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Advancing Agricultural Resilience: Omics Strategies Unveiling Molecular Mechanisms for Disease Resistance In Vegetables

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In modern agriculture, the cultivation of vegetables faces significant challenges due to the relentless onslaught of various diseases that can lead to substantial crop losses. To address these challenges, omics approaches have emerged as powerful tools for understanding the molecular mechanisms underlying vegetable disease resistance. Omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, have emerged as invaluable tools for investigating vegetable disease resistance. The abstract reviews their application in deciphering the complex interactions between plants and pathogens to enhance resistance. Genomic studies identify resistance-associated genes and loci, while transcriptomics reveals defense pathways and regulatory networks. Proteomics unravel dynamic protein changes during interactions, indicating potential biomarkers and defense proteins. Metabolomics elucidates metabolic shifts in resistant plants, highlighting signaling and defense-related metabolites. Integration of omics data enables a comprehensive understanding and modeling of plant-pathogen dynamics. These approaches also expedite breeding via marker-assisted selection and genome editing. Challenges include data integration and functional validation. Nonetheless, omics approaches offer unprecedented insights into vegetable disease resistance, promising sustainable crop protection and food security.

Keywords: Omics approaches, genomics, transcriptomics, proteomics, metabolomics, vegetables, marker-assisted selection, genome editing, sustainable crop protection, food security.

INTRODUCTION

Vegetables provide nutrients and biologically active compounds. They also play a crucial role in economies and considerably contribute to agricultural productivity (Shipman et al., 2021). However, for vegetable crops, there are several obstacles. Crops often experience production decreases, quality declines, and post-harvest loss because of diseases caused by fungus, oomycetes, bacteria, viruses, and root-knot nematodes (Xu et al., 2022). The major problem in vegetable production is the heavy incidences of diseases and pests. Due to the greater susceptibility of vegetable crops to diseases and insect pests, it becomes hard to achieve the maximum yield potential. Indiscriminate use of pesticides for controlling diseases, insect pests, and nematodes is hazardous to the health and environment (Dhall, 2015). Diseases are caused by a variety of plant pathogens, ranging from viroids with a few hundred nucleotides to higher plants. Their impacts might range from minor symptoms to catastrophes that completely devastate vast areas that were planted with food crops (Khan et al., 2023). Crop production is adversely affected when pathogens like bacteria, fungi, and viruses attack. To defend against such attacks, plants have evolved a variety of strategies that include altering gene expression, activating several metabolic pathways, and post-translationally altering proteins. These strategies result in the accumulation of primary and secondary metabolites that are involved in plant defense responses (Gomez-Casati et al., 2016). To understand a crucial fact: plants get sick, plant disease ecology, which is intrinsically interdisciplinary, draws on the divergent disciplines of microbial ecology, epidemiology, plant physiology, and genetics. Plant pathologists have known for

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more than a century that, in vulnerable plants, aggressive microorganisms (such as bacteria, fungi, viruses, and oomycetes) drive disease dynamics (Crandall et al., 2020). The frequency and variety of pests and illnesses that crops are exposed to have been growing for a while. There are three factors in playing. The first is that globalization has never been greater. Long distances must be traveled by plant parts made in one location before they can be consumed in another, making it impossible to completely control diseases and increasing the likelihood that local plants will come into touch with a variety of pathogens. Second, the allele pool for many crops, including R alleles, is typically quite small. This is due to the bottleneck in their domestication process and the monopoly that some elite kinds enjoy in a particular area (Fernandez-Gutierrez & Gutierrez-Gonzalez, 2021). The main strategy adopted for combating phytopathogens is chemical control. Since the 1960s, when the dangers of pesticides were exposed, there has been knowledge about the use and abuse of chemicals (fungicides and pesticides). Preventive measures are founded on the idea that keeping hosts and infections apart is the best way to control disease. There are various forms that this style of management might take. Rules for prohibition and prevention may be established by a government entity (county, state, or country). These quarantines are used in conjunction with inspections.

However, conventional breeding typically includes raising and analyzing vast populations of crops over several generations, which is a time-consuming and labor-intensive operation. When employing biotechnology, genetic engineering (Christou, 2013). Omics approaches allow researchers to decode the genetic code and molecular details of vegetables. Genomics unravels the underlying blueprint, highlighting genes that confer natural defense mechanisms against pathogens. Transcriptomics captures the dynamic orchestra of gene expression during pathogen encounters, revealing how plants coordinate their defenses. Proteomics focuses on the intricate aspects of proteins, uncovering the molecular basis that executes plant immunity. Metabolomics, meanwhile, uncovers the chemical footprints of disease resistance, unveiling the production of compounds that deter pathogens (Razzaq et al., 2021).

Genomics and Disease-Resistant Genes**:** To increase the resistance and productivity of plants, particularly vegetables, genomics and the study of disease-resistant genes are essential. Identifying disease-resistant genes and comprehending the genetics of resistant plants can aid in the development of more resilient and productive vegetable crops (Dong & Ronald, 2019). Researchers have found genes in vegetable crops that give resistance to several diseases by using genomics approaches including genome sequencing and functional genomics. These genes could code for proteins that recognize and kill pathogens, enhancing the plant's natural defense mechanisms (Shahriar et al., 2021). Identification of molecular markers associated to genes for disease resistance is possible by genomics. These markers can be used in breeding plans to more effectively choose plants with preferred features. This technique, known as marker-assisted selection (MAS), makes possible the selection of plants with resistance without must wait for disease challenges, which accelerate the conventional breeding process (Amiteye, 2021). Resistance genes, also known as R genes, are essential parts of a plant's immune system that are necessary in identifying and combating pathogens like bacteria, viruses, fungi, and pests. Genomics has significantly advanced our understanding of how these genes work and how they contribute to plant defense mechanisms has considerably improved (Dong & Ronald, 2019). Genomics allows researchers to identify and catalog R genes within a plant's genome. Researchers can pinpoint the precise sequences that encode R genes using methods like genome sequencing and analysis. Numerous R genes have been found in numerous plant species because of this. Genomics also revealed the genetic diversity present in R genes across different plant varieties and species. This diversity contributes to the plant's ability to recognize a wide range of pathogens, enhancing its overall defense capabilities. Genomics has enabled the identification of effector proteins produced by pathogens. These effectors are recognized by R gene products, initiating the plant's defense response. By studying the interactions between effectors and R genes at the genomic level (Zhang et al., 2022). As pathogens evolve to avoid detection by plant R genes, plants, in turn, evolve new R gene variants to recognize novel pathogen effectors. This ongoing arms race is evident at the genomic level. Comparative genomics allows researchers to compare the R gene repertoire of different plant species. This helps in understanding how plants have evolved different strategies for pathogen recognition and defense. It also aids in transferring knowledge from model plant species to agriculturally important crops (Anderson et al., 2010). Functional genomics techniques, such as transcriptomics and proteomics, can reveal how R genes are activated and how they influence downstream defense pathways. This provides insights into the molecular processes underlying the plant's response to pathogens (Ercolano et al., 2012). Genomics has facilitated the development of targeted approaches for modifying R genes. Techniques like CRISPR-Cas9 can be used to edit R genes, potentially enhancing their activity or introducing novel recognition specificities to improve plant resistance (Gaj et al., 2016).

Transcriptomics of Pathogen Interactions**:** Transcriptomics plays a crucial role in understanding how plants respond to pathogen attacks at the molecular level. It provides insights into which genes are activated or suppressed, and how these responses contribute to the plant's defense mechanisms. Here's how transcriptomics is used to study pathogen interactions in vegetables: Plants have receptor proteins on their cell surfaces that can recognize specific molecules associated with pathogens. These molecules are often called pathogen-associated molecular patterns (PAMPs). When a plant detects PAMPs, it initiates a signaling cascade that leads to changes in gene expression. Pathogen recognition triggers signaling pathways, such as the PAMP-triggered immunity (PTI) and effector-triggered immunity (ETI) pathways. These pathways involve the activation of various protein kinases, phosphatases, and other signaling molecules (Tor et al., 2009). Signaling cascades activate transcription factors (TFs), which are proteins that bind to specific DNA sequences in the promoters of target genes. TFs regulate the expression of downstream genes by either enhancing (activation) or inhibiting (repression) their transcription (Chen & Pugh, 2021). Many genes involved in plant defense are upregulated in response to pathogen attacks. These include genes encoding antimicrobial proteins, enzymes involved in the synthesis of defensive compounds, and proteins that enhance the plant's resistance (Kaur et al., 2022). Phytohormones like salicylic acid (SA), jasmonic acid (JA), and ethylene play crucial roles in mediating plant-pathogen interactions. Different hormones are often associated with specific types of pathogens. For example, SA is often linked to defense against biotrophic pathogens, while JA and ethylene are associated with defense against necrotrophic pathogens (Alazem & Lin, 2015). Pathogens can breach plant cell walls to enter plant tissues. In response, plants activate genes involved in cell wall reinforcement, such as those encoding proteins like chitinases and glucanases. Pathogen interaction can lead to the activation of genes involved in the production of secondary metabolites, such as phenolics, alkaloids, and terpenes, which can have antimicrobial properties (Kongala & Kondreddy, 2023).

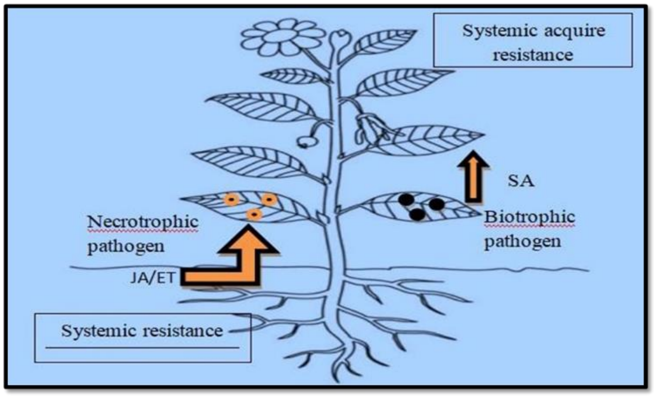

Figure 1. Plant defense pathways against pathogens are linked to interactions with beneficial rhizosphere microbes.

In some cases, plants trigger programmed cell death in response to pathogen attacks. This localized cell death, known as the hypersensitive response (HR), limits pathogen spread. Genes involved in HR, including those encoding proteases and cell death regulators, are upregulated. Successful defense responses can lead to systemic acquired resistance, where the entire plant becomes more resistant to subsequent infections (Balint-Kurti, 2019). MicroRNAs (small RNA molecules) play a role in post-transcriptional gene regulation during plant-pathogen interactions. Some microRNAs can target mRNAs of defense-related genes, influencing their expression levels (Dong et al., 2022).

Plants use different defense responses to deal with different types of pathogens. For successful defense against biotrophic pathogens, plants typically activate the salicylic acid (SA) pathway and produce reactive

Slavokhotova et al. (2021) studied response of cucumber plants to one of the global pathogens, cucumber green mottle mosaic virus (CGMMV), which causes severe symptoms in leaves and fruits. The inbred line of *Cucumis sativus* L. which is highly susceptible to CGMMV, was chosen for inoculation. Transcriptomes of infected plants at the early and late stages of infection were analyzed in comparison with the corresponding transcriptomes of healthy plants using RNA-seq. The changes in the signaling pathways of ethylene and salicylic and jasmonic acids, as well as the differences in silencing response and expression of pathogenesis-related proteins and transcription factors, were revealed. The results show that silencing was strongly suppressed in infected plants, while the salicylic acid and ethylene signaling pathways were induced. The genes encoding pathogenesis-related proteins and the genes involved in the jasmonic acid pathway changed their expression insignificantly.

***Proteomics of Defense Mechanisms*:** In recent years, mass spectrometry-based proteomics has provided scientists with the tremendous capability to study plants more precisely than previously possible. Currently, proteomics has been transformed from an isolated field into a comprehensive tool for biological research that can be used to explain biological functions. Several studies have successfully used the power of proteomics as a discovery tool to uncover plant resistance mechanisms (Liu et al., 2019). There is growing evidence that indicates that the spatial proteome and post-translational modifications (PTMs) of proteins directly participate in the plant immune response. Therefore, understanding the subcellular localization and PTMs of proteins is crucial for a comprehensive understanding of plant responses to biotic stress. In this review, we discuss current approaches to plant proteomics that use mass spectrometry, with particular emphasis on the application of spatial proteomics and PTMs (Chen et al., 2021).

Viruses, bacteria, fungi, and other pathogens can all cause a variety of diseases in potato plants. Proteomics can offer important insights into how potato plants respond to these illnesses and potentially help design disease management methods by revealing the defensive mechanisms at the protein level. Proteomics enables the identification and characterization of PRPs, which are a group of defense-related proteins that are induced in response to pathogen attacks. These proteins play key roles in plant defense by inhibiting pathogen growth or promoting cell death. Proteomic studies can reveal changes in the abundance of PRPs during infection, providing insights into their roles in potato disease resistance. PRPs, a class of defense-related proteins that are activated in response to pathogen infection, can be recognized and characterized with the help of proteomics. By preventing pathogen growth or encouraging cell death, these proteins play important roles in plant defense. Proteomic research can shed light on PRPs' roles in potato disease resistance by revealing variations in their abundance during infection (Dos Santos & Franco, 2023). Researchers can compare the protein expression patterns of healthy and diseased potato plants using proteomics. Researchers can narrow down probable candidates implicated in the plant's defense mechanisms by determining which proteins are upregulated or downregulated as the disease progresses. This knowledge can direct more functional research to support the functions of these proteins in disease resistance.

The signaling pathways that are engaged during pathogen infection can be uncovered by proteomic analysis. These studies frequently lead to the discovery of important regulatory proteins, including transcription factors, kinases, and phosphatases. Understanding these signaling components will help you better understand how potato plants detect pathogen attacks and establish effective defenses (Richter et al., 2016).

Protein-protein interactions can be used to identify protein-protein interactions that are essential for coordinating defensive reactions. Understanding the complicated network of molecular processes that take place during disease defense in potatoes is made easier by identifying connections between defense-related proteins and other cellular elements (Rao et al., 2014). Protein activity and function are significantly regulated by post-translational modifications (PTMs) during disease defense. The stability, location, and interactions of defense-related proteins can be impacted by modifications in PTMs like phosphorylation, ubiquitination, and glycosylation, which can be revealed by proteomic analyses (Friso & van Wijk, 2015).

***Metabolic Changes and Secondary Metabolites*:** The generation of secondary metabolites having antibacterial characteristics is frequently a part of disease defense. Proteomics can shed light on the secondary metabolite biosynthesis-related enzymes as well as alterations in primary metabolism that may affect the body's overall defense response. Potato plants frequently need to divert resources to defense-related processes when pathogen attacks occur. This may entail modifying fundamental metabolic processes to supply energy and precursor molecules for defense-related processes, such as glycolysis and the tricarboxylic acid (TCA) cycle (Jan et al., 2021). In addition to serving as the basis for proteins, amino acids also serve as the building blocks for secondary metabolites. Phenylalanine is one of the amino acids that is employed in the manufacture of phenolic chemicals, which are crucial for plant defense. The synthesis of molecules associated with defense may be affected by modifications in amino acid metabolism (Divekar et al., 2022). Attacks by pathogens can alter the carbohydrates are metabolized and increase the synthesis of sugars and other carbs. These substances can function as signaling molecules and contribute to the induction of defensive mechanisms (Kato & Ishiwa, 2015).

I. ***Phenolic Compounds*:** Phenolic compounds are important secondary metabolites involved in plant defense against pathogens. They have antimicrobial properties and contribute to strengthening the plant cell wall. Proteomics can help identify the enzymes involved in the biosynthesis of phenolic compounds, providing insights into how potato plants increase their production in response to diseases (Oulahal & Degraeve, 2021).

II. ***Alkaloids*:** Potatoes contain certain alkaloid substances that are linked to protection against infections and herbivores. These substances may also be antibacterial and can discourage herbivores (Thawabteh et al., 2019).

III. ***Glycoalkaloids*:** Potatoes produce toxic glycoalkaloids like solanine and chaconine to fend off herbivores and defend themselves against infections. Understanding glycoalkaloids' regulation and manufacture through proteomics is vital for both plant defense and food safety, as large concentrations of these compounds can be toxic to humans (Urugo & Tringo, 2023).

IV. ***Terpenes*:** Terpenes are a wide range of secondary metabolites with the potential for being antibacterial. They are produced from isoprenoid precursors, and proteomic research shows that during pathogen infection, enzymes are involved in their production (Singh & Sharma, 2015).

V. ***Volatile Organic Compounds (VOCs)*:** Plants release VOCs in response to a variety of stressors, such as disease infections. These substances can function as indirect defenses by attracting the diseases' natural competitors or by directly preventing the growth of the pathogens (Brilli et al., 2019).

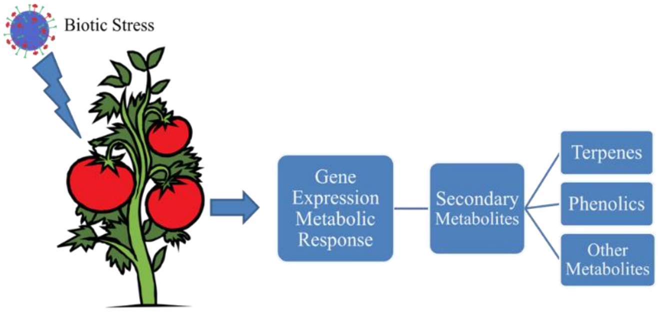

Figure 2. Metabolic changes and secondary metabolites.

The identification of the enzymes and regulatory elements involved in the manufacture of these secondary metabolites is made possible by proteomic investigations. Researchers may be able to modify these substances' levels to improve the potato plant's resistance to illnesses by understanding how they are created and controlled in response to pathogen attacks. Proteomics can also shed light on the complex metabolic linkages and pathways that play a role in the overall defense response of potatoes against different pathogens.

***Omics-Based Disease Resistance Breeding*:** The development of disease-resistant vegetable crops has been greatly aided by omics-based disease resistance breeding, which involves the integration of several high-throughput technologies including genomics, transcriptomics, proteomics and metabolomics. Here are a few instances of vegetable crops that have benefited from breeding for disease resistance using omics-based methods. Tomato (*Solanum lycopersicum*) yellow leaf curl virus (TYLCV) Resistance, Key genes involved in resistance to TYLCV, a viral disease, have been discovered through genomic and transcriptome research. By altering these genes, gene editing techniques have been used to increase resistance (Khan et al., 2022). Late Blight Resistance, Genes linked to resistance to the late blight pathogen Phytophthora infestans have been found using omics techniques. The creation of tomato varieties resistant to blight has benefited from these findings (Zhi et al., 2021). Potato (*Solanum tuberosum*) Late Blight Resistance. The production of potato cultivars with improved resistance to Phytophthora infestans is the result of the improvement of potato late blight resistance through genomes and transcriptomics, like tomatoes (Paluchowska et al., 2022). Potato Virus Y (PVY) Resistance, Omics research has discovered resistance genes to PVY, a virus that affects potato crops. The efforts to create PVY-resistant potatoes have benefited from these discoveries (Liu et al., 2023). Cucumber (*Cucumis sativus*) Downy Mildew Resistance, Key genes and proteins linked to resistance to *Pseudoperonospora c*ubensis caused cucumber downy mildew to have been identified by transcriptomics and proteomics. These discoveries are used in the breeding of cucumbers with enhanced resistance (Olczak-Woltman et al., 2011). Pepper (*Capsicum spp*.) Bacterial Spot Resistance. The discovery of genes and proteins involved in pepper resistance to bacterial spot infections (*Xanthomonas spp*.) has been made possible by omics-based techniques. Using this information, resistant pepper cultivars are being created (Zhu et al., 2021). Lettuce (*Lactuca sativa*) Downy Mildew Resistance, Genes linked to resistance to lettuce Downy mildew (*Bremia lactucae*) have been discovered through genomic and transcriptome research. Using omics-based data, breeding operations are intended to introduce resistant alleles (Parra et al., 2021). Spinach (*Spinacia oleracea*) White Rust Resistance, Candidate genes linked to resistance to white rust (*Albugo occidentalis*) in spinach have been found through genomic analysis. To produce spinach cultivars resistant to illness, these genes are being targeted (Shi et al., 2022). The identification of genes connected to resistance to clubroot disease caused by Plasmodiophora brassicae in diverse Brassica crops has been made possible thanks to genomic investigations (Pang et al., 2018). Sweet Potato (*Ipomoea batatas*) Virus Resistance, breeding efforts for virus-resistant cultivars have been aided by omics-based studies that have helped to understand the molecular basis of sweet potato resistance against numerous viruses. These examples illustrate how omics technologies have been applied to identify genetic markers, genes, and pathways associated with disease resistance in various vegetable crops. This information has been instrumental in accelerating traditional breeding efforts and, in some cases, in the development of genetically edited crops with enhanced disease resistance. While genomics has significantly advanced our understanding of disease resistance in vegetables, several challenges remain, along with exciting future directions for research and application. Here are some challenges and future directions related to disease resistance in vegetables using genomics:

***Challenges*:** Multiple genes with additive, epistatic, and pleiotropic effects are frequently associated with disease resistance. It is difficult to unravel the complex genetic architecture of resistance characteristics. Finding potential genes using genomics is just the beginning. It is essential, but labor-intensive, to functionally validate these genes and comprehend their functions in disease resistance pathways. Vegetables are impacted by a variety of diseases and pests, requiring specialized management strategies. It is difficult to develop broad-spectrum resistance that protects against numerous diseases. Although many have not been sequenced or have reference genomes of poor quality, several vegetable crops have reference genomes. This makes precise genetic studies challenging. Concerns about ethics and regulations are raised by the usage of genetically modified crops. It can be difficult to guarantee consumer acceptability and regulatory approval for these crops.

***Conclusion*:** Understanding the functions of genes in disease resistance pathways will be possible through in-depth functional characterization of candidate genes utilizing methods like CRISPR-Cas9 and RNA interference. An integrated understanding of how genes are produced, controlled, and function during disease resistance responses will be made possible by integrating genomics with transcriptomics, proteomics, and metabolomics. Combining multiple omics data sets will enable the identification of key regulatory hubs and interactions within complex networks underlying disease resistance. Continued advancement in gene editing techniques will enable the precise modification of genes associated with disease susceptibility and resistance, leading to crops with enhanced and tailored resistance.

Studying the genomics of pathogens and their interactions with host plants will provide insights into pathogen evolution and help design more effective resistance strategies. Integration of genomics data into marker-assisted breeding programs will expedite the development of disease-resistant vegetable varieties. Open data sharing and collaboration among researchers globally will accelerate discoveries and enable more comprehensive analyses. Studying the interactions between disease resistance and environmental stressors due to climate change will be crucial for developing resilient vegetable crops. Engaging with the public to promote understanding and acceptance of genetically edited disease-resistant vegetables is important for their successful adoption. Establishing consistent and internationally recognized regulations for genetically edited crops will facilitate their commercialization and global trade.

In conclusion, while challenges exist, genomics holds immense potential for enhancing disease resistance in vegetables. By addressing these challenges and embracing future directions, researchers can contribute to more sustainable and resilient agricultural practices and ensure a more secure food supply.

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REFERENCES

Alazem, M.(2015). Roles of plant hormones in the regulation of host-virus interactions. *Molecular Plant Pathology 16*, 529-540.

Amiteye, S., (2021). Basic concepts and methodologies of DNA marker systems in plant molecular breeding. *Heliyon 7*, 08093.

Anderson, J.P., (2010). Plants versus pathogens: an evolutionary arms race. *Functions of Plant Biology 37*, 499-512.

Balint-Kurti, P., (2019). The plant hypersensitive response: concepts, control and consequences. *Molecular of Plant Pathology 20*, 1163-1178.

Brilli, F., (2019). Exploiting plant volatile organic compounds (VOCs) in agriculture to improve sustainable defense strategies and productivity of crops. *Frontiers in Plant Science 10*, 436279.

Chen, H., (2021). What do transcription factors interact with? *Journal of Molecular Biology 433*, 166883.

Chen, Y., (2021). Exploring the diversity of plant proteome. *Journal of Integrative Plant Biology 63*, 1197-1210.

Christou, P., (2013). Plant genetic engineering and agricultural biotechnology 1983–2013. *Trends biotechnology 31*, 125-127.

Crandall, S.G., (2020). A multi-omics approach to solving problems in plant disease ecology. *PLoS One 15*, 0237975.

Dhall, R., (2015). Breeding for biotic stresses resistance in vegetable crops: a review. *Journal of Crop Sciences Technology 4*, 13-27.

Divekar, P.A., (2022). Plant secondary metabolites as defense tools against herbivores for sustainable crop protection. *International Journal of Molecular Science 23*, 2690. doi: 10.3390/ijms23052690

Dong, O.X., (2019). Genetic engineering for disease resistance in plants: recent progress and future perspectives. *Plant Physiology 180*, 26-38.

Dong, Q., (2022). MicroRNAs and their roles in plant development. *Frontier of Plant Sciences 13*, 824240.

Dos Santos, C., (2023). Pathogenesis-related proteins (PRs) with enzyme activity activating plant defense responses. *Plants 12*, 2226. doi: 10.3390/plants12112226

Ercolano, M.R., (2012). Genetic and genomic approaches for R-gene mediated disease resistance in tomato: retrospects and prospects. *Plant Cell Reports, 31*, 973-985.

Fernandez-Gutierrez, A., (2021). Bioinformatic-based approaches for disease-resistance gene discovery in plants. *Agronomy, 11*, 2259.

Friso, G., (20150. Posttranslational protein modifications in plant metabolism. *Plant Physiology*, *169*, 1469-1487.

Gaj, T., (2016). Genome-editing technologies: principles and applications. *Cold Spring Harb Perspective Biology, 8*, a023754.

Gomez-Casati, D.F., (2016). Omics approaches for the engineering of pathogen resistant plants. *Current Issues in Molecular Biolog,y 19*, 89-98.

Jan, R., (2021). Plant secondary metabolite biosynthesis and transcriptional regulation in response to biotic and abiotic stress conditions. *Agronomy, 11*, 968.

Kato, K., (2015). The role of carbohydrates in infection strategies of enteric pathogens. *Tropical Medicine & International Health, 43*, 41-52.

Kaur, S., (2022). How do plants defend themselves against pathogens-Biochemical mechanisms and genetic interventions. *Physiology and Molecular Biology of Plants, 28*, 485-504.

Khan, A., (2023). Plant disease resistance research at the dawn of the new era. *Phytopathology 113*, 756-759.

Khan, Z.A., (2022). CRISPR/Cas-mediated resistance against viruses in plants. *International Journal of Molecular Sciences 23*, 2303. doi: 10.3390/ijms23042303

Kongala, S.I., (2023). A review on plant and pathogen derived carbohydrates, oligosaccharides and their role in plant's immunity. *Carbohydrate Polymer Technologies and Applications*, *6*, 100330.

Liu, J., (2023). Strategies for engineering virus resistance in potato. *Plants, 12*, 1736.

Liu, Y., (2019). Proteomics: a powerful tool to study plant responses to biotic stress. *Plant Methods, 15*, 135. https://doi.org/10.1186/s13007-019-0515-8

Olczak-Woltman, H., (2011). The genetic basis of resistance to downy mildew in *Cucumis* spp. latest developments and prospects. *Journal of Applied Genetics, 52*, 249-255.

Oulahal, N., (2021). Phenolic-rich plant extracts with antimicrobial activity: an alternative to food preservatives and biocides? *Front Microbiology, 12*, 753518.

Paluchowska, P., (2022). Late blight resistance genes in potato breeding. *Planta 255*, 127. doi: 10.1007/s00425-022-03910-6

Pang, W., (2018). Identification and mapping of the clubroot resistance gene CRd in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*). *Frontiers of Plant Science, 9*, 653. doi: 10.3389/fpls.2018.00653

Parra, L., (2021). Identification and mapping of new genes for resistance to downy mildew in lettuce. *Theoretical and Applied Genetics 134*, 519-528.

Rao, V.S., (2014). Protein-protein interaction detection: methods and analysis. *International Journal of Proteomics, 2014*, 147648.

Razzaq, M.K., (2021). Omics and CRISPR-Cas9 approaches for molecular insight, functional gene analysis, and stress tolerance development in crops. *International Journal of Proteomics, 22*, 1292. doi: 10.3390/ijms22031292

Richter, E., (2016). Proteomic discovery of host kinase signaling in bacterial infections. *Proteomics Clinical Application 10*, 994-1010.

Shahriar, S.A., (2021). Control of plant viral diseases by CRISPR/Cas9: resistance mechanisms, strategies and challenges in food crops. *Plants, 10*, 1264.

Shi, A., (2022). Genome-wide association study and genomic prediction of white rust resistance in USDA GRIN spinach germplasm. *Horticulture Research 9*, uhac069. doi: 10.1093/hr/uhac069

Shipman, E.N., (2021). Can gene editing reduce postharvest waste and loss of fruit, vegetables, and ornamentals? *Horticulture Research 8*. doi.org/10.1038/s41438-020-00428-4

Singh, B., (2015). Plant terpenes: defense responses, phylogenetic analysis, regulation and clinical applications. *Biotechnology, 5*, 129-151.

Slavokhotova, A., (2021). Transcriptomic analysis of genes involved in plant defense response to the cucumber green mottle mosaic virus infection. *Life (Basel) 11*, 1064. doi: 10.3390/life11101064

Thawabteh, A., (2019). The biological activity of natural alkaloids against herbivores, cancerous cells and pathogens. *Toxins (Basel) 11,* 656. doi: 10.3390/toxins11110656

Tor, M., (2009). Receptor-mediated signaling in plants: molecular patterns and programmes. *Journal of Experimental Botany 60*, 3645-3654.

Urugo, M.M., (2023). Naturally occurring plant food toxicants and the role of food processing methods in their detoxification. International *Journal of Food Science, 2023*, 9947841.

Xiao, C., (2019). Quantitative proteomics of potato leaves infected with *Phytophthora infestans* provides insights into coordinated and altered protein expression during early and late disease stages. *International Journal of Molecular Sciences 20*, 136. doi: 10.3390/ijms20010136

Xu, J., (2022). Exploring new strategies in diseases resistance of horticultural crops. *Frontiers in Sustainable Food Systems, 6*, 1021350.

Zhang, S., (2022). Action mechanisms of effectors in plant-pathogen interaction. *International Journal of Molecular Sciences 23*, 6758. doi: 10.3390/ijms23126758

Zhi, X., (2021). Fine mapping of the *Ph-2* gene conferring resistance to late blight (*Phytophthora infestans*) in tomato. *Plant Disease 105*, 851-858.

Zhu, Q., (2021). Identification of key transcription factors related to bacterial spot resistance in pepper through regulatory network analyses. *Gene,s 12*, 1351. doi: 10.3390/genes12091351