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Opinion Article

Systematic Analysis of Changes in the Proteome after Viral Infection

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DESCRIPTION

The interaction of viral and host factors the latter of which dominate their viral counterparts is necessary for the establishment and reproduction of viruses in their host. The sequential influence of viral elements upon host physiology can be revealed by a systemic examination of temporal variations in the expression of host components, revealing crucial viral pathogenesis processes and cues to mitigate them. Transcriptomics, proteomics, and other high-throughput technologies have recently enabled us to acquire significant molecular insights into the relationships between viruses and their hosts. The research also reveals that, in addition to some unique pathways, other viruses also target common pathways and machinery, which serves as the foundation for the development of broad-spectrum antiviral inhibitors or medications. The progressive impact of baculoviral infection on the proteome of Lepidopteran cell line is examined in this study.

Baculoviruses are common in a wide range of biotechnological applications since they are naturally occurring pathogens of over 600 species of insects, the majority of which are Lepidopterans. These are being successfully used as vectors for the expression of thousands of proteins and are also being researched as prospective vectors for gene therapy due to their inability to replicate in mammalian cells. In agriculture and forestry, certain baculoviruses are utilised as effective substitutes for chemical insecticides to control insect pests6. Baculoviruses have a dsDNA genome and reproduce in insect cell nuclei. The life cycle can be roughly divided into three stages: an early stage (0–6 hpi), during which actin-based motility propels the virus in the host nucleus and early viral proteins are transcribed using host RNA polymerase; a late stage (6-24 hpi), during which budded virions are released from the cell envelope and viral DNA is replicated; and a very late stage (>24 hpi), during which the virus forms occlusion bodies in After 18 hours of infection with the Autographa californica Multinucleopolyhedrovirus (AcMNPV), the baculoviral infection causes the host's protein synthesis to cease.

The cutoff of host mRNA expression was then observed between 12 and 18 hours after infection. At various stages of infection, high-throughput transcriptome investigations have revealed differential regulation of a number of host pathways, including stress response, heat shock response, metabolism, protein expression, ER trafficking, etc. However, only a small number of studies have comprehensively examined the impact of baculoviral infection on the host proteome to date. After baculovirus infection at intervals of 6 and 12 hours, the differential proteome of S. frugiperda cells revealed differential regulation of 648 and 413 proteins, respectively. Recent integrated transcriptome and proteomic analyses of Helicoverpa armigera infected fat bodies have revealed the differential regulation of about 450 proteins, particularly those involved in cell metabolism.

The family Coronaviridae of the order Nidovirales contains enclosed single-stranded positive sense RNA viruses known as coronaviruses. They can infect both humans and other animals, such as cows, pigs, mice, and chickens. Typically, they cause respiratory infections, gastrointestinal diseases, and neurological disorders of varied degrees of severity. The first coronavirus to be identified was the Infectious Bronchitis Virus (IBV), which is grouped with the Gamma coronaviruses based on antigenic and genetic similarity. It is a significant poultry infection that is likely endemic in every place where chickens are raised; it has a negative impact on poultry production and results in significant financial losses. All IBV strains have the ability to infect a wide variety of chicken epithelial surfaces, including the trachea, kidney, oviduct, and proventriculus. The host cell's shape, transcription and translation patterns, cell cycle, cytoskeleton, suppression of interferon, and apoptosis pathways are all significantly impacted by coronavirus infection. Inflammation, altered immunological and stress responses, and altered coagulation pathways can all result from coronavirus infection. Such large alterations in the gene expression patterns of host cell hosts are linked to such deep functional and morphological changes in host cells. Microarray technologies have been used in numerous investigations to describe modifications in host gene expression brought on by coronavirus infection. However, viral replication is ultimately controlled by protein expression and Post-Translational Modification (PTM). Transcriptome analyses have a number of drawbacks, including inconsistencies with the levels of expression of the associated proteins and the inability to

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offer information on PTM. Additionally, they only provide a snapshot of gene expression patterns.

Proteomics-based approaches show promise since they can get around some of the problems that transcriptomics-based approaches have. Comparative proteomics analysis has lately become a useful method for determining the host's overall protein profile in response to virus infection. It has been used to research enveloped RNA viruses including influenza, respiratory syncytial, parainfluenza, human metapneumovirus, SARS-CoV, and Mouse Hepatitis Viruses (MHV).

It offers priceless knowledge on the signalling pathways used by cells to either respond to viral infections or manipulate cellular machinery to ensure their own survival.