Global Research journal of Natural Science and Technology (Grjnst)

Volume: 03 - Issue 3 (2025)

p.ISSN: 2790-7643 e.ISSN: 2790-7651

Biochemistry of Plant–Virus Interactions: RNA Silencing, Host Proteins, and Biotechnology-Based Resistance

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Abstract: *Plant–virus interactions involve complex biochemical processes that determine the outcome of infection, resistance, or susceptibility in host plants. This review highlights key molecular mechanisms underlying these interactions, with emphasis on RNA silencing pathways, host protein manipulation, and biotechnology-driven resistance strategies. RNA silencing serves as a primary antiviral defense in plants through siRNAs, miRNAs, and RDR-mediated amplification, while viruses counter this system using viral suppressors (VSRs) that disrupt Dicer activity, AGO function, or small RNA stability. Additionally, viruses exploit host proteins including heat-shock proteins, transcription factors, and post-translational modification machinery to enhance replication and evade immunity. Advances in biotechnology, particularly RNA interference, CRISPR/Cas genome editing, and synthetic biology, offer promising strategies for engineering durable, broad-spectrum virus resistance in crops. Omics technologies further facilitate the discovery of host susceptibility factors, stress-responsive genes, and metabolic shifts associated with viral infection. Together, these molecular insights support the development of innovative and sustainable approaches for plant virus management and improved global crop resilience.*

Keywords: *Plant–virus interactions; RNA silencing; Viral suppressors (VSRs); Host proteins; Antiviral defense; siRNA; miRNA; RDR proteins; CRISPR/Cas; RNA interference (RNAi); Biotechnology-based resistance; Transgenic plants; Omics technologies; Synthetic biology; Viral pathogenesis; Plant immunity; Virus–host co-evolution; Gene editing; Plant defense mechanisms; Molecular plant pathology.*

1. Introduction

There are many reasons why studying the biochemistry of plant-virus interactions is important. First of all, plant viruses are a serious threat to crop production all over the world. By understanding the complex molecular interactions that occur between plants and viruses, it is possible to elucidate efficient molecular strategies that can boost the resistance of plants (Ray & Casteel, 2022; Zanardo *et al*., 2019). Wang (2015) state that these interactions modify the physiological cell processes of the plant so that protein synthesis, nutrient allocation, and immune responses are altered by the virus and by the plant as well in order to help with survival and replication (Osterbaan & Fuchs, 2019). By investigating these interactions at a biochemical scale, we can uncover mechanisms underlying virus-host co-evolutionary dynamics. Both mutualistic and antagonistic interactions can take place in it. Viruses and their vectors use effectors to alter plant physiology which helps the virus or trigger phytovirus immunity (Ray Casteel, 2022). Studying the biochemistry of plant-virus interactions also involves understanding how viruses interfere with plant hormone pathways that regulate growth and defenses. Viruses typically change hormones in plants.

This helps the behaviour of plants. Also, this provides support to the reproduction and dispersal of viruses (Islam *et al*., 2019). By manipulating this hormone, we can learn how to enhance defenses in plants against viruses. Recent technological advancements in transcriptomics and proteomics offer advanced and effective tools to identify new virus-associated functional components. This dynamic development facilitates a molecular characterization of plant responses. These help to recognize host factors that viruses use for replication and movement, which could lead to genetic interventions such as gene editing for virus-resistant crops (Gomaa *et al*., 2024; Souza *et al*., 2019; A. Wang, 2015). Plant virus interactions with host plant are different from the other plant pathogen systems. This is because of a number of peculiar features. Unlike the fungi and bacteria that secrete effector proteins to manipulate plant processes, viruses mainly modulate host cellular mechanisms, such as RNA silencing. When viruses infect plants, the plants mount a complex resistance response that includes RNA silencing and systemic resistance. Furthermore, it can trigger hypersensitive responses the contain the virus to cells that are already infected (Henry *et al*., 2013; S. Zhang *et al*., 2022)

Many viruses' pathogens transmission is assisted by insect vectory involvement. The plant, virus and vector interaction is very complex. Usually, there are mutualistic interactions. In these, the virus and the vector manipulate plant immunity for their own benefit. On the contrary, some pathogens such as fungi party involve the plant tissue or get into it through environmental means, usually with the involvement of soil fauna (Ray & Casteel, 2022). Although viral effectors are present, their action is different from the other effectors from bacterial or fungal pathogens. Paraphrased (40 words): Transcription factors and plant protein degradation pathways are frequent targets of these viruses. However, unlike fungal or bacterial effectors, which interfere with plant physiological activities in the cell, these viruses manipulate them differently (Jameson, 2000; Ray & Casteel, 2022). In many cases, virus infects a plant and causes a complex impact from stunting to chlorosis. They cause changes in the levels of hormones such as cytokinins and auxins causing the seeds to act in a way that benefits the virus (Jameson, 2000).

2. RNA Silencing Mechanisms

Plants possess a naturally occurring defense mechanism against viruses known as RNA silencing. This antiviral response aims for specific destruction of viral RNA, effectively blocking virus replication. This defense uses short interfering RNAs (siRNAs) to direct Argonaute proteins to the viral RNA, leading to its cleavage and suppression (Lopez-Gomollon & Baulcombe, 2022; Vance & Vaucheret, 2001). RNA silencing has the amazing ability to target both RNA and DNA viruses. RNA degradation pathways are another strategy often mediated by RNA-dependent RNA polymerases (RDRs) (Vaistij & Jones, 2009; M.-B. Wang *et al*., 2012). DNA viruses can also be inhibited by RNA-directed DNA methylation pathways which will prevent their transcription and therefore their replication (M.-B. Wang *et al*., 2012). In addition to degrading viral RNAs, RNA silencing in plants can interfere with viral replication and promote antiviral defense through reprogramming epigenetic modifications upon infection by viruses (C. Wang *et al*. 2019).

United States Navy, Italian Navy and Royal Navy, through permits and control in the government, and access to payment channels, much to some competition and government interference and all. VSRs can interfere with various steps of the RNA silencing pathway. They often do this binding with the RNA silencing proteins or the siRNA. Thus, the plant defence gets neutralized (Kontra *et al*., 2016; M.-B. Wang *et al*., 2012). Studies have shown the strong effectiveness of RNA silencing as a defence mechanism against viruses. The existence of specialized RNA silencing pathways that involve the functions of proteins such as Dicer-like 2 (DCL2), Argonaute 2 (AGO2) and other essential proteins activation that strongly enhances virus

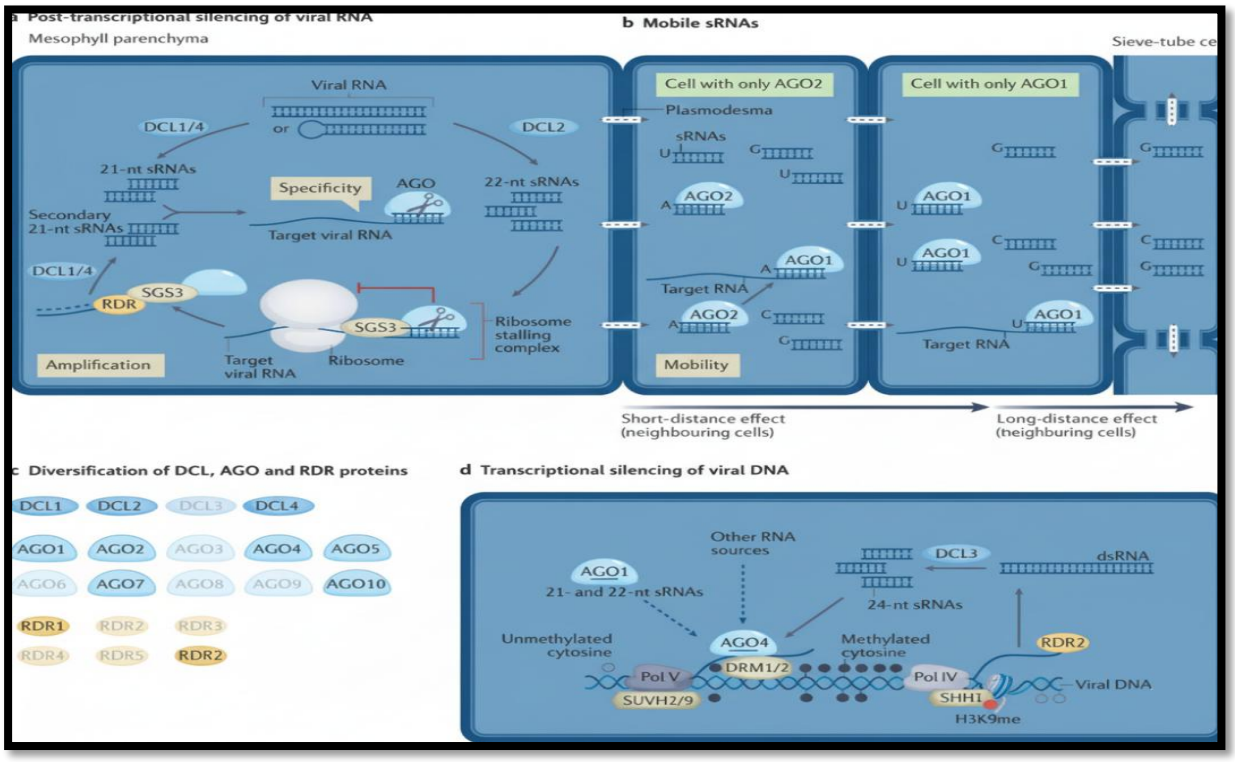
replication but protects plants from lethal viral infection (X. Zhang e al., 2012). Moreover, RDR6 and others generate secondary siRNAs. This amplifies silencing and increases viral resistance. The deficiency of these genes makes the host susceptible to viral infections (F. Li *et al*., 2014).

The Small interfering RNA, micro-RNA and RNA dependent RNA polymerase proteins are important for antiviral defenses in various organisms but especially the plants. Here is an overview of their roles in viral resistance. siRNA refers to a molecule that is essential for the antiviral response by means of RNA interference (RNAi). Dicer-like enzymes are responsible for the formation of double-stranded RNA. Post-processing, siRNAs are merged with Argonaute proteins which form the RISC or RNA-induced silencing complex that inhibits the amplification of viruses by degrading the complementary parts of the viral RNA (roughly 32 words). miRNAs can also participate in antiviral immunity but their action differs somewhat from that of siRNAs. miRNAs don't need to match the base pairs perfectly. Thus, they can control many virus-fighting genes. Viruses benefit from antagonizing host factors (like proteins involved in the interferon pathway) to boost their own survival. Certain miRNAs of plants modulate the antiviral pathways by repressing the expression of RDR proteins, that enhances resistance against the viruses (like miR444 in rice; H. Wang *et al*., 2016). RDR Proteins RDRs are helpful in amplifying the RNA silencing signal. In antiviral defense, RDRs help make double-stranded RNA from the RNA genome or transcripts of viruses. This double-stranded RNA is processed into siRNAs. The amplification process strengthens the RNAi response and increases the plants' capacity to resist viral infections (Xie *et al*., 2004). In rice, RDR1 is upregulated by miR444 after viral infection to increase the antiviral RNA silencing of the plant's signaling cascade (H. Wang *et al*. 2016). A wide range of viral suppressor proteins impede RNA silencing through numerous mechanisms that disrupt the host's antiviral defenses. The effect seems particularly pronounced in plant viruses. These proteins (viral suppressors of RNA silencing, or VSRs) use different approaches to suppress the RNA interference (RNAi) pathway. It is the organism's main defence mechanism against virus infections.

Various VSRs such as p19 from *tombusviruses* bind specifically to small interfering RNAs (siRNAs). The binding of the siRNA by the virus prevents the incorporation of siRNA into the RNA-induced silencing complex (RISC), and the degradation of the viral RNA target (Ye *et al*., 2003). Some viral suppressors interfere with Argonaute proteins, the core parts of the RISC, by acting through direct interactions. For instance, the P1 protein of sweet potato mild mottle virus binds to AGO1 and AGO2 but rather specifically inhibits AGO1 by blocking its access to target

RNAs. This stops the RISC's silencing function from taking place (Kenesi *et al*., 2017). Some VSRs act on any molecules in the RNA silencing pathway upstream of Dicing activities. The P38 protein of the turnip crinkle virus can bind to long double-stranded RNAs and inhibit Dicer processing of those double-stranded RNAs into siRNAs, which are involved in the initiation of RNA silencing (Iki *et al*., 2017). Some VSRs like the p126 protein from Tobacco mosaic virus, are modular in that they have other domains, each of which can independently suppress RNA silencing. Different components of the protein can affect different steps of the RNA silencing pathway thanks to the modular nature of this protein. This makes the virus more resistant (L.-Y. Wang *et al*., 201211). Some viral suppressors rely on the presence of host transcription factors to function. According to Endres *et al*. (2010), the suffocation processes of the potyvirus HC-Pro and carmovirus P38 require the host transcription factor RAV2, inducible by ethylene to block primary siRNAs. VSRs usually have more than one function in viruses. These include moving from one cell to another and assisting in genome replication, alongside silencing host RNA. Due to their multifunctionality, they can meet the demands of both viral infectivity and host defense suppression (Atabekova *et al*., 2023).

Figure 2.1 Mechanisms of Antiviral RNA Silencing in Plants: Post-Transcriptional, Mobile, and Transcriptional Pathways



3. Host Proteins and Viral Manipulation

The Viruses use host proteins to replicate and evade immune responses. They do this by strategically selecting proteins in the host. Viruses normally attack several key proteins and processes. Viral and host proteins undergo a variety of post-translational modifications such as acetylation, that alter chromatin structure, transcription as well as signal transduction. According to Xue *et al*. (2022), these changes are involved in virus attachment, entry, replication, assembly, and release. Viruses affect cell proliferation and metabolism by using host proteins for their own biological purposes, driving (directing) Protein-Protein Interactions. It is important for viruses to contact these structures to replicate and disseminate throughout the host (Gerold *et al*., 2017). Heterogeneous Nuclear Ribonucleoproteins (hnRNPs) may pose a therapeutic potential against the virus as they are being targeted. DNA viruses are designed to take control of both the cellular and metabolic processes, while RNA viruses target certain cellular tasks and intracellular transport (Durmuş & Ülgen, 2017).

Viruses targeting host ribosomes and translation factors for viral protein synthesis suggests role of ribosomal proteins in viral life cycle. These proteins are also post-translationally modified, which

subsequently affects the viral RNA translation and the cellular response of a host. Proteins that bind RNA, such as G3BP1, are often targeted to moderate, stability, translation and immune response to mRNA. Viruses can alter G3BP1 function by degrading, sequestering or redistributing it to complete their lifecycle. Viruses take over the host's PTM process to help them survive. Host PTMs can inhibit virus replication by activation of immune responses and inhibition of viral protein synthesis. these also correlate with the activation of antiviral actions (R. Kumar *et al*., 2020).

These different mechanisms show how a virus and its host cells interact. The virus takes advantage of the host's cellular machinery and processes to successfully infect and propagate itself (Durmuş & Ülgen, 2017; Gerold *et al*., 2017; Jayabalan *et al*., 2023; R. Kumar *et al*., 2020; Miller *et al*., 2020; Xue *et al*., 2022). Heat-shock proteins (HSPs), chaperones, and transcription factors facilitate viral replication by playing an important role in essential interactions and modifications. Heat-shock proteins and chaperones are usually involved with the folding, stabilization and degradation of proteins under stressful cellular conditions. Proteins exploited by viruses for replication; for example, tombusviruses were reported to use host heat-shock proteins and chaperones during viral replication process. The proteins form viral replication compartments and can stabilize viral proteins in complexes which are required for replication (Nagy, 2016; Noueiry & Ahlquist, 2003). Further, eukaryotic translation elongation factor 1A (eEF1A), a protein chaperone, is used by different viruses, including HIV and the West Nile virus, for various viral processes, such as transcription, translation, and assembly (D. Li *et al*, 2013).

The transcription factors play an essential role in regulating viral and host gene expression during infection. Some viruses can take over their host's transcription factors to boost the expression of viral genes needed for replication. Certain pathogenic viruses such as herpes simplex virus and Epstein-Barr virus that employ cellular transcription factors for switching from latent to replicative cycle. The switch is mediated by transcription factors that activate the transcription of viral genes, which begins the viral replication cycle (Garcia-Blanco & Cullen, 1991). Further, viruses target transcription factors to modulate the immune pathways of the host. Thereby helping in immune evasion and viral replication (Giraldo *et al*., 2020). Viruses have developed many ways for their benefits. They manipulate different biochemical pathways of their host to benefit. In general, these cells employ strategies to hijack and subvert critical cellular processes and signaling pathways important for host cells. Viruses use ncRNAs to regulate genes of the host and evade immune surveillance. In order to survive and promote cellular transformation, viral non-coding

RNAs may regulate viral replication; target gene expression in the host and avert host immune responses. Viruses hijack the signaling molecules that control many cellular processes. Adjusting G-protein signaling and MAPK pathways, for example, helps manage host cell survival and cytoskeletal dynamics (Alto & Orth, 2012). Some viruses can manipulate Wnt signalling involved in the regulation of the cell cycle and oncogenesis. Viral tactics include changes to epigenetics, targeting of miRNAs, and alteration of Wnt pathway members, which occasionally results in Wnt signalling activation (Van Zuylen *et al*., 2016). Viruses, particularly RNA viruses, have the ability to use host post-translational modification machinery to their advantage. This includes changing the viral proteins so they are soluble and antigenic and evade immune detection. HIV-1 takes advantage of the host proteasomal degradation mechanisms in order to evade immune attacks and promote its own replication within the host. The system is manipulated by them to degrade the nondestructive host proteins of the virus (Lata *et al*., 2018). DNA viruses have developed ways to inhibit the initial defenses of the host. They alter the levels of host defense proteins by changing the transcription of the respective genes and through protein degradation. Further they also exploit cellular pathways to block defensive mechanisms (Crow *et al*., 2016). Many viruses have exploited the host sumoylation system, which is involved in transcriptional regulation, apoptosis, and cell cycle control. According to Wilson (2017), this could improve viral protein function and support viral infection.

TABLE 3.1 – Viral Suppressors of RNA Silencing (VSRs) and Their Targets

Virus	VSR	Target	Inhibition Strategy
Tombusvirus	p19	siRNAs	Sequesters siRNAs
Potyvirus	HC-Pro	AGO1	Blocks RISC function
TCV	P38	DCL processing	Binds dsRNA

TMV	p126	Multiple	Blocks local & systemic RNAi

4. Biotechnological Resistance Strategies

RNA interference in plants is a powerful tool that engineers viral resistance. In this method, double-stranded RNA (dsRNA) is supplied to plants. This sets off a sequence-dependent gene-silencing mechanism that leads to the destruction of the target mRNA (Ali *et al*., 2010). One successful strategy is to produce transgenic plants that express hairpin loop dsRNA of coding sequences for the viral coat protein. This method was applied to potatoes targeting the coat protein genes of the Potato virus X (PVX), Potato virus Y (PVY) and Potato virus S (PVS). The expression constructs are used to produce small interfering RNAs which target the viral RNA for destruction before any infection. This provides immunity that is pre-programmed. Transgenic potatoes produced with this method showed the remarkable ability to resist the three viruses up to nearly 100% over years of cropping. RNA interference also uses the trans-acting small interfering RNAs or tasiRNAs, or an artificial microRNA or amiRNA. They can specifically silence virus RNA or virus RNAi suppressors. One example of RNAi application is the use of tasiRNA targeting RNAi suppressors such as AC2 and AC4 of Tomato leaf curl New Delhi virus (ToLCNDV), which confers robust resistance in transgenic plants (Singh *et al*., 2015).

The RNAi technology is also useful for non-transgenic plant applications. Economic crises can be avoided with strategic intermediate measures (He & Zhang, 2023). Through environmental monitoring, on-site assessments, and continuous observations, early warning systems help manage potential crises (He & Zhang, 2023). RNA-guided CRISPR-Cas systems have been combined with RNAi for the specific editing of viral genomes or host susceptibility genes: a potential way to develop plant virus resistance (Taliansky *et al*., 2021). RNA interference (RNAi) provides a powerful means for engineering plants that resist viruses. However, the success of these methodologies requires accurate identification of target viral genes and effective silencing without adverse effects on the plant. Researchers are constantly looking to improve these processes. They also want to overcome issues that stem from different resistances and issues related to regulation. CRISPR/Cas and genome editing technology are very helpful for fighting viral infections. The CRISPR/Cas9 system was originally identified as a bacterial adaptive immune mechanism. Now, it can be used for targeted genome editing applications. The CRISPR/Cas9 system can be used in virology research and antiviral therapies (Bayat *et al*., 2018; Chen *et al*., 2018). CRISPR/Cas is applied in virology primarily to directly manipulate and disrupt viral genomes. Scientists have

used this technique successfully to investigate and change herpesviruses, HIV, hepatitis B and other viruses of interest. CRISPR/Cas9 system allows targeted, precise mutagenesis, which can help eliminate proviral DNA and viral replication. These strategies can ultimately facilitate the development of treatments for chronic virus infections where conventional means do not work, as noted by C. Lee, 2019; Okoli *et al*., 2018.

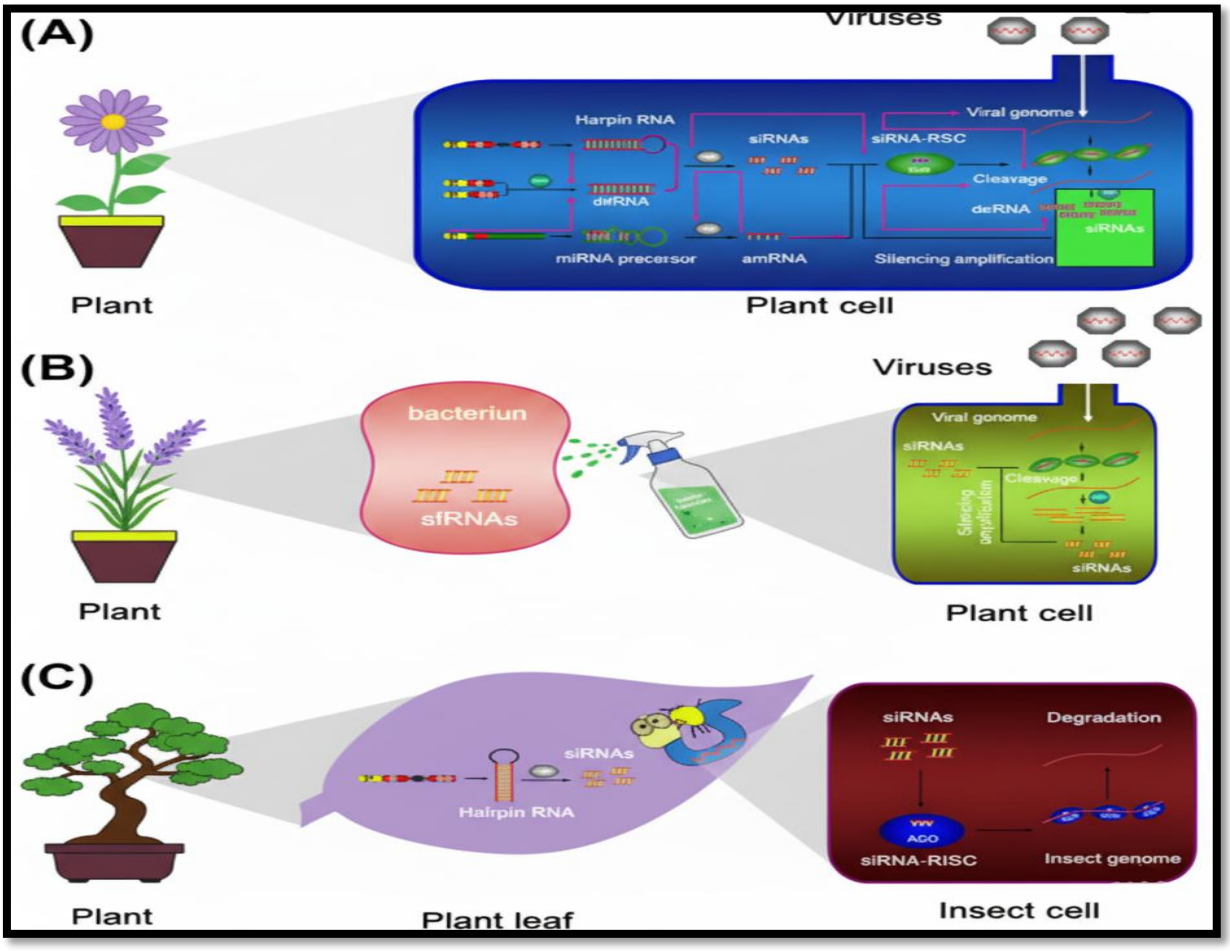
The CRISPR/Cas technology contributes to pathogenic understanding of the viruses and their vaccines' development. Teng *et al*. (2021) suggested the improvement of vaccine vectors and recombinant vaccines through editing orthopoxvirus genomes. The use of CRISPR/Cas systems is also being investigated for their suitability for diagnostics and monitoring the outbreak of disease as they provide efficient tools for rapid detection and planning response to viruses (Bayat *et al*, 2018). The development of CRISPR/Cas technology is further aided by the advancements of delivery systems that allow CRISPR components to be delivered safely and precisely to target cells. Different non-viral delivery systems are being explored for efficient genome editing. Guaranteed biosafety is a prerequisite (Fang *et al*., 2022). Nonetheless, the technology has off-target effect issues and ethical implications. Thus, it should not be permitted unless evaluated by appropriate controls (Ju *et al*., 2017). Creating genetically modified organisms that has traits of native plants helps them defend themselves from pathogens and replicate natural resistance. It is hoped that host-derived resistance genes and trans-genic approaches can confer durable resistance against pests or pathogens in the organisms of concern.

Transgenic approaches, involving the incorporation of new resistance genes into crop plants, have shown considerable potential for enhancing resistance to pests and diseases. Pyramiding the genes in a variety/ hybrid can produce a better result. For example, insecticidal protein-expressing genetically engineered crops possess enhanced resistance against pests from varying orders such as Lepidoptera, Homoptera, and Coleoptera originating from different plant species. Pyramiding, or stacking different resistance genes into one plant, has been suggested to enhance the efficacy and durability of this form of protection (Gatehouse & Gatehouse, 1998). Genes for Host-Derived Resistance. Plant resistance genes have been frequently used for disease control. But the resistance offered by many of these genes is not durable as pathogens quickly adapt to overcome them. The toughness of these resistance genes that impose a fitness cost on pathogens for adaptation can be predicted (Leach *et al*., 2001).

The introgression of these resistance genes, have been done in a susceptible genetic background. The use of polygenic (quantitative) resistance also seems to influence durability

positively. It is likely that polygenic resistance, which combines the effect of several genes giving partial resistance, is more durable than zonogenic resistance (Palloix *et al*., 2009; Pilet-Nayel *et al*., 2017). Non-host resistance is known to be durable as it has a broad spectrum of effectiveness against a large number of pathogens. While transgenic technologies have been used to introduce non-host resistance, it is difficult to develop these traits via conventional breeding (S. Lee *et al*., 2016). A deployment strategy ensures longevity of resistance. Gene pyramiding, sequential use and mixing strategies have been modeled to test their efficacy in the durability of resistance genes. Pyramiding genes combining multiple different genes into a variety—has been identified as the most durable strategy. This is especially the case if the pathogen must mutate to overcome the resistance (Elisabeth Lof *et al*., 2017). For instance, the transgenic tomato plants that express the NPR1 gene from Arabidopsis have shown a high resistance to many fungal and bacterial diseases. These transgenic lines have been stabling over several generations and show the potential of transgenic methods for sustainable crop protection (Lin *et al*., 2004).

Figure 4.1 Applications of RNA Interference (RNAi) in Plant–Virus and Plant–Insect Interactions



5. Applications and Future Directions

Biotechnology-based resistance strategies include the use of genes that enhance resistance to pests, diseases and environmental stresses. One application in this area is the creation of genetically modified (GM) crops that are herbicide-resistant and pest-resistant. Paraphrase this (40 words): Since the commercialization of first biotechnologically derived tomato in 1994, the global area under genetically modified crops enhanced tremendously whereby traits like insect resistance and herbicide tolerance played an essential role in enhancing agricultural productivity and food security (Mall *et al*., 2018).

Crop resilience can be improved by various plant breeding technologies including genetic engineering and genome editing technologies. CRISPR-Cas technology is an example of an innovation that has created crop varieties with resistance to diseases and harsh environments, further increasing yields and sustainability. (Matinvafa *et al*., 2023) Modern biotechnology techniques have been developed that allow for accurate genetic engineering. The use of CRISPR technology can offer promise to produce stress-resilient and high-yield crop varieties (Khan, 2024). Biotechnology has used rapid and precise genetic engineering techniques to enhance diseases resistance in cereals and other crops with clear benefits. These methods help the immune system of crops, providing a rapid and sustainable way to avert disease loss of yields. Agricultural biotechnology has changed the scenario in the case of India by increasing its productivity and socio-economics. According to experts, adoption of GM crops like Bt cotton increased yield, reduced the use of pesticide and improved income. R.K. Kumar *et al*. (2024) further mention that advancements in gene editing technologies, notably CRISPR, help improve crop traits and resilience sustainably. Genetic engineering and genome editing technologies are very important for Africa to tackle its food security challenges and enhance the resilience of crops to various stresses. Efforts such as Nigeria's National Biotechnology Policy have led to the commercialization of biotechnologically enhanced crops and improved agricultural productivity and resilience (Adegbaju *et al*., 2024). The wide application of RNA interference (RNAi) and CRISPR-based technologies in the field has some significant limitations.

TABLE 5.1. Omics Technologies Contributing to Plant–Virus Research

Section: Applications and Future Directions (Omics + Synthetic Biology)

Omics Tool	What it Reveals	Application in Viruses	Benefit

Genomics	Viral/host genes	Host susceptibility genes	Target discovery
Transcriptomics	Gene expression	Viral stress responses	Pathway mapping
Proteomics	Protein interactions	Viral movement proteins	Mechanism insights
Metabolomics	Metabolic shifts	Stress metabolites	Biomarker identification

6. Challenges with RNAi. And CRISPR. Technology

RNAi technologies often face problems with efficiency and specificity. Making sure that the RNAi elements only work on the specified targets without affecting other genes is a global challenge. It is difficult to send RNAi components into the target cell (organism). Researchers are still looking for ways to improve delivery and uptake, as well as stability for use, especially agricultural use (Touzdjian Pinheiro Kohlrausch Távora *et al* 2022). Concerns from the Public and Regulatory Frameworks Like any other biotechnology, the RNAi area is not free of public perception and regulatory issues, especially in terms of guaranteeing public and environmental safety. (Touzdjian Pinheiro Kohlrausch Távora *et al*., 2022)

The ability of CRISPR technology to edit unintended sections of the genome is one of its biggest challenges, popularly called off-target effects. Precision is essential for both plant and human purposes. It is a major concern and has been reported by Hryhorowicz *et al*. in 2023. Like RNAi, the delivery of the CRISPR editing machinery to the cells or organisms to be edited is neither effective nor efficient. The choice of delivery mechanisms and CRISPR systems can affect transformation efficiency (Prado *et al*., 2024). CRISPR technology is subject to intense regulation due to ethical concerns and risk factor related to genome editing mostly with respect to agriculture and human gene therapy (Macarrón Palacios *et al*., 2024; Touzdjian Pinheiro Kohlrausch Távora *et al*., 2022). Species-specific Challenges: The different genome complexities of woody plants can further complicate CRISPR-based solutions to agriculture (Min *et al*., 2022). Omics and synthetic biology have greatly advanced our knowledge of plant-virus biochemical interactions in recent years. They have provided invaluable insights into the complex world of virus attack mechanisms, virus-induced cell changes, and host recognition of virus invasion. Various omics technologies have improved our understanding of molecular mechanisms through which plants respond to viruses and stresses. These technologies include genomics, transcriptomics, proteomics, and

metabolomics (M. Wang *et al*., 2024; Yan *et al*., 2022). The functional analysis of stress-related genes and exploration of metabolic and signalling pathways shall enable a more holistic understanding of plant defence strategies (Murmu *et al*., 2024; Razzaq *et al*., 2021).

The flux of metabolites shows which biochemical pathways change through analysis of metabolite levels, and this analysis gives us accurate estimates of the activities of the population of metabolic pathways. Researchers have identified stress metabolites by observing small molecule profile from plant tissues in response to viral infection (Manickam *et al*., 2023) Combining omics data with synthetic biology has further revolutionized plant virology. Modern technology aids in creation of novel tools for assembling viral infectious clones to aid in functionality characterization of plant viruses, both knew and unknown. With these tools, we can systemically study viruses in relation to their roles in the plant phytobiome and use modified viruses as vectors for gene therapy, leading to engineered crops with enhanced traits (Pasin *et al*., 2019). The study of omics-driven systems biology in synthetic biology may facilitate the development of gene and protein function characterisetion studies for understanding how viruses and plants interact and how this interaction can be modified to enhance plant resistance (Amer & Baidoo, 2021).

7. Conclusion

Merging biochemical expertise with biotechnology is essential for bio-security of viral diseases for following reasons. The merging of Artificial Intelligence Technology and Virology Technology helps in better diagnosis, prevention and treatment of virus. First, biotechnologies help to make new kinds of devices. For example, optical biosensors can help quickly detect viruses that are hard to find. This equipment is necessary for early diagnosis, timely intervention, and prevention of the spread of infectious diseases (Sharma *et al*., 2021). Moreover, next-generation sequencing (NGS) offers the possibility to detect pathogens comprehensively, even in the absence of knowledge of their genome. Thus, it comes as a robust platform for identifying an emerging virus (Gauthier *et al*., 2023).

Besides, vaccine development is improved by biotechnological activities. Progress in genetic engineering along with development of immunostimulants can improve vaccine efficacy and stability against existing and emerging infectious diseases (Abdelaziz *et al*., 2024). Viruses currently affect the global market which is why the development of vaccines is essential. more manufacturing processes can be adapted for the production of biological products owing to

biotechnology. The use of continuous processing models of viral testing and clearance will ensure safety and efficacy of large-scale products. It is essential for the sustainable management of diseases. Understanding how different pathogens interact with each other and host environment can help in developing new antiviral drugs. Nanotechnology combined with biochemistry has resulted in the creation of nanocrystals capable of facilitating targeted drug delivery with improved pharmacokinetics to redress the limitations of available antiviral drugs (Chaturvedi *et al*., 2024). Likewise, knowledge of genetic and molecular basis of viral infection through integrative approaches in bioinformatics and multi-omics can help effective management of these diseases (Elrashedy *et al*, 2025).

Acknowledgment

We would like to express my deepest gratitude to my parents for their unconditional love, constant encouragement, and unwavering support throughout my academic journey. Their guidance and prayers have always been a source of strength and motivation for me. We are also sincerely thankful to my teachers, whose dedication, knowledge, and mentorship have shaped my learning and inspired me to strive for excellence. Their continuous support and valuable guidance played an essential role in the completion of this work.

References

Abdelaziz, K., Yitbarek, A., Helmy, Y. A., Selim, M. S. H., Hodgins, D. C., & Sharafeldin, T. A. (2024). Advances in Poultry Vaccines: Leveraging Biotechnology for Improving Vaccine Development, Stability, and Delivery. Vaccines, 12(2), 134. https://doi.org/10.3390/vaccines12020134

Adegbaju, M. S., Ajose, T., Adegbaju, I. E., Omosebi, T., Ajenifujah-Solebo, S. O., Falana, O. Y., Shittu, O. B., Adetunji, C. O., & Akinbo, O. (2024). Genetic engineering and genome editing technologies as catalyst for Africa's food security: the case of plant biotechnology in Nigeria. Frontiers in Genome Editing, 6. https://doi.org/10.3389/fgeed.2024.1398813

Ali, N., Datta, S. K., & Datta, K. (2010). RNA interference in designing transgenic crops. GM Crops, 1(4), 207–213. https://doi.org/10.4161/gmcr.1.4.13344

Alto, N. M., & Orth, K. (2012). Subversion of cell signaling by pathogens. Cold Spring Harbor Perspectives in Biology, 4(9), a006114. https://doi.org/10.1101/cshperspect.a006114

Amer, B., & Baidoo, E. E. K. (2021). Omics-Driven Biotechnology for Industrial Applications. Frontiers in Bioengineering and Biotechnology, 9. https://doi.org/10.3389/fbioe.2021.613307

Atabekova, A. K., Solovyev, A. G., Solovieva, A. D., Chergintsev, D. A., & Morozov, S. Y. (2023). Role of Plant Virus Movement Proteins in Suppression of Host RNAi Defense.

International Journal of Molecular Sciences, 24(10), 9049. https://doi.org/10.3390/ijms24109049

Barrangou, R., Birmingham, A., Beijersbergen, R. L., Wiemann, S., Smith, A. V. B., & Hornung, V. (2015). Advances in CRISPR-Cas9 genome engineering: lessons learned from RNA interference. Nucleic Acids Research, 43(7), 3407–3419. https://doi.org/10.1093/nar/gkv226

Baulcombe, D. (1999). Viruses and gene silencing in plants. Archives of Virology. Supplementum, 15, 189–201. https://doi.org/10.1007/978-3-7091-6425-9_14

Bayat, H., Naderi, F., Rahimpour, A., Khan, A. H., & Memarnejadian, A. (2018). The Impact of CRISPR-Cas System on Antiviral Therapy. Advanced Pharmaceutical Bulletin, 8(4), 591–597. https://doi.org/10.15171/apb.2018.067

Chaturvedi, A., Shukla, R., & Sharma, S. (2024). Drug Nanocrystals: A Delivery Channel for Antiviral Therapies. AAPS PharmSciTech, 25(3). https://doi.org/10.1208/s12249-024-02754-5

Chen, Y.-C., Sheng, J., Trang, P., & Liu, F. (2018). Potential Application of the CRISPR/Cas9 System against Herpesvirus Infections. Viruses, 10(6), 291. https://doi.org/10.3390/v10060291

Crow, M. S., Lum, K. K., Sheng, X., Song, B., & Cristea, I. M. (2016). Diverse mechanisms evolved by DNA viruses to inhibit early host defenses. Critical Reviews in Biochemistry and Molecular Biology, 51(6), 452–481. https://doi.org/10.1080/10409238.2016.1226250

Durmuş, S., & Ülgen, K. Ö. (2017). Comparative interactomics for virus-human protein-protein interactions: DNA viruses versus RNA viruses. FEBS Open Bio, 7(1), 96–107. https://doi.org/10.1002/2211-5463.12167

Elisabeth Lof, M., De Vallavieille-Pope, C., & Van Der Werf, W. (2017). Achieving Durable Resistance Against Plant Diseases: Scenario Analyses with a National-Scale Spatially Explicit Model for a Wind-Dispersed Plant Pathogen. Phytopathology®, 107(5), 580–589. https://doi.org/10.1094/phyto-05-16-0207-r

Elrashedy, A., Mousa, W., Nayel, M., Salama, A., Zaghawa, A., Elsify, A., & Hasan, M. E. (2025). Advances in bioinformatics and multi-omics integration: transforming viral infectious disease research in veterinary medicine. Virology Journal, 22(1). https://doi.org/10.1186/s12985-025-02640-x

Endres, M. W., Gregory, B. D., Gao, Z., Foreman, A. W., Mlotshwa, S., Ge, X., Pruss, G. J., Ecker, J. R., Bowman, L. H., & Vance, V. (2010). Two Plant Viral Suppressors of Silencing Require the Ethylene-Inducible Host Transcription Factor RAV2 to Block RNA Silencing. PLoS Pathogens, 6(1), e1000729. https://doi.org/10.1371/journal.ppat.1000729

Fang, T., Cao, X., Ibnat, M., & Chen, G. (2022). Stimuli-responsive nanoformulations for CRISPR-Cas9 genome editing. Journal of Nanobiotechnology, 20(1). https://doi.org/10.1186/s12951-022-01570-y

Garcia-Blanco, M. A., & Cullen, B. R. (1991). Molecular basis of latency in pathogenic human viruses. Science, 254(5033), 815–820. https://doi.org/10.1126/science.1658933

Gatehouse, A. M. R., & Gatehouse, J. A. (1998). Identifying proteins with insecticidal activity: use of encoding genes to produce insect-resistant transgenic crops. Pesticide Science, 52(2), 165–175. https://doi.org/10.1002/(sici)1096-9063(199802)52:2<165::aid-ps679>3.0.co;2-7

Gauthier, N. P. G., Chorlton, S. D., Manges, A. R., & Krajden, M. (2023). Agnostic Sequencing for Detection of Viral Pathogens. Clinical Microbiology Reviews, 36(1). https://doi.org/10.1128/cmr.00119-22

Gerold, G., Bruening, J., Weigel, B., & Pietschmann, T. (2017). Protein Interactions during the Flavivirus and Hepacivirus Life Cycle. Molecular & Cellular Proteomics, 16(Suppl 4 1), S75–S91. https://doi.org/10.1074/mcp.r116.065649

Giraldo, M. I., Hage, A., Van Tol, S., & Rajsbaum, R. (2020). TRIM Proteins in Host Defense and Viral Pathogenesis. Current Clinical Microbiology Reports, 7(4), 101–114. https://doi.org/10.1007/s40588-020-00150-8

Gomaa, A. E., El Mounadi, K., Parperides, E., & Garcia-Ruiz, H. (2024). Cell Fractionation and the Identification of Host Proteins Involved in Plant-Virus Interactions. Pathogens (Basel, Switzerland), 13(1), 53. https://doi.org/10.3390/pathogens13010053

Hameed, A., Jander, G., Mansoor, S., Van Eck, J., Bilal, R., Tahir, M. N., & Asad, S. (2017). RNAi-Mediated Simultaneous Resistance Against Three RNA Viruses in Potato. Molecular Biotechnology, 59(2–3), 73–83. https://doi.org/10.1007/s12033-017-9995-9

Henry, E., Coaker, G., & Yadeta, K. A. (2013). Recognition of bacterial plant pathogens: local, systemic and transgenerational immunity. New Phytologist, 199(4), 908–915. https://doi.org/10.1111/nph.12214

Hong, J., Zhang, D., Shi, J., & Yang, L. (2016). Plant Metabolomics: An Indispensable System Biology Tool for Plant Science. International Journal of Molecular Sciences, 17(6), 767. https://doi.org/10.3390/ijms17060767

Hryhorowicz, M., Zeyland, J., & Lipiński, D. (2023). Evolution of CRISPR/Cas Systems for Precise Genome Editing. International Journal of Molecular Sciences, 24(18), 14233. https://doi.org/10.3390/ijms241814233

Iki, T., Tschopp, M.-A., & Voinnet, O. (2017). Biochemical and genetic functional dissection of the P38 viral suppressor of RNA silencing. RNA, 23(5), 639–654. https://doi.org/10.1261/rna.060434.116

Islam, W., Naveed, H., Zaynab, M., Huang, Z., & Chen, H. Y. H. (2019). Plant defense against virus diseases; growth hormones in highlights. Plant Signaling & Behavior, 14(6), 1596719. https://doi.org/10.1080/15592324.2019.1596719

Jameson, P. E. (2000). Cytokinins and auxins in plant-pathogen interactions – An overview. Plant Growth Regulation, 32(2–3), 369–380. https://doi.org/10.1023/a:1010733617543

Jan, A., Adil, S., Ali, T., Ahmed, B., Ahmed, Z., & Hussain, Z. (2025). Desert and medicinal plants as novel sources of antimicrobial agents for crop protection. Planta Animalia, 4(3), 197-218.

Jan, A., Ali, T., Chirag, S., Ahmed, S., Ali, M., Wali, S., ... & Ullah, K. (2025). Eco-Friendly Management of Insect Pests and Plant Diseases Using Botanical Extracts. Global Research Journal of Natural Science and Technology.

Jan, A., Hussain, Z., Ullah, A., Ahmed, Z., Bakhsh, B. P., Latif, A., ... & Ahmed, M. (2025). Sugarcane Whip Smut: A Comprehensive Review of Pathogen Biology, Epidemiology, and Control Measures. Annual Methodological Archive Research Review, 3(5), 211-232.

Jan, A., Razzaq, F., Umair, M., Ullah, I., Shamsullah, S., Uzair, M., Ikram, M., Ayyaz, M., & Ali, T. (2025). Cotton Leaf Curl Disease: Pathogen Diversity, Whitefly Ecology, and Integrated Management Approaches. Planta Animalia, 4(4), 363-371.

Jan, A., Shaikh, G. Y., Ullah, S., Saddam, S., Ali, T., u Rehman, A., ... & Ahmed, M. (2025). In-vitro antifungal activity of medicinal plant extracts against Fusarium oxysporum causing wilt in okra. Indus Journal of Bioscience Research, 3(8), 406-414.

Jayabalan, A. K., Griffin, D. E., & Leung, A. K. L. (2023). Pro-Viral and Anti-Viral Roles of the RNA-Binding Protein G3BP1. Viruses, 15(2), 449. https://doi.org/10.3390/v15020449

Johnson, S. A., Brown, M. R., Lute, S. C., & Brorson, K. A. (2016). Adapting viral safety assurance strategies to continuous processing of biological products. Biotechnology and Bioengineering, 114(1), 21–32. https://doi.org/10.1002/bit.26060

Ju, X., Xu, J., & Sun, Z. S. (2017). CRISPR Editing in Biological and Biomedical Investigation. Journal of Cellular Biochemistry, 119(1), 52–61. https://doi.org/10.1002/jcb.26154

Kenesi, E., Vértessy, B., Carbonell, A., Lakatos, L., & Lózsa, R. (2017). A viral suppressor of RNA silencing inhibits ARGONAUTE 1 function by precluding target RNA binding to pre-assembled RISC. Nucleic Acids Research, 45(13), 7736–7750. https://doi.org/10.1093/nar/gkx379

Khan, N. (2024). Unlocking Innovation in Crop Resilience and Productivity: Breakthroughs in Biotechnology and Sustainable Farming. Innovation Discovery, 1(4), 28. https://doi.org/10.53964/id.2024028

Koeppe, S., Kalischuk, M., & Kawchuk, L. (2023). RNA Interference Past and Future Applications in Plants. International Journal of Molecular Sciences, 24(11), 9755. https://doi.org/10.3390/ijms24119755

Kontra, L., Csorba, T., Turina, M., Tavazza, M., Tavazza, R., Tisza, V., Burgyán, J., Lucioli, A., Moxon, S., & Medzihradszky, A. (2016). Distinct Effects of p19 RNA Silencing Suppressor on Small RNA Mediated Pathways in Plants. PLOS Pathogens, 12(10), e1005935. https://doi.org/10.1371/journal.ppat.1005935

Kumar, R. K., Chitra, M., Kumar, K. R., Alagendran, S., Senthamizhkumaran, V. R., Tyagi, T., & Tyagi, A. (2024). Advances in Agricultural Biotechnology: Enhancing Productivity and

Sustainability in India : A Review. Journal of Scientific Research and Reports, 30(7), 366–383. https://doi.org/10.9734/jsrr/2024/v30i72154

Kumar, R., Nayak, D., Sunil, S., Mehta, D., & Mishra, N. (2020). Role of Host-Mediated Post-Translational Modifications (PTMs) in RNA Virus Pathogenesis. International Journal of Molecular Sciences, 22(1), 323. https://doi.org/10.3390/ijms22010323

Lata, S., Mishra, R., & Banerjea, A. C. (2018). Proteasomal Degradation Machinery: Favorite Target of HIV-1 Proteins. Frontiers in Microbiology, 9(27539). https://doi.org/10.3389/fmicb.2018.02738

Leach, J. E., Bai, J., Vera Cruz, C. M., & Leung, H. (2001). Pathogen fitness penalty as a predictor of durability of disease resistance genes. Annual Review of Phytopathology, 39(1), 187–224. https://doi.org/10.1146/annurev.phyto.39.1.187

Lee, C. (2019). CRISPR/Cas9-Based Antiviral Strategy: Current Status and the Potential Challenge. Molecules, 24(7), 1349. https://doi.org/10.3390/molecules24071349

Lee, S., Whitaker, V. M., & Hutton, S. F. (2016). Mini Review: Potential Applications of Non-host Resistance for Crop Improvement. Frontiers in Plant Science, 7(664). https://doi.org/10.3389/fpls.2016.00997

Li, D., Harrich, D., Wei, T., & Abbott, C. M. (2013). The Unexpected Roles of Eukaryotic Translation Elongation Factors in RNA Virus Replication and Pathogenesis. Microbiology and Molecular Biology Reviews, 77(2), 253–266. https://doi.org/10.1128/mmbr.00059-12

Li, F., Huang, C., Zhou, X., & Li, Z. (2014). Suppression of RNA Silencing by a Plant DNA Virus Satellite Requires a Host Calmodulin-Like Protein to Repress RDR6 Expression. PLoS Pathogens, 10(2), e1003921. https://doi.org/10.1371/journal.ppat.1003921

Lin, W.-C., Lu, C.-F., Yang, N.-S., Wang, J.-F., Cheng, M.-L., Wu, J.-W., Lin, Y.-M., Black, L., Green, S. K., & Cheng, C.-P. (2004). Transgenic tomato plants expressing the Arabidopsis NPR1 gene display enhanced resistance to a spectrum of fungal and bacterial diseases. Transgenic Research, 13(6), 567–581. https://doi.org/10.1007/s11248-004-2375-9

Lopez-Gomollon, S., & Baulcombe, D. C. (2022). Roles of RNA silencing in viral and non-viral plant immunity and in the crosstalk between disease resistance systems. Nature Reviews. Molecular Cell Biology, 23(10), 645–662. https://doi.org/10.1038/s41580-022-00496-5

Ma, J.-B., Ye, K., & Patel, D. J. (2004). Structural basis for overhang-specific small interfering RNA recognition by the PAZ domain. Nature, 429(6989), 318–322. https://doi.org/10.1038/nature02519

Macarrón Palacios, A., Korus, P., Wilkens, B. G. C., Heshmatpour, N., & Patnaik, S. R. (2024). Revolutionizing in vivo therapy with CRISPR/Cas genome editing: breakthroughs, opportunities and challenges. Frontiers in Genome Editing, 6(4). https://doi.org/10.3389/fgeed.2024.1342193

Mall, T., Dhadialla, T. S., Rodrigo, S., & Gupta, M. (2018). Overview of Biotechnology-Derived Herbicide Tolerance and Insect Resistance Traits in Plant Agriculture. Methods in

Molecular Biology (Clifton, N.J.), 1864, 313–342. https://doi.org/10.1007/978-1-4939-8778-8_21

Manickam, S., Kambale, R., Rajagopalan, V. R., Muthurajan, R., Kanagarajan, S., & Rajasekaran, R. (2023). Plant Metabolomics: Current Initiatives and Future Prospects. Current Issues in Molecular Biology, 45(11), 8894–8906. https://doi.org/10.3390/cimb45110558

Matinvafa, M. A., Makani, S., Parsasharif, N., Zahed, M. A., Movahed, E., & Ghiasvand, S. (2023). CRISPR-Cas technology secures sustainability through its applications: a review in green biotechnology. 3 Biotech, 13(11). https://doi.org/10.1007/s13205-023-03786-7

Miller, C. M., Fuchs, G., & Selvam, S. (2020). Fatal attraction: The roles of ribosomal proteins in the viral life cycle. WIREs RNA, 12(2), e1613. https://doi.org/10.1002/wrna.1613

Min, T., Hwarari, D., Li, D., Movahedi, A., & Yang, L. (2022). CRISPR-Based Genome Editing and Its Applications in Woody Plants. International Journal of Molecular Sciences, 23(17), 10175. https://doi.org/10.3390/ijms231710175

Murmu, S., Chaurasia, H., Archak, S., Jha, G. K., Sinha, D., Das, R., & Sharma, S. (2024). A review of artificial intelligence-assisted omics techniques in plant defense: current trends and future directions. Frontiers in Plant Science, 15. https://doi.org/10.3389/fpls.2024.1292054

Nagy, P. D. (2016). Tombusvirus-Host Interactions: Co-Opted Evolutionarily Conserved Host Factors Take Center Court. Annual Review of Virology, 3(1), 491–515. https://doi.org/10.1146/annurev-virology-110615-042312

Noueiry, A. O., & Ahlquist, P. (2003). Brome mosaic virus RNA replication: revealing the role of the host in RNA virus replication. Annual Review of Phytopathology, 41(1), 77–98. https://doi.org/10.1146/annurev.phyto.41.052002.095717

Okoli, A., Okeke, M. I., Tryland, M., & Moens, U. (2018). CRISPR/Cas9—Advancing Orthopoxvirus Genome Editing for Vaccine and Vector Development. Viruses, 10(1), 50. https://doi.org/10.3390/v10010050

Osterbaan, L. J., & Fuchs, M. (2019). Dynamic interactions between plant viruses and their hosts for symptom development. Journal of Plant Pathology, 101(4), 885–895. https://doi.org/10.1007/s42161-019-00323-5

Palloix, A., Ayme, V., & Moury, B. (2009). Durability of plant major resistance genes to pathogens depends on the genetic background, experimental evidence and consequences for breeding strategies. New Phytologist, 183(1), 190–199. https://doi.org/10.1111/j.1469-8137.2009.02827.x

Pasin, F., Menzel, W., & Daròs, J. (2019). Harnessed viruses in the age of metagenomics and synthetic biology: an update on infectious clone assembly and biotechnologies of plant viruses. Plant Biotechnology Journal, 17(6), 1010–1026. https://doi.org/10.1111/pbi.13084

Pilet-Nayel, M.-L., Moury, B., Durel, C.-E., Delourme, R., Caffier, V., Fournet, S., Kerlan, M.-C., & Montarry, J. (2017). Quantitative Resistance to Plant Pathogens in Pyramiding

Strategies for Durable Crop Protection. Frontiers in Plant Science, 8(1813). https://doi.org/10.3389/fpls.2017.01838

Prado, G. S., Lubini, G., Pereira, T. C., Nobile, P. M., Takita, M. A., Santos, L. N. D., Padilha, L., Monteiro-Vitorello, C. B., Boscariol-Camargo, R. L., Cristofani-Yaly, M., Contiliani, D. F., Souza, A. A. D., Rocha, D. C., Creste, S., Maluf, M. P., & Martinati-Schenk, J. C. (2024). CRISPR technology towards genome editing of the perennial and semi-perennial crops citrus, coffee and sugarcane. Frontiers in Plant Science, 14. https://doi.org/10.3389/fpls.2023.1331258

Ray, S., & Casteel, C. L. (2022). Effector-mediated plant-virus-vector interactions. The Plant Cell, 34(5), 1514–1531. https://doi.org/10.1093/plcell/koac058

Razzaq, M. K., Aleem, M., Mansoor, S., Khan, M. A., Rauf, S., Iqbal, S., & Siddique, K. H. M. (2021). Omics and CRISPR-Cas9 Approaches for Molecular Insight, Functional Gene Analysis, and Stress Tolerance Development in Crops. International Journal of Molecular Sciences, 22(3), 1292. https://doi.org/10.3390/ijms22031292

Roonjha, M. A., Roonjho, R., Ali, M., Anas, M., Khalid, H., & Jan, A. (2025). Aphid-Transmitted Plant Viruses: Epidemiology and Integrated Vector Management. International Journal of Agriculture Innovations and Cutting-Edge Research (HEC Recognised), 3(3), 109-126.

Sharma, A., Mishra, R. K., Goud, K. Y., Mohamed, M. A., Kummari, S., Tiwari, S., Li, Z., Narayan, R., Stanciu, L. A., & Marty, J. L. (2021). Optical Biosensors for Diagnostics of Infectious Viral Disease: A Recent Update. Diagnostics, 11(11), 2083. https://doi.org/10.3390/diagnostics11112083

Singh, A., Mukherjee, S. K., Taneja, J., & Dasgupta, I. (2015). Development of plants resistant to tomato geminiviruses using artificial trans-acting small interfering RNA. Molecular Plant Pathology, 16(7), 724–734. https://doi.org/10.1111/mpp.12229

Souza, P. F. N., Carvalho, F. E. L., & Garcia-Ruiz, H. (2019). What proteomics can reveal about plant-virus interactions? Photosynthesis-related proteins on the spotlight. Theoretical and Experimental Plant Physiology, 31(1), 227–248. https://doi.org/10.1007/s40626-019-00142-0

Taliansky, M., Samarskaya, V., Zavriev, S. K., Fesenko, I., Kalinina, N. O., & Love, A. J. (2021). RNA-Based Technologies for Engineering Plant Virus Resistance. Plants, 10(1), 82. https://doi.org/10.3390/plants10010082

Teng, M., Luo, J., Nair, V., & Yao, Y. (2021). Latest Advances of Virology Research Using CRISPR/Cas9-Based Gene-Editing Technology and Its Application to Vaccine Development. Viruses, 13(5), 779. https://doi.org/10.3390/v13050779

Touzdjian Pinheiro Kohlrausch Távora, F., Correa Molinari, H. B., Osiro, K. O., Abrão De Oliveira Molinari, P., Lima De Sousa, N., Márcia Mertz Henning, L., Hunter, W. B., Fátima Grossi De Sá, M., Kobayashi, A. K., De Moraes Rêgo-Machado, C., Chagas Freitas, N., Lima Nepomuceno, A., Cardoso, T. B., Feingold, S. E., Santiago, T. R., Barbosa Monteiro Arraes, F., Chumbinho De Andrade, E., De Assis Dos Santos Diniz, F., & Furtado, L. L. (2022). CRISPR/Cas- and Topical RNAi-Based Technologies for Crop

Management and Improvement: Reviewing the Risk Assessment and Challenges Towards a More Sustainable Agriculture. Frontiers in Bioengineering and Biotechnology, 10(16). https://doi.org/10.3389/fbioe.2022.913728

Vaistij, F. E., & Jones, L. (2009). Compromised Virus-Induced Gene Silencing in RDR6-Deficient Plants. Plant Physiology, 149(3), 1399–1407. https://doi.org/10.1104/pp.108.132688

Van Zuylen, W. J., Rawlinson, W. D., & Ford, C. E. (2016). The Wnt pathway: a key network in cell signalling dysregulated by viruses. Reviews in Medical Virology, 26(5), 340–355. https://doi.org/10.1002/rmv.1892

Vance, V., & Vaucheret, H. (2001). RNA silencing in plants--defense and counterdefense. Science, 292(5525), 2277–2280. https://doi.org/10.1126/science.1061334

Wang, A. (2015). Dissecting the Molecular Network of Virus-Plant Interactions: The Complex Roles of Host Factors. Annual Review of Phytopathology, 53(1), 45–66. https://doi.org/10.1146/annurev-phyto-080614-120001

Wang, C., Li, Z., Zou, J., Yang, Y., Wang, C., & Zhu, S. (2019). Epigenetics in the plant-virus interaction. Plant Cell Reports, 38(9), 1031–1038. https://doi.org/10.1007/s00299-019-02414-0

Wang, H., Kong, X., Fang, R., Yan, Y., Wu, Y., Hamera, S., Chen, X., & Jiao, X. (2016). A Signaling Cascade from miR444 to RDR1 in Rice Antiviral RNA Silencing Pathway. Plant Physiology, 170(4), 2365–2377. https://doi.org/10.1104/pp.15.01283

Wang, L.-Y., Hung, T.-H., Shen, T.-L., Lin, S.-S., Lin, N.-C., & Li, T.-K. (2012). Multiple Domains of the Tobacco mosaic virus p126 Protein Can Independently Suppress Local and Systemic RNA Silencing. Molecular Plant-Microbe Interactions®, 25(5), 648–657. https://doi.org/10.1094/mpmi-06-11-0155

Wang, M., Zhang, S., Li, R., & Zhao, Q. (2024). Unraveling the specialized metabolic pathways in medicinal plant genomes: a review. Frontiers in Plant Science, 15. https://doi.org/10.3389/fpls.2024.1459533

Wang, M.-B., Masuta, C., Shimura, H., & Smith, N. A. (2012). RNA Silencing and Plant Viral Diseases. Molecular Plant-Microbe Interactions®, 25(10), 1275–1285. https://doi.org/10.1094/mpmi-04-12-0093-cr

Wilson, V. G. (2017). Viral Interplay with the Host Sumoylation System. Advances in Experimental Medicine and Biology, 963, 359–388. https://doi.org/10.1007/978-3-319-50044-7_21

Withers, J. B., Torabi, S. F., Ghasempur, S., Tycowski, K. T., Mondol, V., Steitz, J. A., Pawlica, P., & Rosa-Mercado, N. A. (2019). Idiosyncrasies of Viral Noncoding RNAs Provide Insights into Host Cell Biology. Annual Review of Virology, 6(1), 297–317. https://doi.org/10.1146/annurev-virology-092818-015811

Xie, Z., Carrington, J. C., Zilberman, D., Gustafson, A. M., Lellis, A. D., Johansen, L. K., Kasschau, K. D., & Jacobsen, S. E. (2004). Genetic and functional diversification of small

RNA pathways in plants. PLoS Biology, 2(5), e104. https://doi.org/10.1371/journal.pbio.0020104

Xue, M., Feng, T., Chen, Z., Yan, Y., Chen, Z., & Dai, J. (2022). Protein Acetylation Going Viral: Implications in Antiviral Immunity and Viral Infection. International Journal of Molecular Sciences, 23(19), 11308. https://doi.org/10.3390/ijms231911308

Yan, S., Bhawal, R., Yin, Z., Thannhauser, T. W., & Zhang, S. (2022). Recent advances in proteomics and metabolomics in plants. Molecular Horticulture, 2(1). https://doi.org/10.1186/s43897-022-00038-9

Ye, K., Patel, D. J., & Malinina, L. (2003). Recognition of small interfering RNA by a viral suppressor of RNA silencing. Nature, 426(6968), 874–878. https://doi.org/10.1038/nature02213

Yeung, M. L., Jeang, K. T., Bennasser, Y., & Le, S. Y. (2005). siRNA, miRNA and HIV: promises and challenges. Cell Research, 15(11–12), 935–946. https://doi.org/10.1038/sj.cr.7290371

Yoder, J. I., Tomilov, A. A., Wu, B., Tomilova, N., & Gunathilake, P. (2009). Engineering host resistance against parasitic weeds with RNA interference. Pest Management Science, 65(5), 460–466. https://doi.org/10.1002/ps.1696

Zanardo, L. G., Alves, M. S., & De Souza, G. B. (2019). Transcriptomics of plant–virus interactions: a review. Theoretical and Experimental Plant Physiology, 31(1), 103–125. https://doi.org/10.1007/s40626-019-00143-z

Zhang, S., Li, C., Si, J., Han, Z., & Chen, D. (2022). Action Mechanisms of Effectors in Plant-Pathogen Interaction. International Journal of Molecular Sciences, 23(12), 6758. https://doi.org/10.3390/ijms23126758

Zhang, X., Singh, J., Qu, F., Li, D., & Zhang, X. (2012). Temperature-Dependent Survival of Turnip Crinkle Virus-Infected Arabidopsi Plants Relies on an RNA Silencing-Based Defense That Requires DCL2, AGO2, and HEN1. Journal of Virology, 86(12), 6847–6854. https://doi.org/10.1128/jvi.00497-12