

Sequencing the Navel Orangeworm (NOW) Genome to Identify Genes Associated with Detoxification and Insecticide Resistance

Project Leader: May R. Berenbaum/Hugh Robertson

Dept. of Entomology, University of Illinois, 505 S. Goodwin, Urbana, IL 61801-3795
(217) 333-7784, maybe@illinois.edu

PROJECT SUMMARY

Objectives:

- Sequence the navel orangeworm (NOW) genome using Illumina sequencing and manual annotation.
- In addition, continue research on characterizing cytochrome P450 genes that may potentially influence insecticide resistance, as well as research on manipulating the rate of detoxification using phytochemicals present in almonds.

Background and Discussion:

This research effort uses affordable next-generation sequencing techniques to characterize the entire genome of the navel orangeworm, *Amyelois transitella*, and in doing so can provide an immense and useful set of tools for identifying gene targets for biorational chemical control of this pest.

Sequencing the genome will characterize all detoxification enzymes (cytochrome P450s, carboxylesterases and glutathione-S-transferases) that contribute to insecticide detoxification and phytochemical metabolism. This work will provide a rational framework for

insecticide choices and enable growers to optimize their insecticide use and reduce chemical inputs into almond production.

In addition, research will characterize chemosensory protein genes (e.g., odorant binding proteins, olfactory receptors, gustatory receptors) that mediate host finding and larval feeding. This information will aid in the development of oviposition and larval feeding disruption strategies that will further reduce insecticide input; we hope that this work, once completed, will be of use to the entire almond industry and to associated researchers.

To date, we have conducted the first round of genome sequencing, which will yield contigs that represent most of the genome. We are now moving on to generating long-insert genomic libraries that when sequenced will provide the connections needed to link these contigs into scaffolds, which will represent most of the genome in large pieces, suitable for automated gene modeling and annotation.

Lastly, work continues from last year's project (10-ENTO1-Berenbaum) on characterizing cytochrome P450 genes that may potentially influence insecticide resistance, as well as research on manipulating the rate of detoxification using phytochemicals present in almonds

Project Cooperator: Joe Siegel, USDA/ARS, Parlier

For More Details, Visit

- Poster location 36, Exhibit Hall, Session 3; or on the web (after January 2012) at AlmondBoard.com/AICposters
- 2010 - 2011 Annual Report CD (10-ENTO1-Berenbaum); or on the web (after January 2012) at AlmondBoard.com/ResearchReports
- Related Projects: 11-ENTO11-Siegel/Walse