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Title:	Identification & Characterization of conserved microRNAs in Drosophila immune responses
Authors:	<a href="#">Bhatt, Saurabh</a>
Keywords:	Identification & Characterization Drosophila immune microRNAs
Issue Date:	Apr-2022
Publisher:	IISER Mohali
Abstract:	<p>The microRNAs are small non coding RNAs of length ~ 20-22 base pair and are involved in post- transcriptional regulation of gene regulation. They associate with a protein known as Argonaute to form RNA-induced silencing complex (RISC) which repress or degrade mRNAs in a sequence dependent manner. Many miRNAs are known to play key role in many important cellular processes such as metabolism, differentiation, immune system etc. Their role in both innate and adaptive immune responses is very well studied in the past decade. However, not much is known about their role in insect innate responses. Drosophila melanogaster and Bombyx mori provide a good model to study innate immune responses. Being part of closely related order, they can also be used to determine conservation in the role of miRNA in innate immune responses. The current work unravels 79 miRNAs are conserved between the two species with sequence identity of &gt;95%. Major immune response in Drosophila includes hemolymph and fat body. The current work demonstrates that 30 miRNAs out of the 79 are found to be expressing in the hemolymph of Drosophila under normal conditions. Expression of five miRNAs is also validated in Drosophila larval fat body. Infecting Drosophila larvae with gram-negative bacteria like E. coli induces Imd signaling pathway in which the antimicrobial peptide (AMP), Diptericin (Dpt) is up- regulated. The level of up-regulation depends on the time for which the larvae are incubated. Initial expression analysis shows that the levels of miR-184-5p are downregulated during E. coli infection. But several technical issues need to be addressed before this can be established.</p>
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