

Sequencing the Navel Orangeworm Genome

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Introduction

Sequencing the navel orangeworm (*Amyelois transitella*:NOW) genome will allow for innovation in management of this pest. Gene-level knowledge of physiological and behavioral processes in NOW will aid development of more effective management methods.

Targets include:

1. Phytochemical and pesticide detoxification genes.
2. Chemosensory protein-encoding genes, which mediate host plant orientation, oviposition, and pheromone detection.



Methods

An adult female NOW from a laboratory colony (J. Siegel:USDA) was submitted for high-throughput ILLUMINA sequencing. The genome will be assembled using the short-read assembly program SOAPdenovo. Annotation of detoxification and chemosensory genes will be carried out manually.

Results to Date

The NOW genome size is about 400 Mb and has reduced polymorphism. Currently, we have two lanes of 180bp paired-end ILLUMINA reads, and two lanes of 1.5kb shotgun reads. We have constructed a preliminary scaffolded assembly.

Preliminary Examination of Data

The NOW genome shows remarkably reduced polymorphism, which should greatly aid genome assembly. The estimated 400 Mb genome size is comparable to another sequenced lepidopteran genome, the 432 Mb of *Bombyx mori*, the silk moth.

Future Research

1. Continued improvement of assembly by generating paired-end reads from longer fragments, expecting 30x coverage.
2. Post-assembly, automated genome-wide construction of gene models.
3. Examination of genome for local impact: detoxification and chemosensory genes in the context of NOW biology.

Acknowledgments

We thank the Almond Board of California for research funding, Joel Siegel of USDA-ARS for specimens and guidance.