

**Molecular mechanisms of insecticide resistance in the
glasshouse whitefly, *Trialeurodes vaporariorum***

Submitted by

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Abstract

The whitefly *Trialeurodes vaporariorum* Westwood (Hemiptera: Aleyrodidae) is a serious pest of protected vegetable and ornamental crops in most temperate regions of the world. Neonicotinoids, pymetrozine (a feeding blocker), spiromesifen (a tetrionic acid derivative), bifenthrin (a pyrethroid), and pyriproxyfen (a juvenile hormone mimic) are among the most important insecticides used to control this species.

Bioassays were used to quantify responses of recently-collected strains of *T. vaporariorum* to three neonicotinoids (imidacloprid, thiamethoxam, and acetamiprid), pymetrozine, spiromesifen, bifenthrin, and pyriproxyfen. 454 pyrosequencing was exploited to generate the first transcriptome for this species. PCR-sequencing was used to identify mutations in the target proteins of spiromesifen and bifenthrin potentially associated with resistance to these compounds. Microarray sequencing technology was employed to investigate differences in gene expression associated with pyriproxyfen resistance.

Resistance to neonicotinoids was age-specific in expression and consistently associated with resistance to pymetrozine, supporting a hypothesis of metabolic resistance analogous to that in the tobacco whitefly, *Bemisia tabaci*. Bioassays also showed moderate to high level resistance to spiromesifen, bifenthrin and pyriproxyfen in some strains. Analysis of the transcriptome identified genes encoding enzymes involved in the detoxification of xenobiotics (cytochrome P450s, carboxyl/cholinesterases, and glutathione-s transferases) and ones encoding insecticide targets: acetyl-coA carboxylase (ACCase), the target of spiromesifen and the voltage-gated sodium channel protein targeted by pyrethroids. PCR-sequencing revealed a single nucleotide polymorphism in the ACCase gene, which was consistently associated with spiromesifen resistance. Three amino-acid substitutions in the sodium channel of pyrethroid-resistant *T. vaporariorum* were found in positions previously implicated in pyrethroid resistance in *B. tabaci*. Microarray sequencing disclosed that a cytochrome P450 gene (*CYP4G61*) was overexpressed in a strain selected for increased pyriproxyfen resistance. The implications of these results and opportunities for further work are discussed.

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