Developments in the Navel Orangeworm Genome

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Introduction

The sequencing and annotation of the navel orangeworm (*Amyelois transitella*:NOW) genome is well underway. The NOW genome project will allow for innovation in management of this pest. Discovering the genetic basis of pesticide tolerance and host-plant preference aids development of more effective control strategies. Because variation in genes coding for detoxification enzymes can increase pesticide tolerance and host-plant range, these genes can be identified as potential control targets. We focused on discovering the range of detoxification enzymes in the NOW genome, particularly the cytochrome P450 enzymes, which are known to increase pesticide and phytochemical tolerance.

Results to Date

The NOW genome size is estimated to be 400 Mb, with low polymorphism. The current assembly coverage depth is 36X. Manual gene annotation is underway, with focus on detoxification genes. Midgut RNA sequencing shows several 1:1 orthologs to *Bombyx mori* P450 genes transcribed in this tissue. Of these, several NOW-specific blooms are visible, particularly in the CYP6 family.

Figure 1. Comparative estimated size of lepidopteran genomes. Data based on C-value or genome project assemblies for *A. transitella, B. mori, D. plexxipus,* and *H. melpomene.*

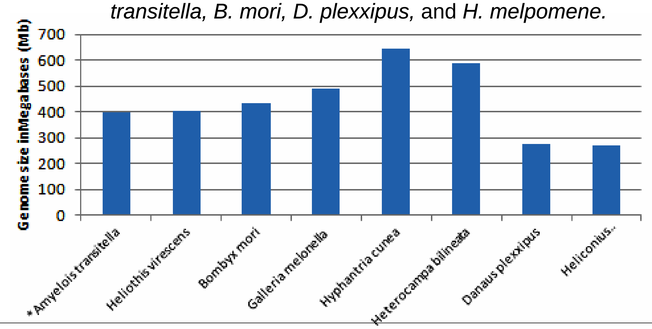
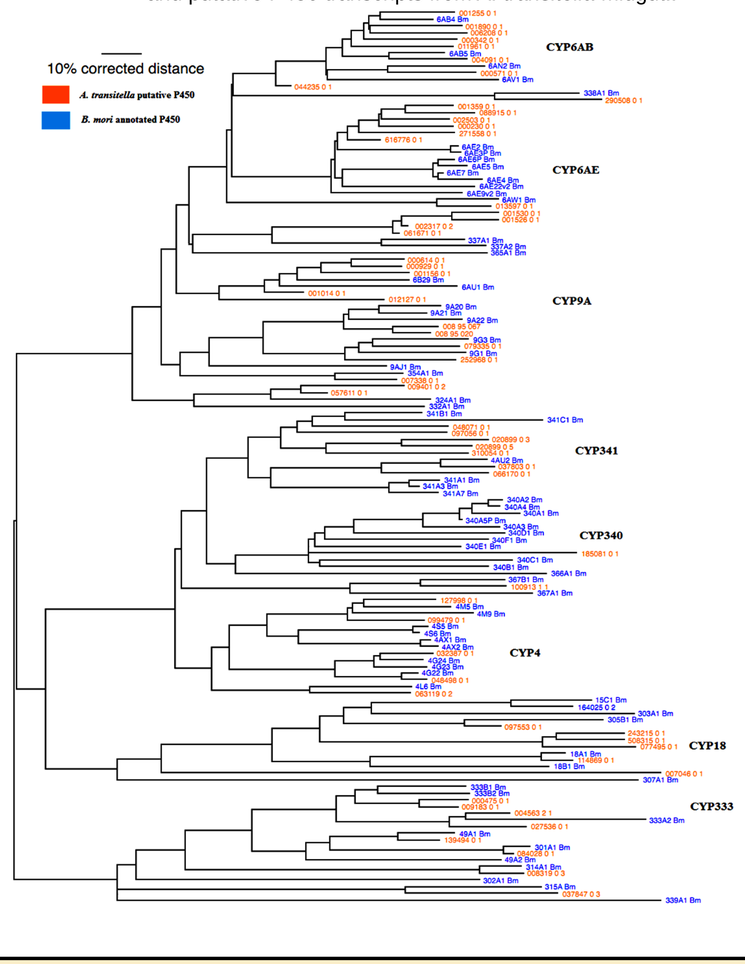


Figure 2. Corrected Distance tree of *B. mori* annotated P450 genes and putative P450 transcripts from *A. transitella* midgut..



Discussion

The NOW genome shows remarkably reduced polymorphism, which should greatly aid genome assembly. The estimated 400 Mb genome size is comparable to other lepidopteran genome sizes. Putative P450 genes transcribed in the midgut are orthologous to others implicated in pesticide, furanocoumarin, and aflatoxin detoxification. These detoxification genes are logical targets for further study, as their nucleotide variation may affect pesticide effectiveness.

Methods

An adult female NOW from a laboratory colony (J. Siegel:USDA) was submitted for high-throughput ILLUMINA sequencing. Resulting reads were assembled using the program SOAPdenovo. Construction of a 10kb mate-pair library will allow for longer- range scaffolding and assembly improvement. Annotation of detoxification and chemosensory genes is being carried out manually. This is complemented by a midgut RNA transcription dataset from ILLUMINA RNAseq. Reads were assembled *de novo* using Trinity and were compared against a database of annotated lepidopteran P450 genes for sequence similarity.

References

Feyereisen, R., 2011. Arthropod CYPomes illustrate the tempo and mode in P450 evolution. Biochim. Biophys. Acta 1814: 19-28.?

Acknowledgments

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