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INTEGRATIVE OMICS FOR PLANT PROTECTION IN FRUIT CROPS: LINKING MOLECULAR DEFENCE TO ORCHARD-LEVEL DISEASE MANAGEMENT

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Graphical Abstract

Abstract

Fruit crop diseases cause substantial annual losses, compromising balance between global nutritional security and economic stability of fruit-growing regions. Failure of conventional disease management strategies calls for pioneering technologies. Omics approach – genomics, transcriptomics, proteomics, metabolomics, phenomics, and metagenomics – revolutionizing fruit pathology by quick pathogen detection and breeding of resistant varieties, emphasizing sustainability. Genomics enables development and identification of resistant genes through Next-Generation Sequencing(NGS) and CRISPR gene editing. Transcriptomics decipher host-pathogen interaction and defence expression, whereas proteomics and metabolomics reveal proteins and secondary metabolites promoting fruit crop resilience. Phenomics integrates AI, machine learning, and modern sensing/imaging technologies for early disease detection and management. Metagenomics allows for biocontrol strategies by characterization of beneficial microbes. Challenges encompass: (a) data integration across omics layers, (b) high costs and limited bioinformatics infrastructure, (c) shortage of skilled personnel, and (d) translating lab insights to field applications. Omics-driven strategies encourage sustainable fruit production by reducing chemical usage and enhancing genetic resistance. Implementation of omics approach at field level could transform fruit orchard protection and nutritional security at a global level. This review highlights the potential advantages of integrative omics for successful disease management in fruit crops.

Keywords: Omics-Fruit Crop Diseases-Disease Resistance-Fruit breeding-Metagenomics

1. INTRODUCTION

Fruit cultivation is vital for global health and nutrition as it provides vitamins, minerals, and antioxidants that are essential in the human diet. It generates economic stability for millions of farming communities and strengthens

food security, standing as a cornerstone of food security and rural development (Harris et al., 2022). The value of global fruit production was estimated to be $619.8 billion in the year 2023-2024(FAOSTAT, 2025). Extensive Annual losses occur globally in fruit cultivation due to various plant diseases (Oerke, 2006). Historical horticultural practices relied on supernatural, religious, or traditional methods for plant protection, which have proven inefficient for fruit orchard management (Martinelli et al., 2015).

Traditional methods dependent on chemical pesticides cause serious environmental and human health issues (Fisher et al., 2018). The Endosulfan disaster, which occurred in Kerala, India, should serve as a reminder of the danger of pesticides to human health (Reshma & Jayalakshmi, 2020). Global pesticide application in agriculture reached 3.73 million tonnes of active ingredients in 2023, which was double the application rates of the 1990s (FAO, 2025). Extreme pesticide use disrupts ecological balance and harms beneficial organisms. This practice contributes to the evolution of pesticide-resistant pathogens (Carvalho, 2017). Conventional breeding methods, such as backcrossing and mass selection, have significant limitations. Breeding for resistance in fruit crops takes 15-30 years (Khan & Korban, 2022). The efficacy of traditional disease control methods is inconsistent owing to the varying environmental conditions (Singh et al., 2020). This necessitates the integration of modern biotechnological methods, such as the multi-omics approach and CRISPR-Cas9 technology, for effective management of diseases in fruit crops (Aroge et al., 2024; Bacha et al., 2025).

The multi-omics approach comprises Genomics, Transcriptomics, Proteomics, Metabolomics, and Phenomics (Fukushima et al., 2009). These approaches provide insight into changes at the molecular level during host-pathogen interaction. Genomics involves the use of Next-Generation Sequencing (NGS) and sequence-specific nucleases such as Zinc finger nucleases(ZFN), Transcription Activator-Like Effector Nucleases(TALEN), and Clustered Regularly Interspaced Short Palindromic Repeats(CRISPR/Cas) for rapid pathogen detection, gene editing, and resistance gene mapping(Yin & Qiu, 2019). Transcriptomics, the quantitative study of ribonucleic acid transcription, is employed for analysis of changes in gene expression during pathogen attack and for identification of pathways in the defence mechanism(Tan et al., 2009). Proteomics refers to the analysis of a collection of proteins formed during host-pathogen interactions. Metabolomics is the characterization of molecular metabolites for the analysis of biochemical changes and metabolic pathways associated with infection response and disease progression(Balotf et al., 2022). Phenomics is the non-invasive monitoring of phenotypical changes in plants using modern sensing technologies, such as hyperspectral imaging, Magnetic Resonance Imaging (MRI), and ultrasound, for the rapid detection of infections in plants (Simko et al., 2016). Integration of different omics approaches provides a comprehensive view of mechanisms in fruit crop disease ecology (Crandall et al., 2020). In addition, metagenomic approaches rely on high-throughput sequencing and bioinformatics for detecting pathogenic microbial genomes and developing biocontrol strategies (Taunk & Goutam, 2021).

The central dogma of molecular biology encompasses the directional flow of genetic information, wherein Deoxyribo-Nucleic Acid (DNA) encodes the hereditary blueprint, which is transcribed to RNA and subsequently translated to proteins that govern cellular functions and biological responses. This concept provides a basis for understanding the molecular mechanisms underlying plant defence and serves as a framework for modern multi-omics approaches in deciphering disease resistance in fruit crops (Kukurba & Montgomery, 2015).

This review discusses the implementation, progress, and difficulties of multi-omics technology systems in fruit crop disease management. The aim of this review is to integrate recent advancements in multi-omics technologies to emphasize their revolutionary capacity to enhance fruit crop disease management, thereby contributing to sustainable fruit production and global nutritional security.

2. OVERVIEW OF OMICS TECHNOLOGY

The term “omics” refers to the collection of high-throughput experimental techniques used to characterize and study the molecules and their functions within a biological system (Joyce & Palsson, 2006). The suffix “ome” in omics means “entirety”, “everything”, “all”. Each omic technology delves into a different layer of biological information, but these layers are not independent in function from each other. They are linked with each other by the central dogma theory and are also disconnected by post-transcriptional, post-translational, and metabolic regulation, which creates irregularities for decoding information between layers. The effectiveness of omics technology lies not in what each technology can detect on its own, but in the analysis of information transfer between various omics layers, which allows for predictive transfer and breakdown of loss of information at each transition.

The pipeline for utilization of multi-omics for disease management in fruit crops by integration of genomics, transcriptomics, proteomics, metabolomics, and phenomics is summarised in **Figure 1**.

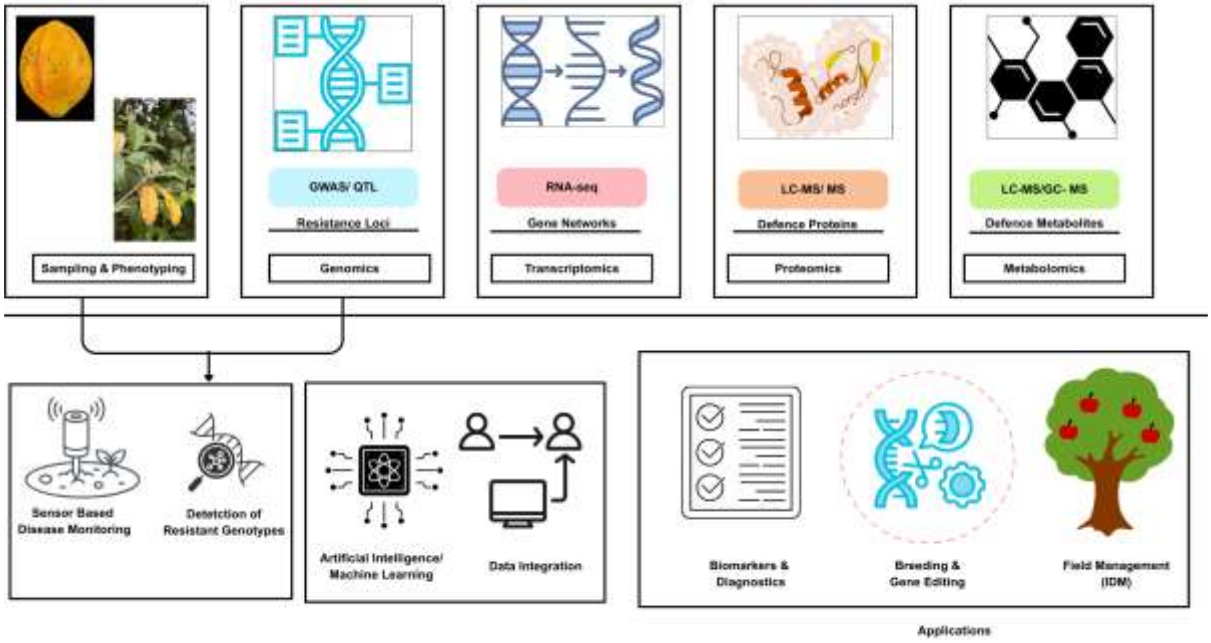

Figure 1.Multi-omics workflow for disease management in fruit crops, illustrating the pipeline from field sampling and phenotyping of symptomatic and healthy tissues through genomics (GWAS/QTL mapping of resistance loci), transcriptomics (RNA-seq–based gene network analysis), proteomics (LC-MS/MS profiling of defence proteins), and metabolomics (LC-MS/GC-MS profiling of defence metabolites), terminating in downstream applications including sensor-based disease monitoring, detection of resistant genotypes, artificial intelligence/machine-learning–driven data integration, biomarker-based diagnostics, resistance breeding and gene editing, and field-level integrated disease management (IDM)

2.1. Genomics

Genomics is the detailed analysis of an organism's genome, including both non-coding regions and genes, and how they interact with each other and with the environment. It provides the static DNA blueprint of resistance potential in terms of disease resistance. (Weissenbach, 2016). Researchers utilized Sanger sequencing for early genome projects in the model plant *Arabidopsis thaliana (Initiative & Copenhaver, 2000)* and for fruit crops like grapevine and papaya (Jaillon et al., 2007; Ming et al., 2008). With the introduction of Next-Generation Sequencing (NGS) – 2nd generation technologies such as Illumina and 454–reduced sequencing costs and increased throughput by enabling millions of parallel sequencing reactions. Researchers employ techniques like Targeting Induced Local Lesions IN Genomes(TILLING) and Ecotype Targeted Induced Local Lesions IN Genomes(Eco-TILLING) to identify allelic variants in mutant and natural gene collections, respectively, which recognize and cut mismatches in the double helix of DNA (Deme et al., 2025). Massive amounts of genomic data generated by NGS are stored by international public repositories, such as GenBank, EMBL, and DDBJ, whereas specialized platforms, such as Phytozome, complement general repositories by focusing on specific plant species with information on their practical use in breeding programs. Molecular markers, such as Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs), are used to study genetic diversity for germplasm enhancement and to identify genes and Quantitative Trait Loci (QTLs) linked to resistance using techniques like Association Mapping and Bulked Segregant Analysis (BSA). The resulting tight linkage markers can be directly employed in breeding strategies such as marker-assisted selection (MAS), 'breeding by design,' and Genomic Selection (M. Perez-de-Castro et al., 2012). Reference genomes for fruit crops such as mango, banana, apple, grape, citrus, papaya, peach, and strawberry are now available, enabling Genome-Wide Association Studies (GWAS) and MAS. However, fruit crop genomes have large structural variants such as transposable elements, inversions, and copy number variants that can disrupt or enhance resistance or susceptibility genes, which evade detection by SNP(Guo et al., 2020). Traditional GWAS approaches use the SNP approach, which fails to detect changes in the genome resulting from structural variations. Even though genomics provides insights into stable genetic loci and evolutionary history, it does not fully capture dynamic regulatory levels such as epigenetics, allele-specific expression, and tissue-specific deployment of resistance. For overcoming these limitations, "**Transcriptomics**" is the technology that analyses and determines the expression of genomic signatures during infection.

2.2. Transcriptomics

Transcriptomics is the study of a complete set of RNA molecules, including Messenger RNA(mRNA), Transfer RNA(tRNA), Ribosomal RNA(rRNA), and other non-coding RNAs, within a cell or tissue at a certain developmental stage or physiological condition(Dong & Chen, 2013). Genomics is considered the static blueprint; whereas, transcriptomics is dynamic and is the transcriptional dialogue between the host and pathogen during infection. Transcriptome unravels which resistance genes are differentially expressed in response to pathogen attack. The transcriptome is a critical link between the genome and proteome, demonstrating the functional ex-

pression of genetic information and detailing the complex networks that govern cellular actions. However, transcriptomic abundance doesn't always necessarily translate into protein abundance due to post-transcriptional regulation(Jia et al., 2018; Vélez-Bermúdez & Schmidt, 2014). Differentially Expressed Genes (DEGs) alone do not account for whether the corresponding proteins accumulate, whether they undergo post-translational modifications or whether the metabolic products generated effectively control the infection site. Therefore, transcriptomic data can be understood only as an estimate of the likelihood of defence response, not as confirmed functional immunity. The answer to these questions is provided by the next layer of omics technology, "**Proteomics**".

Transcriptomic technologies such as reverse transcription quantitative polymerase chain reaction (RT-qPCR), microarray hybridization, bulk RNA sequencing (RNA-seq), Single-Cell RNA sequencing (scRNA-seq), and direct RNA sequencing are used to detect new transcripts, alternative splicing patterns, and gene fusion events, providing insights into the cellular environment beyond genomics (Henke et al., 2026). Transcriptome analysis has evolved from single-gene detection methods, such as Northern Blotting and qPCR, to RNA sequencing. Long Non-Coding(LNC)RNA, which does not consist of any coding sequences, was considered to be transcriptional noise and ignored in transcriptomic analysis studies, but modern research has proved that they also play a role in the regulation of biological processes, abiotic and biotic stress response (Cheng et al., 2021). Modern approaches identify novel transcripts, microRNAs, alternative splicing events, and non-coding regions. These discoveries unravel how promoters, enhancers, and silencers modulate gene regulation. Bulk RNA sequencing averages all cellular defence responses into a single profile, thereby failing to capture the heterogeneous interactions of plant cells with the pathogen. This is because different cells respond differently to the pathogen, with some cells becoming infected, some acting as bystanders, and some mounting a defence response. Single-cell RNA sequencing is an emerging technology that can discover variations at the cellular level, used for understanding the heterogeneity and complexity of RNA transcripts within individual cells(Tzec-Interián et al., 2025). However, scRNA- sequencing requires protoplasting, which itself can induce stress responses, thereby limiting its practical application in the field of fruit pathology. Another alternative approach, which holds promise, is single-nuclei RNA sequencing technology, which does not require protoplasting. As of now, no studies of scRNA sequencing have yet been conducted on any of the fruit crops, making it a distant practical reality in the field of fruit pathology

2.3. Proteomics

Proteomics is considered the investigation of proteomes, or a complete set of proteins produced within a cell, tissue, or organism. It examines how physiological, developmental, and environmental conditions alter protein composition. Proteomics studies elucidate the post-translational modifications(phosphorylation, glycosylation, ubiquitination), protein localization, abundance, activity, and protein interactions for functional and physiological responses (Priya D et al., 2025). Proteomics connects the gap between what a cell can do (encoded in the genome) and what a cell plans to do (decoded by the transcriptome) to the functional ability of the cell/ what it actually does. The proteins that are present and active at the host-pathogen interface regulate defence and infection responses toward the pathogen. Proteomics identifies the defence proteins, but whether these proteins alter the metabolic environment for supressing pathogen growth is determined by the field "**Metabolomics**".

Proteomic analysis employs analytical techniques such as 2-dimensional gel electrophoresis (2-DE) and coupled gel-free shotgun liquid chromatography-mass spectrometry (LC-MS). Modern second-generation proteomic technologies include Multidimensional Protein Identification Technology(MudPIT), Targeted Mass Tags (TMTs), Isotope-Coded Affinity tags(ICATs), and Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) (Hu et al., 2015). Characterisation of protein structures at atomic resolution or near-atomic resolution is done by experimental approaches such as X-Ray Crystallography, Nuclear Magnetic Resonance (NMR) Spectroscopy, and Cryo-Electron Microscopy (Balasco Serrão, 2025; Zha et al., 2026). Structural bioinformatics tools such as Python Molecular Graphics (PyMOL) and Python Prescription (PyRx) are employed to visualise protein structures, determine protein-protein interactions, and examine protein-ligand binding sites(Rosignoli & Paiardini, 2022; Urbanová et al., 2025). The bioinformatics approach for proteomics includes several database search tools for protein identification. A combination of conventional forward database searches with sequence-reversed or randomized target-decoy databases is used for validation and accuracy in proteomic analysis (Matros et al., 2011). These technologies enable the identification of thousands of proteins from complex biological samples, enabling a clearer understanding of protein interaction networks. **Figure 2** depicts how PyMOL and structural protein databases can be used to visualise pathogen virulence factors alongside host PR proteins in fruit crops. Despite technological advances, the number of proteomes available for fruit crops is limited or negligible compared to agronomic crops like rice, wheat, maize, etc. Because of complete, well-annotated proteome databases for fruit crops, researchers depend on homology-based identification and match their data to proteins from the model crop "*Arabidopsis thaliana*". This approach works poorly as proteins undergo evolution rapidly at the host-pathogen interface, which can differ significantly between species. Recent proteogenomic studies in pineapple and sweet cherry revealed hundreds of peptides that were not present in standard annotated proteomes (Ariffin et al., 2024; Xanthopoulou et al., 2022). Therefore, reliable conclusions about defence mechanisms and the identification of defence proteins in fruit crop pathogens are limited, highlighting the urgent need for proteogenomic mapping of fruit crop proteomes.

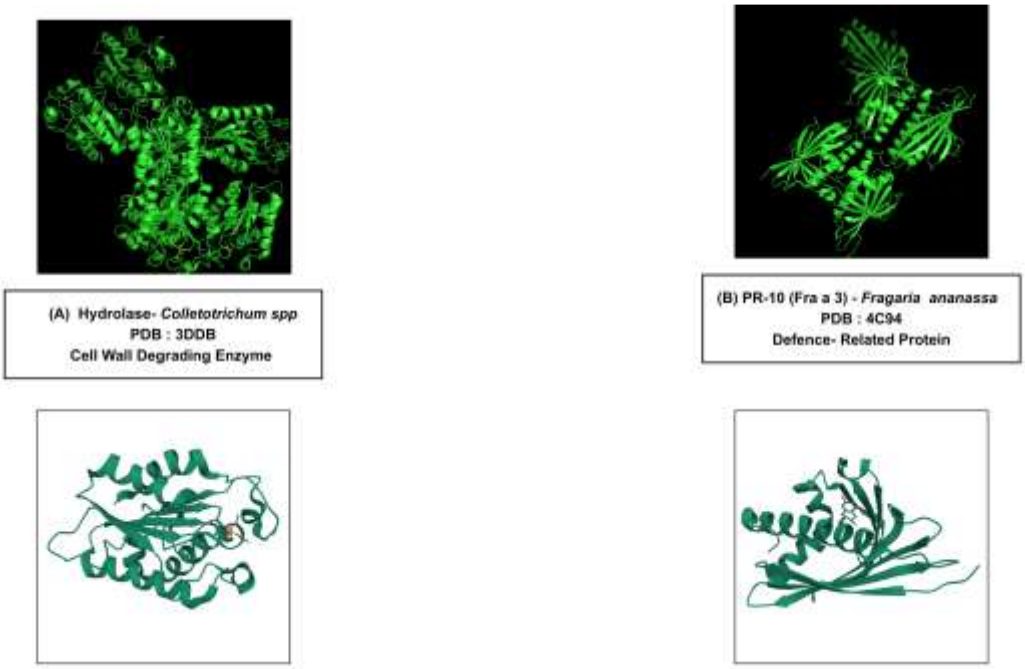

Figure 2.Structural comparison of pathogen and host proteins involved in fruit crop–pathogen interactions, showing the three-dimensional structure of a *Colletotrichum spp*. hydrolase (PDB: 3DDB), a cell-wall-degrading enzyme (A), and the defence-related PR-10 (Fr(Fra a 3) protein from *Fragaria ananassa* (PDB: 4C94) (B), highlighting the contrasting architectures of a fungal virulence factor and a strawberry pathogenesis-related protein.

2.4. Metabolomics

Metabolomics surveys metabolites (low-molecular-weight compounds) in biological systems. These compounds reveal functional and toxicological aspects of the organism. Metabolomics can be considered the functional omics layer responsible for the phenotype. Metabolites are considered the actual mediators of defence, including antimicrobial compounds, signalling molecules, and cell wall reinforcements. Due to functional validity, the identification and estimation of biomarkers can convey a plant's disease resistance or susceptibility. Metabolomic data is also the most variable among all omics layers, fluctuating with time of day, tissue age, and microclimate. Metabolites are mobile in nature, and being volatile or diffusible helps them to function as systemic signals beyond localized infection sites. Remote detection of various physiological changes due to metabolites is done by the technology **Phenomics**, bridging metabolite dynamics with phenotypic stress responses.

The plant metabolome consists of a vast array of primary metabolites, like inorganic ions, carbohydrates, lipids, and amino acids, and secondary metabolites like alkaloids, flavonoids, terpenoids, and phenols (Waris et al., 2022). Vinay et al. (2021) estimated that nearly 200,000 different metabolites exist in plant metabolomes. Primary metabolites are synthesised for developmental growth and structural conservation, whereas secondary metabolites are produced during biotic and abiotic stress conditions. Metabolomic Analysis tools include nuclear magnetic resonance(NMR), liquid chromatography–mass spectrometry (LC–MS), Gas chromatography–mass spectrometry (GC–MS), capillary electrophoresis mass spectrometry (CE–MS), and Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR–MS) (Khakimov et al., 2014). Metabolomic data are mainly obtained using 2 approaches: targeted and untargeted metabolomic analyses. Targeted metabolomics quantifies specific known metabolites, whereas untargeted metabolomics explores all detectable metabolites in a sample; both approaches share similar preparation and chromatographic methods but differ in analytical scope (Han et al., 2023; Waris et al., 2022). Untargeted metabolomics generates copious amounts of metabolome data, most of which remain undetected and chemically unannotated, and are biologically important compounds in interaction studies. Targeted metabolomics enables precise quantification and insights into metabolite synthesis pathways and defence responses, while sacrificing discovery potential and broad metabolomic coverage. Integration of both approaches is required for enhanced metabolic coverage along with functional discovery, precise quantification, and deeper understanding at the pathway level.

2.5. Phenomics

Phenomics studies examine the observable physical, biological, and chemical traits that result from the interaction between genotype and environment. Phenomics is different from the preceding omics layers as it measures the integrated physiological outcome of molecular defence response, not the molecules themselves. Phenomics relies on a combination of genetic, environmental, and time-based factors for the determination of an organism's phenotype (Zavafer et al., 2023). Scientists use modern technologies such as high-throughput imaging, sensor networks, robotics, AI, and machine learning algorithms to discover the complex relationship between the genome, environment, and physiology (Kaya, 2025). Use of AI in phenomics has enhanced the integration and precision of analysis of large-scale phenotypic data, allowing for stress detection and predictive breeding (Yang et al., 2021). Integration of machine learning with phenomics allows accurate modelling and prediction of yield and growth responses to climate-related stresses and management interventions (Khan et al., 2021).

Unmanned Aerial Vehicle (UAV)- based phenomics provides unparalleled scalability, allowing for coverage of hectares per hour, making it ideal for monitoring of large orchards. However, the effectiveness of UAV-based data acquisition depends strongly on flight-path design, flight altitude, camera sensor quality, canopy complexity, and illumination while dense tree crowns, low light intensity in cloudy and rainy conditions, small identifiable targets such as insects or early disease lesions reduce detection accuracy(Popescu et al., 2023). Ground-based phenomic sensors allow for recording fine spatial resolutions up to the millimeter scale and are valuable in detecting structural and physiological changes such as lesion development, pigment changes, and early stress responses, which may be missed by aerial platforms. These sensors can be mounted on handheld devices, tripods, gantries, or tractors. But it is limited by restricted spatial coverage and higher operational complexity, making it less suitable for large-scale field surveillance(Awada et al., 2024).

However, phenomic sensors detect physiological stress responses rather than the pathogen itself. For example, a hyperspectral signature of chlorophyll degradation can be due to various reasons like fungal infection, bacterial infection, nutrient deficiency, or drought stress. Phenomics fails to specify the reason for the physiological response and requires molecular validation from other omics layers. Without such cross-omics integration, phenomics compromises high-resolution phenotypic data due to low diagnostic specificity, constraining its effectiveness for precise disease management.

2.6. Metagenomics

Metagenomics is the analysis of all the genetic material obtained directly from environmental samples for investigation into the composition, diversity, and functional potential of microbial communities without the need for microbial culture (Fadiji & Babalola, 2020). The resistance or susceptibility of a crop is not solely determined by its own genome, transcriptome, or proteome but also by its microbial neighbours – pathogens, commensals, and beneficials all surviving in the same environment. Metagenomics employs direct DNA sequencing of environmental samples, unlike traditional microbiology techniques. This approach helps researchers discover new genes, metabolic pathways, and previously undetectable microbial species (Wu et al., 2022). Metagenomics provides an understanding of the plant-associated microbial communities, which can be pathogenic or non-pathogenic in nature, unveiling their diversity, beneficial or harmful roles, and interactions. Metagenomic studies reveal microbes involved in plant growth promotion and defence mechanisms. The microbiome is fortified with metabolic enrichment pathways, which promote nutrient recycling and bolster the immune response of plants (Di Gianvito et al., 2025). Metagenomics uncovers the hidden microbial allies present in the crop microbiome and covers the ecological dimension, revealing their functional role in stress tolerance and enhancement of plant health and productivity. However, metagenomics is limited due to its correlational nature. Even if the rhizosphere of a crop species shows resistance and has a rich microbiome, metagenomic studies do not distinguish whether the resistance is due to the microbiome or due to the crop cultivar. Confirmation is determined by culture-based isolation and inoculation, along with Koch's postulate-style validation omitted in most metagenomic studies. Integration of metagenomics with **Transcriptomics** and **Metabolomics** helps understand the correlation and pathway of resistance development in a crop due to its mmicrobiome.

Table *1* enlists bioinformatic database repositories used for the storage and retrieval of omics data collected.

Table 1. Public Databases for Multi-Omics Data Retrieval and Analysis

Data Type	Online Resource	Description	Reference	URL
Genomics	Genbank	An annotated collection of all publicly available DNA sequences	(M. Perez-de-Castro et al., 2012)	http://www.ncbi.nlm.nih.gov/genbank/
	PRGdb 4.0	Bioinformatics resource for Resistance Genes	(Sanseverino et al., 2010)	https://prgdb.org/prgdb4/
Transcriptomics	GENEVESTIGATOR	Database for large-scale exploration of global gene expression datasets	(Lim et al., 2022)	https://genevestigator.com/
Proteomics	UniProt	Central repository for protein sequences and functional information	(Wu et al., 2006)	https://www.uniprot.org/
	PRIDE	Annotation and discovery of disease-responsive proteins	(Deutsch et al., 2023)	https://www.ebi.ac.uk/pride/
	STRING	Search Tool for the Retrieval of Interacting Genes/Proteins	(Szklarczyk et al., 2025)	https://string-db.org/
Metabolomics	Metabolights	Open-access repository for metabolomics datasets	(Yurekten et al., 2024)	https://www.ebi.ac.uk/metabolights/

3. Application of Omics in Fruit Crop Disease Management Strategies

3.1. Genomics for Disease Resistance Breeding in Fruit Crops

Gene editing technologies such as CRISPR-Cas9 and TILLING are employed for the development of disease resistance genes in fruit crop species in recent times(Klosterman et al., 2016). Reverse Genetics Approach, such as ECO-TILLING, is utilised for the detection of disease resistance genes in natural populations (Fondong et al., 2016). The first instance of use of genomic technologies for disease management was the creation of transgenic papaya cultivars “Sun Up” and “Rainbow” for resistance to Papaya Ringspot Virus (PRSV) by the insertion of a gene that encodes the viral coat protein of PRSV, which results in Pathogen-Derived Resistance (PDR) in the plant genome by RNA silencing or RNA Interference (RNAi). The PRSV HA 5-1 coat protein gene coated with tungsten particles was transferred into plant embryogenic tissue by us using the gene gun (Gonsalves, 1998). Genome-Wide Association Studies (GWAS) have been done in many fruit crops to uncover which contribute to disease resistance. Whole-genome identify polymorphisms and quantitative trait loci involved in disease resistance. This allows breeders to leverage linkage disequilibrium associated with diverse germplasm for integration into breeding programs (Serrie et al., 2024). Masri and Kiss (2024) predicted 10VvNAC genes that provide tolerance against *Botrytis cinerea* infection in grapevine.

Table 2. Applications of CRISPR Technology for Disease Resistance & Management **in Major Fruit Crops** provides a list of applications of CRISPR-based gene-editing technologies for disease management in fruit crops. The basic principle behind CRISPR-Cas9–mediated editing of resistance and susceptibility loci in fruit crops is depicted in **Figure 3**.

A fundamental limitation of biotechnological approaches lies in their reliance on the effector-susceptibility interface, rather than characterization of resistance alleles uncovered by GWAS. Consequently, even though CRISPR-Cas systems have already been deployed for the elimination of susceptibility genes or effector targets, a reduction in disease incidence has only been reported in controlled conditions. To date, not even a single CRISPR-edited disease-resistant fruit cultivar has been released for commercial cultivation. This gap between laboratory success and commercial cultivation can be attributed to 2 biological bottlenecks, along with standard regulatory hurdles.

- Firstly, most gene knockouts are evaluated in a greenhouse or controlled conditions against one or a few pathogen isolates, whereas the pathogen population encountered across orchards and seasons is genetically diverse and rapidly evolving in nature.
- Secondly, the genes that are edited out can have pleiotropic roles in growth, development, climate resilience, and fruit quality, which only become visible after multi-year and multi-location trials.

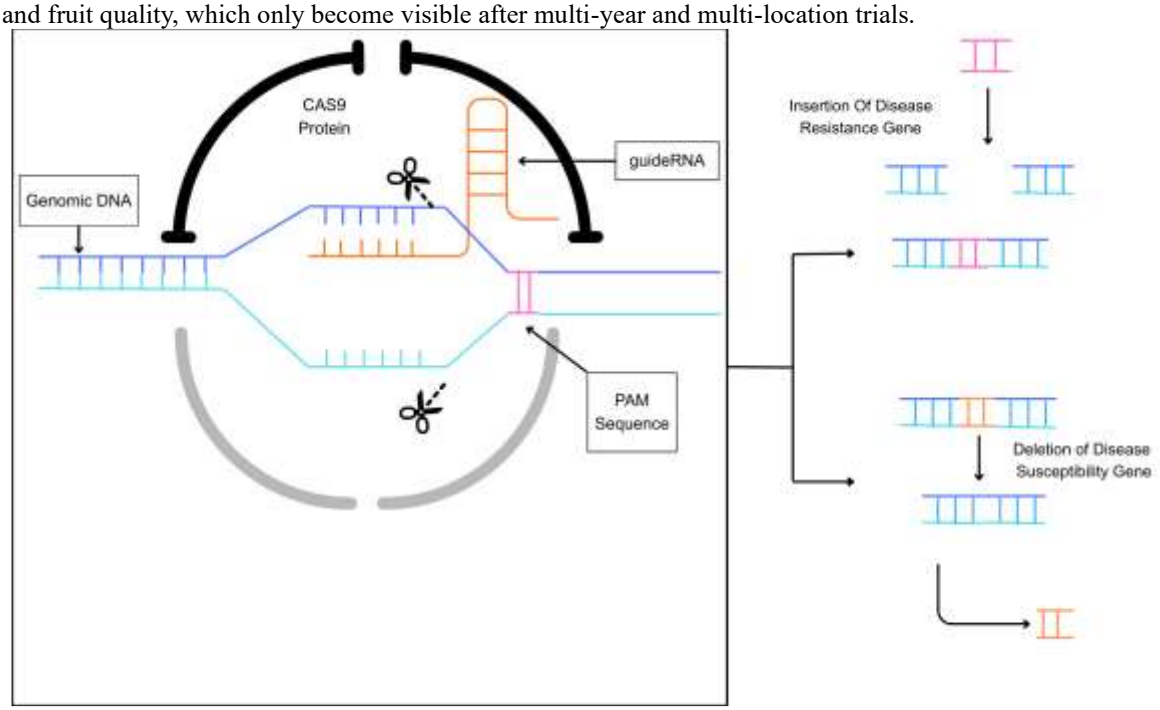

Figure 3. Schematic representation of how CRISPR-Cas9 creates disease-resistant fruit crops. The Cas9-gRNA complex first homes in on a genomic target near a PAM sequence to trigger a localized double-strand break. The subsequent repair process is leveraged to either integrate resistance-granting genes or deactivate genes associated with disease susceptibility.

The field of Genomics should focus on achieving a structural and biochemical understanding of how different alleles confer immunity, resistance, tolerance, and susceptibility, and systematically screen edited lines for long-term horticultural performance and epidemiological durability. Until then, Genomic technologies and CRISPR-based engineering will remain restricted to the creation of preliminary research model lines instead of commercially viable cultivars.

Table 2. Applications of CRISPR Technology for Disease Resistance & Management in Major Fruit Crops

Gene Editing Technology	Fruit Crop Disease	Target Gene	Mechanism	Reference
CRISPR/Cas9	Grapes Powdery Mildew *(Erysiphe necator*)	VvMLO3, VvMLO4	Function mutation of a specific Mildew Locus leading to loss of susceptibility genes	(Moffa et al., 2025)
	Apple Fire Blight (*Erwinia amylovora*)	MdDIPM4 Susceptibility gene	Elimination of Susceptibility protein, thereby denying the pathogen's effector protein a host target	(Pompili et al., 2020)
	Banana Fusarium Wilt (*Fusarium oxysporum f.sp. cubense*)	SIX9 effector gene	Elimination of the effector gene SIX9 of *Fusarium oxysporum* f.sp. *cubense* race 1 Fusarium wilt	(Villao et al., 2025)
	Strawberry Powdery Mildew(*Podosphaera aphanis)*	*Fvb7-1*, *Fvb7-2*, *Fvb7-3*, and *Fvb7-4* genes	Knockout of *Fvb7-1*, *Fvb7-2*, *Fvb7-3*, and *Fvb7-4* genes in the MLO (*Mildew Resistance Locus O*) gene family	(Akter et al., 2024)
CRISPR/Cas12	Citrus Canker (*Xanthomonas citri subsp. citri*)	CsLOB1 promoter gene	Modification of the EBE PthA4 region of the promoter gene, thereby disrupting the pathogen's ability to cause disease	(Jia et al., 2024)
	Strawberry Anthracnose (*Colletotrichum gloeosporioides*)	β-tubulin gene	Rapid DNA amplification and CRISPR/Cas12a-based detection of infected seedlings	(Zheng et al., 2024)

3.2. Transcriptome Analysis for Gene Expression In Fruit Crop Disease Mechanism

Pathogen Infection triggers differential gene expression in plants. This causes degradation of plant cell structures and symptom appearance (Roy et al., 2023). They also unravel the upregulated activity of genes involved in the synthesis of pathogenesis-related(PR) proteins and secondary metabolites during pathogen attack, which determine a plant's susceptibility, tolerance, or resistance (Mohini Kajla et al., 2023; Rahman et al., 2022). Transcriptomics provides a molecular-level snapshot of how pathogen-plant interactions disrupt plant architecture, thereby providing insights into disease progression mechanisms and the identification of genes and pathways responsible for resistance breeding or genetic modifications. Transcriptomic profiling in strawberry by microarray technology has identified genes responsive to Salicylic acid (SA) and Jasmonic acid (JA), clarifying the hormonal control of defence and signalling during infection (Amil-Ruiz et al., 2016). Transcription factors such as WRKY, Basic Helix-Loop-Helix(bHLH), Basic Leucine Zipper(bZIP), MYB, and AP2/ERF(Apetala2/Ethylene-ResponsiveFactor) are crucial in the regulation of biosynthesis of secondary metabolites involved in plant defence (M. Kajla et al., 2023). Transcriptomic studies have also revealed defence pathways, such as the MAPK signalling cascade in apple against *Fusarium proliferatum (Duan et al., 2022)* and the induction of phenylpropanoid biosynthesis in grapevine plants showing resistance to downy mildew (Li et al., 2015). Patil & Tripathi(2024) revealed that differential expression of 15 miRNAs regulates disease resistance, susceptibility, and tolerance of papaya plants to Papaya ringspot virus. Md Saad et al. (2022) Analysed the host-pathogen interaction of *Erwinia mallotivora* with both susceptible and resistant papaya varieties by dual RNA-sequencing to unravel the interaction between co-expression analysis of T3SS effector genes and biotic stress-related transcription factors. Liu et al. (2025) found out that the accumulation of various secondary metabolites, especially terpenoids, in response to pathogen *Cytospora mali* in apple species *Malus sieversii* was linked to upregulation of transcription factors AP2/ERF and WRKY domain. Error! Reference source not found. (adapted from (Amil-Ruiz et al., 2016) depicts the cross-talk between SA and JA pathways triggered by fungal elicitors in strawberry black spot resistance.

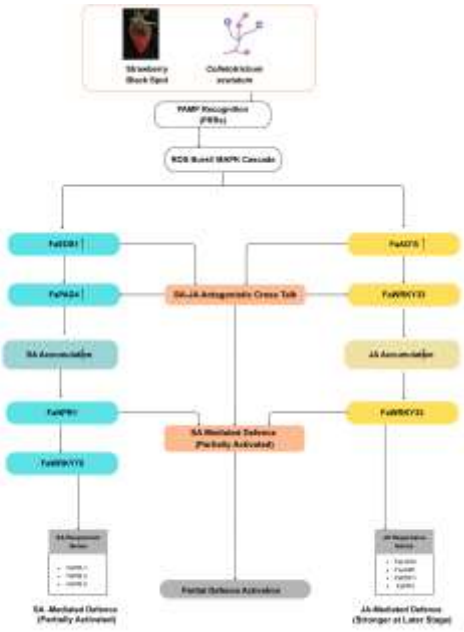

Figure 4.Interaction between strawberries and the pathogen *Colletotrichum. acutatum* triggers a sophisticated hormonal network. By engaging MAPK and WRKY33 signaling, the plant balances Salicylic Acid, Jasmonic Acid, and Ethylene pathways. This integrated response allows the plant to deploy a variety of defensive strategies—Systemic Acquired Resistance, Systemic Defense, and Pathogen Defense—to combat the infection across its entire system

Transcriptomic Research on pathogen-fruit datasets is heavily reliant on correlative data obtained from prediction models of transcription families based on model species. For the establishment of true causality, these correlative network predictions must be integrated with functional validation methods such as chromatin occupancy data, cis-motif enrichment, and reverse-genetics in fruit crop species(Zang et al., 2020).

3.3. Proteomics: Protein Arsenal for Fruit Crop Defence

Pathogen detection in the plant cell occurs through the interaction of pathogen-produced structures, known as Pathogen- or Microbial-Associated Molecular Patterns (PAMPs or MAMPs), with protein structures called Pattern Recognition Receptors (PRRs), which are present in the plant cell. These interactions activate Pathogen-Triggered Immunity (PTI), which comprises the first line of plant defence, resulting in the production of various secondary messengers such as Cyclic Guanosine Monophosphate (cGMP) and Mitogen-Activated Protein Kinases (MAPKs), which are involved in potentiation of further defence responses by the plant (Grandellis et al., 2016). Membrane-bound proteins, such as receptor-like kinases and receptor-like proteins, are responsible for intracellular signal transduction and stimulation of MAPK by activation of a phosphorylation cascade(Reyes Zamora et al., 2024). Pathogens can also evade PTI by secreting specialized effector molecules, which initiate effector-triggered immunity (ETI) upon recognition by plant resistance proteins. Nucleotide-Binding Leucine-Rich Repeat Protein acts as a switch for turning on ETI and controls hypersensitive response, ROS outbursts, and programmed cell death (Wang et al., 2023). Both PTI and ETI promote the synthesis of antimicrobial peptides and defence molecules like pathogenesis-related proteins that significantly contribute to neutralization of pathogen attacks (Putra et al., 2025).

Table *3* discusses the PR protein families involved in PTI/ETI mechanisms across fruit crops, highlighting the importance of proteomics in defence activation. **Figure 5** outlines how both PTI and ETI promote plant defence responses such as PR gene activation and cell wall fortification.

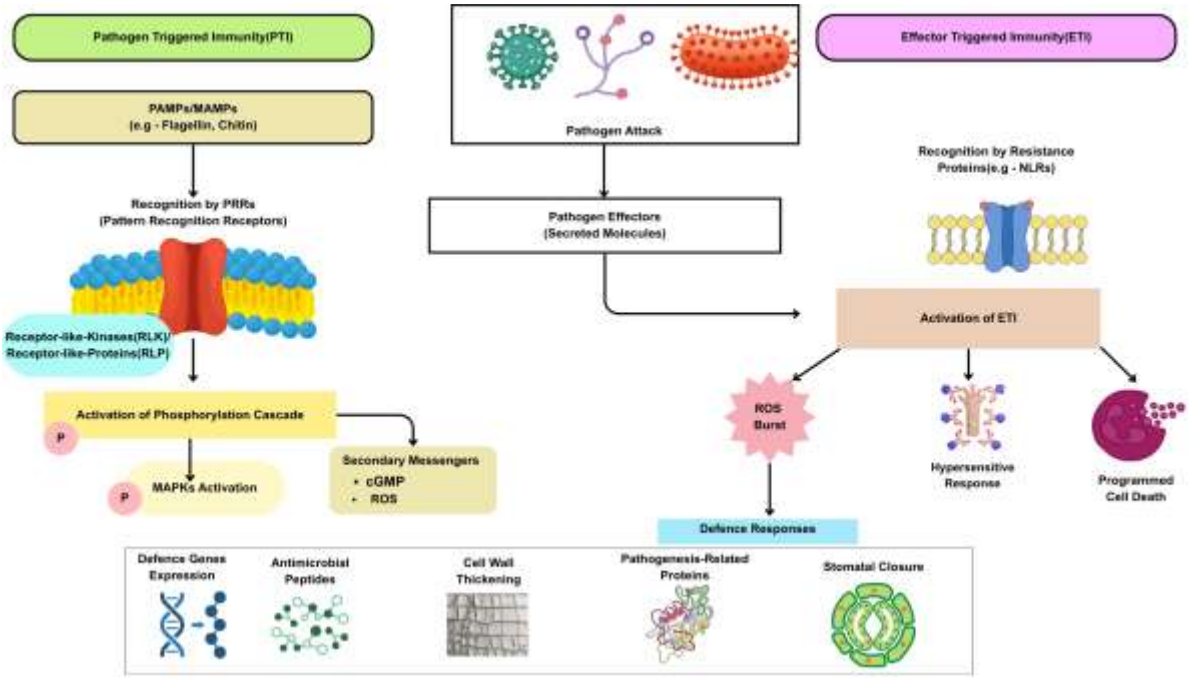

Figure 5. Molecular mechanisms of plant immunity in fruit crops during pathogen attack, depicting pathogen-triggered immunity (PTI) initiated by PAMP/MAMP recognition via PRRs, activation of MAPK cascades and secondary messengers (cGMP, ROS), and effector-triggered immunity (ETI) via NLR proteins, leading to reactive oxygen species (ROS) burst, cell-wall thickening, pathogenesis-related (PR) gene expression, hypersensitive response (HR), and programmed cell death.

Table 3. PR proteins in Fruit Crop Defence

PR Protein Family	Mechanism	Mechanism of Disease Resistance for Fruit Crops	Fruit Crop Disease	Reference
PR 1	SAR Pathway Activation	Reduced susceptibility of Swingle Citrumelo Rootstock	*Candidatus liberibacter asiaticus*	(Wu et al., 2018)
PR 2	B-1,3-Glucanase	Hydrolysis of the fungal Cell Wall	*Fusarium moniliforme* Mango Malformation	(Ebrahim et al., 2011)
PR 3	Endochitinase	Activation of Jasmonic Acid Signalling Pathway	*(Venturia inaequalis*) Apple Scab (*Venturia pyrina*) Pear Scab	(Perchepied et al., 2021)
PR 4	Chitin Binding Protein	Defence response	*Botryosphaeria dothidea* Apple Ring Rot	(Bai et al., 2013)
PR 5	Thaumatin-like protein	Membrane Disruption of Fungus	*Botrytis cinerea* Grape Bunch Rot	(Gkizi et al., 2021)
PR 6	Proteinase Inhibitor	Defence mechanism against fungal pathogens, lowering the susceptibility of infected plants		(Butassi et al., 2022)
PR 7	Subtilisin-like endoprotease	Accessory protein that helps in the dissolution of the cell wall of fungal pathogens		(Campos et al., 2007)
PR 8	Chitinase	Inhibitory effect on spore germination of the fungus	*Botrytis cinerea* Gray mold in apple	(Liu et al., 2013)
PR 9	Peroxidase	Plant Cell Wall Formation and ROS formation against spread of Fungal Pathogens		(Becker et al., 2023)

PR 10	Ribonuclease-like protein	Degradation of Nucleic Acids(DNA/RNA) of Fungus	*Monilinia fructicola* Brown rot in plum	(El-kereamy et al., 2009)
PR 11	Endochitinase	Attack on fungal pathogens in pear		(Han et al., 2025)
PR 12	Defensin protein	Accumulation of ROS species	*Cytospora mali* Apple Dieback	(Jia et al., 2025)
PR 13	Thionin	Membrane Disruption of Fungus	*Fusarium oxysporum*f. sp.*cubense* Banana -Panama Wilt	(Hamed et al., 2018)
PR 14	Lipid Transfer Proteins	Membrane Disruption *p*	Bacterial and Viral Pathogens of *Citrus sp*	(Campos et al., 2007)
PR 17	Aminopeptidase	Defence Response	*Xyllela fastidiosa* Citrus Variegated Chlorosis	(Campos et al., 2007)

Even though 17 PR-Protein families are classified in plants, high-resolution experimental structures are available only for a few fruit crops. Functional annotation of PR- Proteins present in perennial fruit crops is done by computational homology models from model species *Arabidopsis spp.*, tobacco, or cereals. Defence proteins exhibit distinct sequence divergence in critical regions such as active-site loops, glycosylation motifs, and oligomerization interfaces due to post-translational modifications(PTM)(Muleya et al., 2022). This dependence on non-fruit templates misrepresents substrate pockets, membrane-interaction surfaces, and protease- sensitive regions. Moving forward, the field of proteomics should integrate systematic structural profiling of fruit crop defence proteins and PR isoforms with PTM for better mechanistic understanding of proteomic defence.

3.4. Metabolomics: Role of Metabolites in Plant Defence

Pathogen infection in fruit crops initiates the production of secondary metabolites, which are protective in nature. Various metabolites, such as tannins, phenols, terpenes, and sulphur and nitrogen-containing compounds, contribute to plant defence through strengthening of cell walls and eliminating microbial invaders, while also serving as signalling agents to regulate hormonal and genetic defence responses(Khan et al., 2025). The major pathways involved in the production of various secondary metabolites are the shikimic Acid pathway, the malonic Acid pathway, the mevalonic acid pathway, and the phenylpropanoid pathway(M. Kajla et al., 2023). The shikimic acid pathway is involved in the production of aromatic acids like phenylalanine, tyrosine, and tryptophan, which serve as precursors for the production of phenolics, flavonoids, and alkaloids(Ge et al., 2019), whereas the mevalonic acid pathway plays a significant role in the production of terpenes, steroids, and plant hormones. The phenylpropanoid pathway is involved in the synthesis of flavonoids, tannins, coumarins, and lignin through the conversion of phenylalanine, which is derived from the shikimic acid pathway(Araujo et al., 2014). Md Saad et al. (2022) discovered that the compounds formed by the terpenoid biosynthesis pathway and the steroid biosynthesis pathway regulate defence responses against *Erwinia mallotivora* in *Carica papaya cv. Eksotika and Viorica.* Further cases of metabolite-derived disease resistance are mentioned in

Table *4*.

Most metabolome studies in fruit pathology studies are untargeted and correlational: LC-MS or GC-MS workflows identify metabolites that accumulate during infection or in resistant genotypes without establishing whether they are causative agents, metabolic bystanders, or mechanistic drivers of resistance(Kalaignan et al., 2025). For the establishment of a mechanism, LC-MS and GC-MS-based profiling in fruit crops should be done along with NMR, FT-ICR–MS, and Raman Spectrosocopy. This approach will enhance the accuracy and specificity of metabolomic analyses in fruit-pathogen systems, mapping candidate defence metabolites within their chemical environment, providing the foundation for understanding biosynthetic pathways and metabolic targets.

Table 4. Role of Secondary Metabolites in Disease Resistance of Fruit Crops

Metabolite Class	Defence Mechanism	Role in Disease Resistance for Fruit Crops	Reference

Saponins	Plant Defence Induction & Cell Membrane Peroxidation of Fungal Cells	Antifungal activity against *Valsa mali* (Valsa canker) and *Botryosphaeria dothidea* (apple ring rot) in Apple	(Li et al., 2023)
Flavonoids	Structural Fortification of Plant Cell and Membrane Disruption of Pathogen	Prevent the growth of the fungus *Coniella diplodiella,* causing white rot in the Chinese grapes variety	(Tan et al., 2024)
Terpenes	Induction of Systemic Resistance	Toxic effects on fungal pathogens such as *Botrytis cinerea and Colletotrichum gloeosporioides*	(Z. Zhang et al., 2022)
Coumarins (Scoporane)	Phytoalexins and Phytoanticipins	Higher amounts of Coumarin concentration in Citrus latifolia provided resistance against Citrus Black Spot Disease caused by the fungus *Phyllosticta citricarpa*	(P Fernandes et al., 2022)
Stilbenes (Resveratrol)	Phytoalexin	Transgenic grapes expressing stilbene synthase showed disease resistance against the powdery mildew fungus *Erysiphe necator*	(Liu et al., 2019)
Lignin	Plant Cell Wall Fortification	Lignin accumulation in apple roots boosts immunity against *Fusarium solani,* causing apple replant disease	(Zhou et al., 2025)

3.5. Phenomics: Rapid Disease Detection and Assessment of Disease Resistance by Image-Based Phenotyping

A combination of high-resolution imagery data captured using unmanned aerial vehicles(UAVs), satellites, etc., with advanced machine learning models and artificial intelligence, has the potential for rapid non-destructive detection of disease symptoms and phenotypic quantification of resistance (Gomez Selvaraj et al., 2020). Deep Convolution Neural Networks (CNN), a type of deep learning model, are suited for the analysis of large visual datasets obtained through different imaging technologies. This allows for rapid detection of disease symptoms (Sanga et al., 2020). Multispectral imaging analyzes data acquired across five discrete bands, comprising blue, green, red, red edge, and near-infrared (400-1000nm), allowing for the detection of diseases such as apple fire blight, banana fusarium wilt, and grapevine trunk disease. (Bendel et al., 2020; Xiao et al., 2022; S. Zhang et al., 2022). Hyperspectral imaging analyses data across a large number of spectral bands (400-2500nm), allowing for more precise detection compared to multispectral imaging, and is used for early detection of diseases such as Banana Sigatoka (*Pseudocercospora fijiensis)* and apple mosaic disease (Liu et al., 2023; Ugarte Fajardo et al., 2020*).* Thermal imaging measures changes in leaf temperature by detecting changes in infrared radiation, which allows presymptomatic detection of diseases such as banana sigatoka leaf spot and apple fungal mold (Anasta et al., 2021; Lipińska et al., 2022). Chlorophyll fluorescence imaging monitors changes in leaf phytochemistry due to pathogen infection and is used to detect diseases such as White Root Rot in avocado and Bull's Eye Rot in apple (Martínez-Ferri et al., 2015; Pieczywek et al., 2018). Bio speckle imaging measures dynamic fluctuations of laser light scattered from living tissues for the detection of changes in metabolic activity due to diseases such as green mold in citrus and bull's eye rot in apples (Pieczywek et al., 2018; Yang et al., 2024). Phenomics-driven workflows facilitate resistant genotype selection and precision disease management in fruit crops, as illustrated in **Error! Reference source not found.**. Integration of phenomics data with genomics, deep learning models, and Artificial Intelligence has helped farmers for early detection and management of diseases in apple, guava, and papaya (Chao et al., 2020; Gulzar, 2025; Paramesha et al., 2025; Sangeetha et al., 2023).**Figure 6** depicts a phenomics workflow that supports precision disease management by linking field phenotypes to breeding decisions.

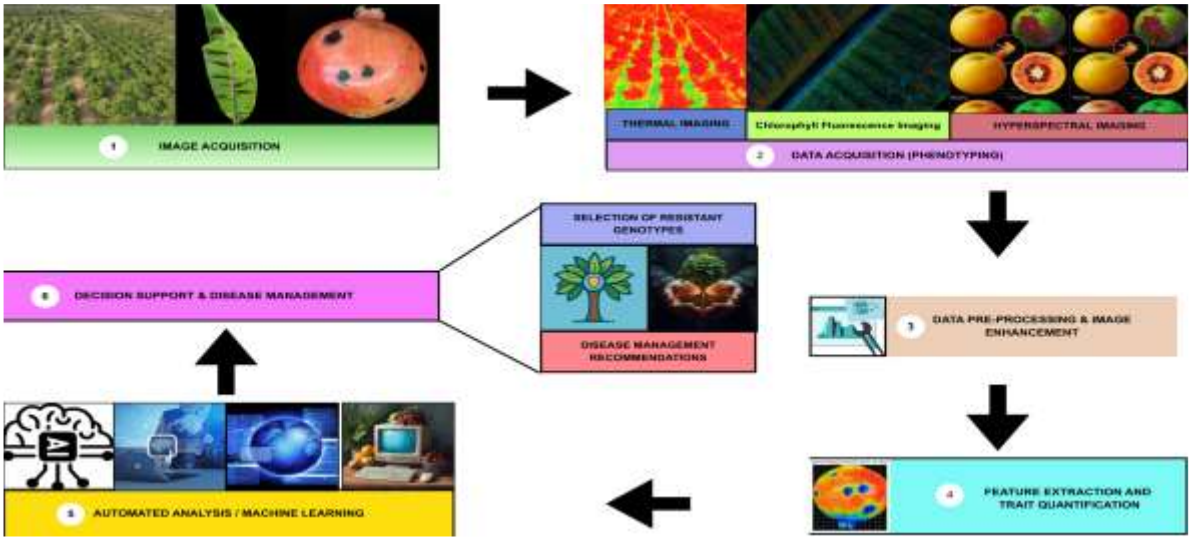

Figure 6. Phenomics workflow from field image acquisition of symptomatic/asymptomatic tissues through thermal/hyperspectral imaging, data acquisition and preprocessing/enhancement, feature extraction and trait quantification using machine learning, and genomic selection of resistant genotypes to support decision-making for integrated disease management.

3.6. Metagenomics: Analyzing Microbial Community Dynamics for Disease Management

Metagenomics reveals the role of plant-microbe interactions in disease suppression by identifying beneficial microbes that enhance fruit-crop defence. High-throughput NGS technologies have improved the analysis of microbial community interactions with the plant and pathogenic microbes, allowing for the characterization of beneficial microbes that are antagonistic to plant pathogenic microbes (Zambounis et al., 2020). Databases like KEGG(Kyoto Encyclopaedia for Genes and Genomes) and COG(Clusters of Orthologous Genes) are utilized for unravelling the microbial metabolic pathway linked to biocontrol properties of the beneficial microbe against the pathogen, allowing for the development of these beneficial microbes as biocontrol agents (Ravinath et al., 2024). Plant growth-promoting rhizobacteria, such as *Kocuria rhizophila*, *Acinetobacter rhizosphaerae*, *Pseudomonas stutzeri*, *Pseudomonas veronii*, and *Stenotrophomonas geniculate,* are present in the soil microbiome of apple orchards and contribute to the bioremediation process in apple trees by bolstering the immune response indirectly (Mendybayeva et al., 2025). Examples of how various microbial organisms provide disease resistance against various fruit crop diseases are listed in

Table *5*.

Table 5. Metagenomic Insights into Microbial Metabolites Involved in Fruit Crop Disease Resistance

Biocontrol Agents	Pathogen Controlled	Fruit Crop Disease	Mechanism of Disease Suppression	Reference
***Debaryomyces hansenii* strain:KP006**	Colletotrichum *gloeosporioides* *Botryodiplodia theobromae*	Mango Anthracnose Mango Stem End Rot	Induction of host resistance and production of antifungal compounds	(Prasad et al., 2024)
Bacillus velezensis	*Trichothecium roseum*	Pink Rot in Citrus	Antifungal effects and production of defence-related enzymes	(Zhu et al., 2025)
Pseudomonas lurida	*Botryosphaeria dothidea*	Apple Ring Rot	Downregulated expression of pathogenicity-related genes and defence activation of the host plant	(Huang et al., 2026)
***Bacillus* sp. GVS2**	*Rotylenchulus reniformis*	Reniform nematode disease in pineapple	Induced Systemic Resistance by activation of jasmonic acid and ethylene signalling pathways	(Soler et al., 2021)
***Yarrowia lipolytica* strain MBC25**	*Botrytis cinerea*	Gray mold in Strawberry	Antifungal activity by secretion of enzymes and metabolites	(Karimi et al., 2025)
***Burkholderia sola* NAU20**	*Colletotrichum gloeosporioides*	Strawberry Anthracnose	Antifungal Activity by accumulation of ROS species and enzymes	(Wang et al., 2025)

Most of the biocontrol claims listed in

Table *5* are based on in-vitro or greenhouse experiments without validation from multi-year field trials across commercial orchards. This is a serious limitation for practical implementation, as disease suppression due to a microbial strain is dependent on soil physicochemistry, rhizosphere, and climate. Multi-omics designs that combine metagenomics with host transcriptomics and metabolomics are absent for fruit crops, leaving this field as a mechanistically poorly understood area requiring systematic study.

3.7. Integrative Multi-Omics Approach in Fruit Crop Disease Management

Due to the complexity of plant systems, a single omics technology is insufficient to explain the complex mechanisms of disease advancement and resistance in plants. Researchers can build interactive networks that model fruit crop- pathogen dynamics by integrating genomics, transcriptomics, proteomics, and metabolomics. The use of a multi-omics approach helps scientists to understand how plant-pathogen interactions occur at a multidimensional level (Sun et al., 2025). This approach provides sustainable and innovative solutions for disease management in fruit crops (Liu et al., 2025). Shen et al. (2019)proposed an integrative multi-omics approach by employing (Bulk Segregant Analysis) BSA- sequencing and RNA sequencing for the identification of resistance genes and QTL (Quantitative Trait Loci) expressed against *Botryosphaeria dothidea* infection in apple. *Fusarium oxysporum f. sp. cubense* causes Panama wilt in bananas, a devastating disease that cannot be controlled by chemical or physical methods after establishment (Villao et al., 2025). Sunisha et al. (2020) transferred antimicrobial genes *Ace*-AMP1 and *pflp* into embryogenic tissues of the banana variety Rasthali Agrobacterium-mediated transformation. The transformants showed enhanced tolerance to the disease. Researchers performed RNA sequencing for analysis of differential gene expression in banana plants and found that transcription factors such as 29 *ERFs*, 18 zinc finger proteins, 12 *WRKYs*, 9 *NACs*, and 5 *MYBs* were produced in response to the infection (Cheng et al., 2021). Metabolomic analysis of *Fusarium*-resistant banana variety Guijiao 9 showed that lipid metabolism, phenylpropanoid metabolism, and cell wall modification played a role in immune response (Tian et al., 2023). Metagenomic studies on a resistant banana cultivar, Anaikomban, demonstrated that the *Bacillus subtilis* isolate AKPS2 exhibited antagonistic properties against the fungus (Ajesh et al., 2025). Elinisa et al. (2025) utilized a deep learning image segmentation model, U-Net, for early detection of Fusarium disease by automated identification of symptoms from field images. Integration of different omics data will help to model crop-pathogen dynamics and provide promising sustainable disease management solutions in fruit crops.

3.8. Artificial Intelligence and Machine Learning for Omics Data Integration

Analysis of multi-omics data poses several challenges due to the data showing hyperdimensionality, intrinsic variability, and tightly coupled variables. Methods like classical univariate and multivariate statistics, which are commonly used for data analysis, have low efficiency in handling omics data. Statistical models such as ANOVA, linear regression, and mixed linear models are reliant on assumptions of linearity, normality, and independence among variables, which do not take into account the complex and unpredictable mechanisms behind disease resistance traits (Niazian & Niedbała, 2020). Machine learning methods, such as Random Forest, SVM, and Neural networks, can be classified as artificial intelligence technology that is used to build prediction models for plant disease diagnosis. The accuracy of the evaluation model is calculated using unbiased metrics such as true positive rate, true negative rate, precision, and recall (Ahmed & Yadav, 2023). Gan et al. (2025) demonstrated that machine-learning-based selection models outperform conventional statistical methods for predicting disease and pest resistance. Traditional machine learning model SVM(Support Vector Machine) provides an accuracy of 70-80%, whereas deep learning models like CNN(Convolution Neural Networks) and RNN(Recurrent Neural Network) achieve an accuracy over 90%(Paramesha et al., 2025). These models integrate different omics layers by joint representations, which allows the discovery of synergistic gene-protein-metabolite networks that are crucial for host-pathogen interactions. But, successful integration also requires effective preprocessing, dimensionality reduction, and validation to ensure biological continuity. Therefore, ML-based feature selection along with domain expertise and experimental validation are critical for converting multi-omics findings into practical breeding and disease management solutions (Cheng & Wang, 2024). As shown in **Figure 7**, convolutional and pooling layers progressively refine image features for the accurate prediction of disease presence in fruit crops

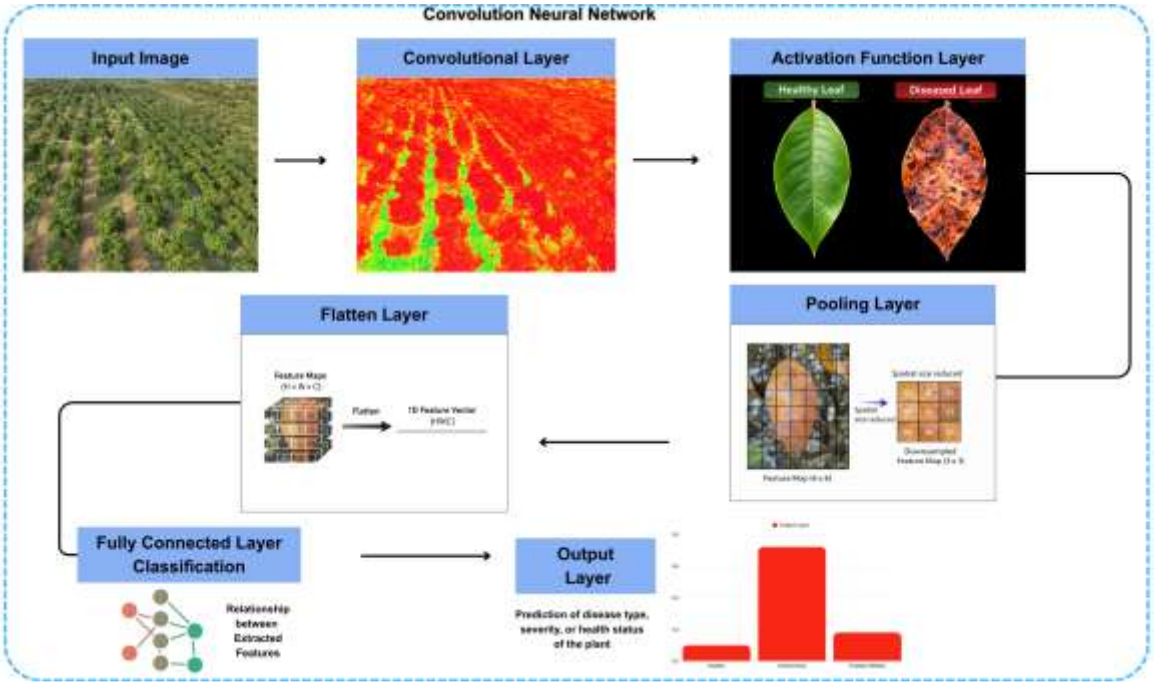

Figure 7. Convolutional neural network (CNN) architecture for hyperspectral image classification in fruit crop disease phenotyping, showing the sequential processing from input field/orchard images through convolutional layers (feature extraction), pooling layers (dimensionality reduction), flattening, fully connected layers (feature integration), and activation/output layers yielding disease type probabilities

3.9. Challenges and Limitations of Omics Technology

Although technology has advanced significantly in the past decade, integrating omics technology for successful disease management in fruit crops will likely take decades to realize. This is due to the several technical, computational, and practical hurdles involved in adopting this technology, which restrict its widespread use. The complexity of the biological data comprising various omics technologies is also a constraint for adoption. The datasets generated by the multi-omics approach are heterogeneous in nature. Therefore, an integrated multi-omics approach for disease management requires multiple bioinformatic tools, experts of different scientific disciplines, and standardized technology with protocols (Fan et al., 2025). The functional validation of newly identified genes, transcripts, and proteins that provide disease resistance is difficult and requires experimental verification. This can sometimes only be done through multiple orchard trials, which resemble biological systems with pathogen challenges, variable environmental conditions, and developmental stages of commercial fruit production. Integration of several omics disciplines for disease management also requires successful collaboration between breeders and researchers of various disciplines. This poses another challenge for the adoption of omics technology due to a lack of skilled personnel.

3.10. Ethical & Regulatory Considerations

Ethical and regulatory frameworks of various government policies pose another hindrance to the adoption of multi-omics technology (Haokip et al., 2023). Farmers are reluctant to adopt different multi-omics approaches for disease management strategies in fruit crops. Consumer non-preference in the EU and the USA towards products of genetically modified crops discourages the adoption of multi-omics technologies by farmers (de Andrés-Sánchez et al., 2025). Farmers are often unaware of the ethical implications of privacy and the sharing of data related to omics technology. If different nations adopt policies that support the application of omics technology, the rate of adoption of this futuristic technology will increase.

3.11. Future Perspectives

The potential for using multi-omics for disease management in fruit crops is enormous and largely remains neglected in both developing and developed nations.

The development of modern gene editing technologies will replace or augment conventional breeding methods in the future. This has high potential for shortening the breeding cycle of fruit crops and rapid development of lines resistant to newly evolved pathogens. This is very important in the case of perennial fruit crops, as major fruit crops have long juvenile phases.

Research and development of bioinformatic tools and computational systems is crucial for the integration of data from various omics technologies. Advanced computers and machines allow for larger data storage, faster analysis, and integration of data for deciphering fruit crop-pathogen relations.

The development of portable, simple, miniature biosensors and sequencing devices will enhance the widespread adoption of multi-omics approaches by scientists and farmers in fruit crops for disease management.
Future advancements in automation, IoT integration, and blockchain technology will improve the adoption rates of multi-omics technologies in fruit cultivation. These innovations will enhance the resilience and sustainability of fruit crops through efficient management of various diseases (Kaya, 2025).
Hands-on training in different omics technologies for upcoming farmers, horticulturalists, researchers, and students will open the door to infinite possibilities for the development of disease-resilient fruit crops, advanced diagnostic precision, and sustainable fruit crop management.
Adoption of policies favourable to the growth of multi-omics technology by nations is crucial for the development of sustainable disease management practices in fruit crops.
Research into multi-omics technology for post-harvest disease management in fruit crops has increased in recent years. Limited research has been conducted on applying multi-omics technology for managing fruit crop diseases at the field level.

4. CONCLUSION

Multi-omics approach - consisting of genomics, transcriptomics, proteomics, metabolomics, phenomics, and metagenomics has transformed the disease management process in fruit crops by providing detailed insights into the molecular and physiological interactions between fruit crops and their pathogens. However, this review identifies a critical limiting factor: the field's focus remains largely on individual omics layers, obscuring the inter-layer functional connections. Lack of a coordinated reference dataset similar to the Cancer Genome Atlas for fruit crops prevents detailed study of pathosystems. Establishment of open-access, standardized multi-omics datasets for 3-4 model fruit pathosystems, such as Fusarium wilt of banana, Papaya Ringspot Virus, due to their economic significance, is the need of the hour.
Global adoption of multi-omics technology for fruit crop disease management is still limited due to technical, financial, and infrastructural constraints. The major hurdles include data integration across various omics platforms, standardization of experimental techniques, and practical field application of multi-omics technologies. Development of computational frameworks that account for the unique challenges of fruit crops, such as long-term epigenetic memory and tissue-level heterogeneity, is required. Socio-ethical considerations and regulatory frameworks of various nations oppose the implementation of multi-omics technology in fruit orchard disease management.
Prioritization of research and development in multi-omics technologies and bioinformatics tools at the global and regional levels is crucial for identifying disease resistance mechanisms, integrating data across various omics disciplines, and accelerating the breeding of resilient fruit crop varieties. Investment in infrastructure, training on multi-omics technologies and bioinformatic tools, and favourable regulatory policies will enable the practical implementation of these technologies for fruit orchard disease management. The continued development of multi-omics technology will revolutionize global fruit crop production systems, bolster food and nutritional security, and transform fruit crop disease management strategies for sustainable production.

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CONFLICT OF INTEREST

The authors declare that they have no conflict of interests.

AUTHOR CONTRIBUTIONS

Joebin Salin: Conceptualization; writing—original draft; data curation; formal analysis; visualization; figure preparation; methodology. **D. Vidhya**: Supervision; conceptualization; writing—review and editing; methodology; validation; project administration**. J. Auxcilia**: Investigation; data curation; writing-original draft; resources; formal analysis. **N. Indra**: Investigation; data curation; writing-review and editing; visualization. **R. Suresh**: Methodology; writing-review and editing; formal analysis; software; data curation. **P. Renukadevi**: Supervision; investigation; writing-review and editing; resources; pathology expertise.

DATA AVAILABILITY STATEMENT

Data supporting this study are available within the manuscript.

DECLARATION OF GENERATIVE AI & AI-ASSISTED TECHNOLOGIES

During the preparation of this manuscript, the authors used Grammarly solely for grammar, spelling, sentence structuring, and readability improvements. Grammarly was not used to generate scientific content, arguments or data; all ideas, interpretations and conclusions are the authors' own. After using Grammarly, the authors carefully

reviewed and edited all suggested changes and take full responsibility for the accuracy and integrity of the manuscript.

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