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sDiv Workshop

”Synthesizing transcriptome data to explore interspecies bee-pathogen molecular interactions that may underpin pollinator decline”
Trans-Bee

1st workshop – October 10-11, 2013

Summary

Participants

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Presentations and identification of datasets

- Honey bee health: from genes to landscapes (C. Grozinger)
- Interaction between pathogens in the honey bee (V. Doublet)
- Toward a better understanding of host responses to parasites: a focus on bee brain transcriptome (C. Alaux & Y. Le Conte)
- Honey bee pathogen and pathway discovery (M. Flenniken)
- The transcriptome of ageing and immunity in honeybee workers (C. Aurori & R. Moritz)
- Viruses in fire ants: from the field to the lab and genomics of infection (F. Manfredini)
- How to solve a problem like *Varroa* (J. Bull)
- Disentangling multiple interactions in the hive ecosystem (F. Nazzi)
- Immune priming in bumblebees: a transcriptomic perspective (M. Lattorff)
- Gene expression differences underlying genotype-by-genotype specificity in bumblebees infected with *Crithidia bombi* (S. Barribeau)
- Ultra-deep profiling of alternatively spliced *Drosophila* Dscam Isoforms (A. Gogol-Doering)
- The green hourglass (I. Grosse)
- Galaxy tools for analyzing bee's transcriptome (O. Bedoya Reina)
- The *Drosophila* model, possibilities and limitations (D. Hultmark)
- Gene expression in honeybees is dramatically altered by deformed wing virus and not microsporidia (D. McMahon & E. Niño)

Focal areas of discussions

From the original idea of analyzing all available bee gene expression data sets in response to pathogens, we re-defined the question to the 'response of the honey bee to *Nosema* and viruses'. We will begin with comparisons of data sets examining virus effects to determine if there are conserved sets of genes or GO pathways regulated across the different studies, despite large differences in experimental and analytical methodology among the studies. We will subsequently move on to comparisons of *Nosema* data sets. Ultimately, we can compare gene expression responses across viruses and *Nosema* to see which honey bee responses might be unique for specific infections and which might be general responses triggered by various stressors.

From the variety of data sets already available, there are multiple differences which could reduce the similarities in the transcriptional responses. We may be able to evaluate the relative contribution of these different factors to variation in transcriptional responses. The variables that differ between the studies include: the genetic background of honey bees; the tissues used for transcriptome; the stage of the bees (larvae, pupae or adults); the time post-infection; the platforms for data collection (microarray vs. sequencing) or the lab that performed the experiment.

A second aim of this project was to create a pipeline for future gene expression studies in honey bees. This pipeline would provide the tools and guidelines for analyzing the data and make easier the comparison with past studies, including data sets used for Trans-Bee. However, because of many issues discussed during this workshop (singularity of datasets, different platforms that require different normalization methods, constant improvement of mapping to the reference genome), it was suggested to compile general recommendations and suggestions for future honey bee transcriptomic studies. These recommendations can be incorporated into a manuscript the Trans-Bee group will submit to a peer-reviewed journal at the end of the project. This 'guidance' would cover a wide range of issues identified during this workshop, such as:

- ✓ The use of individual vs. pool of bees for transcriptomic studies.
- ✓ The timing post infection for transcriptomic studies. What a time course transcriptome would show? What is the ontogeny of immune response across time?
- ✓ The number of replicates per treatments.
- ✓ Mapping methods.

Outputs and plan for the near future

The first workshop allowed a refinement of the original question, focusing on the response of honey bees to two globally spread pathogens (*Nosema* spp. and viruses), for which a significant amount of data has been collected by participants. The presentation and sharing the datasets and their analysis were also discussed. Moreover, the discussions highlighted the need for general recommendations for analysis of transcriptome data in honey bees that will be generated in the future.

The plan for the next months is (i) the collection of all datasets in a single format, and (ii) the analysis of two separate set of gene expression data: one in response to *Nosema*, and one in response to viruses. The second Trans-Bee workshop is now schedule for **April 28-29, 2104**.

Balance

Presentations: 33%
Discussions of presentations: 33%
General brainstorming: 33%

Collaborations

This project set the basis of a strong collaboration between bee biologists and the bioinformatic team of iDiv. New projects related to the Trans-Bee questions were started.