MONITORING INSECTICIDE RESISTANCE IN FIELD POPULATIONS OF THE TARNISHED PLANT BUG USING BIOCHEMICAL AND MOLECULAR APPROACHES

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The extensive and dominant implementation of transgenic cottons, that express Bt toxins for control of lepidopterous pests, have greatly reduced early-season insecticide use for these pests. The tarnished plant bug was a secondary pest on cotton before the introduction of Bt cotton. It has become an economically important pest in recent year in the Mid-south areas. Due to the lack of effective biological control agents, control of tarnished plant bugs in cotton has relied almost exclusively on chemical insecticides, especially the pyrethroids and organophosphates. During the last a few years, many plant bug populations in Arkansas, Louisiana, and Mississippi have developed high resistance to pyrethroid insecticides. To combat pyrethroid resistant plant bug, extension specialists have recommended the use of a series of chemical insecticides, a variety of organophosphorus insecticides. Recently, organophosphate insecticides, such as malathion and acephate, have had reduced efficacy against the tarnished plant bug.

Evolution of insecticide resistance is usually the result of the elevated detoxification enzyme activities that quickly hydrolyze and degrade insecticides in resistant insects. Increased detoxification enzyme production and activity are mostly associated with elevated gene expression and occasionally with gene mutation. In this study, we developed biochemical and molecular approaches to survey and monitor insecticide resistance in the tarnished plant bug.

Bioassay results have shown that esterase and glutathione S-transferase (GST) inhibitors significantly synergize the toxicity of organophosphorus insecticide. Esterase and GST inhibitors have also significantly suppressed esterase and GST enzyme activities *in vitro*. Field populations collected from Mississippi, Louisiana, and Arkansas were subjected to enzyme activity assays with α-naphthyl acetate (1-NA), β- naphthyl acetate (2-NA), ρ-nitrophenyl acetate (PNPA), 1-chloro-2,4,-dinitrobenzene, and acetylthiochroline. Results showed relatively big variations of esterase and GST activities and relatively low variation of acetylcholine esterase activity in the different field populations. A total of 5 esterase cDNAs were cloned and sequenced by using cDNA library and RT-PCR. Real-time PCR examinations of esterase gene expressions revealed different esterase gene expression profiles in different field populations.