Agri Articles
(e-Magazine for Agricultural Articles)
Volume: 05, Issue: 06 (NOV-DEC, 2025)
Available online at http://www.agriarticles.com
©Agri Articles, ISSN: 2582-9882

Proteome Profiling of Insect Saliva under Pathogen Influence

Apoorva Nautiyal, Arshi Zeba, Saumya Makhloga, Gedela Venkata Hima Sameera and *Ishika Joshi
College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand, India
***Corresponding Author's email: ishikajoshi486@gmail.com**

Sap-feeding insects like aphids, whiteflies, and leafhoppers act as key carriers of plant pathogens and are responsible for major yield losses across global agriculture. The efficiency of pathogen transmission is governed by intricate biological interactions between the vector insect, the pathogen, and the host plant. Among these interactions, insect saliva is particularly important, as it enables feeding from vascular tissues and directly mediates pathogen delivery into plants. Growing research indicates that plant pathogens can reprogram the salivary proteome of their insect vectors, modifying effector molecules, detoxification enzymes, and immunity-related proteins, to promote longer feeding periods and improve their acquisition and transmission. Progress in advanced proteomic technologies such as LC-MS/MS and quantitative labeling platforms has allowed scientists to accurately identify salivary proteins whose expression changes during infection and determine their specific roles in vector competence. This knowledge enhances our understanding of the molecular processes that govern disease spread and provides new intervention points for vector management. Technologies like RNA interference, CRISPR-mediated gene disruption, and host plants engineered for effector-triggered immunity can be designed to target crucial salivary components that pathogens rely on. This article summarizes current findings on how pathogens reshape salivary protein profiles in insect vectors, the functional consequences of these changes, and their relevance in crop protection. Incorporating salivary proteomics with modern molecular control approaches can support the development of precise, environmentally friendly strategies that reduce dependency on chemical pesticides and strengthen global food security.

Keywords: Vector competence, LC-MS/MS, Quantitative proteomics, Salivary effectors

Introduction

Insect vectors are central to the spread of numerous destructive plant pathogens, such as viruses, bacteria, and phytoplasmas, that severely affect crop productivity across the globe. The ability of these pathogens to move from one plant to another depends on a delicate and dynamic relationship between the vector insect, the pathogen, and the host plant (Hogenhout *et al*., 2008). A key player in this interaction is insect saliva, which supports the insect's feeding process by helping the stylet penetrate plant tissues, suppressing host defense reactions, and enabling efficient access to nutrient-rich phloem and xylem (Elzinga & Jander, 2013).

Many plant pathogens transmitted by sap-feeding insects have evolved ways to manipulate saliva composition to ensure their own successful acquisition and spread. These pathogens can alter the expression and activity of salivary proteins in the vector, influencing feeding behavior, weakening host immune responses, and creating an environment that favors their multiplication and transmission (Bosque-Pérez & Eigenbrode, 2011). Recent assessments of insecticide performance against sucking pests (Devi *et al*., 2024) emphasize

the importance of understanding vector feeding biology, including salivary proteome changes that influence pest susceptibility. Therefore, decoding how pathogens reshape the salivary proteome of insect vectors is essential for understanding the mechanisms behind efficient pathogen transmission. Variability in pest pressure observed across seasons in solanaceous crops (Singh *et al.*, 2023) highlights the dynamic nature of vector feeding behaviour, reinforcing the importance of understanding salivary protein modulation under pathogen influence.

Recent advancements in proteomic tools, such as LC-MS/MS and quantitative labeling techniques like iTRAQ, have made it possible to identify and compare salivary proteins altered during pathogen infection with high accuracy. These molecular insights can pave the way for new, eco-friendly disease management strategies, including RNA interference-based control and plants engineered for resistance against vector manipulation.
This article delves into current advancements in understanding how pathogens influence salivary proteomes in insect vectors, highlights major discoveries from modern proteomic studies, and explores how this knowledge can contribute to improved control of vector-borne crop diseases.

Table 1. Pathogen-Induced Modifications in Insect Salivary Proteome and Their Functional Roles

Vector Insect	Associated Pathogen	Key Salivary Proteome Changes	Functional Effect on Transmission
Aphids (*Myzus persicae*)	Potato leafroll virus (PLRV)	↑ Detoxification & immunity-suppressing proteins	Enhanced phloem feeding and virus acquisition
Whiteflies (*Bemisia tabaci*)	Tomato yellow leaf curl virus (TYLCV)	↑ Virus-binding proteins in saliva	Improved pathogen retention and inoculation
Leafhoppers (*Macrosteles quadrilineatus*)	Aster yellows phytoplasma	Altered effector protein profiles	Facilitated pathogen delivery and vector competence
Planthoppers (*Sogatella furcifera*)	Southern rice black-streaked dwarf virus	↓ Immunity-related salivary enzymes	Increased feeding success and viral spread

↑ Up-regulation; ↓ Down-regulation

Saliva of Hemipteran and Other Vector Insects

Sap-feeding insects such as aphids, whiteflies, leafhoppers, and planthoppers depend on piercing-sucking mouthparts to access nutrients from a plant's vascular system. Their ability to feed successfully is largely driven by saliva, which is produced in specialized salivary glands and delivered directly into plant tissues through the stylet (Miles, 1999). This saliva is typically divided into two main types based on its function: gelling saliva, which hardens to form a sheath that stabilizes the stylet during plant tissue penetration, and watery saliva, which is secreted into the phloem to facilitate sustained sap uptake (Tjallingii, 2006). Salivary secretions contain a wide range of active proteins, including enzymes and effector molecules that manipulate plant physiological processes. These proteins help the insect suppress host immune responses, maintain sap flow, and extract nutrients more efficiently (Elzinga & Jander, 2013). For example, aphid effectors like Mp10 and C002 are known to interfere with jasmonic acid, based defense pathways, enabling insects to feed for extended periods (Bos *et al.*, 2010). In the case of vector insects, saliva also plays a crucial role in transmitting plant pathogens. Many viruses and phytoplasmas hijack salivary components to move between the insect vector and the plant host, making salivary glands important hubs for pathogen accumulation and interaction (Hogenhout *et al.*, 2008). Therefore, decoding the protein composition and functions of insect saliva is key to understanding how these vectors overcome plant defences and facilitate disease spread. With the support of advanced

proteomic approaches, researchers can now identify and analyze these salivary proteins in detail, offering valuable insights into potential targets for disrupting vector feeding and pathogen transmission.

Pathogen-Induced Modulation of Salivary Proteome

Plant pathogens that rely on sap-feeding insects for transmission often manipulate the salivary protein profiles of their vectors to increase the chances of successful spread. Evidence suggests that both viruses and phytoplasmas can enhance the production of certain salivary effectors that weaken plant defence responses and allow insects to feed for longer periods, ultimately improving pathogen uptake and delivery (DeBlasio *et al*., 2021). For instance, Potato leafroll virus has been shown to alter oxidative-stress-related enzymes in aphid saliva, helping the insects gain better access to the phloem. Tomato yellow leaf curl virus similarly adjusts the salivary proteome of whiteflies, boosting the virus's ability to persist in the insect and be transmitted to new plants. In addition, some pathogens suppress immune-associated proteins in vector salivary glands, making the insects more efficient carriers. Collectively, these findings demonstrate how plant pathogens can reprogram vector physiology at the molecular level to enhance disease spread, offering valuable new targets for strategies aimed at breaking the transmission cycle.

Proteomic Approaches Used in Saliva Analysis

Recent developments in proteomic technologies have significantly enhanced our ability to study salivary proteins in insect vectors, even when only tiny sample volumes are available. To collect saliva, researchers commonly use artificial feeding setups, such as parafilm membranes or liquid diet chambers, that encourage insects to secrete watery saliva into a controlled environment. Once collected, protein separation techniques like SDS-PAGE and two-dimensional gel electrophoresis are used to examine overall protein patterns. More advanced instruments, including LC-MS/MS and MALDI-TOF, enable precise identification of individual salivary proteins. For monitoring changes triggered by pathogen infection, quantitative proteomic approaches such as iTRAQ, TMT, and SWATH-MS have become important tools, allowing sensitive comparison of protein abundance across treatments. In addition, bioinformatics pipelines support the prediction of secreted proteins, identification of potential effectors, and mapping of biological pathways linked to transmission. Together, these technologies provide a robust framework for uncovering how plant pathogens alter salivary composition in their insect carriers, offering new opportunities to disrupt pathogen spread at the molecular level.

Implications for Plant Protection

Decoding how plant pathogens reshape the salivary proteome of insect vectors opens new avenues for advanced and eco-friendly crop protection solutions. Proteins in saliva that suppress plant defense responses can act as strategic targets for RNA interference (RNAi), which can interrupt vector feeding behavior and limit pathogen spread. Host-delivered RNAi (HD-RNAi) and gene-editing tools can be engineered to specifically silence salivary protein-coding genes that are essential for pathogen transmission. Additionally, identifying virulence-related molecules secreted in saliva provides valuable information for breeding or genetically enhancing plants to recognize and counter pathogen-assisted feeding, thus boosting resistance to vector-borne diseases. Salivary proteomics also offers applications in surveillance, enabling the detection of early infection stages and assessment of vector competence in agricultural fields. When combined with integrated pest and disease management approaches, these insights contribute to reduced chemical pesticide use, lower environmental impact, and improved crop productivity. Ultimately, salivary proteome research supports the development of forward-looking strategies that protect both farmers livelihoods and global food systems.

Conclusion

Proteomic studies of insect saliva are shedding light on how plant pathogens cleverly reprogram their insect vectors to improve feeding and maximize their chances of

transmission. Alterations in the salivary protein profile can weaken plant defense systems, help insects reach the phloem more easily, and promote efficient pathogen entry into new hosts. These discoveries emphasize the role of insect saliva as a crucial molecular bridge connecting the vector, the pathogen, and the plant and position it as a promising target for novel disease management tactics. As proteomic tools and molecular techniques continue to advance, researchers have growing opportunities to interfere with the transmission cycle using RNAi-based control, genome editing, or crops bred for enhanced recognition of salivary effectors. Incorporating salivary proteomics into vector management research can contribute to the development of more targeted, environmentally friendly, and durable strategies to combat vector-borne plant diseases and improve agricultural resilience.

References

1. Bos, J. I., Prince, D., Pitino, M., Maffei, M. E., Win, J., & Hogenhout, S. A. (2010). A functional genomics approach identifies candidate effectors from the aphid species Myzus persicae (green peach aphid). *PLoS genetics*, *6*(11), e1001216.
2. Bosque-Pérez, N. A., & Eigenbrode, S. D. (2011). The influence of virus-induced changes in plants on aphid vectors: insights from luteovirus pathosystems. *Virus research*, *159*(2), 201-205.
3. DeBlasio, S. L., Wilson, J. R., Tamborindeguy, C., Johnson, R. S., Pinheiro, P. V., MacCoss, M. J., ... & Heck, M. (2021). Affinity purification–mass spectrometry identifies a novel interaction between a polerovirus and a conserved innate immunity aphid protein that regulates transmission efficiency. *Journal of Proteome Research*, *20*(6), 3365-3387.
4. Devi, D. L., Dasari, S., Sujatha, G. S., Mandal, S. K., Teja, K. S. S., Mishra, R., & Kumar, G. A. (2024). Bioefficacy and economics of newer insecticides against sucking insect pests of cowpea. *International Journal of Advanced Biochemistry Research*, SP-8(8), 1043–1047.
5. Elzinga, D. A., & Jander, G. (2013). The role of protein effectors in plant–aphid interactions. *Current opinion in plant biology*, *16*(4), 451-456.
6. Elzinga, D. A., & Jander, G. (2013). The role of protein effectors in plant–aphid interactions. *Current opinion in plant biology*, *16*(4), 451-456.
7. Hogenhout, S. A., Ammar, E. D., Whitfield, A. E., & Redinbaugh, M. G. (2008). Insect vector interactions with persistently transmitted viruses. *Annu. Rev. Phytopathol.*, *46*(1), 327-359.
8. Singh, J. K., Chauhan, S., Kumar, P., & Kumar, R. (2023). Seasonal Incidence of Insect Pests of Tomato (Lycopersicum esculentum Miller). Int. J. Environ. Clim. Change, 13(10), 1369-1375.
9. Miles, P. W. (1999). Aphid saliva. *Biological reviews*, *74*(1), 41-85.
10. Tjallingii, W. F. (2006). Salivary secretions by aphids interacting with proteins of phloem wound responses. *Journal of experimental botany*, *57*(4), 739-745.