Genome-wide scans and transcriptomic analyses characterize selective changes as a result of chlorantraniliprole resistance in Plutella xylostella

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Abstract

Pesticide resistance in insects is an example of adaptive evolution occurring in pest species and is driven by the artificial introduction of pesticide. The diamondback moth (DBM), Plutella xylostella L. (Lepidoptera: Plutellidae), has evolved resistance to various insecticides. Understanding the genetic changes underpinning the resistance to pesticides is necessary to the implementation of pest control measures. For this reason, we sequenced the genome of 6 resistant and 6 susceptible DBMs, and inferred the genomic regions of greatest divergence between strains using two indices, Fst and $\vartheta\pi$. Among several genomic regions potentially related to insecticide-resistance, a P450 gene, CYP6B6-like, was observed with significant divergence between the resistant and susceptible strains, with, among other SNPs, a missense mutation located near the substrate recognition site (SRS). To characterize the relative effects of directional selection via insecticide tolerance ('strain') as compared to acute exposure of insecticide ('treatment'), four pairwise comparisons were carried out between libraries to determine the differentially expressed genes (DEGs). Most resistant-related DEGs were identified from comparison between strains, and enriched in pathways for exogenous detoxification including cytochrome P450 and ABC transporter. Further confirmation came from the weighted gene co-expression network analysis (WGCNA), which indicated that genes in the significant module associated with chlorantraniliprole-resistance were enriched in pathways for exogenous detoxification, and that CYP6BG1 represented a hub gene in this module. Our study thus provides a genetic foundation underlying selection for pesticide resistance and plausible mechanisms to explain fast evolved adaptation through genomic divergence and altered gene expression in insects.

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