University of Victoria | Graduate Studies

Notice of the Final Oral Examination for the Degree of Master of Science

of

MARK HANSON

BSc (University of Victoria, 2013)

"Immune Evolution in the Immigrans-Tripunctata Clade of *Drosophila*"

Department of Biology

Monday, December 14, 2015
10:00 A.M.
Hickman Building
Room 120

Supervisory Committee:
Dr. Steve Perlman, Department of Biology, University of Victoria (Supervisor)
Dr. Louise Page, Department of Biology, UVic (Member)
Dr. Caroline Cameron, Department of Biochemistry and Microbiology, UVic (Outside Member)

External Examiner:
Dr. Carl Lowenberger, Department of Biological Sciences, Simon Fraser University

Chair of Oral Examination:
Dr. David Scott, Department of Philosophy, UVic

Dr. David Capson, Dean, Faculty of Graduate Studies

Abstract

Drosophila melanogaster has been integral to unravelling the mechanisms of animalian immunity. The diversity of sequenced *Drosophila* have also been used to characterize how immune systems respond to natural selection. However, *Drosophila* is an incredibly speciose lineage, especially so in the subgenus Drosophila. Of the 12 genomes sequenced in 2007, ushering in the era of *Drosophila* comparative genomics, only three were subgenus Drosophila flies, and none from the lesser-characterized Immigrans-Tripunctata clade. Recently, multiple Immigrans-Tripunctata clade *Drosophila* have been sequenced, including the transcriptome of *Drosophila neotestacea*. I investigated the realized immune responses of *D. neotestacea*, to characterize the immune repertoire of this divergent lineage. The signalling pathways of *D. neotestacea* were largely conserved, though there are interesting patterns of evolution in antimicrobial peptides (AMPs). One of these AMPs, a diptericin, was highly dissimilar to diptericins in *D. melanogaster*, and conserved in other subgenus Drosophila flies. This prompted me to characterize the evolution of the diptericin gene family in *Drosophila*. I found that *Drosophila* diptericins have evolved under positive selection, and display intriguing differences in net charge to well-conserved diptericin domains. I assessed the expression profile of this divergent *D. neotestacea* diptericin, and found that it did not respond to *Serratia* bacterial challenge, unlike diptericin in *D. melanogaster*. I also highlight a potential novel drosocin-like AMP conserved throughout the subgenus Drosophila. These results agree that signalling pathways are highly conserved in diverse insects, including *Drosophila*. However seemingly-conserved effectors of the *Drosophila* immune response (such as AMPs) may have previously unappreciated variation in expression and function.