

# D3389: miRNAs in multiple developmental stages in western corn rootworm (*Diabrotica virgifera virgifera*) revealed by deep sequencing

**Tuesday, September 27, 2016**

**09:00 AM - 05:00 PM**

📍 *Convention Center - West Hall C*

**Introduction:** The western corn rootworm (WCR), *Diabrotica virgifera virgifera*, is a major maize (*Zea mays* L.) pest insect, leading to more than \$1 billion annual losses in the United States. To understand the interactions between WCR and host plants and develop efficient pest control methods, the study of gene expression regulation in WCR is urgent. MicroRNAs are non-coding small RNAs that play important roles in post-transcriptional regulation of gene expression across a wide variety of organisms.

**Methods:** In this study, we sequenced small RNAs (17-30 bp) from multiple life stages of WCR. In total, sequencing yielded 8 to 23 million reads from seven samples (egg, three larval instars, pupae, adult males and females).

**Results/conclusion:** The peak of miRNA length was 21nt. After filtering, the 57-80% remaining reads were mapped to the miRNA hairpin sequences of *Tribolium castaneum*. Further analysis revealed 68 miRNA candidates across all developmental stages of WCR. However, using the preliminary genome sequence of WCR, novel miRNAs have not yet to be identified.

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