

sDiv Workshop

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

2nd workshop – April 28-29, 2014

Summary

The primary objective of the Trans-Bee project is to bring together data generators and data analysts to synthesize results on the impact of pathogenic organisms on the honey bee transcriptome, with the aim of providing a functional analysis of this host's response to microbial challenge. For further details on the project and to read the report of the first Trans-Bee workshop, please follow the link: <http://www.idiv-biodiversity.de/sdiv/workshops/workshops-2013/stransbee>.

Participants

- Robert J. Paxton (Martin-Luther-University Halle-Wittenberg, Germany / Project applicant)
- Christina M. Grozinger (Penn State University, USA / Project applicant)
- Vincent Doublet (Martin-Luther-University Halle-Wittenberg, Germany / sDiv Trans-Bee postdoc)
- Mark Brown (Royal Holloway University of London, UK)
- Seth M. Barribeau (ETH Zurich, Switzerland)
- James C. Bull (Swansea University, UK)
- Michelle Flenniken (Montana State University - College of Agriculture, USA)
- Elke Genersch (Länderinstitut für Bienenkunde, Hohen Neuendorf, Germany)
- Andreas Gogol-Doering (iDiv, Germany)
- H. Michael G. Lattorff (Martin-Luther-University Halle-Wittenberg, Germany)
- Dino P. McMahon (Martin-Luther-University Halle-Wittenberg, Germany)
- Francesco Nazzi (Università de Udine, Italy)
- Elina L. Niño (Penn State University, USA)
- Katja Nowick (University of Leipzig, Germany)
- Yvonne Poeschl (iDiv Leipzig, Germany)
- Ronald Van Rij (Radboud University Nijmegen, Nijmegen, the Netherlands)

Presentations by new participants

- “Ongoing transcriptomic studies in bumblebees and their parasites” (by Mark Brown)
- “Viral, bacterial and fungal pathogens of honey bees” (by Elke Genersch)
- “Antiviral defense in flies and mosquitoes: RNAi and beyond” (by Ronald Van Rij)

Focal areas of discussions

The first morning of the workshop was dedicated to presentation of the results of the analyses undertaken in the previous six months. Shortly, these analyses generated the lists of genes obtained from two distinct ways of data exploration: a rank product analysis and a local context finder based analysis. These two separate and complementary analyses provided lists of genes highly regulated by pathogens across studies (rank product) as well as clusters of genes specifically regulated, even if only slightly, by tissue and or pathogen (local context finder).

After presentation of the results, participants discussed the complementarity of the two analyses and suggested some modifications to improve upon them. In addition, major concerns of the participants for the generation of the results were the origin of the datasets and the wide range of parameters that could

influence the results: the platform used to collect the data (microarray vs. sequencing), the age and physiology of bees used in experiments (nurse vs. forager), the tissue used for library preparation (brain, gut, abdomen). New analysis (PCA, see below) and a specific comparison of our results with well characterized transcriptomes from nurse and forager bees available in the literature are now considered.

Outputs and plan for the near future

Potential new datasets have been identified that may be included in the analysis. All datasets will be then re-analyzed together, taking into account the improvements suggested by participant (e.g. increase the number of genes used for analysis by allowing missing value in the rank product analysis, create new clusters for the local context finder analysis (e.g. cluster expression values of genes responding to virus AND Varroa)).

After the acquisition of the new results, the new gene lists will be analyzed using GO terms as originally planned (1st workshop) to provide a functional analysis of the genes regulated by the pathogens. Three additional analyses of the data will be performed. First, a PCA (Principal Component Analysis) of the expression data across the studies will be used to identify the variables (pathogen, tissue used for transcriptome, platform for data collection, duration of the experiment, etc..) that influence most the data. Second, the over-representation of transcription factors in our gene lists and the identification of regulated genes with common promoter binding regions will be tested. Third, the evolutionary rate of immune genes regulated by specific pathogens vs. immune genes regulated by all pathogens or non-regulated immune genes will be compared. These analyses – directly or indirectly – will help us to discriminate between systemic and specific immune responses of honey bees (using online tools such as OrthoDB or ImmunoDB).

Finally, the participants discussed how this work could result in the generation of a manuscript. A timeline for the future analysis and the writing of the manuscript was set up, with a deadline of ms submission by the end of this year. The Trans-Bee participants aimed to submit this work to a journal specialized in genomics, with open access so that the wider scientific community can benefit from the project.

Balance

Presentations: 33%

Discussions of presentations: 33%

General brainstorming: 33%

Collaborations

This second workshop permitted us to identify new datasets from a new collaborator to include in the study.