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Prevention of Honey Bee COlony LOSSes
COLOSS

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Virus Task Force

Proceedings

Halle (Saale), Germany, 5-6 march 2019

Virus Task Force

Topic

- Advances in honeybee virus research (oral presentations)
- Papers under writing
- Preparation of COLOSS meeting in Montreal (Canada)

When

- 5-6 march 2019

Where

- Halle (Saale), Germany

Schedule

5 march 2019

9:00–9:30	Welcome and participant introductions
9:30-10:00	Robert Paxton
10:00–10:30	Coffee/snack break
10:30-13:00	Declan Schroeder Tabea Streicher Anja Tehel Orlando Yanez Nor Chejanovsky
13:00-13:30	Lunch
13:30-15:30	Virus distribution (review discussion)
15:30-16:00	Coffee/snack break
16:00-18:00	Virus distribution (review discussion continued)
19:00-	Social dinner

6 march 2019

8:30-8:45	Bee Lab tour
8:45-10:00	Transmission routes Discussion on the Review paper
10:00-10:30	Coffee/snack break
10:30-12:00	(review continuation)
12:00-13:00	Lunch
13:00-16:00	Reviews completion
16:00- 17:00 END	General discussion, summary and perspectives

ORGANIZER CONTACTS		
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Abstracts

Abstract 1

Ongoing virus research at the University of Halle

(1) Robert J. Paxton
(1) Martin-Luther-University Halle-Wittenberg

I will give an overview of current research projects underway in my group, General Zoology MLU Halle, that address the ecology and evolution of bee-virus interactions.

Abstract 2

Viral host-adaptation of Deformed wing virus to Apis mellifera versus Bombus terrestris

Tabea Streicher
Martin-Luther-University Halle-Wittenberg

Several RNA viruses, which are known to negatively affect the health of managed honey bees (Apis mellifera), are nowadays commonly found in many wild bee species and thus pose a potential threat to the community of pollinators. One of the most commonly found viruses is Deformed wing virus (DWV). Furthermore, negative effects of a DWV infection on Bombus spp. have been detected.

To investigate whether DWV adapts to B. terrestris, we serially passaged replicate lineages of honey bee derived DWV (genotype B) through B. terrestris and, as a reference, through A. mellifera. To test for local adaptation to the respective host, we reciprocally cross-inoculated the final passages in white-eyed pupae of both host species. Pupal mortality and wing deformities of eclosed bees were used as parameters of virus virulence whilst roughly 8 % of the DWV-B genome was sequenced to search for genetic changes that might underpin local adaptation.

A significant increase in viral titre and several parallel evolved nucleotide changes occurred in the independently evolved viral lines in A. mellifera, which suggests local adaptation of DWV-B to the selective regime we imposed on the virus. However, adaptation generally came without a significant increase in virulence (pupal mortality, wing deformities).

Serial passaging DWV-B through B. terrestris caused an initial drop followed by a significant increase in viral titre with ensuing passage, suggesting local adaptation to the new host environment. However, viral sequences showed no genetic difference from the starting inoculum. When B. terrestris selected lines were used to infect A. mellifera, virulence was not diminished. These findings suggest that viral adaptation to B. terrestris came without a cost to the virus in its original host. They further support the current hypothesis that DWV is a multihost pathogen.

Abstract 3

Superinfection Exclusion in Swindon honey bees

Declan Schroeder
University of Minnesota & University of Reading

The arrival of the Varroa mite is often linked to colony losses as it has the ability to vector harmful pathogens, of which Deformed wing virus (DWV) is the one most often associated with Varroa. DWV is currently made up of three master variants, DWV Type A, B and C. Moreover, these master variants can recombine with each other with potentially lethal or protective outcomes for colony health. We recently hypothesized that recombination between DWV master variants protected honey bees from a lethal DWV variant through a process known as Superinfection Exclusion (SIE). Here we report on the outcome of moving Swindon honey bees (type B dominated) into a type A dominated environment. Colony survival and diversity of DWV infection overtime will be presented.

Workshop Summary

The Coloss Virus Task Force is a group of researchers that focusses on viruses infecting the honeybee (*Apis mellifera*) worldwide. The first meeting held in Avignon in 2017 was the starting point of discussions that lead to the writing of two literature reviews on the topic. The first manuscript will give an overview of the viruses infecting the honeybee: describing the diversity of known viruses, their virulence and effects on the host, their distribution as well as the temporal dynamics involved. The second manuscript will focus on the routes of transmission of these viruses, whether within one species or between species of bees (social and solitary). The meetings of the Virus Task Force are also a good opportunity to share expertise and results on virus research.

The workshop started with a morning of presentations by guests and members of the host group (Prof. Robert Paxton, Insect Evolutionary Ecology Group, University of Halle-Wittenberg, Germany). Robert Paxton as well as Tabea Streicher and Anja Tehel, two of his students, gave an overview of the virus research held in his lab. Declan Schroeder presented some of his work on Superinfection exclusion and the phylogeny of the *Deformed Wings Virus* strains, Orlando Yanez spoke about viral particles found in hive products such as honey pollen and was, and finally Nor Chejanovsky presented results of metagenomics analysis on the diversity of viruses detected in different *Apis* species (*mellifera, ligustica, syriaca, intermissa, cerana* and *intermissa*) as well as in *Varroa destructor*. All talks were followed by active and stimulating discussions.

An hour was dedicated to a lab tour with the local head technician Anja Miertsch. The lab tour provided the opportunity for discussions on molecular techniques currently used in bee virus research.

The afternoon of 5th march and the whole day of the 6th march were dedicated to updates and discussions concerning the ongoing work of the group on two reviews. All present members agreed to complete their part of the work before a deadline set for September 2019. It was decided that members who were not present and have not been active will have until 30th of April 2019 to revise and comment on the current manuscripts (available on Googledocs). Members failing to reply by the 30th April will be considered as not interested and therefore will be excluded from the list of authors.