C and relative humidity of 96 ± 3 %. Moisture content (MC) of the pellets was determined daily. The counting of live and dead IJ’s was performed every two days, while infectivity over time was tested by exposing third instar Phyllopaga vetula larvae to IJ’s every two days. The bioassay was replicated 5 times. Survival analysis was performed using Kaplan-Meier graphs and Log-rank test. Initial MC of pellets containing IJ’s collected in WT was 47%, while in pellets with IJ’s collected on PP initial WC was 50%. The median survival time (MST) was 23.0 and 34.5 days, respectively. However, the MST of the control treatment was 28.12 days. P. vetula larvae were little susceptible to infection by IJ stored as WS, but somewhat susceptible to infection by IJ formulated in DE. About 2% of total P. vetula larvae exposed to IJ’s collected from PP were infected, while only 1.2% of the larvae exposed to IJ’s from WT were infected.

POSTER Wednesday 16:30 NE-2
Ecological characterization of Steinernema siamkayai (Rhabditida: Steinernematidae), a warm-adapted entomopathogenic nematode isolate from India
Ramalingam Karthik Raja1,2, Aishwarya Dilip Kumar1, Sivaperumal Sivaramakrishnan1, Seluck Hazir1, Pachiappan Perumal1
1Department of Biotechnology, Periyar University, Salem, Tamil Nadu, India; 2Faculty of Arts and Science, Department of Biology, Adnan Menderes University, 09010 Aydin, Turkey; 3Department of Biotechnology and Genetic Engineering, Bharathidasan University, Tiruchirappalli, Tamil Nadu, India
Correspondence: siramkarthik81@gmail.com

Our study describes basic ecological properties of Steinernema siamkayai Tiruchirappalli strain from India. The effect of temperature on nematode infectivity and development, laboratory host range and foraging behaviour were determined. The data showed that S. siamkayai is a warm-adapted nematode species with larval mortality observed between 15°C and 37.5°C and nematode reproduction occurring between 20°C and 35°C. All insect species used in this study were susceptible to S. siamkayai under laboratory conditions. Sixty infective juveniles (IJ’s) per insect were used and the lepidopterans, Galleria mellonella (100%) and Spodoptera exigua (85%), were the most susceptible species followed by the dipteran, Ceratitis capitata (60%), and lepidopteran, Cydia splandana (55%), and the coleopteran, Tenebrio molitor (45%), whereas the coleopteran, Curculio elephas (25%), was the least susceptible species. S. siamkayai infective juveniles (IJ’s) stood on their tails and jumped and could also attach to a mobile host at a rate of 27 IJs larvae-1 out of 1000 IJs in 10 min. Larval mortality of G. mellonella by S. siamkayai on different substrates (sand, filter paper, filter paper sprinkled with sand) was 100% on all substrates. Number of IJ’s out of 100 Us that penetrated into a G. mellonella host at different soil depths was the highest at the surface (44 IJs larva-1) and the lowest at 5 cm depth (13 IJs larva-1) with no larval mortality observed at 10 cm depth. In addition, the symbiotic bacterium of S. siamkayai was identified as Xenorhabdus stockiae based on genotypic and phenotypic characterisation. Bacterial growth was observed between 15°C and 41°C.
The aim of this study was to determine the biological control effect of entomopathogenic nematodes Steinernema feltiae and Heterorhabditis bacteriophora against melon aphid Aphis gossypii in the laboratory conditions. The experiments were conducted in 10 cm Petri dishes lined with a moistened filter paper. One infested cucumber plant leaf containing approximately 120-150 A. gossypii was placed in each Petri dish and the S. feltiae and H. bacteriophora nematodes were applied with concentrations of 500, 1000 and 1500 infective juveniles/ml. Insect mortality was checked at 3, 5 and 7 days after the treatment. The results showed that S. feltiae was with higher virulence against A. gossypii, than H. bacteriophora and the mortality was related to time, nematode type and concentrations. Seven days after the treatment, 500, 1000 and 1500 IJs/ml applications exhibited 20, 58 and 78% mortality for S. feltiae, and respectively 15, 28, and 46% for H. bacteriophora. In conclusion was determined that A. gossypii can be controlled by S. feltiae, better than H. bacteriophora, but further studies should be conducted in greenhouse and filed conditions.

The new local entomopathogenic nematode - Steinernema feltiae Georgian strain „Geo-nema“ is considered as a significant biological control agent against South American tomato moth, Tuta absoluta (Lepidoptera: Gelechiidae). At present this invasive pest insect causes great damage (80-90%) on tomato plants in greenhouses of Georgia. I-III instars larvae live on leaf surface at development stage. The pest pupation takes place in the soil or within mines of leaf surface. Where the relationship of “host-pathogen” is established by spray nematode suspension on tomato plants, or the soil treatment. The susceptibility of local entomopathogenic nematodes – S. feltiae to T. absoluta in laboratory and greenhouse conditions were established. Determination of invasive ability of S. feltiae has conducted according to recent methods in insect Nematology. The different instars of pest larvae were settled on tomato plants pot culture and were treated with nematode suspension - 500 IJs/ml for invasion 1 spr. mL suspension at 23-25°C and 60–70% RH laboratory conditions. The application was carried out two times with 7 days interval and a sterile water was used in control variants. The infected larvae were detected after 48, 72, 96 hr. Data was analysed with two way ANOVA (p=0.05). The pest mortality index by “Geo-nema” suspension was achieved to 79.2%. The experiments and observations at the stationary plot (200-250 sq,m greenhouse) was planted by Dutch tomato sort - "Rose pinkinikum" were conducted twice with the application rate 25 million IJs/ha. The biological efficacy of nematode suspension achieved to 53.2 – 54.1%.

Root exudates favor friends and hinder foes in the rhizospheric nematode community

J. Hiltpold, G. Jaffue, T. C. J Turlings
1Hawkesbury Institute for the Environment, University of Western Sydney, Penrith, NSW, Australia; 2 FARCE lab, University of Neuchâtel, Neuchâtel, Switzerland
Correspondence: j.hiltpold@uws.edu.au

Root tips exude a large amount of photosynthetic assimilated carbon. Some of these organic compounds are detrimental for root pest organisms whereas some can favor beneficials. Here we tested the effect of pea root cap exudates on three nematodes species commonly found in the rhizosphere. Heterorhabditis bacteriophora is an entomopathogenic nematode (EPN) commonly used as a biological control agent against soil-dwelling arthropods. The soybean cyst nematode (SCN) Heterodera glycines and the root-knot nematode (RKN) Meloidogyne incognita are plant-parasitic nematodes causing severe damage to root systems; they are considered major agricultural pests. Pea root cap exudates induced a reversible stage of quiescence to the three tested species. In the presence of diluted exudates, which reflected concentrations more likely encountered in the environment distal from the root tip, EPNs exhibited a significant increase in the number of oscillations per minute. In contrast, SCN and RKN activity was significantly reduced when the nematodes immersed in the dilution of pea root exudates. When applied with diluted root exudate, EPN showed higher infectiousness than in water. These results suggest that the same compound (or blend of compounds) can simultaneously favor beneficial organisms and hinder pests. Identifying the molecules involved and understanding the mechanisms leading to dramatically different effects on nematodes can help to develop ecologically sound methods to manage both insects, by favoring their natural enemies, and nematode pests, by limiting their activity in the rhizosphere.
strains were isolated in Hokkaido against last instar larvae of wax moth, Galleria mellonella, was evaluated in the laboratory at 10°C, 15°C and 20°C. All strains were observed active host searching behavior and host attractiveness for host odors at 15-20°C. Hksf11s was the only strain that observed active host searching behavior and host attractiveness for host odors. These results suggested that the decrease of host searching behavior under low temperature may be related to host attractiveness for host odors.

**POSTER Wednesday 16:30 NE-7**

Genomic determinants of the entomopathogenic lifestyle from independently arising nematodes

Hillel Schwartz1, Adler Dillman2, Paul Sternberg2
1HHMI and Division of Biology and Biological Engineering, California Institute of Technology, Pasadena CA 91125, USA; 2Department of Nematology, University of California Riverside, CA 92521, USA

Correspondence: hillels@caltech.edu

Entomopathogenic nematodes disperse as infective juveniles to hunt their insect prey. Upon finding a host, they invade its body and release symbiotic pathogenic bacteria that rapidly kill the insect and convert it into a food source, while preventing colonization of the carcass by other microorganisms and predation by other scavengers. This lifestyle has arisen independently at least three times, in two different clades: the Steinernema and of Heterorhabditis nematodes, and Oscheius carolinensis.

To better understand how these nematodes have converged on this shared strategy, we have sequenced the genomes and transcriptomes of five species of Steinernema, four species of Heterorhabditis, and of O. carolinensis. We are seeking genomic traits common to these nematodes but not shared with free-living or with parasitic nematodes, some of them more closely related to these EPNs but not sharing their symbiosis. Comparisons of these species may reveal mechanisms that regulate responses to bacterial interactions and variations that correlate with differences in lifestyle or bacterial compatibility.

In addition to genomic studies of the different EPN species, we are developing H. bacteriophora as a laboratory organism. H. bacteriophora grows well on plates, is reportedly susceptible to RNAi and transgenesis, and can develop as selfing hermaphrodites, and so should be a powerful system for molecular genetic study of symbiosis. When cultured at low density these nematodes develop almost exclusively as females. We have screened for and isolated a constitutively hermaphroditic mutant for use in molecular genetic studies of symbiosis and of sex determination.

**Viruses**

**POSTER Wednesday 16:30 VI-1-STU**

The impact of virus diversity on the evolution of pest resistance

Leon Yu Zheng Li1, Jenny S. Cory2
1Department of Biological Sciences, Simon Fraser University, Burnaby, BC, Canada

Correspondence: leonl@sfu.ca

Pathogen mixtures have long been theorized to reduce the rate of evolution of resistance in host. The goal of this project is to determine whether virus diversity affect the rate of evolution of resistance in pests. Wild-type virus containing mixed variants have been shown to more pathogenic possibly due to varying modes of infection. We hypothesize that there is a decrease in the rate of resistance evolving as virus diversity increases. Using the cabbage looper (Trichoplusia ni) as a model, we have subjected T. ni to multigenerational selection for resistance using single and mixed variants of Autographa californica multiple nucleopolyhedrovirus (AcMNPV). The selection experiment is currently ongoing and we will present the progress made so far. The results will not only provide information on the effect that multiple selection pressure can have on the rate of evolution, but also give us insight into better pest management practices. This better understanding of microbial insecticide usage will allow us to utilize these natural control agents more effectively in the future.

**POSTER Wednesday 16:30 VI-2**

Constitutive and herbivore-induced defenses of soybean inhibits baculoviral disease in the fall armyworm, Spodoptera frugiperda

Ikkei Shikano, Kelli Hoover
Department of Entomology, Pennsylvania State University, University Park, PA, USA

Correspondence: bkh25@psu.edu

Plants play an important role in the evolution of insect-pathogen interactions. Inter- and intraspecific variation in host plant chemistry can strongly influence the susceptibility of caterpillars to baculovirus infection. When baculoviruses are ingested with foliage, plant defenses can interfere with fatal infection by the virus. Here, we investigated the impact of constitutive and induced defenses in soybean on the fitness of Spodoptera frugiperda MNPV (SfMNPV) infecting larvae of the fall armyworm (FAW), S. frugiperda. Soybean genotypes vary markedly in their constitutive and inducible defenses against insect herbivores and we are currently testing 9 different genotypes for levels of plant defenses including protease inhibitors, lyopogenase, and phenylalanine ammonia lyase and the impacts of these defenses on mortal virus infection. We applied SfMNPV to leaf disks of soybean genotypes differing in levels of constitutive defenses, and found that the SfMNPV was ingested on soybeans that have high constitutive defenses. To determine the impact of induced soybean defenses on SfMNPV infectivity, we will induce soybeans by exogenously applying jasmonic acid, a phytomolecule that upregulates plant defenses against chewing herbivores. We predict that SfMNPV ingress with induced foliage will result in lower mortality in FAW, fewer virus progeny and longer time to death, thereby resulting in reduced fitness for the virus. While plant defenses are beneficial for plants in terms of reduced herbivore feeding and growth, our study suggests that plant defenses could negatively impact beneficial microbes that act as potential ‘bodyguards’ for plants.

**POSTER Wednesday 16:30 VI-3-STU**

Three baculoviruses infecting white satin moth (LesapNV), douglas-fir tussock moth (OpMNVP) and pale tussock moth (DapuNPV) cluster together on the phylogenetic tree

Martyna Krejmer1, Lukasz Rabalski2, Iwona Skrzecz3, Jadwiga Ziemnicka4, Boguslaw Szewczyk5
1Intercollegiate Faculty of Biotechnology University of Gdansk and Medical University of Gdansk, Department of Recombinant Vaccines, Gdansk, Poland; 2Institute of Plant Protection, Department of Forest Protection, Sekocin Stary, Poland; 3Institute of Plant Protection, Department of Biological Control and Quarantine, Poznan, Poland

Correspondence: martyna.krejmer@biotech.ug.edu.pl

The white satin moth Leucoma salicis L. (Lepidoptera, Lymantriidae) is a dangerous defolator occurring mainly in
Europe and Asia, but it was also introduced to North America in 1920s. The caterpillars feed principally on the leaves of poplar, cottonwood, aspen and willow trees (family Salicaceae) and are commonly on oak. They attack healthy trees, what makes them the primary pest and can lead to massive defoliations and weakened trees. One of the main natural enemies of this insect is baculovirus, LesaNPV (Leucoma salicis Nucleopolyhedrovirus). For population control of white satn moth the biosticides based on LesaNPV baculovirus can be used. This type of control agents are claimed to be very safe for human and animals, because they do not infect organisms other than arthropods and cannot replicate outside their natural host. It has been reported in the literature that LesaNPV is infective against the close relative of its host, Orgyia pseudotsugata L., but OpMNPV does not infect Leucoma salicis L. According to short nucleotide sequences of three genes (polh, lep-8, pf-2) available in the NCBI database LesaNPV was annotated as Alphabaculovirus group I (Jakubowska et al., 2005). In our studies we have prepared the draft of full genome of LesaNPV which we found highly similar to genome of OpMNPV and DapuNPV. We identified 153 ORFs (open reading frames) in LesaNPV genome, few were not present in OpMNPV (like he65) or were fused from two OpMNPV ORFs (OpB2-OpB3). The phylogenetic relationship of LesaNPV and other baculoviruses will be presented.

**POSTER Wednesday 16:30 VI-4**

Screening field collected Lepidoptera larvae for new virus isolates

Michelle T. Franklin 1, Amy Huang 2, Yan Han 2, Matilda Tabert 3, Martin Erdanson 4, Stefan Richard 3, Deborah Henderson 2

1 Institute for Sustainable Horticulture, Kwantlen Polytechnic University, Langley, BC, Canada; 2 Saskatoon Research Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, Canada; 3 Sylvan Technologies Inc., Fredericton, New Brunswick, Canada

Correspondence: Michelle.Franklin@kpu.ca

Alpha and Betabaculoviruses that target lepidopteran larvae remain underutilized as biosticides, despite their suitability for organic farming and high level of safety for humans and beneficial arthropods. In Canada many economically important brassica crops are grown organically, however lepidopteran pests such as diamondback moth (Plutella xylostella), cabbage looper (Trichoplusia ni), and imported cabbageworm (Pieris rapae) pose a serious threat to these crops. The development of resistance to biologically based products such as Bacillus thuringiensis (Bt) and spinosad have reduced the number of products available to growers for control of these pests. Baculoviruses could offer an effective alternative control for these pests in organic brassica crops. To detect local baculovirus strains, we collected and froze over 3000 larvae of these three species from 17 farms throughout the southwest and interior of British Columbia in 2014. Additional larval collections will take place during the summer of 2015. Larvae from each site collected in 2014 were homogenized and we are beginning to perform assays where homogenized larvae are spread on the leaf surface and fed to healthy second instar larvae of the same species. Mortality is assessed daily and cadaver smears will be examined for the presence of virus particles using microscopy. Cadavers that show signs of viral infection will be fed to healthy larvae to further amplify new isolates and molecular identification will be undertaken for promising isolates. Detection of virus isolates is the first step in the development and commercialization of new baculovirus products and in future could provide growers with new biopesticides.

**POSTER Wednesday 16:30 VI-5**

Culex pippins - associated Tunis virus: A new mosaic virus in common house mosquitoes

Diane Bigot 1, Elisabet Herniou 2, Marion Ballenghien 2, Mylène Weill 2, Céline Ayame 3, Nicolas Gablier 3, PhilippeGayrol 4

1 Institut de Recherche sur la Biologie de l’Insecte, UMR 7261, CNRS, Université François-Rabelais, 37200 Tours, France; 2 Institut des Sciences de l’Evolution de Montpellier, UMR 5554, CNRS, Université Montpellier 2, Place E. Bataillon, 34095 Montpellier, France

Correspondence: diane.bigt@etu.univ-tours.fr

Many viral epidemics emerge from previously unknown viruses. The study of novel potential reservoirs of new viruses could help anticipating such viral emergence. In this perspective mosquitoes are good reservoir candidates because they are efficient viral vectors. Twenty-two common house mosquitoes (three species of the Culex genus) were sampled worldwide in the fields. Based on individual mRNA extraction and cDNA synthesis we obtained to be Illumina sequencing technology, representing 690 million reads. A homemade bioinformatics pipeline was used to characterise potential new complete viruses in these transcriptome data. Two variants of a new RNA virus were found in Culex pippins mosquitoes sampled in Tunisia and their genomes consisted in single-stranded RNA of 6.8kb in size. These two viral sequences referred as Culex pippins Associated Tunis Virus (CpATV) strain Moknine and strain ElHabibia, shared 99.6% nucleotide identity. They were independently sampled six years apart, in 2005 and in 2011. CpATVs are composed of four ORFs, one ORF contained a helicase and a RNA-dependant RNA polymerase domain related to a mosquito Negevirus, two ORFs contained capsids protein domains related to Virgaviroidae (plant viruses) among others. These two CpATVs displayed a mosaic genomic organisation with complex phylogenetic origins, and might therefore belong to a new virus family. Still, the true host or the life cycle of CpATVs is not known at this stage.

**POSTER Wednesday 16:30 VI-6**

Newly sequenced full genome of Nun moth (Lymantria monacha) baculovirus show its high similarity to gypsy moth (Lymantria dispar) baculovirus

Lukasz Rabalski 1, Martyna Krejmer 1, Iwona Skrecz 3, Bartosz Wasa 3, Boguslaw Szweczyk 1

1 Intercollegiate Faculty of Biotechnology University of Gdansk and Medical University of Gdansk, Department of Recombinant Vaccines, 80-822 Gdansk, Kladki Str. 24, Poland; 2 Forest Research Institute, Department of Forest Protection, 05-090 Raszyn, Braci Lesnjej Str. 3, Sekocin Stary, Poland; 3 Medical University of Gdansk, Department of Biology and Genetics, 80-211 Gdansk, Debniki Str. 1, Poland

E-mail address: lukasz.rabalski@biotech.ug.edu.pl

Nun moth (Lymantria monacha) belonging to Lepidoptera, Lymantriidae is currently one of the most important pest of conifers in Poland. Caterpillars of this moth attack older and healthy pines, spruces and larches, but is also able to feed on deciduous trees. Nun moth is widely present throughout Europe. The natural biological control of this pest population is provided by Lymantria monacha Nucleopolyhedrovirus (LymoNPV) from Baculoviridae family. To date little is known about LymoNPV genome and phylogenetic relationship to others baculoviruses. To get better insight into LymoNPV molecular biology and its genetic correlation with other baculoviruses we isolated, sequenced on next generation platform and annotated full genome of Polish LymoNPV strain. In this presentation, after detailed DNA
sequencing and phylogenetic analysis, we show how LymoNPV is related to previously sequenced baculoviruses.

POSTER Wednesday 16:30 VI-7

Comparison among betabaculovirus isolates from Gelechiidae insect family
Gloria P. Barrera1, Juliana A. Gómez2, Mariano N. Belachi2, Pablo D. Ghiringhelli2, Laura Villamizar2
1Corporación Colombiana de Investigación Agropecuaria, Corpoica, Bogotá, Colombia; 2Laboratorio de Ingeniería Genética y Biología celular y Molecular, Área Virois de Insectos (ULGBCM-AVI), Dto. De Ciencia y Tecnología, Universidad Nacional de Quilmes, Provincia de Buenos Aires, Argentina
Correspondence: gbarera@corpoica.org.co

Teclia solanivora (Povolny) and Phthisoriaea operculiella (Zeller) are insect species belonging to the potato tuber moth complex (Lepidoptera: Gelechiidae) and Tutia absoluta (Meyrick) (Lepidoptera: Gelechiidae) is considered an important pest of tomato crop. Two Colombian isolates of granulovirus (GVs) recovered from larvae of T. solanivora and T. absoluta and one isolate of granulovirus of P. operculiella were subjected to molecular and morphological analysis. Molecular identification and phylogenetic analysis of Colombian granulovirus isolates were performed using the combined complete sequence of highly conserved baculovirus genes; late expression factor 8 [lef-8], late expression factor 9 [lef-9] and grulin (gran). The genetic distances of these concatenated genes for species demarcation showed that the K-2 P distance among T. solanivora GV, T. absoluta GV and P. operculiella GV was inferior to 0.015 indicating that they belong to the same baculovirus species. Additionally, the restriction endonuclease analysis (REN) using six enzymes showed similar patterns among GVs isolates from different insect species. Electron transmission images showed similar morphologies of OBs with ovoidal shape containing a single virion. T. absoluta GV OBs had the largest average size between 514 nm x 249 nm, while the average sizes for T. solanivora GV and P. operculiella GV OBs were 448 nm x 252nm and 158nm x 224 nm, respectively. The results showed very similar isolates from Gelechiidae insect family. This could be due to the geographical proximity of where isolates were recovered and the possible presence of the three insects host in the same crop.

POSTER Wednesday 16:30 VI-8

Genome sequence analysis of a two alphabaculoviruses and a betabaculovirus from armymworms of genus Mythimna
Robert L. Harrison1, David A. Theilimmann2, Martin A. Erlanson3
1USDA-Agricultural Research Service, Beltsville, MD, USA; 2Agriculture and Agri-Food Canada, Summerland, BC, Canada; 3Agriculture and Agri-Food Canada, Saskatoon, SK, Canada
Correspondence: Robert.L.Harrison@ars.usda.gov

Noctuid species of the armymworm genus Mythimna Guenée are widespread pests of graminaceous crops and pastures. Baculoviruses have been identified from species of Mythimna and the genomes of an alphabaculovirus from Mythimna (Leucania) separato, LeseNPV, and a betabaculovirus from Mythimna (Pseudaletia) unipuncta, PsunGV-H, have been sequenced. To further characterize the genetic diversity of baculoviruses from Mythimna, we isolated genomic DNA from the occlusion bodies of virus isolates Mythimna (Pseudaletia) sp. NPV R7 (MyspGV#7) and Mythimna (Pseudaletia) sp. GV R8 (MyspGV#8) from the Martignoni baculovirus collection, and also from occlusion bodies of a Mythimna (Pseudaletia) unipuncta NPV isolate MyunNPV-KY310 harvested from M. unipuncta in a Kentucky, USA hayfield. Genomic DNA was subjected to 454 pyrosequencing, and the DNA sequences assembled using CLC Genomics Workbench and Lasergene SeqMan Pro software. The genomes for the three viruses ranged in size from 144,510 to 156,649 bp and contained all the core genes recognized for family Baculoviridae. Phylogenetic inference with concatenated amino acid sequence alignments of 34 core genes and pairwise comparisons of partial lef-8, lef-9, and polh nucleotide sequences revealed that all three of the Mythimna viruses represented currently unrecognized species of Baculoviridae, with MyspGV#7 and MyunNPV-KY310 occurring in different locations in the Alphabaculovirus tree and MyspGV#8 occurring in the Betabaculovirus group. MyunNPV-KY310 was most closely related to LeseNPV, while MyspNPV#7 grouped in a clade with NPVs from Mamestra spp. MyspGV#8 grouped in a betabaculovirus clade containing PsunGV-H, but was distinct from PsunGV-H with Kimura-2-parameter nucleotide distances of 0.25 – 0.82 substitutions/site.

POSTER Wednesday 16:30 VI-9

Genome sequence of Trichoplusia ni granulovirus (TnGV), a novel sequenced betabaculovirus infecting the cabbage looper
Ma. de los Angeles Bivián-Hernández1, Juventino López-Tijomulco2, Jorge E. Ibarra3, Ma. Cristina Del Rincón-Castro4
1Food Department and Graduate Program in Bioinsecticides, University of Guanajuato, Irapuato, GTO, México; 2Department of Biotechnology and Biochemistry, CINVESTAV-Irapuato, Irapuato, GTO, México
Correspondence: mdelrinc@yahoo.com

The cabbage looper, Trichoplusia ni, is a member of the moth family Noctuidae. It is an important pest in Canada, Mexico, and the United States. The cabbage looper feeds mainly on crucifers, cabbage, cauliflower, Chinese cabbage, collards, kale, mustard, radish, rutabaga, turnip, and watercress, among others cultures. It is attacked by numerous natural enemies, including a nucleopolyhedrosis virus (NPV) and a granulovirus (GV). The latter is a Betabaculovirus isolated from the T. ni designated as TnGV, whose genome was sequenced in this work. The 175,360 pb long genome has a G+C content of 39.81% and a total of 178 ORFs coding for polypeptides of at least 50 amino acid residues. From the 178 ORFs, 16 showed early promoters, 13 of which were found in the positive and 3 in the negative strand; 63 ORFs showed late promoters, 43 in the positive strand and 33 in the negative one; 21 ORFs showed enhancer-like motifs, 12 in the positive strand and 9 in the negative one. The TnGV genome showed high synteny with the highly related genomes, such as those of Pseudaelita unipuncta GV, Xestia c-nigrum GV and Helicoverpa armigera GV. Interestingly, 11 ORFs were related to different NPV genes, three to Heliothis virescens ascovirus genes, and one related to a Mythimna separata entomopoxivirus gene. According to this comparison, the TnGV should be recognized as a new species from the genus Betabaculovirus, whose closest relative is PsunGV species, with 98.55% of identity.

POSTER Wednesday 16:30 VI-10-STU

The gene pp31 of Cydia pomonella granulovirus is essential for the production of budded viruses and the establishment of a systemic infection in coding moth
Jacqueline A. Frank, Manuela Gebhardt, Diana Schneider, Jörg T. Wennmann, Johannes A. Jehle
Institute for Biological Control, Julius Kühn Institute (IKI), Federal Research Center on Cultivated Plants, Heinrichstraße 243, 64287 Darmstadt, Germany
Cydia pomonella granulovirus (CpGV-M) (Baculoviridae, genus Betabaculovirus) is the most important commercial biological control agent of codling moth (CM) in orchards worldwide. However, only limited knowledge about the molecular basis of virus host interaction is available. We have initiated studies on CpGV genes, which may play a crucial role during the infection process. Transcriptional analysis revealed that gene pp31 is an early and highly expressed gene in the midgut and fatbody of CM larvae. To examine the role of the pp31 gene during CpGV infection, a knockout mutant was cloned using a gps-tagged CpGV bacmid. After transfection of Cp14R cells neither production of budded viruses nor formation of occlusion bodies was observed for the pp31 knockout mutant. This observation was confirmed by infection studies of CM larvae, which succumbed form infection from a mid-based gfp-CpGV bacmid but not from the knockout mutant. The influence of the deletion pp31 on DNA replication and transcription of different genes will be presented by qPCR. In this study, we showed that occlusion-derived viruses (ODVs) of AdhoNPV have lower binding and fusion ability with midgut epithelial cells than with those of the S-strain. Interestingly, the R-strain (resistant strain) is cross-resistant to both nucleopolyhedrovirus (NPV) and granulovirus (GVs) (betabaculovirus). In the present work detailed analysis of complete sequence (acquired by pyrosequencing) of a Colombian S. frugiperda granulovirus (SFGV) isolate possess two genes encoding to enhancins (ORFs 127 and 132) and four genes encoding to chitinases in its genome, being the betabaculovirus that would express more proteins associated to virulence. The aim of this work was to compare enhancins and chitinases of SFGV with homologous sequences described for other isolates of the family Baculoviridae. Bioinformatic analysis was performed with the deduced amino acid sequences for each gene. The enhancins of SFGV was grouped in phylogenetic cluster of betabaculovirus. The ORF 127 was classified in VEF-2 (viral enhancing factor) and grouped with Helicoverpa armigera granulovirus (VEF-2 and Xestia c-nigrum betabaculovirus VEF-2), and the ORF 132 was classified as VEF-4 grouped with Pseudolita unipuncta betabaculovirus VEF-4, H. armigera betabaculovirus VEF-4 and X. c-nigrum betabaculovirus VEF-4 (bootstrap values=100). All chitinases of SFGV lacked of C-terminal domain KDEL, present in most of baculovirus chitinases. The presence of this domain is related with lytic degradation of the integument of the larvae at the end of the infectious cycle; therefore the SFGV chitinases could be proteins secreted, associated with occlusion bodies and with proteolytic action at the initial stage of viral infection.

Baculoviruses are a large group of viruses pathogenic to arthropods, principally insect from the order Lepidoptera some of which are pests of agricultural importance. The main two genera of these viruses (Alphabaculovirus and betabaculovirus) have been used worldwide in biological control strategies. Related genes with virulence as enhancins and chitinases have been found in baculovirus, mainly in betabaculovirus. Spodoptera frugiperda granulovirus (SFGV) isolate possess two genes encoding to enhancins (ORFs 101, 071, 072 and 134) in its genome, being the betabaculovirus that would express more proteins associated to virulence. The aim of this work was to compare enhancins and chitinases of SFGV with homologous sequences described for other isolates of the family Baculoviridae. Bioinformatic analysis was performed with the deduced amino acid sequences for each gene. The enhancins of SFGV was grouped in phylogenetic cluster of betabaculovirus. The ORF 127 was classified in VEF-2 (viral enhancing factor) and grouped with Helicoverpa armigera granulovirus (VEF-2 and Xestia c-nigrum betabaculovirus VEF-2), and the ORF 132 was classified as VEF-4 grouped with Pseudolita unipuncta betabaculovirus VEF-4, H. armigera betabaculovirus VEF-4 and X. c-nigrum betabaculovirus VEF-4 (bootstrap values=100). All chitinases of SFGV lacked of C-terminal domain KDEL, present in most of baculovirus chitinases. The presence of this domain is related with lytic degradation of the integument of the larvae at the end of the infectious cycle; therefore the SFGV chitinases could be proteins secreted, associated with occlusion bodies and with proteolytic action at the initial stage of viral infection.

Enhancins and chitinases: Analysis of a granulovirus of Spodoptera frugiperda
Paola E. Cuartas1
Correspondence: pcuartas@corpoica.org.co

1Corporación Colombiana de Investigación Agropecuaria, Corpoica, Bogotá, Colombia; 2Centro de Bioinformática, Instituto de Biotecnología-IUBUN, Universidad Nacional de Colombia, Bogotá, Colombia

Correspondence: Jacqueline.Frank@bund.de

Baculoviruses are a large group of viruses pathogenic to arthropods, principally insect from the order Lepidoptera some of which are pests of agricultural importance. The main two genera of these viruses (Alphabaculovirus and betabaculovirus) have been used worldwide in biological control strategies. Related genes with virulence as enhancins and chitinases have been found in baculovirus, mainly in betabaculovirus. Spodoptera frugiperda granulovirus (SFGV) isolate possess two genes encoding to enhancins (ORFs 101, 071, 072 and 134) in its genome, being the betabaculovirus that would express more proteins associated to virulence. The aim of this work was to compare enhancins and chitinases of SFGV with homologous sequences described for other isolates of the family Baculoviridae. Bioinformatic analysis was performed with the deduced amino acid sequences for each gene. The enhancins of SFGV was grouped in phylogenetic cluster of betabaculovirus. The ORF 127 was classified in VEF-2 (viral enhancing factor) and grouped with Helicoverpa armigera granulovirus (VEF-2 and Xestia c-nigrum betabaculovirus VEF-2), and the ORF 132 was classified as VEF-4 grouped with Pseudolita unipuncta betabaculovirus VEF-4, H. armigera betabaculovirus VEF-4 and X. c-nigrum betabaculovirus VEF-4 (bootstrap values=100). All chitinases of SFGV lacked of C-terminal domain KDEL, present in most of baculovirus chitinases. The presence of this domain is related with lytic degradation of the integument of the larvae at the end of the infectious cycle; therefore the SFGV chitinases could be proteins secreted, associated with occlusion bodies and with proteolytic action at the initial stage of viral infection.
whereas SFGV ORF099 shows the highest identity/similarity values with ORF023 of the SfMNPV isolates (or ORF022 in SfMNPV 19). In both cases, the obtained results suggest the occurrence of independent horizontal transfer events during the evolution. Relative similarity and bootscanning analyses supported the occurrence of putative recombination events for SFGV ORF059 and ORF099 with high percentage of permuted trees by bootscanning plot against SfMNPVs and SplitNPV II suggesting a heterologous recombination events involving two different virus species belonging to two genera baculoviruses.

**POSTER Wednesday 16:30 VI-14**

**Establishment of a winter moth, Operophtera brumata, cell line permissive for OpbrNPV replication**

John P Burand, Robert L. Harrison, Matthew Boucher

Department of Microbiology, University of Massachusetts Amherst, MA, USA; USDA Agricultural Research Service, Beltsville, MD, USA

Correspondence: jburand@microbio.umass.edu

The winter moth, Operophtera brumata, is an invasive lepidopteran pest on deciduous tree species in the Northeast United States and Canada. We have recently found the previously identified nucleopolyhedrovirus OpbrNPV in O. brumata in Massachusetts and, as an initial step in developing this virus for the control of winter moth, we have established a cell line from this insect. Embryonated winter moth eggs were dissected, and pieces of embryo were transferred to TNM-FH and ExCell420 media supplemented with fetal bovine serum to establish primary cell cultures. Cultures were incubated at 19°C and sub-cultured using trypsin to produce an embryonic cell line, designated iBBL-ObE1. The initial infection of this cell line was accomplished at passage 15 using occlusion-derived virus, and appearance of occlusion bodies (OBs) inside the nuclei of infected cells occurred with one week post infection. OBs recovered from infected cells were confirmed to be OpbrNPV by PCR and were infectious when fed to winter moth larvae.

**POSTER Wednesday 16:30 VI-15**

**AcMNPV infection process in Trichoplusia ni midgut**

Muhammad Afzal Javed, Stephanie Harris, David A. Theilmann, Martin A. Erlandson

1Saskatoon Research Centre, Agriculture and Agri-Food Canada, Saskatoon, SK, S7N 0X2 Canada; 2Pacific Agri-Food Research Centre, Agriculture and Agri-Food Canada, Summerland, BC, V0H 1Z0 Canada

Correspondence: Afzal.javed@agr.gc.ca

Baculoviruses infect a wide range of insect hosts, including important crop pests and as such are potentially excellent tools for biocontrol of these pests. *Autographa californica* multiple nucleopolyhedrovirus (AcMNPV) is the type species for the genus *Baculoviridae*. AcMNPV infection consists of two distinct phenotypes, budded viruses and occlusion derived viruses (ODVs). Previously, it has been shown that AcMNPV infection starts upon oral ingestion of occlusion bodies (OBs) by larvae. OBs dissolve in the alkaline environment of the lepidopteran larval midgut to release ODVs that bind to and enter midgut epithelial cells. Foci of AcMNPV infection form in the midgut; however, it is not clear if these foci of infection form from primary infections or progeny virions spreading to neighboring midgut cells. We report details of AcMNPV infection in midgut tissue using AcMNPV viruses expressing reporter fluorescence proteins, GFP or V393-3x-mCherry fusion proteins, and a gpd4 knockout virus. Oral infection of *Trichoplusia ni* larvae with GFP-recombinant AcMNPV, surrogate for wild type virus, showed that the anterior part of midgut is more heavily infected compared to the posterior midgut. Initially, individual midgut cells are infected and subsequently infection spreads to neighboring cells in midgut epithelial layer. The spread of the infection from primary infected cells is dependent upon gp64. Tracheoles and hemocytes are subsequently infected at approximately 48 hour post infection. Midgut infection declines by 72 hours post infection.

Using a SFP10 specific antibody, SFP10 expression was only weakly visible in AcMNPV-P10 mutant infected SF cells in comparison to the SNPV infection. To determine if the low BV titre and reduced polyhedra were a result of SFP10 expression, siRNA was used to reduce P10 synthesis, which resulted in a significant increase in both polyhedrin expression and polyheda formation. There was also a partial increase in BV titre. These data suggested that P10 has clear species specific roles.

**POSTER Wednesday 16:30 VI-17-STU**

**Multiple amino acid residues of Autographa californica MNPV P143 are responsible for ribosomal RNA degradation in Bombyx mori cells**

Rina Hamajima, Michihiro Kobayashi, Motoko Ikeda

Graduate School of Bioagricultural Sciences, Nagoya University, Chikusa, Nagoya 464-8601, Japan

Correspondence: sgu_qj@yahoo.co.jp

BM-N cells derived from the silkworm, *Bombyx mori*, are permissive for homologous *B. mori* NPV (BmNPV), while non-permissive for *Autographa californica* multiple NPV (AcMNPV). We previously showed that the ribosomal RNA (rRNA) degradation is induced in AcMNPV-infected BM-N cells, and triggered by P143 of AcMNPV (Ac-P143). In this study, we analyzed Ac-P143 to identify the amino acid residues responsible for rRNA degradation. P143 is a DNA helicase essential for viral DNA replication. To determine whether DNA helicase activity of P143 is involved in the rRNA degradation, we
examined rRNA of BM-N cells infected with AcMNPV temperature sensitive mutant 8 (ts8) defective in DNA helicase activity of P143 at non-permissive temperature [33°C]. The result showed that rRNA degradation was induced at both permissive and non-permissive temperature, indicating that DNA helicase activity of P143 is not associated with rRNA degradation in AcMNPV-infected BM-N cells. Next, we constructed mutated Ac-P143s containing amino acid residue substitutions with corresponding those of BmNPV P143 that does not trigger the rRNA degradation, and analyzed using transient expression assay. The results demonstrated that six to eight amino acid residues of Ac-P143 located within the region related to restriction of NPV replication in B. mori cells are responsible for the rRNA degradation of BM-N cells. Our analysis using single cell based assay further demonstrated that eight amino acid residues are also involved in restriction of NPV replication in BM-N cells.

POSTER Wednesday 16:30 VI-18

**Autographa californica** multiple nucleopolyhedrovirus ORF11 and ORF78 are essential for budded virus production, occlusion-derived virus envelopment, and occlusion body formation

Xue Ying Tao1,2, Woo Jin Kim1, Jong Hoon Kim1, Pang Ying3, Ha Kyu Baik4, Yeon Ho Je5
1State Key Laboratory of Food Science and Technology, Nanchang University, Nanchang, China; 2Jiangxi-OA Joint Research Institute, Nanchang University, Nanchang, China; 3College of Agriculture and Life Science, Seoul National University, Seoul, Republic of Korea; 4Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea.

Correspondence: woojin.kim@snu.ac.kr

ORF11 and ORF78 of Autographa californica multiple nucleopolyhedrovirus (AcMNPV) are highly conserved genes of unknown function. To determine the role of these genes in baculovirus replication cycle, two AcMNPV mutants, Ac11KO and Ac78KO with ac11 and ac78 deleted, were constructed, respectively. Microscopy, titration assays, and Western blot analysis revealed that budded viruses (BV) were not produced in Ac11KO-transfected S9 cells. However, qPCR analysis demonstrated that the deletion of ac11 did not affect viral DNA replication. Electron microscopy showed that there was no nucleocapsid in the cytoplasm or plasma membrane of Ac11KO-transfected cells, which demonstrates that the defect in BV production in Ac11KO-transfected cells is due to the inefficient egress of nucleocapsids from the nucleus to the cytoplasm. Also it was observed that the nucleocapsids in the nucleus were not enveloped to form occlusion-derived viruses (ODV) and their subsequent embedding into occlusion bodies (OBs) was also blocked in Ac11KO-transfected cells. These results demonstrate that ac11 is essential for BV production and ODV envelopment. Ac78KO-transfected cells produced a single-cell infection phenotype, indicating that no infectious BVs were produced. The defect in BV production was also confirmed by both viral titration and Western blotting. However, viral DNA replication was unaffected, and OBs were formed. An analysis of BVs and ODVs revealed that Ac78 is associated with both forms of the virions and is an envelope structural protein, and also plays an important role in the embedding of ODV into the OB, which is essential for the viral life cycle.

POSTER Wednesday 16:30 VI-19-STU

**Effects of lacking non-essential genes of BmNPV**

Hitomi Taka1, Chikako Oso1, Masanao Sato1, Shin-ichiro Asano1, Hisanori Bando2
1Graduate School of Agriculture, Hokkaido University, Sapporo, Japan; 2Institute for Advanced Biosciences, Keio University, Tsuruoka, Japan.

Address for Correspondence: hban@abs.agr.hokudai.ac.jp

Nucleopolyhedroviruses (NPV, a member of the family Baculoviridae) produces copious amounts of polyhedrin protein by the end of a replication cycle forming a lot of polyhedra in the nuclei of infected-host insect cells. This characteristic feature of NPV is a beneficial trait as the gene expression vector. To further develop baculoviral applications, deep insight into the functions and interactions of viral gene products concerning the expressive expression of Polh is necessary.

We constructed a comprehensive knockout virus library of BmNPV T3 and showed 86 genes out of 141 BmNPV T3 genes were dispensable for expression of the polyhedrin gene and production of infectious viral progenies (Ono et al., 2012). In BmNPV genome, there were 10 regions containing only non-essential genes (non-essential gene clusters, NEGCs). In order to analyze the effects when these clusters were deleted, we constructed BmNPV bacmids lacking each NEGC and analyzed the expression of GFP under the control of the polyhedrin gene promoter.

Out of ten BmNPV bacmids lacking one of the NEGCs, only one bacmid lacking bm32-bm38 cluster was deficient in production of GFP and/or infectious progeny viruses in transfected cells. This results showed some combinations of non-essential genes have important role for expressing Polh. In addition, we constructed BmNPV bacmids lacking the 7 non-essential genes (bm32-bm38) in various combinations. We report here results from phenotypic analysis of these multiple-gene knockout bacmids.

POSTER Wednesday 16:30 VI-20-STU

**Relevance of BmSyndecan-1 for BmNPV proliferation**

Mamoko Uda1, Masanao Sato1, Shin-ichiro Asano1, Hisanori Bando2
1Graduate School of Agriculture, Hokkaido University, Sapporo, Japan; 2Institute for Advanced Biosciences, Keio University, Yamagata, Japan.

Correspondence: m-uda@abs.agr.hokudai.ac.jp

Baculovirus is a well-known natural pathogen to insects. It is a well-studied virus but not much is known about the entry mechanisms particularly secondary infection and attachment to general cell surface molecules via non-specific electrostatic interaction is most probable. Baculoviruses are insect specific virus and cannot replicate in mammalian cells. However Autographa californica multiplenucleopolyhedrovirus (AcMNPV), belonging to genus Alphabaculovirus, can enter the mammalian cells. Recently it was reported that AlphacNPV utilized part of heparin sulfate chain of Syndecan-1 when entering the mammalian cells (Makkonen et al., 2014). This was the first report that baculovirus may utilize some specific molecule as their receptor. At present we have no information if the mechanism of baculovirus entering mammalian cells applies to the cases in insect cells. We here studied this topic in the infection of Bombyx mori nucleopolyhedrovirus (BmNPV) to BmN cells of silkworm. Syndecan-like transcript variant-1 (BmSyndecan-1) and Syndecan-like transcript variant-2 (BmSyndecan-2) have been detected in the silkworm. First we investigated whether BmSyndecan-1 was required in BmNPV proliferation in BmN cells using RNAi technology to knock down the objective gene. So far the knocking down of BmSyndecan-1 showed no significant effect on virus proliferation in BmN cells. We are now conducting RNAi targeting other molecules i.e. BmSyndecan-2.
Applications of DnaB mini-intein to baculovirus expression system

Won Seok Gwak, Sung Min Bae, Tae Young Shin, Seung Hee Lee, Yong Oh Ahn, Soo Dong Woo
Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea
Correspondence: sdwoo@cbnu.ac.kr

Recombinant proteins including a polypeptide fusion partner, termed affinity tag, to facilitate the purification of the target polypeptides are widely used. When designing up- and downstream processing strategy for a protein, the inclusion of an affinity tag might be attractive for a number of additional reasons. However, the disadvantage of affinity tags is that, in many studies, the tag must be removed from the target after the purification process. Recently, the Synchocystis sp. PCC6803 DnaB mini-intein (Ssp DnaB mini-intein) is widely used in Escherichia coli expression systems as the solution of this problem. The Ssp DnaB mini-intein can be induced simply by shifting of pH and temperature, offering a benefit to cleave a peptide bond without using a protease or chemical reagent. Although the utility of this novel tag is widely studied in E. coli, there is no report yet in baculovirus expression vector system (BEVS). In this study, we generated several baculoviruses to express foreign proteins with Ssp DnaB mini-intein. The optimal conditions for the Ssp DnaB mini-intein in BEVS and the characteristics of recombinant proteins having Ssp DnaB mini-intein were analyzed. In conclusion Ssp DnaB mini-intein was good tag also in BEVS with more advantages.

Production of porcine parvovirus virus-like particles using baculovirus in the silkworm larvae

Seung Hee Lee, Sung Min Bae, Tae Young Shin, Won Seok Gwak, Yong Oh Ahn, Soo Dong Woo
Department of Agricultural Biology, College of Agriculture, Life & Environment Science, Chungbuk National University, Cheongju 361-763, Korea
Correspondence: sdwoo@cbnu.ac.kr

Porcine parvovirus (PPV), a member of the genus Parvovirus, family Parvoviridae, is a significant causative agent in porcine reproductive failure, causing serious economic losses in the swine industry. We have studied usefulness of recombinant porcine parvovirus virus-like particles (PPV-VLPs) as an efficient recombinant vaccine. PPV is a non-enveloped virus and its capsid is assembled from three viral proteins (VP1, VP2, and VP3). The major capsid protein, VP2 is the main target protein for neutralizing antibodies in PPV. When VP2 was expressed in large amounts, it assembled into virus-like particles (VLPs) similar in size and morphology to the original virions. In this study, we generated the recombinant Bombyx mori nucleopolyhedrovirus (BmNPV) to express the VP2 protein. Expression of the VP2 protein was analyzed by SDS-PAGE and Western blot approximately 64 kDa in insect cells and larvae. The formation of VLP by recombinant VP2 was confirmed through transmission electron microscopy examination that diameters ranging from 20 to 22 nm. Additionally, Classical Swine Fever Virus (CSFV) E2 epitope sequences were inserted into the VP2 capsid protein each of N-term, C-term or both sides [PPV-VLP(CSFV)2] to expand the utility of PPV-VLP as a vaccine. Production of the PPV-VLP(CSFV) was analyzed by approximately 65 kDa and also identified by transmission electron microscopy.

Amsacta moorei entomopoxvirus (AMEV), the most studied member of Betanalphapoxvirus genus, isolated from the larvae of the Amsacta moorei moth and consists of cellular and humoral immune responses. Cellular response usually requires hemocyte spreading behavior, which is accompanied by cytoskeletal rearrangement. A glycolytic enzyme, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), catalyzes an oxidation reaction of glyceraldehyde-3-phosphate to change in to 1,3-biphosphoglycerate in the cytosol. Another function of GAPDH in mammalian cell is to bind C-terminal of α-tubulin to facilitate cytoskeletal rearrangement. An immunoprecipitation of viral protein, CpBV-CrV1, against hemocyte lysate revealed that CpBV-CrV1 binds to GAPDH, identified by MALDI-TOF analysis. dsRNA specific to GAPDH inhibits hemocyte spreading function, while RNAi treatments of other glycolytic genes had no effect on spreading. The common molecular motif of CpBV-CrV1 and alpha-tubulin at C-terminal supported the IP analysis. To test the role of α-tubulin motif in CpBV-CrV1, point mutations of CpBV-CrV1 were applied that’s result in loss of the biological activity of CpBV-CrV1. Furthermore immunofluorescence assay indicates CpBV-CrV1 colocalized with tubulin in hemocytes collected from P lutetia xyllostella parasitized by cotesia plutellae. This result suggests that GAPDH plays a critical role in hemocyte spreading behavior during infection of AMEV in Ld652 cells occurs in the presence of α-amanitin, while CrV1 binds to GAPDH, identified by MALDI-TOF analysis. dsRNA specific to GAPDH inhibits hemocyte spreading function, while RNAi treatments of other glycolytic genes had no effect on spreading. The common molecular motif of CpBV-CrV1 and alpha-tubulin at C-terminal supported the IP analysis. To test the role of α-tubulin motif in CpBV-CrV1, point mutations of CpBV-CrV1 were applied that’s result in loss of the biological activity of CpBV-CrV1. Furthermore immunofluorescence assay indicates CpBV-CrV1 colocalized with tubulin in hemocytes collected from P lutetia xyllostella parasitized by cotesia plutellae. This result suggests that GAPDH plays a critical role in hemocyte spreading behavior during
Immune challenge, and it is a molecular target of a pathogenic virus.

**POSTER Wednesday 16:30 VI-25**

The use of zinc-based fixatives for high-fidelity histomorphology and molecular histochemical techniques on arthropod tissue

*Damien M. Laudier*

Laudier Histology, New York City, NY
Correspondence: dmlaud@laudierhistology.com

Producing good histological preparations of arthropod tissues is often problematic. Studies that require high-fidelity morphological preservation for histomorphometric measurements, qualitative/quantitative histopathology and spatial localization of histochromic events; inconsistent or poor histologic preparations can render samples useless for light microscopy analysis. The underlying causes of this variability are not always conclusive. The choice of a tissue fixative is a significant factor in determining the quality outcome of an arthropod histologic preparation. Zinc-based fixatives have proven to provide exceptional morphological preservation, retention of DNA/RNA integrity and antigenic properties of vertebrate tissue. However, the application of zinc-based fixatives on arthropod tissues has been limited. Focusing on class Insecta and class Arachnida, this study compares histological preparations of select tissue types such as neuronal, ocular, digestive and reproductive. Specimen samples were fixed immediately post-sacrifice with various zinc-based fixatives, or with commonly used formaldehyde-based fixatives (zinc-free) for comparison. Following fixation, all tissue samples were comparably processed, embedded and sectioned. Staining was either tinctorial or with an antigenic marker identifying a particular protein expression via immunohistochemical technique. The results illustrate that zinc-based fixatives are highly effective in maintaining high-quality tissue integrity for simple and complex histological investigations and are empirically superior to conventional fixatives.

**THURSDAY – August 13th**

**SYMPOSIUM PAPER Thursday 8:00 125**

Advances in entomopathogenic nematode dispersal and host-finding behavior

*David Shapiro-Ilan*; Edwin E. Lewis

1USDA-ARS, SEFTNRL, Byron, GA, USA; 2Department of Entomology and Nematology, University of California, Davis, USA
Correspondence: David.Shapiro-Ilan@ars.usda.gov

Successful infection by entomopathogenic nematodes (EPNs) depends on being able to disperse and find the host. Therefore, to expand our understanding of epn ecology and leverage their use in biocontrol, it is imperative that we elucidate the behavioral mechanisms behind EPN movement and host-finding. Some recent findings and topics that will be discussed include enhanced dispersal from nematode infected hosts, the discovery of novel cues that induce epn movement such as electromagnetic signals (Ilan et al. 2013), and group movement behavior (moving together in pack) (Shapiro-Ilan et al. 2014).


---

**SYMPOSIUM PAPER Thursday 8:30 126**

Sex, age and following the leader drive infection dynamics of entomopathogenic nematodes

*Ed Lewis*; David Shapiro-Ilan; Yohandra Gonzales; Danica Maxwell

1Department of Entomology and Nematology, University of California – Davis, Davis, CA, USA; 2USDA-ARS, SEFTNRL, Byron, GA, USA
Correspondence: eelewis@ucdavis.edu

Entomopathogenic nematodes (EPNs) employ a mass-attack strategy when they infect a host. This strategy is favored because, in most cases, a single infective juvenile (IJ) is unable to overcome host defenses, and for EPNs in the genus *Steinernema*, females and males are needed for reproduction. It is likely that EPNs move in groups to facilitate this sort of strategy. But, even in a mass attack, one individual must be first to invade, and others must follow. Three questions are addressed here. (1) Which individuals invade first? (2) How many individuals follow? and (3) How long does the infection window stay open? Behavioral differences among individual IJs have been documented numerous times, and can be used to address these questions. Males and females differ in responses to hosts; males have been dubbed the colonizing sex. Old IJs respond differently to hosts than do young IJs; risk-sensitive foraging theory suggests that IJs with less lifespan remaining might take more risks than younger IJs. The interplay between individuals’ behavior and group dynamics is our focus in this work.

---

**SYMPOSIUM PAPER Thursday 9:00 127**

Impact of infection behaviour on lethal male fighting in *Steinernema*

Apostolos Kapranas, Abigail M. D. Maher, Annemie Zenner, Kate O’Callaghan, Christine T. Griffin

Biology Department, Maynooth University, Maynooth, County Kildare, Ireland
Correspondence: christine.griffin@nuim.ie

Males of certain species of *Steinernema* fights and kill each. The combat takes place within the killed host insect, a valuable resource that was previously colonised by infective juveniles (IJs) and killed with the aid of their bacterial symbiont. The host cadaver is thus a closed system in which the number and relatedness of competitors for adult male nematodes is determined by the infection behaviour of the IJs. The recent discovery of lethal fighting in these entomopathogenic nematodes provides a useful invertebrate model for testing theoretical predictions regarding factors such as group size and relatedness of individuals on the outcome of fighting. According to the theory of kin selection, individuals should show less aggression towards close relatives. We tested the effect of relatedness on aggression in groups of *S. longicaudum*, using nine inbred lines, and examined how competitor male group size and relatedness influence male mortality rates. In a series of *in vitro* experiments we found that both relatedness and competitor male group size influenced male mortality rates. Higher relatedness led to
Cooperative secretion of virulence factors by pathogens can often lead to social conflict as cheating mutants that benefit from collective action, but do not contribute to it, can arise and locally outcompete cooperators within hosts. Since cooperation is important for the virulence of invertebrate pathogens such as Bacillus thuringiensis social biology might be applied to the maintenance and improvement of biocontrol agents. Entomopathogenic nematodes (EPN) are ideal candidates here: EPN depend partly on symbiotic bacteria to infect and kill hosts and both bacteria and nematode secrete diverse virulence factors. Critically, effective EPN strains are hard to maintain without serial propagation in vitro (passage), and this can lead to attenuation. We tested whether cooperation is important for the maintenance of virulence in the EPN Heterorhabditis floridensis. As predicted, the potential for social conflict dramatically affected EPNs; low relatedness (high multiplicity of infection), which is expected to increase the success of cheats, led to reduced virulence, lower reproductive rates and premature extinction of all replicates in that treatment within 7 passages. Cooperation also requires strong global (between-host) competition. Contrary to expectation, our attempt to increase between-host competition led to reduced virulence. We conclude that it was difficult to manipulate between-host competition without affecting relatedness. Importantly, passage treatments that maintained high relatedness led to stable virulence and increased nematode reproductive rates, suggesting selection experiments aimed at nematode improvement might benefit from taking social interactions into account.
bassiana in association with sweetcorn (Zea mays). The first set of experiments focused on plant growth effects, using the invasive inoculation method developed for endophytes (Epichloë) of perennial ryegrass. The second set assessed rhizosphere community structure and function was assessed using a DGGE and MicroResp analysis. Significant differences between the isolates studied were observed during various plant-host interactions, suggesting that phenotypic diversity may play a role in the plant associated life history strategy, with important ecological implications.

CONTRIBUTED PAPER Thursday 8:45 132
Light affect sporulation patterns of the mite pathogenic fungus Neoseiulus floridana

Ingeborg Klingenberg, Maren Pindal Holthe, Aruppillai Suthaparan, Karin Wustrum, Torfinn Torp

1Norwegian Institute for Agricultural and Environmental Research (Bioforsk), Norway
2Norwegian University of Life Sciences, Department of Plant Sciences, Norway

Correspondence: ingeborg.klingen@bioforsk.no

A controlled microcosm experiment was conducted to examine how light affects the sporulation pattern of the mite pathogenic fungus Neoseiulus floridana during a 24 h cycle over a period of eight days. This was done by inoculating two spotted spider mites (Tetranychus urticae) with N. floridana and placing them on strawberry plants for death and sporulation. Spore discharge was observed by using a spore trap. Two light regimes were tested: Plant growth light of 150 µmol m<sup>-2</sup> s<sup>-1</sup> for 12 h supplied by high pressure sodium lamps (HPS), followed by either: i) 4 h of 50 µmol m<sup>-2</sup> s<sup>-1</sup> light with similar lamps followed by 8 h darkness or ii) 4 h of 50 µmol m<sup>-2</sup> s<sup>-1</sup> red light followed by 8 h darkness. The red light treatment resulted in a greater numbers of spores over a longer period of time than the light supplied by HPS. A clear difference in hourly spore discharge pattern between the two different light treatments was seen and a significant interaction effect between light treatment and hour in day during the 24 h cycle was observed. The spore discharge peak for the red light treatment is reached within the red light hours and the dark hours. The spore discharge peak for the light supplied by HPS lamp is reached within the dark hours. The results suggest that light affects the sporulation of the beneficial fungus N. floridana indirectly through multitrrophic interactions between the plant (strawberry), the herbivore (T. urticae) and the beneficial (N. floridana).

CONTRIBUTED PAPER Thursday 9:00 133
Environmental safety of Canadian Metarhizium S54 for the northern crayfish, Orconectes virilis, and phantom midge larva, Chaoborus americanus

Ann E. Hajek
Department of Entomology, Cornell University, Ithaca, USA
Correspondence: ajeh4@cornell.edu

Sampling has been conducted at a site in New York State over 18 years to follow the Lymantria dispar population and its associated pathogens and parasitoids. The dominant pathogen was Entomophaga maimaiga, which was temporally density dependent and associated with rain. Lymantria dispar nucleopolyhedrovirus infections were only very abundant during the early years of the study, when L. dispar populations were at higher population densities and E. maimaiga was just moving into this area. Four species of parasitoids were present throughout the years but rarely co-infected with E. maimaiga. The literature reports cyclicity (5 or 10 year) in L. dispar population in the more southerly mid-Atlantic region, but at this site, no cycles occurred; after an initial population collapse, the L. dispar population did not increase to densities causing any defoliation over the 18 years of this study.

CONTRIBUTED PAPER Thursday 9:30 135
Importance of mechano-signal for fungus removal in Drosophila grooming

Aya Yanagawa, Tsutomu Hata, Tsuyoshi Yoshimura, Frederic Marion-Poll

1Kyoto University, Uji, Japan; 2CNRS, Laboratoire Evolution, GénoMics, Comportement et Ecologie, Gif-sur-Yvette, France; 3AgroParisTech, Département Sciences de la Vie et Santé, Paris, France
Correspondence: ayanagawa@rish.kyoto-u.ac.jp

Insects remove and clean microbes from their surface grooming themselves, which is considered as a behavioral defense against pathogen/parasite infection in some cases. Insects like Drosophila melanogaster, which live in an environment littered...
Insect susceptibility to a pathogen can be influenced by maturation of the insect and its reproductive history since tradeoffs can occur between immunity and physiological factors. Additionally, as insects age their ability to combat a pathogen can decrease through a process called immunosenescence. The fungal pathogen Metsarhizium brunneum is being developed to control the Asian longhorned beetle (Anoplophora glabripennis), an invasive wood-borer. Since A. glabripennis take 1-2 weeks to mature after eclosion and can be long-lived, we wanted to determine how age, maturation and mating would impact their susceptibility to M. brunneum. Mature and older (both virgin and mated) and young (only virgin) beetles were inoculated with M. brunneum. The presence of M. brunneum in the hemolymph was quantified and beetles were monitored daily for death. There was a cost of reproduction for mature beetles but not the oldest beetles. Our results contrast with other studies which found immunosenescence in older invertebrates in many different systems. Our findings have important implications for understanding how mating and age can impact susceptibility to a fungal pathogen.

CONTRIBUTED PAPER Thursday 9:45 136-STU
Older beetles are stronger than young: Influence of mating and age on susceptibility to a fungal pathogen
Joanna J. Fisher, Ann E. Hajek
Department of Entomology, Cornell University, Ithaca, USA
Address for Correspondence: jjf236@cornell.edu

---

Yersinia entomophaga: A biopesticidal bacterium active against a wide range of insect pests
Mark Hurst1, Colin Ferguson2, Sarah Mansfield1, Richard Townsend1, Sean Marshall, Sandra Jones1, Jayanthi Swaminathan1, David Wright1, Michael Wilson2, Derick Wilson1, Maureen O’Callaghan1
1Innovative Farm systems, AgResearch, Lincoln Research Centre, New Zealand; 2Innovative Farm systems, AgResearch, Invermay Agricultural Centre, New Zealand; 3Innovative Farm systems, AgResearch, Ruakura New Zealand
Correspondence: mark.hurst@agresearch.co.nz

The bacterium Yersinia entomophaga was isolated from larvae of the New Zealand grass grub, Costelytra zealandica (Coleoptera: Scarabaeidae), from New Zealand soils. Y. entomophaga has activity towards a number of Coleopteran and Lepidopteran pests with the main activity against members of the Scarabaeidae, where LD50 is of approximately 5 x 10^5 bacteria/larva have been determined. Once ingested, death typically occurs within 2-5 day post infection. The main virulence determinant of Y. entomophaga is an insect active toxin complex termed the Yen-TC, that is highly active against members of the Scarabaeidae and the diamondback moth (Plutella xylostella). The bacterium can be economically fermented in large volumes, producing >1 x 10^10 cells/mL within 24 hours. Media and tools have been defined to alter the levels of Yen-TC production and enabling the selective detection of the bacterium post application to the environment. Formulated Y. entomophaga has shown field efficacy when applied as a bait formulation against ground dwelling lepidoptera (Wiseana sp.). The same bait proved more effective (80% control) than the insecticide alpha-cypermethrin for the control of Black beetle (Heteronychus arator), a pasture pest originating from South Africa. Spray developments are in progress for another New Zealand pastoral pest the “plantain moth complex” family Geometridae, Scopula rubaria and Epyaxa rosearia which causes significant damage plantain crops. A range of Y. entomophaga based formulations and delivery systems (e.g. baits, sprays, granules, seed treatments) are being developed.

CONTRIBUTED PAPER Thursday 8:15 138
Yersinia entomophaga: A biopesticidal bacterium active against a wide range of insect pests
Mark Hurst1, Colin Ferguson2, Sarah Mansfield1, Richard Townsend1, Sean Marshall, Sandra Jones1, Jayanthi Swaminathan1, David Wright1, Michael Wilson2, Derick Wilson1, Maureen O’Callaghan1
1Innovative Farm systems, AgResearch, Lincoln Research Centre, New Zealand; 2Innovative Farm systems, AgResearch, Invermay Agricultural Centre, New Zealand; 3Innovative Farm systems, AgResearch, Ruakura New Zealand
Correspondence: mark.hurst@agresearch.co.nz

---

Bacillus thuringiensis culture filtrate to Meloidogyne incognita
Dai Shih and Kunio Fukuoka
Department of Entomology, Tokyo University of Agriculture & Technology, Tokyo, Japan
Address for Correspondence: koike@obhiro.ac.jp

Bacillus thuringiensis has been used as an effective bio-insecticide because it produces the proteins Cry and Cyt, which are highly toxic to insects in certain situations. Root-knot nematode Meloidogyne incognita, is an important plant parasite, it prefers to attack the root of its host plant and can cause extensive damage to a wide variety of economically important crops. Recently, B. thuringiensis strains have the nematicidal activity against root knot nematode was proved. So we focus on using B. thuringiensis as a nematicide to control the Meloidogyne incognita.

In this study, the nematocidal effect of B. thuringiensis was identified by using bacteria culture filtrate (CF) treated second-stage nematode (J2) and egg sac. J2 suspensions (0.1 ml) were placed into wells of a 24-well tissue culture plate (50J2/well) containing 0.9 ml of bacteria CF. Liquid LB was used as the control. The effect of bacteria CF on the viability of J2 was determined after 12h. Bacteria CF from B. thuringiensis strain significantly increased the percentages of J2 motility compare to untreated control. Also, we inoculated bacteria CF of six strains of B. thuringiensis on M. incognitate egg sac by co-culture method for 24h, and removed the egg sac into sterilized water. 3 days after inoculation, counted the quantity of hatched J2 in the bacteria CF and un-hatched eggs in the egg sac to calculate the hatchability of egg. B. thuringiensis strains reduced the hatchability of egg (from 28.4% to 63.9%) compare to the untreated control.

CONTRIBUTED PAPER Thursday 8:00 137-STU
Toxicity of Bacillus thuringiensis culture filtrate to Meloidogyne incognita
Jihelina Qu1,2, Daigo Auchi1, Shin-ichiro Asano1, Masanori Koike2
1The United Graduate School of Agricultural Sciences, Iwate University, Iwate Japan; 2Department of Agro-environmental Science, Obihiro University of Agriculture & Veterinary Medicine, Obihiro, Japan; 3Department of Applied Bioscience, Graduate School of Agriculture, Hokkaido University, Sapporo, Japan
Address for Correspondence: koike@obhiro.ac.jp

Bacillus thuringiensis has been used as an effective bio-insecticide because it produces the proteins Cry and Cyt, which are highly toxic to insects in certain situations. Root-knot nematode...
A native virulent Bacillus sphaericus C3-41(CP 000 817) was isolated and identified from Rabbannahalli village of Yadgiri district, Karnataka, India. The isolates from different geographical origins have different degree of toxicity and persistency in nature. There is vast scope to identify and further characterize native B. sphaericus against mosquito, we made an attempt to characterize the pathogenicity and protein analysis of native B. sphaericus against C. quinquefasciatus. B. sphaericus was subjected for pathogenicity against mosquito larvae from various time of incubation, temperature and liquid media and protein analysis by SDS PAGE. Bioassay of B. sphaericus incubated for four day recorded the highest mortality of 100 per cent each at 750 ppm and 1000 ppm 48 hr after the treatments. Bioassay of B. sphaericus incubated at different temperature recorded, highest mortality at 30°C with 100 per cent 48 hr after the treatment. Among the media tested for bioassay, Egg yolk media recorded maximum mortality with 76.00 per cent and 100 per cent at 24 hr and 48 hr after treatments respectively. Further, the presence of large amount of B. sphaericus toxins proteins Bin A (41 KDa) and Bin B (52 KDa) were observed in SDS-PAGE, thus supporting its lethal potency against mosquito larvae. Therefore, it is highly likely that B. sphaericus isolate could serve as most potent bio-mosquitocide and play major role in dropping mosquito-vector diseases.

The coconut rhinoceros beetle (Oryctes rhinoceros; CRB) is a major pest of coconut and oil palm, but the discovery of Oryctes rhinoceros nudivirus (OrNV) in the 1960s has enabled the successful management of populations in Pacific Island Countries (PICs). Augmentative release of OrNV continues to be an important mechanism for CRB management in both coconut and oil palm growing regions. For ~40 years after adoption of this biocidal strategy, no new outbreaks of CRB were reported from uninfested palm growing countries and islands in the Pacific ensuring continuity of palm based village economies. However, the situation has recently changed. For first time in ~40 years, CRB invasion into completely new areas has been reported in the Pacific, being detected first in Tumon Bay in Guam 2007, followed by Port Moresby in PNG 2010, Honolulu in Hawaii 2013, and Honiara in Solomon Islands 2015. Additionally, Pacific areas with established CRB populations (e.g. Palau) have reported increased severity and frequency of CRB damage. Common to all these areas is the high incidence of severe palm damage, not seen since the introduction of OrNV. Initial attempts to introduce OrNV into the Guam CRB population were unexpectedly unsuccessful, raising the possibility that the CRB-G population that invaded Guam could be tolerant or resistant to the commonly applied OrNV isolates. Analysis of several CRB populations has demonstrated that the CRB-G biotype is also found in Hawaii, Palau, and recently (February 2015) in Port Moresby (PNG), with Honiara (Solomon Islands) still to be confirmed. We will discuss current results in relation to what is known about these new invasions and potential implications for the future.

The coconut rhinoceros beetle, an economically important pest of coconut palms, is effectively managed by application of its natural pathogen, the Oryctes nudivirus (OrNV). The traditional method of producing OrNV in infected larvae is labor intensive, and suffers from inconsistencies in virus titer and purity. In vitro production of OrNV in the susceptible and permissive anchorage-dependent DSIR-HA-1179 insect cell line can overcome these disadvantages. While production of OrNV in cell monolayers grown in T-flasks or Cell Factories is possible, the approach would not be cost-effective at industrial level. Roller Bottle Systems (RBS), with larger growth surface areas and capable of holding larger culture volumes in a more dynamic environment, would be a better option for scaling up purposes. DSIR-HA-1179 cells grown in 490 cm² RBS filled with 60 ml of TC-100 culture medium added with 10% fetal bovine serum yielded a maximum of 1.5 x 10⁸ cells/ml, which was comparable to yields reached in T-flasks under the same culture conditions (1.7 x 10⁸ cells/ml). Infection in RBS of cells in their early exponential growth phase (5 x 10⁵ cells/ml) at multiplicity of infection of 1 TCID₅₀/cell, produced OrNV volumetric and cell-specific yields of 2.1 x 10⁷ TCID₅₀/ml and 250 TCID₅₀/cell respectively, which was an improvement over those produced under identical culture and infection conditions in T-flasks (volumetric and cell-specific yields of 6.8 x 10⁶ TCID₅₀/ml and 102 TCID₅₀/cell, respectively). Thus, the roller bottle system has proven to be a robust alternative for the industrial production of OrNV.
Common bean, Phaseolus vulgaris, is an important food and cash crop in Africa. However, its production is seriously affected by the bean stem maggot (BSM), Ophiomyia phaseoli (Tyron) on Phaseolus vulgaris (L). Bertah Mutune,1,2 Sunday Ekesi,3 Saliou Niassy,2 Vivienne Matiri,2 Christine Bi,2 Nooy K. Maniania2
1International Centre of Insect Physiology and Ecology (icipe), P. O. Box 30772-00100, Nairobi, Kenya; 2Jomo Kenyatta University of Agriculture and Technology (JKUAT), P.O. Box 62000-00200, Nairobi, Kenya
Correspondence: nmaniania@icipe.org

- O8. ha−1) + PsiSNPV = 6×1012 O8. ha−1. Applications were performed in 200 L water ha−1 after 5:00 PM. Chlorantraniliprole was very efficient to control BVC, but not SBL, while B. thuringiensis reduced both populations. Both viruses significantly reduced SBL and VBC populations seven and 10 days after spraying, respectively. After 15 days, the number of larvae in the plots treated with the viruses was lower (VBC < 6.9 and SBL < 0.1) and statistically similar to the control plots. Defoliation was significantly reduced in all treated plots compared to the control plots during the 18 days of the field trial. Defoliation ranged from 10% (one week after application) to 18% (18 days after application) in the NPV treated plots, whereas in the control plots it ranged from 14% to 31% after one week and 18 days after application, respectively. Accumulated defoliation in the plots treated with B. thuringiensis and chlorantraniliprole was less than 10%.

Oriental fruit fly, Bactrocera dorsalis (Hendel) (Diptera: Tephritidae) has been identified as one of the three most important agricultural pests in South East Asia. In India, it causes losses up to 80% on mango alone. In this study three isolates of B. bassiana and three commercial mycoinsecticides were screened against larva, pupa and adults of B. dorsalis. The isolates ITCC No. 6628 and B. NCIPM were found pathogenic to adult stage with LC50 2.5×10−3 and 7.5×10−3 conidia /ml, respectively. While, ITCC No. 6645 found effective against adult stage at 1.2×10−3 and 3×10−3 larvae stage with LC50 9×10−3 conidia /ml. However, the three commercial mycoinsecticides prove their efficacy only on adult stages with 26.6%, 40% and 46.6% mortality for, Bio-power1, Bio-magic®, Bio-catch1, respectively. Significant differences between treatments and control were recorded accompanied by observation of mycosis on the cadavers.

Synergies Enabling the Registration and Adoption of Biological Pest Controls - The Role of Governments, and Academic Programmes and Industry

Facilitating the registration and adoption of biological pest controls in Canada
Tobias Laengle
Pesticide Risk Reduction Program, Agriculture and Agri-Food Canada, St. John’s, NL, Canada
Correspondence: tobias.laengle@agr.gc.ca

Biological pest control products, which include microbial, pheromones, and other non-conventional pest controls, can help growers develop and maintain advanced Integrated Pest Management practices that complement ecosystem services provided by intact agricultural ecosystems. Recognizing the limited availability of these types of products in Canada, in 2005 Agri-Food Canada’s Pesticide Risk Reduction Program (PRRP) began taking an active role in encouraging and assisting companies with the registration of biological pest controls. Meanwhile, biological pest control products, also referred to as biopesticides, have been gaining momentum worldwide, and many of the major players in the agriculture inputs industry have entered the biopesticides field with significant investments. As part of the symposium “Synergies enabling the registration and adoption of biological pest controls – the role of governments, academic programmes, and industry”, this talk will outline how the PRRP contributes to and builds on this global trend. The PRRP optimizes growers’ ability to access and use innovative new technologies by providing support along the innovation chain by (i) supporting research on biopesticides development, (ii) assisting and advising AAFC researchers with the commercialization of products, (iii) providing regulatory support to priority biopesticides identified through a grower-directed process, and (iv) supporting IPM projects to demonstrate the successful integration of biopesticides into integrated production systems. Successful examples will be used to illustrate this work of Pesticide Risk Reduction Program.
In the EU, microbiological control agents are currently registered by Regulation (EC) No 1107/2009, while macrobiological control agents are not included in this regulation. The active substance (based on an isolate of a microorganism), is approved by the EU and the decision applies to all 28 member states. The formulated product is, however, authorised at national level. The complete procedure is often long lasting. **EU has an explicit wish to support IPM, including the use of biological control. Academia in EU can contribute to registration and adoption of biological control in several ways:**

1) Joint research and innovation programs involving several research teams from different countries as well as private companies. Collaboration between research teams and SMEs (small to medium sized enterprises) is strongly encouraged in projects financed by the EU.

2) Networks and working groups related to the subject and sometimes even initiated with the explicit purpose to contribute to registration and adoption of biological control.

I will give a few examples of both types of activities. An example of particular relevance is the working group established in 2013 in order to suggest to the EU how to implement the ‘low risk’ concept for compounds to be approved. This work includes that we suggest to the EU how to define criteria for microorganisms to qualify for being considered as ‘low risk’ and also, how a ‘fast lane’ for registration can be implemented for such microorganisms.
Infection of lepidopteran cells by the baculovirus AcMNPV results in two virion forms, budded virus (BV) and occlusion derived virus (ODV). BV is required for the systemic spread of the virus and attaches to and enters cells by receptor mediated endocytosis mediated by the viral envelope glycoprotein GP64. ODV are required inter-host transmission and bind and enter the host columnar midgut epithelial cells via a receptor mediated membrane fusion event mediated by at least seven per os infectivity factors (PIFs). Previous studies have shown that both BV and ODV are infectious for tissue culture cells. Compared to BV however, ODV have very low infectivity for tissue cells and it is unknown if it requires the PIF complex. To determine if tissue culture infection by ODV requires the PIF complex we generated seven PIF gene knockout viruses, pif0-6. In addition, to ensure any infection observed was not due to GP64 mediated processes each of the pif knockout viruses was generated in a genomic backbone that contained a deletion of gp64. Occlusion bodies were purified transfected cells and ODV were alkali liberated and used for infection assays. Tissue culture infection of ODV, derived from pif- gp64 double knockouts, was compared to ODV isolated from gp64 knockout viruses. Initial results with pif0 and pif4 knockouts have shown that infectivity was low for both pif knockouts and the control virus, but no difference was observed in infection levels. These initial results suggest that the ODV infection of tissue culture cells do not utilize the PIF complex and an alternate entry mechanism must exist.

Typically the interaction between parasitoids and baculoviruses exploiting the same host is a competitive one and the survival of the parasitoid larva is dependent on the timing of parasitization and/or infection. The negative impact on parasitoid development is typically a result of baculovirus infection exhausting the metabolic resources of the host before the parasitoid completes its larval development. However, there are exceptions to this general case and examples of betacabulovirus and entomopoxvirus infections causing direct toxicity to or inhibition of parasitoid development have been described. It has been demonstrated that a protein from the hemolymph of virus-infected hosts is responsible for inhibition of development and killing of the parasitoid larvae. Among a large collection of baculoviruses isolated from geographic populations of bertha armyworm (Mamestra configurata) are strains of both MacoNPV-A and MacoNPV-B species that contain cassettes of four to six genes that are highly homologous to XecGV genes. MacoNPV-A and MacoNPV-B isolate infections in T. ni larvae were assessed for negative impacts on the development of the braconid parasitoid, Cotesia vanessae. Those MacoNPV viruses containing a cassette of XecGV genes inhibit the development of C. vanessae larvae in T. ni larvae. Development of AcMNPV recombinant viruses showed that a single XecGV gene homologue in MacoNPV viruses is responsible for the inhibition of parasitoid development. In vitro assays showed that the purified recombinant protein is toxic to C. vanessae larvae. Potential gene flow between distantly related viral species as well as competition between baculoviruses and parasitoids play a significant role in bertha armyworm ecology.

Tsetse flies (Diptera; Glossinidae) are naturally infected by Glossina hystricosus viruses (family Hytrosaviridae), a large dsDNA virus pathogenic specifically to the Glossina spp. The virus infections are largely asymptomatic but in G. pallidipes, asymptomatic infection can convert to symptomatic infection that is characterized by salivary gland hypertrophy syndrome (SGH), leading to reproductive dysfunction of infected flies which lead in several cases to the collapse of insect factory. Over the last decade researches were conducted to develop a virus management strategy to control and/or eliminate this virus from tsetse mass rearing facilities. The management strategies relies on: collecting information on the virus transmission; understanding tsetse biology and rearing system; using available antiviral drugs to reduce the virus replication and infection; modifying tsetse feeding system to a clean feeding system to interrupt the virus transmission and combining the use of clean feeding system with antiviral drugs. This management system leads to the elimination of the salivary gland virus from the factory for food and feed.”
Prior reports have demonstrated that orally delivered valacyclovir suppresses hytrosavirus (GpSGHV) levels in Glossina pallidipes colonies. Due to the complex nature of this insect-virus interaction, we decided to conduct parallel studies using the MdSGHV/Musca domestica system. Unlike GpSGHV, the MdSGHV expresses an acute infection within three days post-challenge, showing both typical SGH symptoms and virus-induced female sterility in 100% of the treated flies. Accordingly, a series of bioassays were conducted. Flies were injected with valacyclovir and MdSGHV then fed adult food and water amended with valacyclovir. An array of controls determined the impacts of the virus or valacyclovir on female fitness. A second set of bioassays were conducted that included 48h pretreatment of females with a 10% sucrose with and without valacyclovir. These flies were subsequently injected with the virus + valacyclovir cocktail and fed valacyclovir-amended water and adult food. To date, observations have demonstrated that the valacyclovir, at best, only partially suppresses the onset of SGH symptoms. Females treated with valacyclovir and virus fall into three categories: normal SGH, partial or aborted SGH, and no visible SGH. It should be noted that those that failed to display hypertrophy failed to develop eggs; these results suggest that the immediate early genes of MdSGHV may be mediating the virus-induced female sterility. It should be noted that the valacyclovir controls produced a normal complement of eggs, and all virus controls produced pronounced SGH and total female sterility. Ongoing experiments using a combination of conventional qPCR and RT-qPCR will provide quantitative data to these bioassays.

**CONTRIBUTED PAPER Thursday 15:15 154**

**Pathogen-host interaction of deformed wing virus (DWV) and the honey bee (Apis mellifera)**

Sebastian Guder, Elke Genersch

Institute for Bee Research, Molecular Microbiology and Bee Pathology, Hohen Neuendorf, Germany

Correspondence: gisderse@rz.hu-berlin.de

Deformed wing virus (DWV) is a viral pathogen of the European honey bee and is present in the majority of honey bee colonies worldwide. Vertical transmission by larval food, eggs or drone sperm causes true covert infections and progeny emerge without symptoms of a DWV infection. Outbreaks of clinical DWV-infections are associated with Varroa mite (Varroa destructor) infestation and cause overt infections with characteristic symptoms such as crippled wings and shortened abdomens. Varroa mites feed on honey bee pupae’s hemolymph and ingest DWV. Since it is a highly variable virus, different variants develop or a certain virus variant can propagate to a high copy number in mite cells. The DWV mutants were transmitted to the brood when the mite feeds again on honey bee larvae. Emerging bees have elevated virus levels and overt infections always correlate with the detection of DWV-RNA in brains of crippled bees. But also asymptomatic adults can be DWV-positive in their brains leading to the assumption that several DWV-mutants may lead to chronic overt infections with sublethal impairments such as learning disabilities of adult honey bees.

**CONTRIBUTED PAPERS Thursday 14:00 – 16:15**

**Bacteria 3**

**Cyt1Aa-BinA chimera highly toxic to anopheine, aedine, and culicine larvae including those tolerant or resistant to**

**Lysinibacillus sphaericus**

Dennis K. Bideshi1,2, Hyun-Woo Park1,2, Robert H. Hice2, Margaret E. Federici1,2

1Department of Entomology, University of California, Riverside, USA; 2Department of Natural and Mathematical Sciences, California Baptist University, Riverside, USA

Correspondence: brian.federici@ucr.edu

Two naturally occurring mosquitoicidal bacilli, Bacillus thuringiensis subsp. israelensis (Bi) and Lysinibacillus sphaericus (Ls), are the active ingredients of commercial larvicides used for controlling nuisance and vector mosquitoes. Bi’s high insecticidal activity is due to synergistic interactions among its four major proteins (Cry4Aa, Cry9B, Cry11Aa, and Cyt1Aa), whereas Ls’s principal toxicity is caused by the binary mosquitoicidal crystal, Bin, containing Bina, a toxin domain, and Bina a midgut-binding domain. Although used in many countries for over three decades, resistance to Bi is very rare. However, Bin resistance levels greater than 20,000-fold have occurred where Ls has been used intensively for mosquito control. Bi’s Cyt1Aa is a lipophilic protein of low toxicity that binds to midgut microvilli, and in previous studies we showed that it delays the evolution of resistance to Bi Cry proteins and Ls Bin, and can overcome resistance to these when selected for in the laboratory. In the present study, we assayed Cyt1Aa as a broad-spectrum targeting domain by fusing it to Bina. Here we show that the Cyt1Aa-Bina chimera accumulates in a parasporal body in 4Q7, an acrystalliferous strain of Ls, which is normally sensitive to Ls Bin. Our results suggest Cyt1Aa may prove useful as a targeting protein for other insecticidal proteins used to control dipteran vectors and possibly for dipteran and non-dipteran agricultural pests.

**CONTRIBUTED PAPER Thursday 14:15 157**

**Effect of single versus multiple promoters and a high plasmid copy number on the synthesis and assembly of Cyt1Aa crystals in Bacillus thuringiensis**

Hyun-Woo Park1,2, Robert H. Hice2, Brian A. Federici2

1Department of Entomology, University of California, Riverside, USA; 2Department of Natural and Mathematical Sciences, California Baptist University, Riverside, USA

Correspondence: hyunwoo.park@ucr.edu

Cyt1Aa is a major mosquitoicidal protein synthesized during sporulation of Bacillus thuringiensis subsp. israelensis, making up more than 50% of this species parasporal body. This high level of Cyt1Aa synthesis is due to several molecular traits including three strong sporulation-dependent promoters, a strong transcription termination sequence, and an associated 20-kDa helper protein. Although Cyt1Aa’s toxicity is low compared to this species Cry proteins, it nevertheless plays an important role in the biology of B. thuringiensis subsp. israelensis in that it synergizes the toxicity of the latter proteins, namely Cry11Aa, Cyt1Aa and Cry4Aa, and delays the evolution of resistance to these. In the present study, we evaluated the effects of using different cyt1Aa promoter combinations and plasmid copy number on synthesis of Cyt1Aa. Using the 4Q7 (plasmid-cured) strain of B. thuringiensis subsp. israelensis as an experimental host, a plasmid copy number of two or three yielded no Cyt1Aa, whereas a copy number of four
yielded only small crystals, even when expression was driven by one of the wild type promoters. However, using all three wild type promoters and a plasmid copy number of 20 yielded Cyt1A crystals 10-fold larger than those produced by one promoter and a plasmid copy number of four. In general, high levels of Cyt1Aa synthesis resulted in a significant reduction of spores per unit medium and imperfectly formed crystals. Cyt1Aa crystal synthesis using the same expression systems was also evaluated using a B. thuringiensis subsp. israelensis mutant strain that does not produce Cyt1Aa. Very similar results were obtained when the same expression constructs were evaluated in this mutant Cyt1A-minus strain.

CONTRIBUTED PAPER Thursday 14:30 158
The island of mosquitocidal toxins in Bt strain 2160-1 identified by whole genome sequencing and proteogenomic analysis
Jim X. J. Fang1,2, Y. Zhou3, P. T. Gong2, Y. J. Wei1, Y. Zhang1
1The HITAR Institute Canada Inc., Richmond, Canada; 2Hainan Institute of Tropical Agricultural Resources, Sanya, China; 3Institute of Life Sciences, Jiyang College of Zhejiang A&F University, Zhuji, China
Correspondence: jim.x.j.fang@hitar.org

The Bacillus thuringiensis strain 2160-1 has previously been identified as being highly toxic to mosquito larvae and a viable alternative to strains currently used commercially to control these insects. In a genome-wide scan, we predicted a sets of toxins in plasmids clustering in the region where likely formed a toxic island that included 10 toxin-like genes. Proteogenomic analysis proved the presence of the island of mosquitocidal toxins in Bt. Strain 2160-1, which included newly discovered toxins and previous identified five putative insecticidal toxin genes [Cry4Cb, cry30Aa, cry350Aa, cry4Ab and cry4Ba] in this strain. Our findings might provide new insights into the toxic protein island of Bacillus thuringiensis and the role of pathogenicity.

CONTRIBUTED PAPER Thursday 14:45 159
Engineering of Bacillus thuringiensis Cry proteins to improve the activity against western corn rootworm
Ruth Cong, Hana Ali, Michi Izumi Willcoxon, Yi Zheng, Jingtong Hou, Mark Nelson1, Ericka Bermudez, Mark McDonald, Takashi Yamamoto
Plant Protection, Ag Biotechnology, DuPont Pioneer, Hayward, CA and Wilmington, DE
Correspondence: ruth.cong@Pioneer.com

A new 133-kDa Bacillus thuringiensis Cry protein active against Western corn rootworm (WCRW) was discovered. This protein was designated as Cry8Hb1 by Bacillus thuringiensis Toxin Nomenclature Committee. The peptide sequence deduced from the cloned gene indicates a typical three domain-type Cry toxin. Trypsin digestion of Cry8Hb produced the 65-kDa matured toxin along with a 55-kDa fragment. This trypsin digestion pattern is similar to those of Coleoptera-active Cry proteins such as Cry3. The 55-kDa fragment is a result of nicking the Alpha 3-4 loop of Domain I by trypsin. Unexpectedly, it was found that the activity of Cry8Hb against WCRW was enhanced significantly by fusing Escherichia coli maltose binding protein (MBP) to the 75-kDa N-terminal portion of Cry8Hb including the leader sequence and matured toxin. Similar activity improvements were observed with the other corn rootworm-active proteins such as Cry88B. It appears that the activity enhancement is a result of increased solubility of the MBP fusions of those Cry toxins at pH 7 or slightly acidic pH similar to the environment within the corn rootworm midgut. Solubility of a Bt Cry toxin can be modified by DNA shuffling technology introduced by Stemmer (1994, Nature, 370:389-391). To evaluate this concept, a synthetic Cry3-type protein termed IP3-1 was designed by computer-aided protein-engineering using Cry3-family protein sequences and used as the starting material to conduct single-gene, mutagenesis DNA shuffling. The shuffling produced six highly active IP3 variants showing good solubility in a neutral pH buffer.

CONTRIBUTED PAPER Thursday 15:00 160
Laboratory-selected western corn rootworm colony resistant to mCry3A
Jian-Zhou Zhao, Meghan Oneal, Nina Richman, Analiza Alves, Stephen Thompson
DuPont Pioneer, Johnston, U.S.A
Correspondence: Joe.Zhao@Pioneer.com

Bt maize plants expressing various insecticidal Cry protein genes for western corn rootworm (Diatrobota virgifera virgifera, WCRW) management have provided significant value to growers over the past 10 years. Developing insect colonies resistant to Bt traits through laboratory selections can provide valuable resources for research and development of novel traits. We developed a laboratory-selected WCRW colony with a high level of resistance to mCry3A using purified protein and maize events expressing high levels of mCry3A. The resistance ratio (RR) to mCry3A was >90-fold in diet based bioassays. The beetles of the resistant colony were used to make reciprocal crosses with a susceptible laboratory colony to test the inheritance of resistance. Analysis of 12-day relative survival results for the F1 larvae indicated that resistance to mCry3A was inherited autosomally and was incompletely recessive.

CONTRIBUTED PAPER Thursday 15:15 161
A new Cry1Ac toxin of Bacillus thuringiensis highly toxic to Manduca sexta and Trichoplusia ni
Yaritza Reinoso-Pozo1, Cristina Del Rincon-Castro2, Jorge E. Ibarra2
1Department of Biotechnology and Biochemistry, CINVESTAV-Irapuato, Mexico; 2Life Sciences Division, University of Guanajuato, Irapuato, Mexico
Correspondence: jibarra@ira.cinvestav.mx

For the control of insects pest in agriculture different strategies to reduce the environmental impact produced by chemical insecticides have been used. Bacillus thuringiensis is a Gram-positive bacterium which produces crystal inclusions composed by Cry proteins that are toxic to a limited number of target insect larvae. In this study was performed a characterization of a native B. thuringiensis strain called LB1-1200 which showed high toxicity in preliminary experiments against Trichoplusia ni and Manduca sexta larvae. Analysis of the flagellin sequence, plasmids pattern and REP-PCR showed that LB1-1200 strain belongs to the kurstaki serovar and microscopy investigation showed the presence of bipyramidal crystals. The presence of cry genes in LB1-1200 was studied using a PCR strategy with a set of degenerate primers and only one cry1Ac gene was identified. The LC50 using spore-crystal mixture of LB1-1200 against M. sexta y T. ni was 3.581 and 11.458 ng/cm², respectively. A comparison with the reference strains B. thuringiensis kurstaki HD-73, which also contains only a cry1Ac gene, showed much lower toxicity levels than LB1-1200 (21.873 and 108.671 ng/cm², respectively). Sequence analysis of the Cry protein derived from LB1-1200 cry1Ac gene showed three different amino acid substitutions, two in the toxic region (domain III) and one in the non-toxic C-terminal region of the protein. These substitutions are not present in the rest of the Cry1Ac proteins reported to date. Site direct mutagenesis experiments
were performed to determine if these substitutions are related to the high toxicity of the LBIT-1200 strain.

CONTRIBUTED PAPER Thursday 15:30 162
Rapid evolution and genetic basis of resistance to Cry1F in a lab-selected Asian corn borer and its cross-resistance to other Cry toxins
Yueqin Wang, Yidong Wang, Zhenying Wang, Kanglai He
State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protect, Chinese Academy of Agricultural Sciences, Beijing, China
Correspondence: hekanglai@caas.cn

The Asian corn borer, Ostrinia furnacalis (Guenée), is one of the most economic insect pests of maize targeted by Bt maize that has been tested in confined field trials in China. The evolution of resistance by the target insect and its management strategies should be clarified before Bt maize commercialization. It is important for characterizing resistant strains, which will provide the only way to empirically validate proposed management strategies. ACB-FR, a strain of the Asian corn borer, originated from field collection of Xi’an, Shaanxi Province was selected for resistance by exposure to Cry1F toxin incorporated into artificial diet in the laboratory. The susceptibility of selected strain to Cry1F toxin was declined with the selection pressure increased. The selected strain developed more than 52-fold resistance to Cry1Ie after 14 generations of selection. However, it showed lower level of cross-resistance to Cry1Ab, Cry1Ac and Cry1Ah, but it did not cross-resistance to Cry1Le. Bioassay results of F1 reciprocal crosses between ACB-FR and unselected strains showed that the inheritance of resistance to Cry1F was autosomal without maternal effect. Dominance D calculated on the basis of LC50s suggested that resistance to Cry1F toxin was incompletely recessive. Backcrossing studies indicated that resistance to Cry1F toxin was polygenic in ACB-FR.

CONTRIBUTED PAPER Thursday 15:45 163
Evaluation of Bt corn with stacked genes for resistance to the Asian corn borer
Tiantao Zhang, Fan Jiang, Zhenying Wang, Kanglai He
State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing, China
Correspondence: klhe@ippcaas.cn

Transgenic Bacillus thuringiensis (Bt) crop could provide an effective way to control the insect pests. Preventing insect pests from developing resistance to Bt toxins produced by transgenic crops is a major challenge for agriculture. Theoretical models suggest that plants including two dissimilar Bt toxin genes have the potential to delay resistance more effectively than single-toxin plants used sequentially or in mosaics. To test these predictions, transgenic corn plants carrying Cry1Ac or Cry1Ie were obtained, and breeding stacked to two gene corn. To evaluate the resistance of the stacked Bt corn to Asian corn borer (ACB), laboratory bioassays were carried out by exposing susceptible or different resistant ACB neonates to fresh Bt corn whorl, immature tassels, fresh silks, ears and husk. The mortality of ACB neonates indicated that multiple transgenic hybrids have more effective insecticidal efficacy to both susceptible and resistant ACB. Furthermore, field trials were also conducted with artificial infestations of ACB at mid whorl and silk stages.
# AUTHOR INDEX

Abstract numbers only = oral presentation e.g. 111
Abstract numbers preceeded by division codes = poster presentations e.g. BA-1
Abstracts followed by ‘STU’ are student presentations e.g. BA-1-STU

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abd-Alla, Adly</td>
<td>MC-6-STU</td>
</tr>
<tr>
<td>Abdel-Baky, Nagdy F.</td>
<td>DB-6-STU, DB-7, DB-8-STU, FU-10-STU, FU-28,</td>
</tr>
<tr>
<td>Abdelaaffar, Heba M.</td>
<td>VI-21-STU, VI-22-STU</td>
</tr>
<tr>
<td>Abreo, Eduardo</td>
<td>BA-20-STU</td>
</tr>
<tr>
<td>Adegawa, Satomi</td>
<td>FU-18-STU, FU-24-STU, NE-6-STU, 137-STU</td>
</tr>
<tr>
<td>Ahn, Yong Oh</td>
<td></td>
</tr>
<tr>
<td>Aiuchi, Daigo</td>
<td></td>
</tr>
<tr>
<td>Aktories, Klaus</td>
<td></td>
</tr>
<tr>
<td>Ali, Ghulam</td>
<td></td>
</tr>
<tr>
<td>Ali, Hana</td>
<td></td>
</tr>
<tr>
<td>Al-Shuraym, Laila A.M.</td>
<td></td>
</tr>
<tr>
<td>Altier, Nora</td>
<td></td>
</tr>
<tr>
<td>Alvarez, Fabiana</td>
<td></td>
</tr>
<tr>
<td>Alves, Analiza</td>
<td></td>
</tr>
<tr>
<td>Amtoft-Wyns, Anja</td>
<td></td>
</tr>
<tr>
<td>Anderson, Peter</td>
<td></td>
</tr>
<tr>
<td>Araujo, Claudinéia A. S.</td>
<td></td>
</tr>
<tr>
<td>Arif, Basil</td>
<td></td>
</tr>
<tr>
<td>Arnold, Pieter A.</td>
<td></td>
</tr>
<tr>
<td>Aroian, Raffi V.</td>
<td></td>
</tr>
<tr>
<td>Asano, Shin-ichiro</td>
<td></td>
</tr>
<tr>
<td>Asgari, Sassan</td>
<td></td>
</tr>
<tr>
<td>Atayme, Célestine</td>
<td></td>
</tr>
<tr>
<td>Avery, Pasco B.</td>
<td></td>
</tr>
<tr>
<td>Banerje, Rahul</td>
<td>BA-17</td>
</tr>
<tr>
<td>Banyuls, Nuria</td>
<td>74</td>
</tr>
<tr>
<td>Barbarin, Alexis M.</td>
<td>146</td>
</tr>
<tr>
<td>Barney, William</td>
<td></td>
</tr>
<tr>
<td>Barrera, Gloria P.</td>
<td></td>
</tr>
<tr>
<td>Barreto, Emiliano</td>
<td></td>
</tr>
<tr>
<td>Bass, David</td>
<td>8, 68</td>
</tr>
<tr>
<td>Bateman, Kelly S.</td>
<td>51, 65-STU, 66, DB-3</td>
</tr>
<tr>
<td>Baxter, Simon W.</td>
<td>13</td>
</tr>
<tr>
<td>Bayram, Serife</td>
<td>149</td>
</tr>
<tr>
<td>Becnel, James J.</td>
<td>7, 38, 116</td>
</tr>
<tr>
<td>Behle, Robert W.</td>
<td>102, MC-18</td>
</tr>
<tr>
<td>Behie, Scott W.</td>
<td>112</td>
</tr>
<tr>
<td>Bekkaoui, Diana</td>
<td>34-STU, 149</td>
</tr>
<tr>
<td>Bel, Yolanda</td>
<td>BA-16</td>
</tr>
<tr>
<td>Belaich, Mariano</td>
<td>VI-7, VI-13</td>
</tr>
<tr>
<td>Béliveau, Catherine</td>
<td>119</td>
</tr>
<tr>
<td>Bellam, Haripriya</td>
<td>MC-17-STU</td>
</tr>
<tr>
<td>Bellicanta, Giovanni</td>
<td>74</td>
</tr>
<tr>
<td>Bennett, Martyn</td>
<td>68</td>
</tr>
<tr>
<td>Benuzz, Massimo</td>
<td>28</td>
</tr>
<tr>
<td>Bermudez, Ericka</td>
<td>159</td>
</tr>
<tr>
<td>Bernhardt, Tanja</td>
<td>19</td>
</tr>
<tr>
<td>Bettucci, Lina</td>
<td></td>
</tr>
<tr>
<td>Bickley, Lisa K.</td>
<td></td>
</tr>
<tr>
<td>Bideshi, Dennis K.</td>
<td></td>
</tr>
<tr>
<td>Bidochka, Michael J.</td>
<td></td>
</tr>
<tr>
<td>Bigot, Diane</td>
<td>117-STU, VI-5-STU</td>
</tr>
<tr>
<td>Bii, Christine</td>
<td>143</td>
</tr>
<tr>
<td>Bilgo, Etienne</td>
<td>76</td>
</tr>
<tr>
<td>Bishwajeet, P.</td>
<td>144</td>
</tr>
<tr>
<td>Biswas, Siddhartha</td>
<td>53-STU</td>
</tr>
<tr>
<td>Bivián-Hernandez, Ma. de los Angeles</td>
<td></td>
</tr>
<tr>
<td>Björnson, Susan</td>
<td>MI-1</td>
</tr>
<tr>
<td>Björkman, Maria</td>
<td></td>
</tr>
<tr>
<td>Blissard, Gary W.</td>
<td></td>
</tr>
<tr>
<td>Bojorque, Verónica F.</td>
<td>MC-12</td>
</tr>
</tbody>
</table>
Desjardins, Christopher A. 38
Devine, Gregor J. 31
Diabate, Abdoulaye 76
Dias, Luciana P. FU-7-STU
Dillman, Adler NE-7
Dillon, Aoife B. 75
Dilipkumar, Aishwarya NE-2
Djoumad, Abdeldajjed 119
Do Nascimento, Ricardo M. FU-2
Domanska, Barbara BA-11-STU
Dominic, Anto Raja MI-2
Donly, Cam 150
dos Santos, Karine FU-14
Downes, Sharon 10, BA-17
Drezen, Jen-Michel 119
Dubovskiy, I.M. MC-19
Dunlap, C.A. BA-3-STU
Dunn, Alison 47

E
Ebeling, Julia DB-2-STU
Ebssa, Lemma 123
Eigenbrod, Marina 37-STU
Eilenberg, Jørgen 47, DB-5, FU-5-STU, 147
Ekesi, Sunday 18, MC-13, 143
El-Ayoubi, Mustapha 54
Elbashir, Mohammed I. 144
Elkabir, Entisar MI-1
Elkinton, Joseph S. 106-STU
Endo, Haruka 11, BA-14-STU
Enkerli, Jürg FU-5-STU, FU-23-STU
Ens, Shao 64
Erlandson, Martin VI-4, VI-8, VI-15, 150, 151

Escrice, Baltasar BA-16, BA-18
Espinel, Carlos 78, MC-7
Etebari, Kayvan 30, 31
Euerle, Chris FU-4

F
Fabrick, Jeffrey A. 44
Fang, Jim X. J. BA-8, 158
Faria, Marcos FU-6, MC-16
Fast, Naomi M. 41-STU
Faury, Nicole 155
Federici, Brian A. 156, 157
Fei, Zhangjun 70
Feng, Dongmei BA-19
Feng, Ming-Guang 94, 95-STU, 96-STU, 97-STU, 98-STU, MC-2, 138
Ferguson, Colin FU-8
Fernandes, Alesandra M. FU-8, FU-14, FU-17-STU
Fernández-Navarro, Mariana BA-1-STU
Ferré, Juan BA-16, BA-17
Ferreira, Paulo FU-7-STU
Ferreira, Rodrigo B. FU-8
Fick, Will BA-9
Figueiredo, Camila S. 136-STU
Fisher, Joanna J. 48
Floate, Kevin D. BA-4-STU
Flor-Weiler, L.B. BA-3-STU, MC-18
Folgarait, Patricia J. 24, FU-12, MC-14
Fong, Ryan 16
Fonseca, Fernando C. A. 15
Foster, J.M. 92
Foster, Jeremy 85-STU, 86-STU
Foster, R. Nelson FU-8
Franceshini, Sergio 28
Frank, Jacqueline A. VI-10-STU
Franklin, Michelle T. VI-4
Franz, Alexander W. E. 30
Freeman, Mark A. 6, 52
Fritsch, Eva 105-STU, MC-4-STU
Fünfhaus, Anne DB-1-STU, DB-2-STU

G
Galtier, Nicolas 117-STU, VI-5-STU
Gandelman, Olga DB-3
Gao, Yulin BA-5
Garcia, Lorena MC-7
Garcia-Gonzalez, Eva DB-1-STU
Garcia-Suárez, Rosalina BA-2-STU
Gardescu, Sana FU-22
Gariglialba, Erika MC-7
Guan, John F.
Gatsoquinnis, Christos
Gauthier, Debbie
Gayral, Philippe
Gebhardt, Manuela
Geden, C.
Gelderman, Mandy
Gensersch, Elke
Ghiringhelli, Pablo D.
Ghosh, Kaya
Giraddi, R. S.
Gisler, Sebastian
Glare, Travis
Glupov, V. V.
Gobinath, Chandrakasan
Goble, Tarryn Anne
Goffré, Daniela
Goldberg, Jonathan M.
Golo, Patricia S.
Gómez, Demian
Gómez, Juliana A.
Gomis-Cebolla, Joaquin
Gong, P. T.
Gonzales, Yohandar
González, Paula
Gordon, Karl J. H.
Grammare, Pierre M.
Grant, Michelle
Graves, Leo
Greenwood, Spencer J.
Griffin, Christine T.
Griffin, Samantha
Grijalba, Erika
Grisdale, Cameron J.
Grisi, Isabella
Grossi-de-Sa, Maria Fatima
Grøva, Lise
Guan, Xiong
Guan, Yi
Gueli Alletti, Gianpiero
Guevara, Judith
Guo, Shuyuan
Guo, Suxia
Guo, Yajie
Gürkan, M. Oktay
Guzmán-Franco, Ariel W.
Gwak, Won Seok
Gwynn, Roma L.

H
Haas, Jeffrey A.
Hajek, Ann
Hamajima, Rina
Hamilton, Kristina
Hampton, John
Han, Bing
Han, Yan
Han, Yue
Hanson, M. A.
Hapeshi, Alexia
Harris, Stephanie
Harris, Sue E.
Harrison, Robert L.
Hasler, James
Hata, Toshimitsu
Hazir, Selcuk
He, Kanglai
Healey, Joe
Heckel, David G.
Hegedus, Dwayne
Hegedus, Dwayne
Heiman, David
Henderson, Deborah
Henkens, Marleen
Hernández-Dominguez, Carmela
Hernández-Martínez, Patricia
Hernández-Rodríguez, Carmen S.
Hernio, Elizabeth A.
Herrero, Salvador

Gu, 90
GU, 117-STU, VI-5-STU
GEB, 105-STU, VI-10-STU
Geden, 153
GIS, BA-7
GE, DB-1-STU, DB-2-STU, MI-2, 154
Ghiringhelli, 139
Goble, 38
GOF, FU-8
GO, VI-7
Goring, 58, VI-16-STU
GREEN, 67
GRI, 31, 127
GRIF, BA-12
GRIJ, 78
Grisdale, 41-STU
GRIS, BA-6
GROSSI, 15
GROVA, 64
GUAN, 98-STU
GUEL, 37-STU, 69
GUEVAR, MC-7
GUO, 13
GU, 11, MI-3
GU, 90
GU, 117-STU, VI-5-STU
GEB, 105-STU, VI-10-STU
Geden, 153
GIS, BA-7
Hesketh, Helen
Hey, Timothy
Hice, Robert H.
Hicks, Ruth
Hiltzold, I.
Holthe, Maren Pindse
Holyoake, Andrew
Hoover, Kelli
Hou, Dianhai
Hou, Jingtong
Hu, Zhihong
Hua, Dong-hui
Huang, Amy
Huang, Fangneng
Huang, Ning
Huang, Wei-Fone
Huang, Zhihong
Hulse, Rosaline
Humber, Richard A.
Hurst, Mark
Hussain, Mazhar

I
Ibarra, Jorge E.
Ikeda, Motoko
Imamura, Kazuhiro
Inan, Cihan
Ince, Ikbal Agah
Inglis, Susan
Inoue, Maki N.
Inouye, Kuniyo
Iron, Sarah
Ishii, Minehiro
Issi, Irma V.
Iwanicki, Natasha
Iwata, Kento
Izumi Wilcoxon, Michi

J
Jackson, Mark
Jackson, Trevor A.
Jaffuel, G.
Jakka, Siva R. K.
Jakubowskà, Agata K.
James, Bill
James, William J.
Jan, Eric
Janmaat, Alida F.
Jaronski, Stefan
Javed, Muhammad Afzaal
Je, Yeon Ho
Jech,erry E.
Jehle, Johannes A.
Jenkins, Nina E.
Jensen, Annette B.
Jiang, Fan
Jiang, Kun
Jin, Jie
Johnson, Dan
Johnson, Karyn N.
Johnson, S.N.
Jones, Sandra
Jun, Young Soon
Jurat-Fuentes, Juan Luis

K
Kabaluk, J. Todd
Kakhdzse, Manana
Kalmath, Basavaraj S.
Kamalakannan, Siva
Kapranas, Apostolos
Karitithi, Henry M.
Karpinski, Anne
Karthik Raja, Ramalingam
Katkar, Gajanand
Katsuma, Susumu
Kawchuk, Larry
Kaya, Harry K.
Keeling, Patrick J.
Kerr, Rose
Keyser, Chad A.
Kikuta, Shingo

J

47
156, 157
51
82, 124, NE-5
132
131-STU
VI-2
55, 120
159
55, 120
BA-15
VI-4
45
30
7
60
68
FU-14, FU-15, FU-16,
FU-17-STU
63, MC-1, 138
31

BA-1-STU, BA-2-STU,
161, VI-9
VI-17-STU
BA-14-STU
VI-23
59
52
104-STU, VI-11-STU
BA-23
56, VI-16-STU
FU-18-STU, FU-24-STU
MI-4
FU-23-STU
VI-11-STU
16, 159

81, FU-22
MC-15, 140

NE-5
45
32-STU
BA-17
10
72
20, BA-7
FU-8, FU-13, 133
VI-15
BA-13-STU, VI-18
FU-8
37-STU, 69, 80-STU,
105-STU, MC-4-STU,
VI-10-STU
74
DB-5
163
BA-15
FU-1
133
35-STU
82
138
DB-6-STU, DB-7,
DB-8-STU
45, 89

NE-4-STU
139
MC-20
127
33-STU
12
NE-2
139
57-STU
133
122
5
101, 110, FU-8
BA-20-STU
Kim, Jong Hoon  
Kim, Woo Jin  
Kim, Yonggyun  
King, Linda A.  
Kleespies, Regina G.  
Klingen, Ingeborg  
Knispel, Henrique  
Kobayashi, Michihiro  
Koga, Hironori  
Koike, Masanori  
Kokusho, Ryuhei  
Koppenhӧfer, Albrecht M.  
Kostromytska, Olga S.  
Kraus, Bruna M.  
Krejmer, Martyna  
Krell, Peter J.  
Kristmundsson, Árni  
Kuhn, Lisa  
Kumar, Sunil  
Kunimi, Yasuhisa  
Kyei-Poku, George

L  
Labrousse, Carole  
Ladurner, Edith  
Laengle, Tobias  
Lai, Qingying  
Landmann, F.  
Lane, Thomas  
Lang, Alexander E.  
Larem, Andreas  
Lau, Sabina  
Laudier, Damien M.  
Leclerque, Andreas  
Lee, Seok Hee  
Lee, Seung Hee  
Lee, Siu Fai  
Leite, Luis G.  
Lemes, Ana Rita N.  
Lemieux, Vincent

BA-13-STU, VI-18  
BA-13-STU, VI-18  
14, 36-STU, VI-24-STU  
56, VI-16-STU  
37-STU, 47  
FU-23-STU, 132  
DB-1-STU  
VI-17-STU  
BA-23  
FU-18-STU, FU-24-STU,  
NE-6-STU, 137-STU  
57-STU  
123  
123  
MC-16  
VI-3-STU, VI-6  
53-STU, 58  
52  
119  
36-STU, VI-24-STU  
104-STU, 115, VI-11-STU  
FU-11, MI-3

Lemos, Manoel Victor F.  
Leng, Song  
Leung, Joyce P. S.  
Lewis, Edwin E.  
Li, Ao  
Li, Leon Yu Zheng  
Li, Lin  
Li, Xianchun  
Li, Zhaofei  
Libro, Silvia  
Lightner, Don  
Li-Leger, Erica  
Lima, Anabele A.  
Lin, Jian  
Linde, Andreas  
Liu, Chenxi  
Liu, Sijun  
Liu, Yang  
Liu, Zhaoxia  
Loose, Jennifer S. M.  
Lopes, Rogário B.  
López-Tiajomulco, Juventino  
Lovett, Brian  
Lu, Hsiao-Ling  
Lucena, Wagner A.  
Luck, Ashley N.  
Luke, Belinda  
Luo, Sijiani  
Luo, Xiaoxia  
Lupo, Sandra  
Luttrell, Randall G.  
Luz, Christian  

M  
MacDonald, Paul R.  
Macedo, Cristina  
Madhani, Hiten D.  
Maguchi, Yohsuke  
Mahan, Rod J.  
Maharramov, Jafar  
Maher, Abigail M.D.  
Mahon, Rod

BA-9, BA-10  
16  
20  
125, 126, NE-1  
60  
VI-1-STU  
64  
44  
70  
85-STU  
88  
FU-25  
BA-6  
BA-21  
MI-2  
BA-5  
64, 73  
53-STU, 58  
17  
DB-1-STU  
MC-16, FU-6  
VI-9  
76-STU, 100-STU, FU-3-STU  
99-STU, FU-4  
15  
86-STU  
75  
55  
BA-21  
FU-20  
BA-22  
FU-14, FU-15, FU-16,  
FU-17-STU  
107-STU  
BA-6  
38  
NE-6-STU  
10  
49  
127  
BA-17
Malania, Iatamze, NE-4-STU
Maniania, Nguya K., 18, MC-13, 143
Manker, Denise C., 27
Mansfield, Sarah, MC-1, MC-2, 138
Mantouvane, Fernando, FU-11
Marfetán, J.A., MC-14
Marfetán, Jorge A., FU-12
Marion-Poll, Frederic, 135
Marshall, Sean D.G., MC-1, MC-2, 138, 140
Martin, Randy, 148
Martinez, Gonzalo, FU-20
Martins, Erica, BA-6
Martins, Irene, FU-6
Martins-de-Sa, Diogo, 15
Marucci, Suzana C., BA-10
Matiru, Viviene, 143
Maxwell, Danica, 126
Mayerhofer, Johanna, FU-5-STU
McCaskill, David, BA-12
McDonald, Mark, 159
McGraw, Benjamin A., 123
McKinnon, Aimee, 131-STU
McMullen, John G. II, 87-STU
Meagher, Robert, 45
Meijia, Cindy, 49, 50-STU
Meki, Irene K., 33-STU
Mendoza, Artemio Mendoza, 131-STU
Meusch, Dominic, 90
Meyling, Nicolai V., 26, 101, FU-5-STU, FU-23-STU, FU-26
Michalski, M.L., 92
Mikaia, Nona, NE-3
Millard, Andrew, 93
Mitra, Alok, 63
Mizuki, Eiichi, BA-23
Moffitt, Jessica, 30
Moldovan, Anna I., MC-6-STU
Molotievski, Natalia, MC-6-STU
Munteanu, Monnheimer, Laurin R., 69
Montalva, Cristian, FU-14, FU-15, FU-16
Monterroso, Armando, MC-12
Moore, Aubrey, 140
Moore, Carmina, FU-8
Moore, Dave, 75
Moreira, Helio, BA-6
Morga, Benjamin, 103
Mori, Gustavo Maruyama, FU-2
Morinerat, Rose, BA-6
Mou, Yani, 17
Muermann, Martin, BA-7
Mulley, Geraldine, 93
Mumbai, Mercy, MC-13
Munday, Peter, DB-3
Muratoglu, Hacer, VI-23
Murphy, Graeme, 77
Murugan, Kadarkarai, MC-20
Mutune, Beritah, 143
Myers, Judith H., 107-STU
Nagoshi, Rodney, 45
Nagy, Éva, 58
Nakai, Madoka, 104-STU, 115, VI-11-STU
Nakajima, Natsuko, BA-14-STU
Nana, Paulin, MC-13
Nandalochana, Janitha B., FU-8
Narva, Ken, BA-12
Nelson, Mark, 159
Nelson, Tracey, MC-1
Neunemann, David, 32-STU
Niassy, Saliou, 143
Nicolson, Laurel, FU-8
Nielson-LeRoux, Christina, DB-5
Niu, Jinzhi, 50-STU
Norli, Hans R., FU-26
Nunn, Adam J., 75
O'Callaghan, Kate, 127
O'Callaghan, Maureen, MC-1, 138
Oikawa, Fuka, FU-24-STU
Okumura, Shiro, BA-23
Oneal, Meghan, 160
<table>
<thead>
<tr>
<th>Name</th>
<th>Number</th>
<th>Pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ono, Chikako</td>
<td>VI-19-STU</td>
<td></td>
</tr>
<tr>
<td>Oppert, Cris</td>
<td>89</td>
<td></td>
</tr>
<tr>
<td>Orozco, Rousel</td>
<td>62-STU, 88</td>
<td></td>
</tr>
<tr>
<td>Ozdemir, Esengul</td>
<td>34-STU, 149</td>
<td></td>
</tr>
<tr>
<td>Pan, Kai</td>
<td>120</td>
<td></td>
</tr>
<tr>
<td>Park, Hyun-Woo</td>
<td>156, 157</td>
<td></td>
</tr>
<tr>
<td>Park, Youngjin</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td>Parmentier, Laurian</td>
<td>49</td>
<td></td>
</tr>
<tr>
<td>Passarelli, A. Lorena</td>
<td>30</td>
<td></td>
</tr>
<tr>
<td>Patel, Anant</td>
<td>21, 111</td>
<td></td>
</tr>
<tr>
<td>Patil, B.V.</td>
<td>139</td>
<td></td>
</tr>
<tr>
<td>Pauchet, Yannick</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>Pelegrini, Patricia B.</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>Pelz, Juliana</td>
<td>19</td>
<td></td>
</tr>
<tr>
<td>Peng, Donghai</td>
<td>BA-21</td>
<td></td>
</tr>
<tr>
<td>Pereira, Roberto M.</td>
<td>23</td>
<td></td>
</tr>
<tr>
<td>Perera, Omatthage P.</td>
<td>89, 116, BA-22</td>
<td></td>
</tr>
<tr>
<td>Pérez-Martinez, José M.</td>
<td>MC-12</td>
<td></td>
</tr>
<tr>
<td>Periquet, Georges</td>
<td>119</td>
<td></td>
</tr>
<tr>
<td>Perlman, Steve J.</td>
<td>2, 84-STU</td>
<td></td>
</tr>
<tr>
<td>Perumal, Pachiappan</td>
<td>NE-2</td>
<td></td>
</tr>
<tr>
<td>Philipp, Jasmin</td>
<td>80-STU</td>
<td></td>
</tr>
<tr>
<td>Pijalman, Gorben P.</td>
<td>59</td>
<td></td>
</tr>
<tr>
<td>Piot, Niels</td>
<td>49</td>
<td></td>
</tr>
<tr>
<td>Polanczyk, Ricardo A.</td>
<td>BA-9, MC-8</td>
<td></td>
</tr>
<tr>
<td>Pond, Michelle</td>
<td>DB-3</td>
<td></td>
</tr>
<tr>
<td>Ponnuraj, Jeyakumar</td>
<td>44</td>
<td></td>
</tr>
<tr>
<td>Pontieve, Cindy</td>
<td>118</td>
<td></td>
</tr>
<tr>
<td>Poppinga, Lena</td>
<td>DB-1-STU, DB-2-STU</td>
<td></td>
</tr>
<tr>
<td>Possee, Robert D.</td>
<td>56, VI-16-STU</td>
<td></td>
</tr>
<tr>
<td>Potin, Olivier</td>
<td>75</td>
<td></td>
</tr>
<tr>
<td>Potvin, Léna</td>
<td>BA-12</td>
<td></td>
</tr>
<tr>
<td>Prabhuraj, A.</td>
<td>139</td>
<td></td>
</tr>
<tr>
<td>Praça, Lilian</td>
<td>BA-6</td>
<td></td>
</tr>
<tr>
<td>Pupin, Breno</td>
<td>FU-7-STU</td>
<td></td>
</tr>
<tr>
<td>Purse, Beth</td>
<td>47</td>
<td></td>
</tr>
<tr>
<td>Pushparaj, Charlotte</td>
<td>141</td>
<td></td>
</tr>
<tr>
<td>Qi, Jiaheling</td>
<td>137-STU</td>
<td></td>
</tr>
<tr>
<td>Queiroz, Paulo</td>
<td>BA-6</td>
<td></td>
</tr>
<tr>
<td>Quitugua, Roland J.</td>
<td>140</td>
<td></td>
</tr>
<tr>
<td>Raad, Maya</td>
<td>129-STU</td>
<td></td>
</tr>
<tr>
<td>Rabalski, Lukasz</td>
<td>VI-3-STU, VI-6</td>
<td></td>
</tr>
<tr>
<td>Rämert, Birgitta</td>
<td>FU-26</td>
<td></td>
</tr>
<tr>
<td>Rangel, Drauzio E. N.</td>
<td>FU-7-STU</td>
<td></td>
</tr>
<tr>
<td>Rännbäck, Linda-Marie</td>
<td>FU-26</td>
<td></td>
</tr>
<tr>
<td>Raunser, Stefan</td>
<td>90</td>
<td></td>
</tr>
<tr>
<td>Raymond, Ben</td>
<td>4, 128</td>
<td></td>
</tr>
<tr>
<td>Raza, Fahreen</td>
<td>56</td>
<td></td>
</tr>
<tr>
<td>Reddy, Gadi V. P.</td>
<td>FU-13</td>
<td></td>
</tr>
<tr>
<td>Rehner, Stephen</td>
<td>FU-13</td>
<td></td>
</tr>
<tr>
<td>Reineke, Annette</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>Reinoso-Pozo, Yaritzato</td>
<td>161</td>
<td></td>
</tr>
<tr>
<td>Renault, Tristan</td>
<td>155</td>
<td></td>
</tr>
<tr>
<td>Richard, Stefan</td>
<td>VI-4</td>
<td></td>
</tr>
<tr>
<td>Richtman, Nina</td>
<td>160</td>
<td></td>
</tr>
<tr>
<td>Ridgway, Hayley</td>
<td>131-STU</td>
<td></td>
</tr>
<tr>
<td>Rivas, Federico</td>
<td>FU-20, MC-15</td>
<td></td>
</tr>
<tr>
<td>Rivera, Hugo Fernando</td>
<td>MC-7</td>
<td></td>
</tr>
<tr>
<td>Rizhamadze, Irene</td>
<td>NE-4-STU</td>
<td></td>
</tr>
<tr>
<td>Roberts, Donald W.</td>
<td>110, FU-8</td>
<td></td>
</tr>
<tr>
<td>Robertson, Mairi</td>
<td>22</td>
<td></td>
</tr>
<tr>
<td>Rocha, Luiz F. N.</td>
<td>FU-14</td>
<td></td>
</tr>
<tr>
<td>Rodrigues de Castro, Thiago</td>
<td>FU-5-STU</td>
<td></td>
</tr>
<tr>
<td>Rodrigues, Juscelino</td>
<td>FU-17-STU</td>
<td></td>
</tr>
<tr>
<td>Romagnoi, E.M.</td>
<td>BA-3-STU</td>
<td></td>
</tr>
<tr>
<td>Rooney, A.P.</td>
<td>BA-3-STU</td>
<td></td>
</tr>
<tr>
<td>Rooney, Alejandro P.</td>
<td>MC-18</td>
<td></td>
</tr>
<tr>
<td>Ros, Vera I.D.</td>
<td>108-STU, 109</td>
<td></td>
</tr>
<tr>
<td>Ross, Stuart</td>
<td>51</td>
<td></td>
</tr>
<tr>
<td>Rostas, Michael</td>
<td>FU-27-STU, MC-15, 129-STU</td>
<td></td>
</tr>
<tr>
<td>Roux, Louise-Marie D.</td>
<td>67</td>
<td></td>
</tr>
<tr>
<td>Roy, Helen</td>
<td>47</td>
<td></td>
</tr>
<tr>
<td>Royalty, Reed N.</td>
<td>27</td>
<td></td>
</tr>
<tr>
<td>Ruan, Lifang</td>
<td>BA-21</td>
<td></td>
</tr>
<tr>
<td>Ruiz de Escudero, Inigo</td>
<td>BA-16</td>
<td></td>
</tr>
<tr>
<td>Ruiz, Carolina</td>
<td>78</td>
<td></td>
</tr>
<tr>
<td>Ruiz, Gregory M.</td>
<td>48</td>
<td></td>
</tr>
<tr>
<td>Ruiz-Vega, J.</td>
<td>NE-1</td>
<td></td>
</tr>
<tr>
<td>Rusakovich, Georgiy I.</td>
<td>39</td>
<td></td>
</tr>
</tbody>
</table>
Tabashnik, Bruce E. 44
Tabert, Matilda VI-4
Taka, Hitomi VI-19-STU
Tanaka, Shiho 11, BA-20-STU
Tang, Li 96-STU
Tao, Xue Ying VI-18
Tay, Wee Tek 10
Taylor, Bryony 75
Taylor, Nick 51
Teng, Chao-Yi 88
Teng-Nelson, Kathy
Theilmann, David A. 53-STU, VI-8, VI-15, 150, 151
Thomas, Matthew B. 74
Thompson, Stephan MC-6-STU
Tokarev, Yuri S. 39, MI-4
Toprak, Umut 34-STU, 149
Torchin, Mark E. 48
Torp, Torfinn 132
Townsend, Richard
Treat, Scott
Turlings, T.C.J.
Tyler, Charles R.

Uchida, Haruaki 115
Uda, Momoka VI-20-STU
Undorf-Spahn, Karin

Vaaje-Kolstad, Gustav
Vacari, Alessandra M.
Vachon, Vincent
van Aerle, Ronny
van der Werf, Wopke
van Houte, Stineke
van Oers, Monique M.
Vaquero, Maclean
Vera-Velasco, Natalia M.
Verbruggen, Bas

Verdejo, Eva Fortea BA-12
Vidal, Stefan 21, 111
Villamizar, Laura FU-19, VI-7, VI-12, VI-13
Visnovsky, Gabriel 141
Vlak, Just M. 33-STU, 59, 114, DB-5
Vogel, Heiko 32 - STU
Volkoff, Anne-Nathalie 119

Wasag, Bartosz VI-6
Waterfield, Nick 93
Wei, Y.J. 158
Weill, Mylène VI-5-STU
Weis, Michael 150
Weiss, Louis M. 9
Wennmann, Jörg T. 37-STU, 69, VI-10-STU
Werner, Manuel 80-STU
Wessman, Per MC-15
West, Michelle BA-11-STU
Westrum, Karin FU-23-STU, 132
Whelan, Thomas A. 41-STU
Wiebe, Craig 133
Wilches, Diana BA-4-STU
Williams, Adam K. 10
Williams, Bryony A. P. 8, 40-STU
Williams, Thomas 40-STU
Willis, Leslie G. 150  
Wilson, Derick 138  
Wilson, Michael MC-1, 138  
Wiredu-Boakye, Dominic 40-STU  
Wirth, Margaret C. 156  
Wisch, Luca N. MC-5-STU  
Woo, Soo Dong DB-6-STU, DB-7, DB-8-STU, FU-10-STU, FU-28, VI-21-STU, VI-22-STU  
Wright, David 138  
Wright, Glenda M. 67  
Wu, Kongming BA-5  
Wu, Shaohui 123, FU-13  
Wu, Songging 17  
Wu, Tzongyuan 121  
Wu, Yidong BA-5  

X  
Xiao, Gengfu 120  
Xiao, Yutao MC-11-STU  
Xie, Weiping 16  
Xiong, Yueting 17  
Xu, Xiaoping BA-12  
Xu, Zhuoying 17  

Y  
Yamamoto, Takashi 16, 159  
Yanagawa, Aya 135  
Yang, Kai 60  
Yaroslavtseva, O.N. MC-19  
Yin, Yunqiang 91  
Ying, Pang BA-13-STU, VI-18  
Ying, Sheng-Hua 94  
Yoshiga, Toyoji NE-6-STU  
Yoshimura, Tsuyoshi 135  
You, You 16  
Young, Sarah 38  
Yuan, Meijin 60  
Yuan, Yu BA-15  

Z  
Zeng, Qiandong 38  
Zenner, Annemie 127  
Zhang, Chunlu BA-19  
Zhang, Feiping 17  
Zhang, Jie 61  
Zhang, Lingling 17  
Zhang, Long-Bin 96-STU  
Zhang, Nan BA-19  
Zhang, Ni BA-21  
Zhang, Tiantao 163  
Zhang, W. F. BA-8  
Zhang, Xuewen 61  
Zhang, Y. 158  
Zhang, Yanfang 55  
Zhang, Zhe 133  
Zhao, Haizhou 60  
Zhao, Jian-Zhou 160  
Zheng, Jinshui BA-21  
Zheng, Shuning DB-4  
Zheng, Yi 159  
Zhong, Silin 70  
Zhou, Fengqiao 55  
Zhou, Y. BA-8, 158  
Zhu, Jing 97-STU  
Zhu, Xiaoli 17  
Ziemnicka, Jadwiga VI-3-STU  
Zou, Shuangquan 17  
Zucchi, Maria I. FU-2  
Zydenbos, Sue MC-1
Acknowledgments

Your conference bag was sewn by the Common Thread Co-op, Vancouver, BC (www.commonthreadcoop.ca) from upcycled street banners donated from British Columbian municipalities. Please enjoy and re-use it.

The SIP 2015 Meetings Logo was created by Laura Ulrich, a lover of both art and science and a Simon Fraser University student in Burnaby British Columbia. Having almost completed her B.Sc. in Biological Sciences, she is planning on attending the University of Toronto in Mississauga to study in the Biomedical Communications graduate program. Her blog, Monsters and Molecules (https://monstersandmolecules.wordpress.com), is a crossroads between art and science as she shares her journey to become a professional scientific illustrator. The logo was inspired by the Canadian west coast’s geographical splendor and First Nations cultural heritage. The totem pole is based on one of the nine found in Vancouver’s Stanley Park, telling a story through the characters they depict.

Thanks to those for contributing their skills and time to the conference

Joanna Wong  Patrick Savage  Alexandra Toner  Sophie Ruau  Erica Li-Leger
Lucas Witsch  Joyce Leung  Leon Li  Heather Coatsworth  Markus Clodius
Joyce Lam  Harprit Khakh  Luke Kho  Elizabeth Ruberg  Amanda Lemky
Coel Ediger  Amanda Abbot  Yan Han  Justin Foslien  Matilda Tabert
Jorge Macias  Anthony Illiev  John Konyk  Cheryl Erlandson  Martin Brown
Less Willis  Mairi Robertson  Steve Freeman  Bryan Elder  Jane Theilmann
Chris Hinz  Michelle Franklin
The Society for Invertebrate Pathology acknowledges the support of the following: