# Proteomics for Insect- Pest Management in Cotton

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## ABSTRACT

Cotton production worldwide is severely threatened by a range of insect pests, leading to significant yield losses and economic impact. Traditional pest control methods, including chemical pesticides, face limitations such as resistance development, environmental concerns, and non-target effects. Proteomics — the large-scale study of proteins, their structures, and functions — offers a powerful tool for advancing insect-pest management strategies in cotton. By analysing the protein profiles of both pests and cotton plants under biotic stress, researchers can identify key molecular targets involved in pest resistance, host-pathogen interactions, and stress responses. This knowledge enables the development of innovative approaches such as pest-resistant genetically engineered cotton varieties, novel biopesticides, and improved Integrated Pest Management (IPM) practices. This article explores the current advances in proteomic technologies applied to cotton pest management, highlights major discoveries, and discusses future prospects for harnessing proteomics to create sustainable and effective pest control solutions.

## INTRODUCTION

Insect pest management is a critical aspect of cotton cultivation, as insect pests like the cotton bollworm complex and in sucking pest like whiteflies, aphids etc., can cause significant yield losses. Traditional pest control strategies, such as chemical insecticides, have drawbacks including resistance development, environmental concerns, and effects on non-target organisms. As a result, sustainable pest management approaches, like the use of proteomics, are gaining attention.

Proteomics is the large-scale study of proteins, which are the functional molecules in cells. By analysing the proteome (the complete set of proteins expressed in a cell, tissue, or organism at a given time), scientists can gain insight into the biological processes and pathways that are active in pests and their interaction with cotton plants. This knowledge can be leveraged to develop targeted strategies for pest management, including the identification of new molecular targets for pest control or enhancing plant resistance to pests.

**Host- pest interactions**

Higher plants successfully colonize herbivore-rich environments by developing complex anti-herbivore feeding mechanisms. When plants detect physical or chemical signals from insects, such as oral and oviposition secretions, they can alter their proteins and metabolites in response. The primary defence pathways involve jasmonate (JA), ethylene, and salicylic acid, with the JA signalling pathway playing a particularly crucial role in plant resistance. In cotton plants, JA mediates defences against pests like *Helicoverpa armigera* and influences the growth of *Aphis gossypii*. Upon herbivory, cotton plants activate defence proteins such as protease inhibitors, lectins, and pathogenesis-related proteins. Proteomic studies have been instrumental in identifying these changes, revealing that cotton plants produce protease inhibitors in response to *Helicoverpa armigera* feeding. These inhibitors interfere with the insect's digestive enzymes, impairing its ability to process plant material and thus hindering its growth.

*Adelphocoris suturalis* Jakovlev is the primary field pest in *Bt* cotton cultivated areas. Lu *et al.* (2024) studied the cotton defence mechanisms triggered by *A. suturalis* feeding by utilizing LC-QTOF-MS. They analyzed cotton metabolomic changes induced by *A. suturalis*, and identified 496 differential positive ions (374 upregulated, 122 downregulated) across 11 categories, such as terpenoids, alkaloids, phenylpropanoids, flavonoids, isoflavones, etc. Integrated metabolome and proteome analysis highlighted significant upregulation of 17 (89%) proteases in the α-linolenic acid (ALA) metabolism pathway, concomitant with a significant increase in 14 (88%) associated metabolites. Conversely, 19 (73%) proteases in the fructose and mannose biosynthesis pathway were downregulated, with 7 (27%) upregulated proteases corresponding to the downregulation of 8 pathway-associated metabolites.

The cotton leaf hopper is a major pest in cotton, causing a hopper burn in leaves. In this study, Alagarsamy *et al.* (2024) compared the proteomic analysis of NDLH2010 (Resistant) and LRA5166 (Susceptible) varieties, infected with leaf hopper, was employed using a nano LC-MS/MS approach. A total of 1402 proteins varied significantly between leaf hopper-infected and control plants. The resistant and susceptible genotypes had differentially expressed proteins (DEPs) of 743 and 659, respectively.

The cotton bollworm (*Helicoverpa armigera*) is a major pest that damages cotton bolls, leading to significant crop and productivity losses. Despite its impact, the cotton plant's response to bollworm infestation is not fully understood. Kumar *et al.* (2016) conducted a genome-wide study of cotton bolls infested with bollworms using transcriptomic and proteomic approaches, validating their findings with semi-quantitative real-time PCR. The study revealed that 39% of the transcriptome and 35% of the proteome were differentially regulated during infestation. Notably, 36% of regulated transcripts and 45% of proteins were involved in signalling and redox regulation. Defence-related hormones and signalling molecules were activated, while growth-related processes were suppressed. About 26% of up-regulated proteins were linked to defence, while over 50% of down-regulated proteins were related to photosynthesis and growth. The study also found increased expression of biosynthesis genes for jasmonate and ethylene, along with suppression of salicylate, indicating a shift toward defence-focused hormone regulation. These insights highlight a selective mechanism that prioritizes defence over growth, offering potential for developing bollworm-resistant cotton varieties.

### Insect proteomics

When feeding on a resistant cotton plant, insects produce specific proteins to overcome the plant's defences and survive. The expression of these proteins varies between different insect species and can also differ depending on the cotton variety. Insects that successfully adapt to these cotton varieties will form a resistant population. Suppressing or silencing the genes responsible for protein expression eliminates the resistant insect population.

Singh *et al.* (2024) studied the proteome data of four different developmental stages of cotton mealybug. Differential expression of proteins (DEPs) was studied among six different groups of which, maximum DEPs (550 up-regulated and 1118 down- regulated) were obtained when the quantifiable proteins of Egg+first nymphal were compared with second nymphal instar. From this proteomics data fifteen potential target genes were predicted for insect pest management. Further, these fifteen genes were explored and evaluated the for RNAi based pest control and optimisation of dsRNA delivery system in cotton mealybug.

## CONCLUSION

Proteomics offers a powerful tool for advancing insect pest management in cotton by providing insights into insect physiology, resistance mechanisms, and plant-insect interactions. By leveraging this knowledge, researchers can develop targeted pest control strategies that are sustainable, environmentally friendly, and effective in combating insect pests in cotton cultivation. This approach could reduce reliance on chemical insecticides and contribute to the long-term sustainability of cotton production.

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