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# OMICS APPROACHES ASSISTED WITH ARTIFICIAL INTELLIGENCE AS A TOOL AGAINST BIOTIC STRESS TOLERANCE IN PLANTS- A REVIEW

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**Abstract:**
With increasing human population the entire world is facing the problem of food production. Feeding of growing population becoming more difficult due to unpredictable change in climate condition creating pressure on crop production to agriculture community. Plant faces range of biotic stresses which affect growth and development at various stages and interferes cellular, molecular and development processes which reduces agriculture crop productivity. Therefore there is a need to develop sustainable approaches or solutions to address such issues. This can be achieved by using multi omics approaches that help in grasping the molecular mechanism involved in stress resistance mechanism, characterize plant biomolecular pool which help in maintaining response to variable environmental condition. It will provide better understanding of integrated omics approach along with the adoption of artificial intelligence algorithms to understand complex omics data for improving plant tolerance to biotic stress and identify possible targets for enhancing resistance through recombinant DNA technology or plant breeding approaches. Therefore this review provide perception into multi-omic approaches, their limitations and how omics assisted by artificial intelligence present a valuable tool in understanding host pathogen interactions and provide a way for effective crop development strategies under the scenario of climate change.

**Keywords:** Climate change, Biotic stress, Omics, Crop production, Artificial Intelligence.

## 1. INTRODUCTION

It is analysed that world population will reach 9.7 billion by 2050 and to feed such huge population the demand for food supply is also rising. In order to overcome this issue innovative solutions and interdisciplinary research to support food supply by increasing agricultural productivity is the need of the hour (Fukase and Martin, 2020). These problems are moreover enhanced by the available biotic stress present in the environment as plants interact with various biotic stresses like insects, bacteria, viruses, fungi, weeds etc in the environment. Their interaction affects various physiological activity in plants which are also beneficial for regulating plant activity but in some cases they are also harmful for the plants causing diseases Schirawski and Perlin 2018; Crandall et al. 2020).

Microbial illnesses and pest infestations cause significant yield decreases in food crops worldwide. Substantial loss of 30.3%, 22.6%, 21.5 %, 21.4%, 17.2% in rice, maize, wheat, soyabean and potatoes respectively was reported (Savary et al., 2019). Plant infections can be highly destructive, causing output reductions of up to 50% in some areas. They notably affect small-scale farmers and provide significant financial difficulties. Both human health and species diversity are affected by the occurrence of plant diseases which increase the cost of disease control strategies (Ristaino et al., 2021). Similarly the sustainability of crop production, good human health and food security reported to be affected by the outbreak of new pest and diseases (Anderson et al., 2004) Emerging plant diseases are predicted to become more common and severe in the upcoming years due to the shifting distribution of pathogens brought on by climate change and increased international trade ((Bebber et al., 2013).Heavy losses in economic yield of coffee was reported in Central America due to severe outbreak of Hemileia vastatrix's (Avelino et al., 2015).

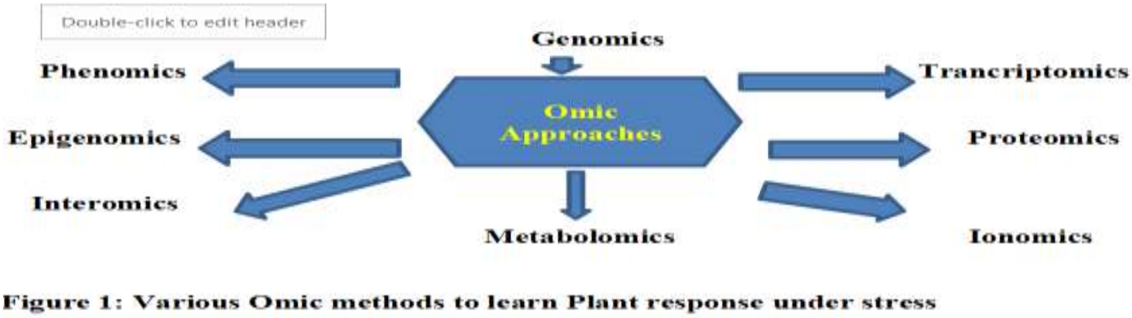
Due to declining agricultural productivity as a result of these environmental stresses there is a huge pressure on the agriculture sector to develop resilient crop with improved yield. (Wu et al., 2024). Pattern Recognition Receptors are activated in response to stress that help in the identification of Pathogen -Associated Molecular Patterns which activates immunity in plants. Several compounds like salicylic acid, jasmonic acid, and ethylene and reactive oxygen species are produced that help in the regulating the expression of genes involved in production of mitogen-activated protein kinase, heat shock proteins and help plant to maintain homeostasis under stress condition (Nicaise et al. 2009; Zhang et al. 2021). These changes affect crop productivity by modulating plant growth, development and physiology there by affecting yield (Song et al., 2026). Understanding plant resilience under biotic challenges can be revolutionized by integrating omics methods, which include transcriptomics, genomes, proteomics, metabolomics, and phenomics. These are specific to the developmental stage and vary according to cell and tissue location in an organism (Griffin 2004). By analysing complex relationship between biological molecules and their function against stress this multi-omics paradigm enables researchers to develop more successful crop enhancement solutions as they provide both host and pathogen profiling exposing regulatory networks and co-evolutionary processes that are frequently overlooked by single omics methods (Li et al, 2019).

This review will intend to provide deep understanding of interaction between host and pathogen by employing multi-omics approaches. Researchers can find important regulatory molecules, understand function of effector proteins and discover pathways of disease resistance or vulnerability by combining transcriptomics, proteomics, and metabolomics. The review also focuses on the computer based tools—from statistical frameworks to machine learning and deep learning techniques—that make it easier to integrate these various datasets.

## 2. OMIC APPROACHES

At molecular level plant responses to stress can be determined by omics approaches as given in Figure 1. With the help of genomics tools and techniques like whole genome sequencing genome-wide association and CRISPR/Cas genetic variation and stress responsive genes can be identified. Similarly Next generation sequencing techniques identifies change in expression of genes under stress condition and transcription factors, stress inducible genes analysed by qRT-PCR and microarrays (Roychowdhury et al., 2023). Stress specific proteins, post translational modification using SILAC is another techniques of Proteomics. Likewise another omic approach that is Metabolomics may use Liquid chromatography -mass spectrometry, nuclear magnetic resonance spectroscopy, and Gas chromatography–mass spectrometry techniques to determine the biochemical status in plants under stress environment and also determines presence of osmolyte, scavenging compounds of reactive oxygen species, and stress responsive secondary metabolites. Change in gene expression which are heritable studied by Epigenomics (Al-Amrani et al., 2021). Phenomics is used to achieve high-throughput phenotypic analysis under stress condition. Ionomics uses Inductively Coupled Plasma Mass Spectrometry to analyze the elemental makeup of plant tissues under stress. (Gupta et al., 2023).

**Figure 1: Various Omic methods to learn Plant response under stress**



### 2.1 Genomics

Genes and regulatory elements resulted from DNA sequencing and their characterization (Saeed et al., 2022). The genome of the plant is a dyanamic environment that has the capacity to adapt in the biotic stress condition. Recent advancement in genomics lead to the identification of loci that govern quantitative traits and complex traits that are controlled by gene regulatory networks. Like according to current pan-genomic studies in rice resistance to fungal disease are associated with lineage specific genes that are not present in reference genome. Most commonly studied genome is Rice because of its relatively smaller genome size (~ 430 Mb). Similarly Arabidoposis thaliana a model genetic plant has also shown itself to be a useful tool for figuring out the essential regulatory pathways of plant stress response due to its variety of mutations and transgenic populations (Shinozaki and Yamaguchi-Shinozaki, 2022). Genetic architecture of complex traits are better studied by Genome Wide Association analysis. It have been successfully utilized in several crops like maize, rice, tomato, peach, lettuce, sesame to provide resources for agricultural functional genomics and inventories of allelic variations, and related genotype–phenotype relationships and also identified haplotypes for earlier unknown pathways (Liu et al., 2019).

These genes can offer the targets required for CRISPR/Cas9 editing and precision breeding, laying the groundwork for comprehending how transcription of these genes takes place (Omidiran et al., 2024; Qi et al., 2024). The availability of annotated resources has made the field of comparative genomics more feasible, due to the identification of genetic markers and gene of interest through genetic engineering and gene editing technology. Pan genomics explores variability at genetic level and evolutionary pathway to identify genes linked with stress tolerance against biotic stress (Naithani et al., 2023). The new subject of epigenomics combines genomics and epigenetics, which deals with heritable changes that go beyond DNA sequences. With epigenomic mechanisms reacting to stressors and environmental conditions, this integration determines how gene regulate plant cell response against stress. To examine these occurrences throughout embryonic stages or evaluate variations brought on by plant diseases, genome-level studies are required. (Callinan and Feinberg, 2006; Muthamilarasan et al., 2019). Genome editing has been revolutionized by the ground-breaking CRISPR-Cas9 technology, which originated in bacteria as a defensive pathway towards viruses. This allows specific change in gene sequence without introducing the gene of interest allowing plant adaptation to stress condition. The most utilized technique is CRISPR/Cas9 that makes the use of single guide RNA to mark particular DNA sequence causing cleavage which get repaired by non-homologous end joining and homology directed repair (Ajithkumar et al., 2025). This multiplexing technique speed up conventional plant breeding method and allow us to design news stress tolerant varieties. Eukaryotic genomes are widely edited by CRISPR-Cas systems, offering prospects to engineer crop plants for increased resistance to biotic stress. (Kumar and Jain, 2015). It has been reported that by this method gene structure of acetolactate synthase enzyme was modified to provide tolerance to herbicide in rice. Genome-wide linkage mapping has been successfully performed in maize to study gene that provide resistance to northern leaf blight (Kaur et al., 2022).

### 2.2 Transcriptomics

Transcriptome represent entire set of RNA transcript within a specific cells or tissue in an organism and transcriptomics allows analysis of genes transcription in response to environmental stimuli over a certain time frame (Raza et al., 2021). This allows examination of variations in gene expression, offering insights into the roles of certain genes. Transcriptomics studies was first subjected to study interaction between potato and Phytophthora infestans (Birch et al. 1999). After that many plant pathogen interaction trancriptome analysis was carried out (Meng et al. 2014; Chen et al. 2021 Qiu et al. 2023;). With the help of transcriptomics gene function can be predicted explaining host pathogen interaction. controlling their enzyme activities and gene expression, plants start a cascade as a signalling response to stresses. When stressors are present, they undergo metabolic changes that increase the transcription of genes involved in management of stress (Wang et al., 2020). DNA and RNA sequencing are high throughput sequencing techniques available nowadays that allows to access response of fruit crops under biotic stress. These approaches allows gene expression profiling for next generation sequencing. Several studies have been reported where scRNA sequence is used to study cellular diversity under stress condition (Choudry et al., 2024).Similarly in Arabidopsis, rice, maize, and soybean these technologies have been used to study stress tolerance mechanism (Khalid et al., 2019). Transcriptomics approach has successfully used in tomato by (Lie et al., 2019) and when the RNA sequencing data from the susceptible and resistant variety of tomato were analysed 209 and 809 genes in response to TYLCV infection showed distinct expression pattern. Similarly in soyabean against nematode infection micro array analysis was created to determine genomic expression of two distinct nematodes. Similarly two population one is compatible and other is incompatible were examined for pre and post parasitic infection on exposure to resistant soyabean genotype, potential parasitism genes showing differential gene expression across two grups were observed. (Mosa et al., 2019).

**2.3 Proteomics**

It involves identification, measurement and profiling of protein by giving information on change in protein expression in response to environmental stress and also provide information about their structure, function, modification and interaction with other proteins ( Kumar et al., 2023). Proteome vary depending on tissue type, age and how it respond the stress condition. Proteins play a key role in developing stress tolerant phenotypes by regulating cellular homeostasis and physiological processes under stress condition (Hasan et al., 2024). It examines the function of proteins involved in the stress response and how they might be used to develop techniques for making plants relatively resistant to strain, in addition to streamlining the identification of plant phenotypes (Singh et al., 2021; Rani et al., 2021). Proteomics allows understanding of variation that occurred after protein synthesis, by interaction with other proteins and change in protein expression under different stress condition. Also helped in identification of biochemical markers and regulatory proteins involved in plant adaptation under stress condition (Liu et al., 2019). Understanding how plant resistance functions and identifying the molecular mechanisms that control susceptibility or resistance are crucial in biotic stress situations. Recent research has demonstrated the strong relationship between a plant's spatial proteome and post-translational modifications and its immune response (Katam et al., 2020). Structural, sequence, and phosphor proteomics represents classes of proteomics that study expressed proteins (Aizat et al.,2018). Different techniques are used to examine protein structures such as electron microscopy, X-ray diffraction, nuclear magnetic resonance (NMR), crystallization, and computer-based modelling (Lie et al., 2005)). Protein functions most commonly studied by Protein microarrays and yeast two hybrid assay (Lueong et al., 2014). Using techniques of proteomics like 2-Dimensional gel electrophoresis, gel free shotgun method protein content in rice kernels has been studied (Koller et al., 2002). Some proteomics techniques like liquid chromatography based separation are used to detect as TFs, kinases, and transport proteins whose abundance is low (Ghosh et al., 2014). Studies on comparative proteomics have been reported to improve crop yield in wheat by comparing proteome of Dasypyrum villosum and wheat scientist have concluded that protein found in Dasypyrum villosum are important for improving wheat yield under stress condition (Wang et al., 2021). The proteomes of chili peppers that are susceptible to and resistant to Fusarium oxysporum sp. were compared. Wilt illness in capsicum was studied using two dimensional electrophoresis. They found proteins from pathogen that produce reactive oxygen species, lignin that break plant cell wall and removal of ROS using integrated proteomics by host in Tamarindus indica. (Pandey et al., 2019; Yadav et al., 2022) and differential expression of proteins, some of which play crucial role in plant defence mechanism using tools of bioinformatics were observed, thereby explaining the function of proteomics to analyse protein and find genes which could be used in future to develop resistant cultivars. (Mariyam et al., 2023b).

**2.4 Metabolomics and Biotic Stress**

Metabolomics is one of the emerging approach that help us to understand how plants respond under stress condition by studying their metabolites. Researchers can pinpoint particular metabolites that are essential to plant defence mechanisms by examining the metabolic pathways that are changed under stressful circumstances. Metabolites involved in plant defence mechanism are easily analysed by using invaluable techniques of liquid and gas chromatography. Therefore it allows high-throughput wide evaluation of metabolities as compare to genomics and transcriptomics in plant system expressed under stress condition and can help in developing innovative techniques and approaches to improve plant resilience(Carrera et al., 2021) On exposure of plants with any of the biotic stress caused by pest, pathogen and herbivorous a defence system activates that cause reprogramming of specific metabolite is involved in improving survival. They also provide information on plant’s adaptive strategies of coping such issues (Fernández et al., 2022). It was reported that in response to pathogen attack Arabidopsis thaliana and Solanum lycopersicum activates their defensive mechanism by producing phytoalexins and other antimicrobial compounds. Production of phenolic compounds in response to fungal infection has also reported that provide structural immunity to the plants as well also showed antimicrobial activity (Daayf et al., 2012) as indicated in Table 1. Plant resistance is further influenced by genetic factors via quantitative trait loci (QTLs). For example, detoxifying mycotoxins

produced by infections is one of the resistance features linked to the Qfhs.ndsu-3BS locus in wheat. These QTLs provide information about the genetic foundations of plant defense by correlating with distinct metabolomic signatures (Srivastava et al., 2013)
The production of these metabolites vary depending upon the plant tissue and its exposure level to pathogens. Like expression of defence related metabolites are higher in roots due to their direct exposure with soil borne pathogen as compare to leaves. In case of Quercus species their conc of L-proline increased in roots as compare to leaves on exposure to Phytophthora cinnamomi and with reduced level of D-glucose and D-fructose sugar (Fernández et al., 2022) this differential metabolic response protects the general health and survival of plants. Differential expression of metabolites have also reported in seeds, flowers and leaves of Brassica juncea which played a important role in making plant resistant to pathogen (Farag et al., 2024) such studies provide valuable information for crop improvement programme.

**Table 1. Mechanism of chemical defence produced in different crops in response to biotic stress**

| **Plant** | **Type of Secondary metabolite produced** | **Target pathogen** | **Effect** | **Reference** |
|---|---|---|---|---|
| A. thaliana | Phenolic compounds | Pseudomonas syringae | Antifungal and antibacterial effect | Soylu et al., 2006 |
| A. thaliana | Phtolexins | Plectosphaerella cucumerina | Antibacterial effect | Fernández et al., 2022 |
| Solanum lycopersicum | Phytoalexins, such as rishitin | Botrytis cinerea | Support plant survival | Bulasag et al., |
| Hordeum vulgare | flavonoids, phenylpropanoids, fatty acids and terpenoids | Fusarium head blight | Hinder pathogen multiplication and cell structure | Kumar et al., 2016 |
| Zea mays | Terpenes | Spodoptera frugiperda | Minimize plant damage | Wang et al., 2022 |

Variable population within the same crop species show expression of different metabolites under stress condition like as compare to susceptible genotypes resistant cultivars reported to produce higher level of flavonoids and terpenoids (Zhu et al., 2022, Mashabela et al., 2023) Genetic diversity therefore play an important role in varietal development that can withstand biotic stress providing better yield under bad climatic condition (Razzaq et al., 2022). Breeders can quickly produce crops that are more resilient to pests, diseases, and herbivores by choosing particular metabolic features that confer resistance. Metabolomics thus makes precise breeding easier, encouraging the creation of adaptable crops for sustainable agriculture (Litvinov et al., 2021). Expression of metabolites under stress condition affect crop physiology affecting physiological process like photosynthesis and respiration and optimize energy use during stress, supporting survival of plant (Ribeiro et al., 2022). By combining metabolomics with other omics approaches new effective strategies can be developed for crop management and improvement (Wishart et al.,2019).

**2.5 Epigenomics, Ionomics and Interactomics**

Epigenomics involves chemical modification of DNA and associated histone proteins without changing the sequence of DNA to regulate gene expression. It is dynamic and very from cell to cell type. It can be done by methylation of DNA, histone and alteration of chromatin. In DNA methylation methyl group is added on the cytosine residue without alteration in the base sequence. This causes the repression of transcription of stress responsive genes thereby preserving energy and optimizing stress signalling, or mobile genetic elements, which are frequently reactive to stress and have the potential to destabilize the genome if left unchecked.
The change in gene expression due to epialleles are heritable, these alleles help plant to adapt under stress condition and provide resistance to diseases. The stress memory remain in the plant and provide adaptive

benefits under variable stress conditions. These epilalleles can be utilized for developing crops that are resistant to stress without DNA sequence alteration and provide an efficient method for crop improvement without involving foreign DNA (El-Sappah et al., 2021). Another mechanism of epigenomics is Histone modifications which are done by acetylation, methylation, phosphorylation and ubiquitination of histone protein required for chromatin activity and gene regulation. When plants are subjected to stress condition some histone proteins are activated like H3 lysine 4 trimethylation and H3K27me3 that increase the transcription. Depending upon the residue on which methylation occur and level of methylation gene expression are regulated like methylation of H3K4me3 is related to gene activation, whereas H3K27me3 and H3K9me2 are involved in gene silencing (Le et al., 2025). These epigenomic modification help in activating stress responsive genes more efficiently and also creates stress memory for future exposure to stresses as in Arabidopsis and rice methylataion of regulatory gene induce tolerance against stress (Bhadouriya et al., 2021). In response to stress MAPKs induce dephosphorylation to induce or compress gene expression immediately (Patel et al., 2024). These modification produce a code of histone that activates expression of stress tolerant genes and allow plant to acclimatise to changing environmental condition (López-Hernández et al., 2025). Similarly chromatin remodelling allows understanding of mechanism behind gene expression under stress condition (Long et al., 2024). One of the most used complex is Switch/Sucrose-Non-Fermentable (SWI/SNF) driven by ATP to reposition nucleosome and allow specific genes to express against stress by exposing their DNA sequence and affect leaves architect, flowering time and root architect (Chen et al., 2024). Similarly research on ionomes provide valuable information which allow control on plant genome function. Ionic characteristics of plants are provided by comprehensive database The Purdue Ionomics Information Management System (PIIMS) which are used in analysis of genetic variation, allow identification of resistant genotypes also used in genome wide mapping (Kumari et al., 2015, El-Esawi et al., 2020). Ionomics can be combined with high throughput analysis such as bioinformatics that help in providing deeper understanding of host-pathogen interactions (Ali et al., 2022).
Another interdisciplinary approach that provide comprehensive understanding of plant system by combining multiple omic approaches like genomics, transcriptomics, proteomics, metabolomics, and epigenomics is Interomics (Chen et al., 2024). They provide insight how signaling pathway alter gene regulation under stress condition and allow plant adaptation (Sahoo et al., 2020). This also provide information for resilient crop development under climate change. Table 2 indicates different single omics approaches against different pathogens.

**Table 2: Indicates different single omic approaches used against different plant pathogen (Balotf et al., 2025)**

| Name of Pathogen | Target Crop | Omic Approach Used |
|---|---|---|
| Fusarium graminearum | Wheat | Genomics |
| Ralstonia solanacearum | Potato | Genomics |
| Heterodera filipjevi | Wheat | Genomics |
| Scleromitrula shiraiana | Mulberry | Genomics |
| Xanthomonas translucens | Small grain cereals | Genomics |
| Phytophthora infestans | Potato | Trancriptomics |
| Sclerotinia sclerotiorum | Pea | Trancriptomics |
| Hyaloperonospora arabidopsidis | Arabidopsis | Trancriptomics |
| Rhizoctonia solani | Wheat | Trancriptomics |
| Ralstonia solanacearum | Tomato | Trancriptomics |
| Magnaporthe oryzea | Rice | Proteomics |
| Clavibacter michiganensis | Tomato | Proteomics |
| Verticillium dahlia | Cotton | Proteomics |
| Botryosphaeria dothidea | Poplar | Proteomics |
| Stagonospora nodorum | Wheat | Metabolomics |
| Fusarium tucumaniae | Soybean | Metabolomics |
| Rhizoctonia solani | Rice | Metabolomics |
| Colletotrichum theobromicola | Strawberry | Metabolomics |
| Pyricularia oryzae | Rice | Metabolomics |

## 3. LIMITATION OF SINGLE OMIC APPROACHES

The expression of any genotype is affected by GXE interaction which is influenced by environmental factors therefore it is very difficult to made conclusion from only genomic data. Their relationship can be investigated by using transcriptomics, proteomics and metabolomics. There is a complex connection between these two levels. Like mRNA has introns and exons, introns are removed by alternate splicing and only the coding sequences are translated into proteins demonstrating the intricacy of cellular reactions to stress (McManus et al., 2015). There are several factors that affect translation through interaction with micro RNA (Liu et al. 2016). Non coding RNA like micro RNA and long non-coding RNAs is play crucial part in regulation of gene but they are not focussed in most transcriptomics studies (Ozsolak and Milos 2011). Like miRNA control protein synthesis in response to stress signal by binding to complementary sequences in mRNA causing m RNA degradation and translation inhibition. Similary long non-coding RNAs enhance or inhibit translation process by interacting with translation machinery in response to stress (Giland Ulitsky 2020). The reliance on good quality, annotated genomes is a technical drawback of transcriptome data. The accessibility of target organism reference genome that provide base for forming and annotation of expressed genes, is crucial to the precision and thoroughness of transcriptome investigations (Bakkeren et al. 2016). Using transcriptomic approach it is difficult to get complete genome of non cultural pathogens due to non availability of DNA of high molecular weight for sequencing but Unlike short-read sequencing methods long read sequencing method depth information required for complete genome assembly(Naranjo-Ortiz and Gabaldon 2020). Similarly compared to transcriptome data, proteome data show a stronger link with biological function (Bludau and Aebersold 2020). However, the large variance in protein concentrations within biological samples is a significant difficulty in proteomic analysis. In complex combinations, these concentrations can vary greatly, masking low-abundance proteins with high-abundance proteins (Righetti and Boschetti 2020). Understanding plant-pathogen interactions is severely hampered by this restriction since the low detection rate may make it more difficult to identify important pathogen effectors and virulence factors. It is challenging in shortgun proteomics to differentiate between proteins isolated from different species having common evolutionary ancestors such as a host and its pathogen in plant pathosystems, due to loss of the direct relationship to the original proteins. When two species have extremely similar or identical peptide sequences, this problem is most noticeable (Hubler et al. 2019). For instance, it is impossible to definitively attribute two peptides that are linked to a specific protein to a single species if their sequences are identical in the host and pathogen. The principle of parsimony, however, requires that all three peptides be ascribed to the host protein if a third peptide specific to the host is found, ignoring the potential that the pathogen variation may also be present (Gupta et al., 2015). This is where transcriptomics comes in handy since mRNA sequencing can more readily distinguish between transcripts originating from hosts and pathogens by identifying species-specific portions of the mRNA sequence.

Due to high variability and complexity of metabolic compounds it is difficult to study plant pathogen interaction in spite of highly efficient detection techniques that detects presence of thousand metabolites in a sample like mass spectrometery. Because metabolite extraction frequently leaves residual proteins in samples, post-extraction metabolite interconversions can distort the results (House et al. 2024). These difficulties demonstrate the necessity of strong workflows and improved extraction methods to guarantee an accurate depiction of metabolic phenotypes in research. Therefore there is a need to adopt multi-omic approaches to study the biological system.

## 4. INTEGRATION OF MULTI OMIC APPROACHES

Utilization of multi omic approaches allow to understand biological process deeply and molecular interaction involved in the production of phenotype. They help in determining the key proteins involved in host pathogen interaction as well as in identification of key factors involved in plant diseases resistance and susceptibility and help in disease identification at early stage (Kahar et al.,2024). One prominent example of this is the R package mix Omics which uses different statistical approaches like Canonical correlation analysis , sparse partial least square discriminant analysis to analyse data from different omic layers to understand biological processes (Rohart et al., 2017). Similarly another tool is multi omics factor analysis that help in coorelating data from different omic data. MOFA models the latent components explain observed data in good way while taking uncertainties into account by using a probabilistic framework (Argelaguet et al. 2018). For integration of multi omic data for network pathway bioinformatics can be used. By using tools like Cytoscape, Pathway Commons and Reactome GSA it is possible to map genes, proteins and metabolites by

integrating data from multi omic dataset and help to analyse how change in one data can influence data from other omic layers (Griss et al. 2020). In the case where variable data of huge dimension such as plant-pathogen interactions, integrating multi-omics data is a potent but computationally demanding undertaking. The scale, data format, and noise profile of each omics layer vary, requiring strong computational techniques to harmonise and comprehend them. Data cleaning, scaling and encoding from many systems presents a significant difficulty (Jan et al., 2025). This entails eliminating batch effects, managing missing values, and effectively adjusting numerical features across different omics layers—all of which require a lot of resources when dealing with big size of sample and time (Goh et al., 2017; Schumann et al., 2025). Furthermore, when the number of samples and features increases, data integration techniques like similarity network fusion, Bayesian inference, or latent factor models (like MOFA2 and iClusterPlus) need a significant amount of processing power and memory (Subramanian et al., 2020).
For carrying out these investigations, cloud-based platforms or high-performance computing (HPC) environments are frequently necessary. For example, depending on the dataset complexity and used parameters, training deep learning models for feature extraction or multi-omics integration using DIABLO (Singh et al. 2019) from the mix Omics R package may take several hours to days. Smaller labs may not have the capacity to meet these needs, which emphasises the necessity for teamwork or cloud-based options like CyVerse Terra (Li et al. 2020). Additionally, a lot of integration tools rely on complicated dependencies and need sophisticated R or Python scripting, which presents extra challenges for scientist lacking computational knowledge (Morabito et al. 2025). Therefore, access to sufficient computing infrastructure and interdisciplinary expertise is just as important to the success of multi-omics research as experimental design. Table 3 illustrates integrated omics approaches used to tackle plant pathogen.

**Table 3: Multi-omic approaches used to study host pathogen interaction (Balotf et al., 2025)**

| Name of Pathogen | Target Crop | Omic Approach Used |
|---|---|---|
| Phytophthora infestans | Potato | Transcriptomics + Proteomics |
| Cladosporium fulvum | Tomato | Transcriptomics + Proteomics |
| Spongosporasubterranea | Potato | Transcriptomics + Proteomics |
| Magnaporthe oryzea | Rice | Transcriptomics + Proteomics |
| Ustilago maydis | Maize | Transcriptomics + Metabolomics |
| Fusarium graminearum | Wheat | Transcriptomics + Proteomics + Metabolomics |

## 5. AI BASED OMIC APPROACHES AND ITS APPLICATION

### 5.1 Artificial Intelligence an overview

Artificial Intelligence makes the use of computer to carry out tasks related to human intelligence like learning, to make decisions and solve problems. Machine learning as a subset of artificial intelligence make use of algorithms and models based on statistics statistical that allow computer to do operation without defining ever step. Similarly within machine learning there is a specialized field known as deep learning entails using deep architectures with several layers to automatically extract hierarchical features while training artificial neural networks to resemble the biological neurons of human brain. Data collection is the initial phase of machine learning particularly when it comes to sequencing data like RNA sequencing studies. For training data representation supervised machine learning use diverse features such as physiochemical properties and sequence information of amino acid (Sperschneider et al., 2018). Selection of algorithm is a important step in machine learning. There are different categories of machine learning algorithms, supervised method depends on training examples to develop correlation between input and output. Unsupervised methods does not depend on known outcomes to determine data pattern, while semi-supervised learning used both labelled and unlabelled information to handle input data. In plant omics data analysis machine learning is a method of choice over traditional methods as it can handle large amount of complex data. Although high throughput sequencing techniques provide information on plant stress responses but uncertainity, non independence among variables have emerged as a challenge in plant omics data(Singh et al., 2016). These difficulties have been effectively overcome by ML, particularly DL, which offers precise assessments of plant traits influenced by interactions between genotype and environment (Arsenovic et al., 2019). Decision tree based ensemble models as one of the method of machine learning helped in prediction of genome and allow analysis of plant omic data by integrating (Gokalp and Tasci, 2019). ML techniques are particularly notable in transcriptomics for improving the detection of differential expressed genes (Wang et al., 2018). For interpretation of model identification of set of genes, explainable Artificial Intelligence is advised due to the potential limits of expression analysis (Sabbatini and Calegari, 2023). In order to learn biological dynamics from big datasets and support conventional modelling techniques, the integration of machine learning along conventional biological information is highlighted (Gilpin et al., 2020). Connecting multi-view biological data requires the use of a variety of machine learning techniques, like tree-based approaches, network-based fusion methods, kernel methods, matrix factorization models, and deep neural networks (Li et al., 2016). The ability of machine learning to perform multivariate analysis is useful for taking into account multiple variables at once, which can result in the identification of novel biomarkers and the creation of prediction models. (Reel and others, 2021). Its use in enhancing agronomic characteristics in omic assisted plant science research is clear, but there are still obstacles in the way of fully using the promise of integrating multiomics data, with scaling issues being a significant barrier (Noor et al., 2019). Advanced techniques for selection of particular feature and extraction of information are required because highly complex omics data. To enhance accuracy ML has revolutionized gene regulatory network integrating multi omics data (Koand Brandizzi, 2020).

### 5.2 Application

Omic techniques assisted by AI provide deeper understanding of plant responses to stresses by combining AI with advanced molecular techniques. As compare to traditional approaches which fail to interpret complex gene, protein and metabolite network it provide smart innovative solutions. These approaches provides important component , biomarkers, pathway that are important in plant defense response. AI combined with multi omic data emerged as a a powerful tool for optimizing crop production, develop resistant crops and provide sustainable food supply (Yan and Wang, 2023).

#### 5.2.1 Application in Genomics

Algorithms used in machine learning play a crucial aspect in determining genes related to stress resistance enabling breeder to enhance production of crop (Liang et al.,2011). SVM and its variants are reported to help in identification of proteins that provide resistance against diseases (Pal et al., 2016). Similarly EFFECTORP has also reported to be effective in determing fungal effector protein (Sperschneider et al. 2016). ML algorithm also provide information on disease susceptible genes that help in adopting effective agricultural practices (Yang and Guo, 2017). It also solves cellular heterogeneity and recognize new cell types. It has been successfully employed in classifying cell types, explaining regulatory networks of genes and integrating multimodal data (Raimundo et al., 2021). Due to the presence of amplified artifacts and low genome coverage in single cell RNA sequencing technique adoption of SIMLR algorithm is recommended (Lin et al., 2017), that provide understanding of complex single cell genomics. To completely utilize the power of machine learning in single cell genomics of plants further research is needed to explore more plant species in order to accelerate the breeding programme.

#### 5.2.2 In Transcriptomics

Machine learning approaches and meta analysis has been utilized to lay out maize genotypes on the basis of expression of genes in response to biotic stress.. Several genes are identified that encode several enzymes like (S)-beta-macrocarpene synthase, zealexin A1 synthase, polyphenol oxidase I, chloroplastic, pathogenesis-related protein 10, CHY1, chitinase chem 5, barwin that provide resistance against biotic stress were reported (Nazari et al., 2023)

#### 5.2.3 In Proteomics and Metabolomics

In case of proteomics AI has been successfully utilized Random Forest algorithm by using sequence data and network attributes to predict host pathogen protein-protein interaction (Yang et al., 2019). Karan and colleagues (2023) using machine learning model studied microbial interactions and with 95% accuracy on experimental datasets predict interaction between rice and blast fungus. Evaluations against additional pathogen-host datasets verified the model's specificity to rice and pathogenic fungus Magnaporthe. grisea. Similarly network clustering algorithm was also used to study incomplete metabolite content of 216 plants where unsupervised machine learning algorithm was used for classification. This study was reported to cluster plants according to their known evolutionary relationships, highlighting the significance of metabolite content as a taxonomic marker (Liu et al., 2017). Additionally, the study revealed previously unidentified species-metabolite correlations and explored how metabolite content could be used to determine nutritional and medicinal qualities in plants. Transfer learning was used to identify metabolism related genes in tomato (Moore et al., 2020)

### 5.2.4 In Phenomics

Several Deep learning techniques of machine learning have been utilized for management of several crops like rice, wheat, tomato and potato. DL-based video detection system that use as Faster R-CNN and YOLO v3 were successfully utilized to detect pest and diseases in crops (Li et al. 2020). Early recognition of tomato leaf spot was reported using MobileNetv2-YOLOv3 model by (Wang and Liu 2021). Hyperspectral imaging approach has been utilized for field detection of potatoes disease (Polder et al., 2019). For counting and localizing agricultural pest deep learning approach with high effectiveness was devised by (Chen and Yuan 2019). List of AI-based tools to address biotic stress in plants were given in Table 4. These algorithm were also employed to identify epistatic and gene-environment interaction in rice and barley affecting agronomic and quality traits (Xu et al., 2015, 2018). Table 4 represent different AI based tools for disease prediction.

**Table 4. List of AI-Based tools used against plant biotic stress**

| AI-based tools | Characteristics | Algorithm used | Description |
|---|---|---|---|
| DRPPP | Protein sequence | Support Vector Machine | Forecast proteins in providing resistance in plants against diseases |
| prPred | bidirectional long short term memory | light gradient boosting | Forecast proteins in providing resistance in plants against diseases |
| StackRPred | pairwise energy content of residues | Ensemble learning | Forecast proteins in providing resistance in plants against diseases |
| ResCap | Sequence compositional properties | Support Vector Machine | Forecast of gene involved in providing resistance to plant |
| Effector P 3.0 | Protein sequence features Ensemble | Ensemble learning | Determine effector proteins of fungus and oomycetes |
| InterSPPI | Protein sequence features; network encoding | Random Forest | Forecast protein- protein interaction Arabidopsis thaliana and pathogens |

## 6. CHALLENGES AND FUTURE PROSPECTS

The evolution of machine learning and availability of advanced biological data have created a new dimension in providing deep understanding of complex biological information. But there is a huge challenge in combining the plant molecular data into machine learning. As compare to traditional plant molecular methods, method involve in machine learning are highly specific. While machine learning (ML) tries to build predictive models, it's important to understand that each ML algorithm has unique strengths and limitations that affect predictive effectiveness under particular circumstances. Because of these biological and technical differences, machine learning model developed for one dataset may not be able to spread well to others. Omic datasets provide huge amount of information but when data from multi omic approaches are integrated using noise and sparsity it face limitations (Joyce and Palsson, 2006). Oversampling and under sampling approaches are used to overcome the issue of imbalanced datasets (Maimon and Rokach, 2005). More challenges were there in case of handling big data of plant system which diifer in size, variety, value where approaches of machine learning need to adapt to handle data from multi omic datasets. Due to the black box nature of deep learning approach, it is very challenging to interpret complex data , therefore researcher should have deep understanding of biological importance of the model in terms of its accuracy and available biological knowledge. We should realize the potential of AI in understanding of plant defence mechanism and their role in crop improvement by collaborating, agriculture scientist, omic researcher and data scientist. Integration of multi omic data with AI seems to be one of the promising approach for early detection of pest and diseases for agricultural crops provide sustainability and food security over changing climatic condition. AI-assisted multi omic approaches help to observe and identify small changes that occurred in molecular profiles of plants providing visible symptoms before the disease arrive. Further understanding of plant defence mechanism can be further enhanced by combining phenotypic methods with AI assisted omic techniques. By using genetic, molecular and environmental variables machine learning and deep learning approaches can provide a solution for predicting diseases based on input variables so preventive measures can be taken. It can also help plant breeders for developing disease resistance varieties through identification of specific genetic markers and pathways related to resistance. It can also allows precise application of pesticides, reducing the negative effects on environment thereby provide effective disease management. Due to changing climatic condition plants faces several stresses affecting their overall growth and productivity therefore by applying AI assisted omic techniques one can determine how these factors additively affect plant defence mechanism, therefore provide a holistic approach for development of climate resilient crops.

## 7. CONCLUSION

It is concluded that the interaction between host and pathogen is highly complex which cannot be explained using only single omic approach. Therefore integrations of multiomic approaches provide a better and comprehensive understanding of the complex biological system. By using extraction and fusion strategies heterogenous omic data can be aligned like deep generative models can be used to stimulate response of pathogen across variable environmental condition (Rivero-Garcia et al. 2024; Yanand Wang 2023.). More focuss should be done on interpretation of models to ensure complete usage of AI. In order to evaluate the reliability of analysis based on AI standards should be established. By overcoming these challenges complex plant pathogen interactions can be studied proving AI can be effective tool in accelerating plant science research.

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## 9. CONFLICT OF INTEREST

There is no conflict of interest to declare.

## REFERENCES

1. Al-Amrani, S., Al-Jabri, Z., Al-Zaabi, A., Alshekaili, J., & Al-Khabori, M. (2021). Proteomics: Concepts and applications in human medicine. World Journal of Biological Chemistry, 12, 57–69. https://doi.org/10.4331/wjbc.v12.i5.57.
2. Ali, S., Tyagi, A. and Bae, H (2021). Ionomic approaches for discovery of novel stress-resilient genes in plants. Int. J. Mol. Sci. 22, 7182.
3. Argelaguet, ., Velten, B., Arnol, D., Dietrich, S., Zenz,T., Marioni, J.C.,Buettner, F., Huber, W. and Stegle, O. (2018). Multi omics factor analysis a framework for unsupervised integration ofmulti-omics data sets. Mol Syst Biol, 14:e8124. 10.15252/msb.20178124.
4. Anderson, P. K., Cunningham, A. A., Patel, N. G., Morales, F. J., Epstein, P. R., & Daszak, P. (2004). Emerging infectious diseases of plants: Pathogen pollution, climate change and agrotechnology drivers. Trends in Ecology & Evolution, 19(10), 535–544. https://doi.org/10.1016/j.tree.2004.07.021.
5. Arsenovic, M., Karanovic, M., Sladojevic, S., Anderla, A. and Stefanovic, D. (2019).Solving current limitations of deep learning based approaches for plant disease detection. Symmetry, 11 (7), 939.
6. Aizat, W. M., & Hassan, M. (2018). Proteomics in systems biology. Advances in Experimental Medicine and Biology, 1102, 31–49.

7. Avelino, J., Cristancho, M., Georgiou, S., Imbach, P., Aguilar, L. and Bornemann, G. (2015). The coffee rust crises in Colombia and Central America(2008–2013): Impacts, plausible causes and proposed solutions. Food Security, 7, 303–321. https://doi.org/10.1007/s12571-015-0446-9.
8. Balotf, S., Wilson, R. and Hemmati, R., (2025). Plant-pathogen interactions: Making the case for multi-omics analysis of complex pathosystems. Stress Biology, 5, 66. https://doi.org/10.1007/s44154-025-00260-7.
9. Bakkeren, G., Joly, D.L. and Duplessis, S.(2016).Genomics research on non-model plantpathogens: Delivering novel insights into rust fungus biology. Front Plant Sci ,7:216.10.3389/fpls.2016.00216.
10. Bebber, D. P., Ramotowski, M. A., & Gurr, S. J. (2013). Crop pests and pathogens move polewards in a warming world. Nature Climate Change, 3(11), 985–988. https://doi.org/10.1038/nclimate1990.
11. Bulasag, A. S., Camagna, M., Kuroyanagi, T., Ashida, A., Ito, K., Tanaka, A., Sato, I., Chiba, S., Ojika, M., & Takemoto, D. (2023). Botrytis cinerea tolerates phytoalexins produced by Solanaceae and Fabaceae plants through an efflux transporter BcatrB and metabolizing enzymes. Frontiers in Plant Science, 14, 1177060.
12. Birch, P. R., Avrova, A. O., Duncan, J. M., Lyon, G. D., & Toth, R. L. (1999). Isolation of potato genes induced during an early stage of the hypersensitive response to Phytophthora infestans. Molecular Plant-Microbe Interactions, 1212, 356–361. https://doi.org/10.1094/MPMI.1999.12.4.356.
13. Bludau, I. and Aebersold, R. (2020). Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nat Rev Mol Cell Biol,21:327–340. 10.1038/s41580-020-0231-2.
14. Bhadouriya, S. L., Mehrotra, S., Basantani, M. K., Loake, G. J., & Mehrotra, R. (2021). Role of chromatin architecture in plant stress responses: An update. Frontiers in Plant Science, 11, 603380. https://doi.org/10.3389/fpls.2020.603380.
15. Callinan, P. A., & Feinberg, A. P. (2006). The emerging science of epigenomics. Human Molecular Genetics, 15(Suppl_1), R95–R101.
16. Crandall, S. G., Gold, K. M., Jiménez-Gasco, M. D. M., Filgueiras, C. C., & Willett, D. S. (2020). A multi-omics approach to solving problems in plant disease ecology. PLoS ONE, 15, e0237975. https://doi.org/10.1371/journal.pone.0237975.
17. Carrera, F. P., Noceda, C., Maridueña-Zavala, M. G., & Cevallos-Cevallos, J. M. (2021). Metabolomics: A powerful tool for understanding plant abiotic stress. Agronomy, 11, 824.
18. Chen, X., He, C., Xu, H., Zeng, G., Huang, Q., Deng, Z., Qin, X., Shen, X., & Hu, Y. (2024). Characterization of the SWI/SNF complex and nucleosome organization in sorghum. Frontiers in Plant Science, 15, 1430467. https://doi.org/10.3389/fpls.2024.1430467.
19. Chen,J.(2024). Comparative interactomics build the bridges from micromolecules to biological behaviour and morphology. Crop Des, 3,100078.
20. Chen, L. and Yuan, Y. (2019). "Agricultural disease image dataset for disease identification based on machine learning," in Big Scientific DataManagement: First International Conference, BigSDM 2018, Beijing, China, November 30– December 1, 2018, Revised Selected Papers 1. (Springer International Publishing), 263–274.
21. Chen, H., King, R., Smith, D., Bayon, C., Ashfield, T., Torriani, S., Kanyuka, K., Hammond-Kosack, K., Bieri, S., & Rudd, J. (2023). Combined pangenomics and transcriptomics reveals core and redundant virulence processes in a rapidly evolving fungal plant pathogen. BMC Biology, 21, 24. https://doi.org/10.1186/s12915-023-01520-6.
22. Choudry, M. W., Riaz, R., Nawaz, P., Ashraf, M., Ijaz, B., & Bakhsh, A. (2024). CRISPR-Cas9-mediated understanding of plant abiotic stress-responsive genes to combat changing climatic patterns. Functional & Integrative Genomics, 24(4).
23. Daayf, F., El Hadrami, A., El-Bebany, A. F., Henriquez, M. A., Yao, Z., Derksen, H., El-Hadrami, I., & Adam, L. R. (2012). Phenolic compounds in plant defense and pathogen counter-defense mechanisms. Recent Advances in Polyphenol Research, 3, 191–208.
24. Duruflé, H. and Déjean, S.(2023). Multi-omics data integration in the context of plant abiotic stress signaling. In Plant Abiotic Stress Signaling; Springer: New York, NY, USA, pp. 295–318.
25. El-Sappah, A.H., Yan,K., Q., Huang,Q., Md.M., Islam,Md.M.,Li, Q.,Wang, Y., Wang, M.S. Khan, X. Zhao, R.R., Mir, J., Li, K.A., El. and Tarabily, M.(2021). Abbas Comprehensive mechanism of gene silencing and its role in plant growth and development. Front. Plant Sci, 12,Article 705249, 10.3389/fpls.2021.705249.

26. El-Esawi, M. A., Sinha, R. P., Chauhan, D. K., Tripathi, D. K., & Pathak, J. (2020). Role of ionomics in plant abiotic stress tolerance. In Plant life under changing environment (pp. 835–860). Academic Press.
27. Farag, M. A., Goyal, V. & Baky, M. H. (2024). Comparative metabolome variation in Brassica juncea organs from two varieties using SPME and GCMS techniques coupled to chemometrics. Scientific Reports, 14, 19900.
28. Fukase, E. & Martin, W. (2020). Economic growth, convergence, and world food demand and supply. World Development, 132, 104954. https://doi.org/10.1016/j.worlddev.2020.104954.
29. Gil, N. and Ulitsky, I. (2020). Regulation of gene expression by cis-acting long non-codingRNAs. Nat Rev Genet, 21:102–117. 10.1038/s41576-019- 0184-5.
30. Griss, J., Viteri, G., Sidiropoulos, K., Nguyen, V., Fabregat, A. and Hermjakob, H (2020).ReactomeGSA-efficient multi-omics comparative pathway analysis. Mol Cell Proteomics,19:2115–2125. 10.1074/mcp.TIR120.002155.
31. Gilpin, W., Huang, Y. and Forger, D. B. (2020). Learning dynamics from large biological data sets: machine learning meets systems biology. Curr. Opin. Syst. Biol, 22, 1–7. doi: 10.1016/j.coisb.2020.07.009.
32. Griffin, J. L. (2004). Metabolic profiles to define the genome: Can we hear the phenotypes? Philosophical Transactions of the Royal Society B: Biological Sciences, 359, 857–871. https://doi.org/10.1098/rstb.2003.1411.
33. Ghosh, D., & Xu, J. (2014). Abiotic stress responses in plant roots: A proteomics perspective. Frontiers in Plant Science, 5, 66977.
34. Gokalp, O. and Tasci, E. (2019). "Weighted voting based ensemble classification with hyper-parameter optimization," in 2019 Innovations in Intelligent Systems and Applications Conference (ASYU). 1–4 (IEEE).
35. Goh. WWB., Wang, W. and Wong, L. (2017).Why batch effects matter in omics data, and how to avoid them. Trends Biotechnol, 35:498–507.10.1016/j.tibtech.2017.02.012.
36. Gupta, S., Kaur, R., Sharma, T., Bhardwaj, A., Sharma, S., Sohal, J. S., & Singh, S. V. (2023). Multi-omics approaches for understanding stressor-induced physiological changes in plants: An updated overview. Physiological and Molecular Plant Pathology, 126, 102047. https://doi.org/10.1016/j.pmpp.2023.102047.
37. Gupta, R., Lee, S.E., Agrawal, G.K., Rakwal, R., Park, S., Wang, Y., Kim. and S.T. (2015). Understanding the plant-pathogen interactions in the context of proteomics-apoplasticproteins inventory. Front Plant Sci, 6:132864. 10.3389/fpls.2015.00352.
38. Hasan, M. M., Rahman, M. A., Corpas, F. J., Rahman, M. M., Jahan, M. S., Liu, X., Ghimire, S., Alabdallah, N. M., Wassem, M. and Alharbi, B. M.,(2024). Salt stress tolerance in rice (Oryza sativa L.): A proteomic overview of recent advances and future prospects. Plant Stress, 11, 100307.
39. Hubler, S.L., Kumar, P., Mehta, S., Easterly, C., Johnson, J.E., Jagtap, P.D. and Griffin, T.J.(2019).Challenges in peptide-spectrum matching: a robust and reproducible statistical framework for removing low-accuracy,high-scoringhits.J Proteome Res, 19:161-173.10.1021/acs.jproteome.9b00478.
40. House, R.J., Soper-Hopper, M.T., Vincent, M.P., Ellis, A.E., Capan, C.D, Madaj, Z.B., Wolfrum, E.,Isaguirre, C.N., Castello, C.D. and Johnson A.B .(2024). A diverse proteome is present and enzymatically active in metabolite extracts. Nat Commun, 15:5796. 10.1038/s41467-024- 50128-z.
41. Joyce, A. R. and Palsson, B.Ø. (2006). The model organism as a system: integrating'omics' data sets. Nat. Rev.Mol. Cell Biol, 7 (3), 198–210. doi: 10.1038/nrm1857.
42. Jan, R., Hussain, A., Assad, A., Khurshid, S. and Macha, M.A. (2025) Challenges with multi-omicsdata integration. In: Multi-Omics in Health and Diseases. Elsevier, pp223–242. 10.1016/B978-0-443-13595-8.00010-6,
43. Karan, B., Mahapatra, S., Sahu, S. S., Pandey, D. M. and Chakravarty, S. 2023).Computational models for prediction of protein–protein interaction in rice and Magnaporthe grisea. Front. Plant Sci, 13, 1046209. doi: 10.3389/fpls.2022.1046209.
44. Kahar, G., Haxim ,Y., Waheed, A., Bozorov, T.A., Liu, X., Wen, X., Zhao, M.and Zhang, D. (2024).Multi-omics approaches provide new insights into the identification of putative fungal effectors from Valsa mali. Microorganisms, 12:655. 10.3390/microorganisms12040655.

45. Ko, D. K. and Brandizzi, F. (2020). Network-based approaches for understanding gene regulation and function in plants. Plant J, 104 (2), 302–317. doi: 10.1111/tpj.14940.
46. Kumari, A., Das, P., Parida, A. K., & Agarwal, P. K. (2015). Proteomics, metabolomics, and ionomics perspectives of salinity tolerance in halophytes. Frontiers in Plant Science, 6, 537.
47. Koller, A., Washburn, M. P., Lange, B. M., Andon, N. L., Deciu, C., Haynes, P. A., Hays, L., Schieltz, D., Ulaszek, R., Wei, J., et al. (2002). Proteomic survey of metabolic pathways in rice. Proceedings of the National Academy of Sciences of the United States of America, 99, 11969–11974.
48. Kumar, A., Mishra, H., Sharma, D., Sharma, D., Rahim, M. S. and Sharma, M. (2018). Pivotal role of bZIPs in amylose biosynthesis by genome survey and transcriptome analysis in wheat (Triticum aestivum L.) mutants. Scientific Reports, 8(1).
49. Kumar, V. & Jain, M. (2015). The CRISPR–Cas system for plant genome editing: Advances and opportunities. Journal of Experimental Botany, 66(1), 47–57. https://doi.org/10.1093/jxb/eru429.
50. Kumar, A., Yogendra, K. N., Karre, S., Kushalappa, A. C., Dion, Y.& Choo, T. M. (2016). WAX INDUCER1 (HvWIN1) transcription factor regulates free fatty acid biosynthetic genes to reinforce cuticle to resist Fusarium head blight in barley spikelets. Journal of Experimental Botany, 67, 4127–4139.
51. Kaur, B., Sandhu, K. S., Kamal, R., Kaur, K., Singh, J., Röder, M. S. & Muqaddasi, Q. H. (2021). Omics for the improvement of abiotic, biotic, and agronomic traits in major cereal crops: Applications, challenges, and prospects. Plants, 10(10).
52. Katam, R., Shokri, S., Murthy, N., Singh, S. K., Suravajhala, P. and Khan, M.N.(2020). Proteomics, physiological, and biochemical analysis of cross-tolerance mechanisms in response to heat and water stresses in soybean. PLoS ONE, 15(6), e0233905.
53. Khalid, N., Aqeel, M. & Noman, A. (2019). System biology of metal tolerance in plants: An integrated view of genomics, transcriptomics,metabolomics, and phenomics. In Plant metal functional omics: A system-wide perspective (pp. 107–144).
54. Liu, Y., Beyer, A. and Aebersold, R, (2016), On the dependency of cellular protein levels onmRNA abundance. Cell, 165:535–550. 10.1016/j.cell.2016.03.014.
55. Liu, K., Abdullah, A. A., Huang, M., Nishioka, T., Altaf-Ul-Amin, M. and Kanaya, S. (2017). Novel approach to classify plants based on metabolite- content similarity. BioMed. Res. Int, doi: 10.1155/2017/5296729.
56. Litvinov, D. Y., Karlov, G. I. & Divashuk, M. G. (2021). Metabolomics for crop breeding: General considerations. Genes, 12, 1602.
57. Liu, H.-L. & Hsu, J.P. (2005). Recent developments in structural proteomics for protein structure determination. Proteomics, 5, 2056–2068.
58. Li, D., Wang, R., Xie, C., Liu, L., Zhang, J. and Li, R.(2020). A recognition method for rice plant diseases and pests video detection based on deep convolutional neural network. Sensors, 20 (3), 578.
59. Liang, Y., Zhang, F., Wang, J., Joshi, T., Wang, Y. and Xu, D. (2011). Prediction of drought-resistant genes in Arabidopsis thaliana using SVM-RFE. PloS One,6 (7), e21750.doi: 10.1371/journal.pone.0021750.
60. Lin, C., Jain, S., Kim, H. and Bar-Joseph, Z. (2017). Using neural networks for reducing the dimensions of single-cell RNA-Seq data. Nucleic Acids Res. 45 (17), e156–e156. doi: 10.1093/nar/gkx68.
61. L i, B., Gould, J., Yang, Y., Sarkizova, S., Tabaka, M., Ashenberg, O., Rosen,Y., Slyper,M.,Kowalczyk, M.S. and Villani, A.C. (2020). Cumulus provides cloud-based data analysis for large-scale single-cell and single-nucleus RNA-seq. Nat Methods, 17:793–798.10.1038/s41592-020-0905-x.
62. Liu, Y., Lu, S., Liu, K., Wang, S., Huang, L. & Guo, L. (2019). Proteomics: A powerful tool to study plant responses to biotic stress. Plant Methods, 15, 1–20.
63. Li, L., Snyder, J. C., Pelaschier, I. M., Huang, J., Niranjan, U. N. and Duncan, P., (2016). Understanding machine-learned density functionals. Int. J. Quantum Chem. 116 (11), 819–833.
64. Liu, H.-J. and Yan, J. (2019). Crop genome-wide association study: a harvest of biological relevance. Plant J, 97: 8-18. https://doi.org/10.1111/tpj.14139.
65. Long, Y., Wendel, J. F., Zhang, X. & Wang, M. (2024). Evolutionary insights into the organization of chromatin structure and landscape of transcriptional regulation in plants. Trends in Plant Science, 29, 638–649. https://doi.org/10.1016/j.tplants.2023.11.009.

66. López-Hernández, L., Toolan-Kerr, P., Bannister, A. J. & Millán-Zambrano, G. (2025). Dynamic histone modification patterns coordinating DNA processes. Molecular Cell, 85, 225–237.https://doi.org/10.1016/j.molcel.2024.10.034.
67. Lueong, S. S., Hoheisel, J. D. & Alhamdani, M. S. S. (2014). Protein microarrays as tools for functional proteomics: Achievements, promises and challenges. Journal of Proteomics & Bioinformatics, 7, 4.
68. Mashabela, M. D., Tugizimana, F., Steenkamp, P. A., Piater, L. A., Dubery, I.A. & Mhlongo, M. I. (2023). Metabolite profiling of susceptible and resistant wheat (Triticum aestivum) cultivars responding to Puccinia striiformis f. sp. tritici infection. BMC Plant Biology, 23, 293.
69. Maimon, O. and Rokach, L. (2005). Data Mining and Knowledge Discovery.Handbook Vol. 2 (New York: Springer).
70. Mariyam, S., Upadhyay, S. K., Chakraborty, K., Verma, K. K., Duhan, J. S. and Muneer, S.(2023). Nanotechnology: A frontier in agricultural science and a novel approach in abiotic stress management and convergence with new-age medicine—A review. Science of the Total Environment, 169097.
71. Moore, B. M., Wang, P., Fan, P., Lee, A., Leong, B. and Lou, Y. R. (2020). With in and cross-species predictions of plant specialized metabolism genes using transfer learning. In silico Plants, 2 (1), diaa005. doi: 10.1093/insilicoplants/diaa005.
72. Morabito, A., De Simone, G., Pastorelli, R., Brunelli, L. and Ferrario,M. (2025). Algorithms and tools for data-driven omics integration to achieve multilayer biological insights: anarrative review. J Transl Med,23:425. 10.1186/s12967-025-06446-x.
73. McManus, J., Cheng, Z. and Vogel, C. (2015) Next-generation analysis of gene expressionregulation–comparing the roles of synthesis anddegradation. Mol Biosyst ,11:2680–2689. 10.1039/c5mb00310e.
74. Meng, H., Sun, M., Jiang, Z., Liu, Y., Sun, Y., Liu, D., Jiang, C., Ren, M., Yuan, G. & Yu, W. (2021). Comparative transcriptome analysis reveals resistant and susceptible genes in tobacco cultivars in response to infection by Phytophthora nicotianae. Scientific Reports, 11, 809. https://doi.org/10.1038/s41598-020-80280-7.
75. Mosa, K. A., Ismail, A. & Helmy, M. (2017). Introduction to plant stresses. In Plant stress tolerance: An integrated omics approach (pp. 1–19).
76. Muthamilarasan, M., Singh, N. K. & Prasad, M. (2019). Multi-omics approaches for strategic improvement of stress tolerance in underutilized crop species: A climate change perspective. Advances in Genetics, 103, 1–38.
77. Naranjo-Ortiz, M.A. and Gabaldón, T. (2020). Fungal evolution: cellular,genomic and metabolic complexity. Biol Rev, 95:1198–1232. 10.1111/brv.12605.
78. Nazari, L., Aslan, M.F. and Sabanci, K.(2023).Integrated transcriptomic meta-analysis and comparative artificial intelligence models in maize under biotic stress.Sci Rep 13, 15899.https://doi.org/10.1038/s41598-023-42984-4.
79. Naithani, S., Gupta, P., Preece, J., D'Eustachio, P., Elser, J. L., Garg, P., Dikeman, D. A., Kiff, J., Cook, J., Olson, A., Wei, S., Tello-Ruiz, M. K., Mundo, A. F., Munoz-Pomer, A., Mohammed, S., Cheng, T., Bolton, E., Papatheodorou, I., Stein, L., Ware, D.& Jaiswal, P. (2019). Plant Reactome: A knowledgebase and resource for comparative pathway analysis. Nucleic Acids Research. https://doi.org/10.1093/nar/gkz996.
80. Noor, E., Cherkaoui, S. and Sauer, U. (2019). Biological insights through omics data integration. Curr. Opin. Syst. Biol, 15, 39–47.
81. Nicaise, V., Roux, M. & Zipfel, C. (2009). Recent advances in PAMP-triggered immunity against bacteria: Pattern recognition receptors watch over and raise the alarm. Plant Physiology, 150, 1638–1647. https://doi.org/10.1104/pp.109.139709.
82. Ozsolak, F. and Milos, P.M. (2011). RNA sequencing: advances, challenges and opportunities. Nat Rev Genet,12:87–98. 10.1038/nrg2934.
83. Omidiran, O., Patel, A., Usman, S., Mhatre, I., Abdelhalim, H., DeGroat, W., Narayanan, R., Singh, K., Mendhe, D. & Ahmed, Z. (2024). GWAS advancements to investigate disease associations and biological mechanisms. Clinical and Translational Discovery, 4, e296. https://doi.org/10.1002/ctd2.296.
84. Pastor-Fernández, J., Sánchez-Bel, P., Gamir, J., Pastor, N., Sanmartín, N.,Cerezo, M., Andrés-Moreno, S. and Flors, N.(2022). Tomato Systemin Induces Resistance against Plectosphaerella cucumerina in

Arabidopsis through the Induction of Phenolic Compounds and Priming of Tryptophan Derivatives. Plant Sci. 321, 111321.
85. Pandey, V., Gupta, A. K., Singh, M., Pandey, D. & Kumar, A. (2019). Complementary proteomics and genomics approaches identify potential pathogenicity/virulence factors in Tilletia indica induced under the influence of host factor. Scientific Reports, 9(1), 553.
86. Pal, T., Jaiswal, V. and Chauhan, R. S. (2016). DRPPP: A machine learning based tool for prediction of disease resistance proteins in plants. Comput. Biol. Med. 78, 42– 48. doi: 10.1016/j.compbiomed.2016.09.008.
87. Patel, A. B., He, Y. & Radhakrishnan, I. (2024). Histone acetylation and deacetylation: Mechanistic insights from structural biology. Gene, 890, 147798. https://doi.org/10.1016/j.gene.2023.147798.
88. Polder, G., Blok, P. M., De Villiers, H. A., van der Wolf, J. M. and Kamp, J. (2019).Potato virus Y detection in seed potatoes using deep learning on hyperspectral images.Front. Plant Sci. 10, 209.
89. Qiu, M., Tian, M., Yong, S., Sun, Y., Cao, J., Li, Y., Zhang, X., Zhai, C., Ye, W. & Wang, M. (2023). Phase-specific transcriptional patterns of the oomycete pathogen Phytophthora sojae unravel genes essential for asexual development and pathogenic processes. PLoS Pathogens, 19, e1011256. https://doi.org/10.1371/journal.ppat.1011256.
90. Raimundo, F., Meng-Papaxanthos, L., Vallot, C. and Vert, J. P. (2021). Machine learning for single-cell genomics data analysis. Curr. Opin. Syst. Biol. 26, 64–71.doi: 10.1016/j.coisb.2021.04.006.
91. Razzaq, A., Wishart, D. S., Wani, S. H., Hameed, M. K., Mubin, M. & Saleem, F. (2022). Advances in metabolomics-driven diagnostic breeding and crop improvement. Metabolites, 12, 511.
92. Rani, M., Mangat, H. K., Pathak, R. K. & Yadav, I. S. (2021). Harnessing the potential of omics for prevention and management of complex crop plant diseases. Journal of Protein & Proteomics, 12(3), 227–245.
93. Raza, A., Su, W., Hussain, M. A., Mehmood, S. S., Zhang, X. and Cheng, Y.(2021). Integrated analysis of metabolome and transcriptome reveals insights for cold tolerance in rapeseed (Brassica napus L.). Frontiers in Plant Science,12, 721681.
94. Reel, P. S., Reel, S., Pearson, E., Trucco, E. and Jefferson, E. (2021). Using machine learning approaches for multi-omics data analysis: A review. Biotechnol. Adv, 49,107739. doi: 10.1016/j.biotechadv.2021.107739.
95. Righetti, P.G. and Boschetti, E. (2020). Low-abundance plant protein enrichment with peptide libraries to enlarge proteome coverage and related applications.PlantSci.290:110302.10.1016/j.plantsci.2019.110302.
96. Ribeiro, C., Stitt, M. and Hotta, C.T.(2022) How stress affects your budget—Stress impacts on starch metabolism. Front. Plant Sci, 2022, 13, 774060.
97. Rivero-Garcia, I., Torres, M. and Sánchez-Cabo, F. (2024). Deep generative models in single-cell omics. Comput Biol Med, 176:108561 .1016/j.compbiomed.2024.108561.
98. Ristaino, J. B., Anderson, P. K., Bebber, D. P., Brauman, K. A., Cunniffe, N. J. and Fedoroff, N. V. (2021). The persistent threat of emerging plant disease pandemics to global food security. Proceedings of the National Academy of Sciences, 118(23), e2022239118. https://doi.org/10.1073/pnas.2022239118.
99. Rohart, F., Gautier, B., Singh, A. and LêCao, K-A (2017). mixOmics: An R package for 'omics feature selection and multiple data integration. PLoS Comput Biol,13:e1005752.10.1371/journal.pcbi.1005752.
100. Roychowdhury, R., Das, S. P., Gupta, A., Parihar, P., Chandrasekhar, K., Sarker, U., Kumar, A., Ramrao, D. P. & Sudhakar, C. (2023). Multi-omics pipeline and omics-integration approach to decipher plant's abiotic stress tolerance responses. Genes, 14, 1281. https://doi.org/10.3390/genes14061281.
101. Sahoo, J.P., Behera, L., Sharma, S.S., Praveena, J.,Nayak, S.K. and Samal, K.C.(2020). Omics Studies and Systems Biology Perspective towards Abiotic Stress Response in Plants. Am. J. Plant Sci. 11, 2172–2194.
102. Savary, S., Willocquet, L., Pethybridge, S. J., Esker, P., McRoberts, N. & Nelson, A. (2019). The global burden of pathogens and pests on major food crops. Nature Ecology & Evolution, 3(3), 430–439. https://doi.org/10.1038/s41559-018-0793-y.
103. Sabbatini, F. and Calegari, R. (2023). "Explainable clustering with CREAM," in Proceedings of the International Conference on Principles of Knowledge Representation and Reasoning. 19 (1), 593–603.

104. Srivastava, V., Obudulu, O., Bygdell, J., Löfstedt, T., Rydén, P., Nilsson, R., Ahnlund, M., Johansson, A., Jonsson, P. and Freyhult, E. (2013). OnPLS integration of transcriptomic, proteomic and metabolomic data shows multi-level oxidative stress responses in the cambium of transgenic Populus plants. BMC Genomics, 14, 893.
105. Subramanian, I., Verma, S., Kumar, S., Jere, A. and Anamika, K. (2020) Multi-omics data integration, interpretation, and its application. Bioinformatics Biol Insights,14:1177932219899051.10.1177/1177932219899051.
106. Singh, A., Shannon, C.P., Gautier, B., Rohart, F., Vacher, M., Tebbutt, S.J. and LêCao K,A.(2019).DIABLO: an integrative approach for identifying key molecular drivers from multi-omicsassays. Bioinformatics, 35:3055–3062. 10.1093/bioinformatics/bty1054.
107. Schumann, Y., Gocke, A. and Neumann, J.E. (2025). Computational methods for data integration and imputation of missing values in omics datasets. Proteomics.25:e202400100. 10.1002/pmic.202400100.
108. Schirawski, J. & Perlin, M. H. (2018). Plant–microbe interaction 2017—The good, the bad and the diverse. International Journal of Molecular Sciences, 19(5), 1374. https://doi.org/10.3390/ijms19051374.
109. Singh, A., Ganapathysubramanian, B., Singh, A. K. and Sarkar, S. (2016). Machine learning for high-throughput stress phenotyping in plants. Trends Plant Sci. 21 (2),110–124. doi: 10.1016/j.tplants.2015.10.015.
110. Singh, R. K., Sood, P., Prasad, A. & Prasad, M. (2021). Advances in omics technology for improving crop yield and stress resilience. Plant Breeding,140(5), 719–731.
111. Sperschneider, J., Gardiner, D. M., Dodds, P. N., Tini, F., Covarelli, L. and Singh, K. B. (2016). EffectorP: predicting fungal effector proteins from secretomes using machine learning. New Phytol. 210 (2), 743–761.doi: 10.1111/nph.13794.
112. Song, F., Yang, Q., Huang, J., Guo, Z., Li, Y.& Deng, W. (2026). Plant drought stress: Physiological, biochemical and molecular mechanisms. Plant Stress, 19, 101153. https://doi.org/10.1016/j.stress.2025.101153.
113. Soylu, S. (2006). Accumulation of cell-wall bound phenolic compounds and phytoalexin in Arabidopsis thaliana leaves following inoculation with pathovars of Pseudomonas syringae. Plant Science, 170, 942–952.
114. Saeed,F., Chaudhry, U.K., Bakhsh,A., Raza,A., Saeed,Y. and Bohra, R.K. Varshney Moving beyond DNA sequence to improve plant stress responses Front. Genet, 13 (2022), Article 874648,10.3389/fgene.2022.874648.
115. Shinozaki,K. and Yamaguchi-Shinozaki,K.(2022). Functional genomics in plant abiotic stress responses and tolerance: from gene discovery to complex regulatory networks and their application in breeding. Proc. Jpn. Acad Ser. B, 98,pp. 470-492, 10.2183/pjab.98.024.
116. Wang, W., Wang, X., Liao, H., Feng, Y., Guo, Y., Shu, Y. & Wang, J. (2022). Effects of nitrogen supply on induced defense in maize (Zea mays) against fall armyworm (Spodoptera frugiperda). International Journal of Molecular Sciences, 23, 10457.
117. Wang, X. and Liu, J. (2021). Multiscale parallel algorithm for early detection of tomato gray mold in a complex natural environment. Front. Plant Sci. 12, 620273.
118. Wang, M., White, N., Grimm, V., Hofman, H., Doley, D. and Thorp, G.(2018).Pattern-oriented modelling as a novel way to verify and validatefunctional–structural plant models: a demonstration with the annual growth module of avocado. Ann. Bot, 121 (5), 941–959. doi: 10.1093/aob/mcx187.
119. Wang, G., Li, X., Dong, J., Jin, R., Yang, L., Huo, L., Chen, L., Zhao, W. & Gao, X. (2021). Proteomics unravels new candidate genes of Dasypyrum villosum for improving wheat quality. Journal of Proteomics, 245.
120. Wishart, D. S. (2019). Metabolomics for investigating physiological and pathophysiological processes. Physiological Reviews, 99, 1819–1875.
121. Wu, Y., Liu, J., Zhao, L., Wu, H., Zhu, Y., Ahmad, I. & Zhou, G. (2024). Abiotic stress responses in crop plants: A multi-scale approach. Journal of Integrative Agriculture. https://doi.org/10.1016/j.jia.2024.09.00.
122. Xu, H., Jiang, B., Cao, Y., Zhang, Y., Zhan, X. and Shen, X. (2015). Detection of epistatic and gene-environment interactions underlying three quality traits in rice using high-throughput genome-wide data. BioMed. Res. Int. doi: 10.1155/2015/ 135782.

123. Xu, Y., Wu, Y. and Wu, J. (2018). Capturing pair-wise epistatic effects associated with three agronomic traits in barley. Genetica,146, 161–170. doi: 10.1007/s10709-018-0008-0.
124. Yan, J. and Wang, X. (2023). Machine learning bridges omics sciences andplant breeding.Trends Plant Sci, 28:199–210. 10.1016/j.tplants.2022.08.018
125. Yang, S., Li, H., He, H., Zhou, Y. and Zhang, Z. (2019). Critical assessmentand performance improvement of plant–pathogen protein–protein interaction prediction methods. Briefings Bioinf, 20 (1), 274–287. doi: 10.1093/bib/bbx123.
126. Yang, X. and Guo, T. (2017). Machine learning in plant disease research.doi: 10.18088/ejbmr.3.1.2017.pp6-9.
127. Yan, J. and Wang, X. (2023). Machine learning bridges omics sciences and plant breeding. Trends Plant Sci, 28 (2), 199–210. doi:10.1016/j.tplants.2022.08.018.
128. Zhu, J., Tang, X., Sun, Y., Li, Y., Wang, Y., Jiang, Y., Shao, H., Yong, B., Li, H. & Tao, X. (2022). Comparative metabolomic profiling of compatible and incompatible interactions between potato and Phytophthora infestans. Frontiers in Microbiology, 13, 857160.
129. Zhang, X., Wang, Z., Jiang, C. & Xu, J.R. (2021). Regulation of biotic interactions and responses to abiotic stresses by MAP kinase pathways in plant pathogenic fungi. Stress Biology, 1, 1–19. https://doi.org/10.1007/s44154-021-00004-3.