



Omics-driven strategies for integrated insect-pest and disease management

Shravan Manbhar Haldhar^{1#} and Prabhu Narayan Meena¹

Summary

Agriculture is increasingly challenged by insect-pests and diseases that threaten global food security, farmer livelihoods, and ecosystem stability. Conventional management strategies, particularly chemical pesticides, have offered short-term solutions but are constrained for resistance development, environmental contamination, and health concerns. This has created an urgent need for innovative, sustainable, and knowledge-driven approaches to crop protection. In this context, omics technologies, including genomics, transcriptomics, proteomics, metabolomics, biopesticides, microbial consortia and microbiomics, have emerged as transformative tools for integrated insect-pest and disease management (IPDM). Omics approaches offer a comprehensive understanding of biological systems by deciphering host-pathogen-pest interactions. Genomics enables the identification of resistance genes and virulence factors, while transcriptomics reveals dynamic gene expression during stress or infection. Proteomics and metabolomics uncover functional proteins and metabolites involved in defense responses, offering insights into biochemical pathways for crop protection. Microbiomics highlights the role of beneficial microbes in enhancing plant immunity and suppressing pests, opening avenues for bio-based interventions. Integration of omics data supports eco-friendly strategies such as molecular diagnostics for early detection, RNA interference (RNAi)-based pest control, and marker-assisted breeding for resistant varieties. Furthermore, omics-driven insights facilitate the development of biopesticides and microbial consortia that complement traditional IPM practices. Beyond pest control, omics contributes to reducing chemical dependency, enhancing biodiversity, improving soil and water health, empowering farmers with knowledge, and advancing climate-smart agriculture. Thus, omics technologies represent a paradigm shift in insect-pest and disease management, enabling a transition from reactive, pesticide-dependent practices to proactive, knowledge-intensive solutions. Their integration into IPDM frameworks promises resilient crops, reduced ecological footprints, and sustainable food security for future generations.

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Introduction

Agriculture faces unprecedented challenges from insect-pests and diseases that threaten global food security, farmer livelihoods, and ecosystem stability. Conventional management approaches, particularly the reliance on chemical pesticides, have historically provided short-term relief but are increasingly constrained for pesticide resistance, environmental contamination, and human health concerns. These limitations underscore the urgent need for innovative, sustainable, and knowledge-intensive strategies to manage pests and diseases effectively (Sharma et al. 2025).

In this context, omics technologies, genomics, transcriptomics, proteomics, metabolomics, and microbiomics have emerged as transformative tools that can revolutionise IPDM. Omics approaches

generate large-scale datasets that capture the complexity of biological systems, offering a holistic understanding of host-pathogen-pest interactions. Genomics enables the identification of resistance genes in crops and virulence factors in pests and pathogens, while transcriptomics reveals dynamic gene expression patterns during infection or stress. Proteomics and metabolomics unravel functional proteins and metabolites involved in defense responses, providing insights into biochemical pathways that can be harnessed for crop protection. Microbiomics highlights the role of beneficial microbes in enhancing plant immunity and suppressing pests, opening avenues for bio-based interventions (Kumar et al. 2025).

By integrating omics data, researchers can design precise, eco-friendly strategies such as molecular diagnostics for early detection, RNA interference (RNAi)-based pest control, and marker-assisted breeding for resistant varieties. Omics-driven insights also facilitate the development of biopesticides and microbial consortia that complement traditional IPM

¹ICAR-National Research Institute for Integrated Pest Management, New Delhi-110058

#Corresponding author: SM Haldhar E-mail: haldhar80@gmail.com

practices. This convergence of cutting-edge molecular science with field-level management strengthens crop resilience and aligns with the goals of sustainable agriculture (Ilieva et al. 2025; Askew et al. 2024).

Thus, omics technologies represent a paradigm shift in insect-pest and disease management, enabling a transition from reactive, chemical-dependent practices to proactive, knowledge-driven solutions. Their integration into IPDM frameworks promises to safeguard crop productivity while minimizing ecological footprints, ensuring food security for future generations. Omics tools bridge this gap by offering molecular-level diagnostics, predictive insights, and targeted interventions, allowing researchers to decode complex interactions among crops, pests, pathogens, and beneficial microbes, which strengthening IPDM strategies (Heeb & Jenner 2019).

Omics for IPDM: key goals and contributions

1. Reduces chemical dependency

Minimizes reliance on synthetic pesticides by integrating cultural, biological, and mechanical controls. Helps prevent pesticide resistance and pest resurgence through molecular insights into pest-pathogen interactions (Kumar et al. 2025). Protects pollinators and beneficial insects, as recent studies highlight pesticide-induced declines in pollinator health and reproduction (Sharma et al. 2025).

2. Enhances biodiversity

Encourages natural predators and parasitoids via habitat management informed by omics-driven ecological monitoring. Promotes crop diversification and intercropping to disrupt pest cycles and enhance resilience (FAO, 2025). Supports soil microbial diversity by reducing chemical overuse, with omics revealing microbial community shifts under IPM practices (Ilieva et al. 2025).

3. Improves soil and water health

Avoids pesticide runoff that contaminates water bodies, safeguarding aquatic biodiversity. Preserves soil organisms, which are essential for nutrient cycling and structure, as shown in soil microbiome studies (Pandey & Saharan 2025). Reduces toxic residues that compromise long-term soil fertility, ensuring sustainable productivity.

4. Empowers farmers with knowledge

Relies on monitoring, forecasting, and omics-based diagnostic tools rather than indiscriminate spraying. Encourages farmer training in pest identification, threshold-based interventions, and RNAi-based biocontrol strategies (Kumar et al. 2025). Builds resilience through adaptive, site-specific strategies supported by digital agriculture platforms.

5. Supports climate-smart agriculture

Reduces greenhouse gas emissions associated with pesticide production and application by shifting toward bio-based solutions (Heeb & Jenner 2019). Enhances carbon sequestration by maintaining healthy, undisturbed soils and promoting microbial-driven soil functions. Aligns with global biodiversity and climate frameworks, notably the Kunming-Montreal Global Biodiversity Framework, which sets ambitious targets

for sustainable agriculture and biodiversity conservation.

Omics approaches for integrated pest and disease management

1. IoT-based monitoring of pest and disease
2. RNA interference (RNAi)-based pest control
3. Plant-pathogen interaction for pest management
4. Marker-assisted breeding for resistant varieties
5. Endophytes for pest and disease control
6. Development of biopesticides
7. Promoting microbial-driven soil functions
8. Promoting crop diversification and intercropping to disrupt pest cycles and enhance resilience

1. IoT-based monitoring of pest and disease

Integrated Pest and Disease Management (IPDM) depends on early detection, regular monitoring, and timely implementation of interventions. Conventional tools such as pheromone traps, sticky traps, and field scouting provide valuable insights but are limited in scale, precision, and automation. Recent advances in Internet of Things (IoT) technologies, wireless sensors, cloud computing, and artificial intelligence (AI) have transformed pest and disease surveillance. When combined with *omics* approaches, IoT systems enable molecular-level diagnostics linked to field-level monitoring, creating a holistic framework for crop protection. Effective monitoring forms the backbone of IPM, as it allows real-time tracking of pest populations and crop health, supporting informed decisions on management strategies. Among traditional tools, pheromone traps remain more effective than light or sticky traps in capturing specific insect species.

Biotic stresses such as diseases and insect pests significantly reduce crop productivity, and remote sensing (RS) has emerged as a powerful tool for detecting stress responses. RS technologies exploit changes in plant pigmentation, morphology, and photosynthetic activity, which alter energy absorption and reflectance patterns (Prabhakar et al. 2012). For example, Prabhakar et al. (2012) assessed leafhopper damage in cotton using hyperspectral RS, categorizing plants into five infestation levels based on chlorophyll and relative water content. Xu et al. (2007) applied reflectance spectra to evaluate leaf miner damage in tomato, while Hillnhutter et al. (2011) mapped cyst nematode symptoms in beet using RS integrated with GIS. Machine learning (ML) has further enhanced predictive capabilities: Kaur et al. (2022) used deep learning to forecast diamondback moth abundance in cabbage, and Li et al. (2024) applied transfer learning CNN models to detect pests in tea plantations, safeguarding leaf quality.

The integration of RS with AI and ML expands the ability to identify and quantify pest- and disease-induced changes in plant biomass, pigment composition, and vigor (Pinter et al. 2003). Small et al. (2015) demonstrated that historical weather data could predicted late blight outbreaks in tomato and potato, leading to a web-based decision support system (DSS). RS can also detect physiological changes such as

chlorosis, necrosis, wilting, and leaf rolling. Techniques like fluorescence spectroscopy, fluorescence imaging, and near-infrared (NIR) spectroscopy have successfully diagnosed fire blight in pear plants before visible symptoms appeared (Spinelli et al. 2006).

Emerging innovations such as electronic nose (E-nose) systems complement RS by detecting volatile organic compounds (VOCs) released during pest or disease stress. These systems, combined with fluorescence imaging, enable early diagnosis by identifying subtle changes in odor profiles and tissue fluorescence. Fuentes et al. (2018) used E-noses to differentiate fire blight from blossom blight in apple trees, while Lins et al. (2009) distinguished citrus canker-infected leaves from chlorosis-affected healthy leaves. ML algorithms, particularly support vector machines (SVM), have shown strong performance in predicting pest and disease occurrence. Bhatia et al. (2020) combined SVM with logistic regression to detect powdery mildew in tomato, while Xiao et al. (2019) applied long short-term memory (LSTM) networks to correlate weather data with insect population dynamics. More recently, Christakakis et al. (2024) developed a smartphone application using Python-based REST API, PostgreSQL, and Keycloak for real-time pest detection, successfully tested against *Tuta absoluta* insect in tomato fields.

Monitoring larval age distribution is critical for predicting outbreaks and optimizing insecticide application timing. RS contributes by estimating pest developmental stages through accumulated degree days. Yones et al. (2012) identified optimal management windows for cotton leafworm (*Spodoptera littoralis*) using satellite RS, while Nansen et al. (2015) showed that temporal changes in body reflectance patterns of maize weevil (*Sitophilus zeamais*) and large flour beetle (*Cynaus angustus*) correlated with responses to entomopathogenic nematodes and plant-derived insecticides. Infrared photography has also been applied to assess black fly and scale infestations in citrus, as well as whitefly damage in cotton. Early mite infestations in cotton were detected through multispectral RS by monitoring canopy color and appearance changes.

ML-based models are increasingly used to forecast pest outbreaks with greater accuracy than traditional statistical methods. Holzinger et al. (2023) reported improved prediction of major tomato pests using ML, while Gonzalez et al. (2022) developed a DSS for thrips management in tomato, reducing insecticide use. AI algorithms also support early warning systems: Murmu et al. (2022) classified fruit fly species based on wing patterns and predicted aphid outbreaks in soybean using deep learning. Bourhis et al. (2021) emphasized AI's role in optimizing monitoring infrastructure to enhance aphid forecasting.

Traditional insect monitoring methods, such as suction traps, are labour-intensive and require expert taxonomic skills, creating bottlenecks. AI-driven image recognition and ML offer scalable alternatives. Aphids, notorious for yield losses and viral transmission, have been systematically monitored using AI and ML

approaches (Batz et al. 2023). Park et al. (2023) employed deep learning models (MRCNN, YOLOv3, Detectron2) on unmanned ground vehicles equipped with cameras to detect *Riptortus pedestris*, a major soybean pest. In the context of invasive species, Halubanza (2024) developed a CNN-based MobileNet v2 model that achieved high precision in identifying locust species (*Locusta migratoria* at 91% and *Nomadacris septemfasciata* at 85%), underscoring the importance of AI in early warning systems for pest invasions.

2. RNA interference (RNAi)-based pest control

Integrated Pest and Disease Management (IPDM) emphasizes strategies that are environmentally sustainable, economically viable, and socially acceptable. Conventional approaches—such as chemical pesticides, cultural practices, and biological control—remain important but face limitations due to resistance development and ecological concerns. The emergence of *omics* technologies, including genomics, transcriptomics, proteomics, and metabolomics, has transformed pest management by providing molecular-level insights into host–pathogen interactions. Within this framework, RNA interference (RNAi) has gained attention as a highly promising tool, enabling precise gene silencing through the application of double-stranded RNA (dsRNA).

Originally discovered in *Caenorhabditis elegans* in the late 1990s, RNAi has since been adapted for agricultural use. In pest management, dsRNA molecules are designed to match essential pest gene sequences. Once inside the pest, these molecules trigger degradation of target mRNA, suppressing gene expression and disrupting critical biological functions. RNAi is increasingly recognized as a safer alternative to conventional pesticides due to its high specificity, adaptability, and minimal ecological footprint (Mahanta et al. 2025). dsRNA has shown effectiveness against diverse pest species, delivered either through topical sprays or transgenic plants. However, large-scale application remains challenging, with key issues including dsRNA design, delivery systems, cellular uptake, environmental stability, biosafety, and production costs (Mendoza-Alatorre et al. 2025).

Mechanistically, RNAi functions by selectively degrading messenger RNA (mRNA), preventing synthesis of corresponding proteins (Askew et al. 2024; Fan et al. 2022). The process begins when dsRNA is recognized by the ribonuclease III enzyme Dicer-2, which cleaves it into small interfering RNAs (siRNAs) of 21–25 nucleotides, typically with 3' overhangs (Niu et al. 2024). These siRNAs are incorporated into the RNA-induced silencing complex (RISC), where Argonaute-2 mediates sequence-specific cleavage of complementary mRNA targets (Flynt et al., 2021). Because of its ability to silence specific genes, RNAi has been widely applied in insect pest management to disrupt essential physiological processes such as development, metabolism, and reproduction (Keppanan et al. 2024). Experimental studies have demonstrated significant gene knockdown and observable phenotypic

effects, underscoring RNAi's potential in crop protection.

RNAi efficiency depends on several factors, including dsRNA length and composition. Short dsRNAs (<27 nt) often show reduced silencing compared to longer molecules (>60 nt) (He et al. 2020). Target gene selection is also critical. More than 90 genes have been successfully silenced across over 30 insect species, primarily those involved in homeostasis, reproduction, metabolism, detoxification, and cellular integrity (Keppanan et al. 2024).

A novel extension of RNAi is symbiont-mediated RNAi (SMR), which exploits natural insect–microbe associations. In this approach, symbionts are genetically engineered to continuously produce dsRNA, serving as both producers and delivery agents (Taracena et al., 2015; Leonard et al., 2020). For example, engineered *Serratia symbiotica* has been used to express dsRNA targeting the *C002* and *EcR* genes in pea aphids (*Acyrtosiphon pisum*), resulting in effective gene silencing (Elston et al. 2023). Other symbionts, such as *Rhodococcus rhodnii* and BFo2 in *Frankliniella occidentalis*, have also been modified to produce dsRNA, leading to significant larval mortality (Whitten et al. 2016). While promising, SMR raises ecological concerns, including the potential uncontrolled spread of engineered symbionts and risks of horizontal gene transfer.

For RNAi to be effective, dsRNA must successfully enter target cells. This requires crossing epithelial barriers such as the peritrophic matrix and midgut epithelium before incorporation into the cytoplasm (Darif et al., 2023). Uptake can occur through clathrin-mediated endocytosis, receptor-mediated transport, or passive diffusion. However, biological barriers reduce RNAi efficiency. dsRNA-specific nucleases (dsRNases) present in insect saliva, hemolymph, and digestive tracts degrade dsRNA before silencing can occur (Li et al. 2024; Chen et al. 2021). Additionally, gut pH and other physicochemical factors contribute to premature dsRNA breakdown, further limiting effectiveness (Yang et al. 2022).

Unlike conventional agrochemicals, RNAi operates at the mRNA level in a sequence-dependent manner, offering unmatched precision and selectivity. This allows farmers to target specific pathogens, nematodes, and insect pests while minimizing harm to non-target species. RNAi-based crop protection can be achieved through two main strategies:

- **Plant-Incorporated Protectants (PIPs):** Transgenic plants engineered to express dsRNA targeting pest or pathogen genes.
- **Spray-Induced Gene Silencing (SIGS):** Exogenous application of dsRNA sprays, absorbed directly by pathogens or taken up by plant cells and transferred to interacting pests.

Both approaches highlight RNAi's versatility as an alternative to conventional pesticides. dsRNA can also act as a resistance suppressor, countering resistant insect or weed strains. Commercially, dsRNA-based products are expected to fall into four categories: (i)

direct control agents, (ii) resistance factor repressors, (iii) development disruptors, and (iv) growth enhancers (Zotti & Smagghe 2015; San-Miguel & Scott 2016).

3. Plant-pathogen interaction for pest management

Pathogen-derived elicitors are molecular signals that facilitate successful invasion and colonization of host tissues. In response, plants produce recognition molecules that detect these pathogenic cues and activate defense mechanisms (Gupta et al., 2015). A thorough understanding of this bidirectional communication—both before and after infection—is essential for designing effective disease management strategies and safeguarding agricultural productivity. Plant immune responses are broadly categorized into pattern-triggered immunity (PTI) and effector-triggered immunity (ETI). These defense layers involve the generation of reactive oxygen species (ROS), hypersensitive cell death, activation of mitogen-activated protein kinase (MAPK) cascades, calcium-dependent protein kinases, and regulation through phytohormones (Balotf et al. 2021). The advent of high-throughput omics technologies—including genomics, transcriptomics, proteomics, metabolomics, and epigenomics—has revolutionized our ability to study plant–pathogen interactions at a systems level. These approaches enable comprehensive profiling of biomolecules, providing insights into gene expression dynamics, protein–protein interactions, metabolic reprogramming, and epigenetic modifications during infection (Hayden et al., 2014). Genomic and transcriptomic analyses have facilitated the identification of resistance (R) genes, susceptibility (S) genes, and pathogenicity-related factors. Meanwhile, proteomic and metabolomic studies reveal downstream changes in defense pathways and metabolic adjustments in plants under pathogen attack.

By integrating multi-omics datasets, researchers can unravel complex signaling networks and temporal regulation of host responses, offering a holistic view of plant immunity (Van Emon 2016; Kumar et al. 2023). This integration has transformed the study of host–pathogen interactions, enabling scientists to decode the molecular mechanisms that determine resistance or susceptibility. Ultimately, omics-guided insights provide a powerful foundation for next-generation plant protection strategies, supporting the development of resilient crop varieties and sustainable disease management practices.

a. Genomics

Advances in genome sequencing and annotation have provided unprecedented insights into genome architecture, evolutionary dynamics, and the functional basis of host–pathogen interactions. Comparative analyses of plant and pathogen genomes have enabled the identification of key genes associated with virulence, resistance, and immunity, thereby clarifying the genetic foundations of susceptibility and defense. Whole-genome sequencing of plant pathogens has been particularly valuable in revealing mechanisms of pathogenicity, adaptation, and evolutionary strategies

(Lee et al. 2005). For example, sequencing of *Phytophthora infestans*, the causal agent of potato late blight, uncovered a highly dynamic genome characterized by repeat-rich regions and rapidly evolving effector gene clusters, highlighting its remarkable adaptability (Haas et al. 2009; Maurice et al. 2019; Zhang et al. 2021).

On the host side, genomics has facilitated the discovery of resistance (R) genes and susceptibility (S) genes that regulate immune responses. The genome of *Arabidopsis thaliana* has served as a model for studying nucleotide-binding leucine-rich repeat (NLR) gene families, which play a central role in pathogen recognition. Similarly, rice genomics has guided breeding programs that stack multiple R genes, such as *Xa21* and *Pi9*, to confer broad-spectrum resistance against bacterial and fungal pathogens (Ercoli et al. 2022).

Comparative genomics of pathogen populations and host cultivars has further illustrated the co-evolutionary arms race between avirulence (Avr) genes and R genes, with selective pressures driving effector diversification. For instance, the effector *AvrXa7* from *Xanthomonas oryzae* pv. *oryzae* was identified through comparative analysis and shown to interact with the rice *Xa7* resistance gene, triggering defense responses (Loper et al. 2012; Mena et al. 2022). Recent comparative studies of *Diaporthe* species have also provided insights into pathogenic strategies, with transcriptomic analyses of *Diaporthe caulivora* during host infection revealing mechanisms of virulence and host adaptation (Mena et al. 2022).

Collectively, these genomic investigations underscore the importance of sequencing and comparative analysis in unraveling the molecular basis of plant–pathogen interactions. By identifying critical genes and pathways, genomics not only enhances our understanding of host immunity and pathogen evolution but also provides actionable knowledge for breeding disease-resistant crop varieties.

b. Proteomics

Proteomics has greatly advanced our understanding of plant–pathogen interactions by enabling the identification of resistance proteins, pathogenesis-related proteins, effector molecules, and their post-translational modifications. The apoplast, where much of the host–pathogen communication occurs, serves as a critical site for molecular exchange between plant cells and invading microbes (Stotz et al., 2014; Guerra-Guimarães et al. 2015). Because these interactions involve the protein complements of both host and pathogen, proteomic investigations are inherently complex. To overcome these challenges, lesion-mimic mutants have been employed to identify proteins associated with defense responses (Kim et al. 2008).

For example, Tahara et al. (2003) examined proteins of *Xanthomonas axonopodis* pv. *passiflora* released in response to passion fruit leaf extracts. Their study revealed enhanced expression of several proteins, including a putative membrane-associated protein, an inorganic pyrophosphatase, and a hypothetical protein resembling the *Salmonella*

typhimurium yciF gene. Similarly, Marra et al. (2006) conducted a three-way proteomic analysis involving bean plants, pathogenic fungi (*Rhizoctonia solani* or *Botrytis cinerea*), and the biocontrol fungus *Trichoderma atroviride*. Their work demonstrated that plant proteomes expressed pathogenesis-related proteins and potential resistance genes during interactions, while *T. atroviride* produced proteins homologous to hydrophobins and ABC transporters. Pathogen proteomes, in contrast, showed upregulation of virulence factors such as cyclophilins when interacting with the plant alone or in the presence of the antagonist.

These findings highlight the power of proteomics in identifying key gene products from both host and pathogen that play pivotal roles in disease development and resistance (Fernandez & Novo 2011). By coupling proteomic data with bioinformatics tools, researchers can unravel complex molecular associations, identify novel protein targets, and design strategies for early disease detection and crop protection. Ultimately, proteomics provides a comprehensive framework for understanding plant–microbe interactions and contributes to the development of innovative disease management approaches.

c. Transcriptomics

Transcriptomic approaches have greatly advanced our understanding of gene expression and regulation in plants (Herrera-Estrella, 2014). Techniques such as DNA microarrays, subtractive libraries, expressed sequence tags (ESTs), serial analysis of gene expression (SAGE), and RNA sequencing (RNA-seq) have enabled researchers to link complex biological processes to large-scale transcriptome responses under diverse conditions (Gao et al. 2013). By comparing transcriptomic datasets across cell types or treatments, RNA-seq facilitates the discovery of novel genes, splice variants, and differentially expressed transcripts, thereby providing deeper insights into plant responses to biotic and abiotic stresses (Loraine et al. 2013).

Transcriptome profiling has revealed genes that play pivotal roles in shifting plant–microbe interactions from mutualistic to pathogenic, offering valuable perspectives on disrupted associations (Rathnasamy et al. 2023). For instance, Jiang et al. (2019) examined *Citrullus lanatus* roots infected with *Fusarium* and treated with *Bacillus velezensis* F21. Their study demonstrated that infection triggered systemic resistance, activating ripening-related genes, transcription factors, and disease-resistance pathways, thereby confirming the role of biocontrol agents in priming host immunity. Similarly, Zhao et al. (2020) investigated the biocontrol fungus *Coniothyrium minitans*, which parasitizes *Sclerotinia sclerotiorum*. Transcriptomic analysis revealed activation of diverse proteins and secondary metabolites that contributed to suppression of the pathogen.

Recent advances in single-cell transcriptomics have further refined our understanding of plant–microbe interactions. Studies on legume–rhizobia symbiosis have uncovered early dynamics at the cellular level,

showing transient defense responses in epidermal cells and cortex-specific gene expression patterns that highlight tissue-specific functions. Distinct nodule structures—indeterminate and determinate—were shown to compartmentalize nitrogen fixation processes, with glutamine synthetase genes enriched in infected cells and asparagine synthesis occurring in uninfected cells (Cervantes-Perez et al. 2024; Yin et al. 2023).

Together, these findings underscore the transformative role of transcriptomics in decoding plant–microbe interactions. By revealing gene networks, regulatory pathways, and tissue-specific responses, transcriptomic studies not only enhance our understanding of plant immunity but also provide actionable knowledge for developing biocontrol strategies and improving crop resilience.

d. Metabolomics

Metabolomics focuses on the identification, quantification, and interpretation of small molecules involved in metabolic pathways, offering insights into cellular processes, phenotypic traits, and responses to environmental or genetic changes (Xu et al. 2022). When combined with other functional genomics approaches, metabolomics provides a deeper understanding of host–pathogen interactions (Allwood et al. 2010). During infection, plants often reprogram their metabolome at the site of invasion, initiating localized responses that can extend to adjacent tissues and trigger systemic defense mechanisms (Arbona & Gomez-Cadenas 2016).

For example, infection of resistant and susceptible rice cultivars with *Xanthomonas oryzae* pv. *oryzae* revealed distinct metabolite profiles, including differences in acetophenone, xanthophylls, alkaloids, carbohydrates, and lipids (Sana et al., 2010). Similarly, Kage et al. (2017) reported that a tolerant wheat variety accumulated defense-related metabolites such as coumaroyl putrescine and coumaroyl agmatine during fusarium head blight. The study linked these compounds to the activity of the *agmatine coumaroyl transferase* (ACT) gene, which contributes to resistance against *Fusarium graminearum*. In ginseng, metabolomic analyses following *Fusarium solani* infection revealed dynamic changes in saponins, sugars, and organic acids that varied with infection duration (Smith et al. 2006). More recently, Dong et al. (2023) identified 365 metabolites in wheat during fusarium head blight, including nucleotides, lipids, amino acids, carbohydrates, flavonoids, and hydroxycinnamate derivatives. The abundance of defense-related metabolites was shown to differ across resistant and susceptible varieties, underscoring the complexity of metabolic responses.

Despite its promise, metabolomics faces several limitations. The vast diversity and structural complexity of plant and microbial metabolites—many of which remain uncharacterized pose challenges for accurate identification and functional annotation, particularly in non-model species. Moreover, the metabolome is highly dynamic, influenced by environmental conditions,

developmental stage, and tissue type, making it difficult to distinguish infection-induced changes from baseline variation. Quantification is often relative rather than absolute, and the absence of authentic standards for many secondary metabolites restricts precision. Integration with other omics layers (genomics, transcriptomics, proteomics) is further complicated by differences in data structure and temporal resolution. Reproducibility also remains a concern due to the lack of standardized protocols for sample preparation, instrument calibration, and data normalization.

Nevertheless, metabolomics continues to be a powerful tool for unraveling host–pathogen interactions. When combined with functional genomics and computational modelling, it provides a holistic view of plant defense mechanisms and pathogen virulence strategies, ultimately contributing to the development of sustainable crop protection approaches.

e. Plant-phenomics

Plant phenomics refers to the high-throughput characterization of complex plant traits, providing insights into how specific genotypes perform under varying environmental conditions. It also serves as a powerful imaging-based tool for capturing intricate features relevant to crop selection and improvement (Kumari et al. 2024). In recent years, several advanced phenotyping platforms have been developed that allow early-stage evaluation of crop performance in both controlled laboratory settings and natural field environments. These include robotics, spectroscopy, image analysis, non-invasive imaging, and high-performance computing, all of which enable precise and rapid assessment of plant traits (Xiao et al., 2022).

Phenomics has proven particularly valuable in studying plant–pathogen interactions. For example, thermal imaging in *Arabidopsis thaliana* infected with *Pseudomonas syringae* detected localized stomatal closure and subtle changes in leaf surface temperature before visible symptoms appeared, offering insights into early defense responses. Similarly, chlorophyll fluorescence imaging has been used in *Nicotiana benthamiana* to monitor declines in photosystem II efficiency following infection with *Phytophthora infestans*, correlating strongly with pathogen load (Chaerle et al. 2004). In wheat (*Triticum aestivum*), hyperspectral imaging has enabled discrimination between resistant and susceptible genotypes to stripe rust (*Puccinia striiformis*), facilitating rapid screening in breeding programs (Bock et al. 2010).

By integrating phenotypic datasets with transcriptomic and metabolomic analyses, researchers have been able to identify genotype-specific responses and potential resistance markers. Although challenges remain such as standardizing protocols, managing large datasets, and ensuring reproducibility—these examples demonstrate how plant phenomics enhances our understanding of host–pathogen dynamics. Ultimately, phenomics provides a critical bridge between genotype and phenotype, supporting the development of disease-resilient crops and advancing sustainable agriculture.

4. Marker-assisted breeding for resistant varieties

The integration of omics technologies with marker-assisted breeding offers a transformative pathway for developing crop varieties resistant to pests and diseases. This synergy strengthens integrated pest management (IPM) frameworks, ensuring sustainable agricultural productivity and food security. The foundations of crop breeding were laid with the discovery of Mendelian inheritance, but the field has advanced dramatically with the advent of modern genomics. In recent years, innovative approaches such as genomic selection, speed breeding, and high-throughput phenotyping (HTTP) have accelerated the pace of crop improvement. Biotechnological interventions, including genetic engineering and gene transformation, have further expanded the breeder's toolkit, enabling the incorporation of desirable traits with precision. Techniques such as whole genome sequencing (WGS), gene identification, and molecular marker development have proven effective in enhancing cisgenesis, intragenesis, mutation breeding, and polyploidy programs (Murovec et al. 2017).

Conventional breeding, while foundational, is often slow and resource-intensive. It requires multi-year replicated trials across diverse environments to evaluate the genetic potential of candidate genotypes (Voss-Fels et al., 2019). Molecular breeding, supported by advanced genomic studies, has significantly improved efficiency by reducing the time required to fix traits and identify superior lines. Plants, with their short generation times and large populations, are particularly amenable to manipulation through crossbreeding and selfing (Stetter et al. 2016).

One of the most notable innovations is "speed breeding," a non-GMO approach that enables multiple generations of crops within a single year. By manipulating environmental conditions and extending photoperiods, researchers can achieve four to six generations annually in crops such as wheat, barley, and canola (Watson et al. 2018; Voss-Fels et al. 2019). This technique has alleviated the bottleneck of long generation times, allowing rapid trait fixation and accelerating the release of improved varieties.

The urgency of these innovations is underscored by global challenges. Crop yields are increasingly

threatened by biotic and abiotic stresses, while the world's population is projected to reach ten billion within the next three decades (Hickey et al. 2019). Speed breeding, combined with genomics-assisted breeding (GAB), provides a powerful solution to these challenges by enabling rapid development of resilient varieties.

Modern crop improvement now relies on a diverse set of tools that merge classical breeding with cutting-edge technologies. Molecular markers allow precise identification of resistance genes, such as those conferring stripe rust resistance in wheat (Farrakh et al. 2016). GAB has proven effective in enhancing resilience, as demonstrated by pearl millet resistant to downy mildew (Rai et al. 2008) and pulses with improved drought tolerance (Mitrofanova & Khakimova 2017). Double haploid techniques accelerate trait fixation, producing barley lines with enhanced drought and cold tolerance (Wójcik-Jagła et al. 2020) and maize hybrids with improved yield under stress (Serumaga et al. 2018).

Next-generation sequencing (NGS) has expanded the breeder's arsenal, exemplified by soybean pangenome studies that revealed structural variations linked to agronomic traits (Li et al., 2014). Machine learning (ML) applications, including digital imaging and hyperspectral analysis, have facilitated high-throughput disease detection, such as bacterial blight in rice (Lu et al. 2017), yellow rust in wheat (Zhang et al. 2019), and potato Y virus in potato (Polder et al. 2019). Genome editing tools like CRISPR have introduced precision breeding, enabling the development of crops with targeted traits, such as high-amylopectin waxy corn (Waltz, 2016a).

Collectively, these innovations speed breeding, molecular markers, NGS, ML, and CRISPR have revolutionized crop improvement. They not only accelerate the breeding cycle but also enhance resilience against pests, diseases, and climate stresses. By integrating omics approaches with marker-assisted breeding, agriculture is better positioned to meet the dual challenges of food security and environmental sustainability.

Table 1. Examples of tools aiding breeding in food crop improvement

Tool	Crop	Purpose	References
Molecular markers	Wheat	Stripe rust resistance	Farrakh et al. 2016
GAB	Pearl millet	Improved' against downy mildew disease	Rai et al. 2008
GAB	Pulse	Drought tolerance	Mitrofanova & Khakimova 2017
Double Haploid	Barley	Drought and cold resilience	Wojcik-Jagła et al. 2020
Double Haploid	Maize	Improved yield under drought stress	Serumaga et al. 2018
NGS	Soybean	Pangenome	Li et al. 2014
Digital Images (ML)	Rice	Bacterial blight disease assessment	Lu et al. 2017
Hyperspectral imaging (ML)	Wheat	Detection of yellow rust	Zhang et al. 2019
Hyperspectral imaging (ML)	Potato	Potato Y virus detection	Polder et al. 2019

CRISPR	Maize	High-amylopectin waxy corn	Waltz 2016
Speed Breeding	Wheat, barely, chickpea, canola, soybean, sorghum, millets, rapeseed, sugarcane, tomato, and potato	Reducing generation time	Hickey et al. 2019

Wild and relative species gene pool keeps unique traits that can be exploited by direct selection for use in combination breeding or improvement through advanced methods. They also constitute priceless pools that contain gene (s) conferring improved adaptations to stressed environments and are also resistant to diseases and insects or have further nutritional and medicinal

properties. Therefore, there is a crucial need to promote the systematic utilization of a wild gene pool in deliberate breeding work for developing genotypes having biotic and abiotic stress resistance or tolerance and their conservation as related species (Haldhar and Samadia, 2017).

Table 2. Different genotypes of underutilized horticulture crop resistant to insect pests in arid and semi-arid regions of India

S. No.	Crop Name	Insect Species	Resistance Genotypes	Reference
1.	Ber, <i>Z. mauritiana</i>	Stone weevil, <i>A. imalayanus</i>	Resistant: Kali, Katha, Illaichi and Tikadi Moderately resistant: Akharota, Dandan, Gola, Goma Kirti, Sanaur-1, Seb, Umrans and ZG-3	Haldhar et al. 2018c
		Fruit fly, <i>C. vesuviana</i>	Resistant: The ber cultivars such as Tikadi, Katha and Illaichi Moderately resistant: BS-75-1, Safeda, Dandan, Gola, Goma Kirti, Jogia, Narma, Mundia, Reshmi, Seb, ZG-3, Umrans and Akharota	Haldhar et al. 2018a
		Fruit borer, <i>M. scyroides</i>	Resistant: Safeda, Tikadi, Darakhi and Illaichi Moderately resistant: BS-75-1, Gola, Goma Kirti, Seb and Umrans	Haldhar et al. 2023a
2.	Indian Cherry, <i>C. myxa</i>	Tingid bug, <i>D. cheriani</i>	Resistant: AHCM-22, AHCM-25 and AHCM-34 Moderately resistant: AHCM-14, AHCM-30 and AHCM-31	Haldhar et al. 2019
3.	Jamun, <i>S. cumini</i>	Fruit borers, <i>M. scyroides</i> and <i>D. aprobola</i>	Resistant: GJ-26, GJ-27, GJ-19, GJ-17 and GJ-15 Moderately resistant: GJ-3, GJ-6, GJ-7, GJ-9, GJ-13, GJ-16, GJ-18, GJ-20, GJ-23, GJ-24 and GJ-25	Haldhar et al. 2016
4.	Datepalm, <i>P. dactylifera</i>	Fruit borers, <i>B. amydraula</i> and <i>A. sabella</i>	Resistant: Migra, Tayer, Javantri and Medjool	Haldhar et al. 2021
5.	Pomegranate, <i>P. granatum</i>	Mite, <i>T. punicae</i>	Resistant: HP Collec., Speen Sacarin, Gule Shah Rose Pink and AHPG-C3 Moderately resistant: Sur Sukker, Tujetis EC 4347, Bassin Seedless, Dholka, Uthkal, Agah, Achik Dana and Goma Khata	Haldhar et al. 2022
6.	Snapmelon, <i>C. melo</i> L. var. <i>Momordica</i>	Fruit fly, <i>B. cucurbitae</i>	Resistant: IC-430190, DKS-AHS 2011/4, and DKS-AHS 2011/3 Moderately resistant: IC-430160, IC-430162, IC-430175, IC-430179, IC-430180, IC-430185, IC-369788, and DKS-AHS 2011/2	Haldhar et al. 2018b
7.	Musk melon, <i>C. melo</i>	Fruit fly, <i>B. cucurbitae</i>	Resistant: AHMM/BR-1, RM-50 and AHMM/BR-8 Moderately resistant: MHY-5, D. Madhu and P. Sarabati	Haldhar et al. 2013

Source: Haldhar et al. 2023b

5. Endophytes for pest and disease control

Endophytes, microorganisms that colonize internal plant tissues without causing disease, have emerged as promising allies in integrated pest and disease management (IPDM). These symbiotic microbes

inhabit roots, stems, and leaves, where they co-evolve with host plants and contribute to mutual survival through nutrient exchange and enhanced fitness (Shen et al., 2019). Their persistence inside plant tissues, despite chemical and physical defense barriers, reflects

sophisticated adaptations that secure their ecological niche (Kusari et al. 2011). Initially described as cryptic colonizers capable of living within plants without visible symptoms (Azevedo 1998), endophytes are now recognized as phylogenetically diverse groups that interact dynamically within the endosphere and rhizosphere (Evangelisti et al., 2014). Beyond their ecological role, they enhance crop productivity, disease resistance, and tolerance to abiotic stress, thereby stabilizing yields (Govindarajan et al. 2008). Their versatility includes producing bioactive metabolites, improving nutrient acquisition, and modulating plant stress responses. In this way, endophytes act as hidden layers of defense against biotic stresses (Bhagat et al. 2016; Carvalho et al. 2018). Many of their metabolites, initially linked to pathogen resistance, also affect herbivorous insects (Gundel et al. 2020), positioning them as natural entomopathogens and eco-friendly tools for pest suppression. Considering that pests cause global yield losses of nearly 15% in major crops (Filho & Macedo 2011), endophytes represent a valuable resource for sustainable agriculture.

Applications of Endophytes in disease Control:

Endophytes combat pathogens through direct and indirect mechanisms. Direct strategies include competition for space and nutrients, as well as secretion of antimicrobial compounds (Adeleke & Babalola 2022). Indirectly, they activate systemic resistance pathways and upregulate stress-responsive genes (Sood et al. 2021). For instance, *Pseudomonas fluorescens* suppresses soil-borne pathogens such as *Fusarium* and *Rhizoctonia* while enhancing host immunity (Dimkic et al. 2022; Nazir et al. 2024). Competitive exclusion is particularly important since endophytes and pathogens often occupy overlapping niches within plant tissues (Hameed et al. 2025; Kashyap et al. 2023). Strains like *P. fluorescens* and *P. aeruginosa* produce potent bioactive compounds including 2,4-diacetylphloroglucinol, phenazine-1-carboxylic acid, pyoluteorin, pyrrolnitrin, and hydrogen cyanide, all effective against phytopathogenic fungi (Lashin et al. 2021). Similarly, extracts of *Beauveria bassiana* exhibit strong insecticidal activity against cotton leafworm and aphids, while *Trichoderma harzianum* suppresses *Magnaporthe grisea* (Abdullah et al. 2019). Mycoparasitism is another mechanism, exemplified by *Lecanicillium* spp., which reduce powdery mildew and rust fungi (Ownley et al. 2010). Endophytic fungi isolated from mangroves in Indonesia also demonstrated antagonism against *Fusarium oxysporum*, with *Colletotrichum* and *Aspergillus fumigatus* producing volatile antifungal agents such as cyclohexanone and phenyl alcohol (Suciatmih & Rashmansyah 2013).

Endophytes in Insect Management: Beyond pathogen suppression, endophytes contribute to plant defense against insect herbivores, an equally critical component of biotic stress management (Pandey et al. 2019). One mechanism involves modulation of volatile organic compounds (VOCs), which act as toxins, repellents, or attractants for natural predators of pests (Brosset & Blande 2022). For example, *Streptomyces* sp. ES2

exhibited toxicity against *Spodoptera littoralis*, causing morphological and histopathological deformities due to compounds such as cyromazine, 4-nitrophenol, and diazinon (Diab et al. 2023). Genomic and metabolomic analyses have further identified endophytes with biocontrol potential. *Burkholderia contaminans* NZ, for instance, suppresses *Macrophomina phaseolina* in jute through melanin synthesis and pyrrolnitrin inhibition (Zaman et al. 2021). Similarly, colonization of maize by *Metarhizium robertsii* enhanced plant growth, altered defense gene expression, and reduced the growth rate of black cutworm larvae (Ahmad et al. 2020). These findings highlight the dual role of endophytes as plant growth promoters and natural biopesticides.

6. Development of biopesticides

Biopesticides, derived from living organisms or natural products, are increasingly recognized as sustainable alternatives to chemical pesticides due to their specificity, biodegradability, and reduced environmental footprint. The integration of omics approaches into biopesticide development has accelerated the identification of microbial strains, bioactive metabolites, and molecular pathways that underpin pest suppression and disease resistance, thereby strengthening IPDM frameworks (Ayilara et al. 2023).

Genomic sequencing of beneficial microbes such as *Bacillus thuringiensis*, *Pseudomonas fluorescens*, and *Trichoderma* spp. has revealed biosynthetic gene clusters encoding antimicrobial peptides, lipopeptides, and secondary metabolites with pesticidal properties. Comparative genomics enables researchers to pinpoint strain-specific traits that confer biocontrol efficacy, such as siderophore production, chitinase activity, or volatile organic compound synthesis. Metagenomics, which analyzes microbial communities directly from environmental samples, has expanded the pool of candidate organisms by uncovering unculturable microbes with potential biopesticidal activity. Soil and rhizosphere metagenomic studies have identified novel polyketide synthase and non-ribosomal peptide synthetase gene clusters that suppress pathogens like *Fusarium* and *Phytophthora*. These insights allow the design of microbial consortia or engineered strains with enhanced pest suppression capabilities (Mawcha et al. 2024).

Transcriptomic profiling of plants treated with biopesticides provides valuable information on host defense activation. RNA-seq analyses reveal upregulation of pathogenesis-related (PR) proteins, jasmonic acid and salicylic acid signalling pathways, and genes involved in reactive oxygen species detoxification. Proteomics complements transcriptomics by identifying proteins secreted by biocontrol agents that directly inhibit pathogens or modulate plant immunity. For example, proteomic studies of *Trichoderma* spp. have identified secreted enzymes like glucanases and proteases that degrade pathogen cell walls, while bacterial proteomics has revealed effector proteins that trigger induced systemic resistance. Together, transcriptomics and proteomics provide mechanistic clarity on biopesticide action,

guiding the selection of strains and formulations with consistent field performance (Jain et al. 2021).

Metabolomics has emerged as a powerful tool for characterizing bioactive compounds produced by microbes and plants. Using LC-MS/MS and NMR spectroscopy, researchers can profile secondary metabolites that exhibit antifungal, antibacterial, or insecticidal activity. Metabolomic studies have identified compounds like surfactin, iturin, fengycin (from *Bacillus subtilis*), pyrrolnitrin (from *Pseudomonas fluorescens*), and volatile terpenoids (from endophytic fungi), which serve as potent biopesticides. Importantly, metabolomics also helps in understanding synergistic interactions among metabolites, enabling the design of multi-component formulations that target diverse pests and pathogens. Furthermore, metabolomics can be applied to plants treated with biopesticides to monitor changes in metabolic pathways, such as enhanced accumulation of phytoalexins or flavonoids, which contribute to disease resistance (Parveen & Rashtrapal 2024).

Omics-guided discovery has accelerated the pipeline for biopesticide development. Once candidate strains or metabolites are identified, formulation science ensures their stability, shelf-life, and field efficacy. Advances in encapsulation technologies, such as nano-formulations and polymer-based carriers, protect microbial viability and control release of bioactive compounds. Omics data also guide strain compatibility in consortia-based biopesticides, ensuring synergistic interactions rather than antagonism. Moreover, omics approaches help in monitoring biopesticide persistence in soil and plant tissues, addressing regulatory concerns about safety and environmental impact (Marrone 2025).

Despite significant progress, several challenges remain in translating omics discoveries into commercially viable biopesticides. Variability in field performance due to environmental factors, regulatory hurdles, and limited farmer awareness hinder widespread adoption. Omics approaches can help overcome these challenges by identifying biomarkers for biopesticide efficacy, enabling rapid quality control and certification. Additionally, genome editing tools like CRISPR-Cas can be employed to enhance biocontrol traits in microbial strains, guided by omics insights. Synthetic biology offers opportunities to engineer microbial chassis that produce tailored biopesticidal compounds with improved stability and specificity. Future research should also focus on integrating omics data with precision agriculture technologies, such as remote sensing and AI-driven pest forecasting, to optimize biopesticide application timing and dosage (Marrone 2019).

The development of omics-based biopesticides aligns with global efforts to reduce chemical pesticide use and promote sustainable agriculture. Policymakers can leverage omics data to establish science-based regulations that ensure safety while facilitating innovation. Capacity building among farmers through extension services and training is essential to promote

adoption. Public-private partnerships can accelerate commercialization by bridging the gap between laboratory research and field deployment. Importantly, omics approaches provide evidence for the ecological benefits of biopesticides, such as reduced non-target effects, improved soil biodiversity, and mitigation of pesticide residues in food chains (Trimmer 2024).

7. Promoting microbial-driven soil functions

Soil microbial communities are central to ecosystem functioning, influencing nutrient cycling, plant health, and resilience against pests and diseases. Integrated Pest and Disease Management (IPDM) increasingly recognizes the importance of harnessing microbial-driven soil functions to reduce reliance on chemical inputs and promote sustainable agriculture (Tiwari et al. 2024)). The advent of omics technologies genomics, transcriptomics, proteomics, metabolomics, and metagenomics, has revolutionized our ability to study soil microbiomes, uncovering their roles in plant defense, nutrient acquisition, and pathogen suppression. By integrating multi-omics approaches, researchers can decode the complexity of soil microbial networks and design strategies that enhance beneficial interactions, thereby strengthening IPDM frameworks (Chao et al. 2024).

Genomic sequencing of beneficial microbes such as *Bacillus*, *Pseudomonas*, and *Trichoderma* has revealed biosynthetic gene clusters responsible for producing antimicrobial peptides, lipopeptides, and secondary metabolites that suppress pathogens. Metagenomics, which analyzes microbial communities directly from soil samples, has expanded our understanding of unculturable microbes and their functional potential (Contreras-Cornejo et al. 2024). Studies have shown that metagenomic profiling can identify novel genes involved in nitrogen fixation, phosphorus solubilization, and biocontrol activities, thereby linking microbial diversity to soil health and crop productivity. For instance, metagenomic surveys of rhizosphere soils have uncovered microbial consortia capable of producing siderophores and volatile organic compounds that inhibit pathogens such as *Fusarium* and *Rhizoctonia*. These insights allow the development of microbial inoculants tailored to specific soil conditions and crop requirements (Niazi et al. 2023; Jain et al. 2024).

Transcriptomic analyses provide dynamic information on gene expression patterns in soil microbes under stress or during plant-pathogen interactions. RNA-seq studies have revealed how beneficial microbes activate plant defense pathways, including salicylic acid and jasmonic acid signaling, upon colonization. Proteomics complements transcriptomics by identifying proteins secreted by soil microbes that directly inhibit pathogens or modulate plant immunity. For example, proteomic studies of *Trichoderma* spp. have identified secreted enzymes such as glucanases and proteases that degrade pathogen cell walls, while bacterial proteomics has revealed effector proteins that trigger induced systemic resistance (Eshel et al. 2021). Together,

transcriptomics and proteomics provide mechanistic clarity on how soil microbes contribute to pest and disease suppression, guiding the selection of strains with consistent field performance (Kimotho & Maina 2024).

Metabolomics enables the characterization of bioactive compounds produced by soil microbes and plants. Using LC-MS/MS and NMR spectroscopy, researchers can profile metabolites such as surfactin, iturin, fengycin (from *Bacillus subtilis*), pyrrolnitrin (from *Pseudomonas fluorescens*), and volatile terpenoids (from endophytic fungi), which serve as potent biopesticides. Metabolomic studies also reveal how microbial metabolites influence nutrient cycling, for example by enhancing phosphorus solubilization or nitrogen fixation. Importantly, metabolomics helps in understanding synergistic interactions among metabolites, enabling the design of multi-component formulations that target diverse pests and pathogens. Furthermore, metabolomic profiling of plants treated with microbial inoculants has shown enhanced accumulation of phytoalexins and flavonoids, contributing to systemic resistance (Sahoo et al. 2025).

The integration of genomics, transcriptomics, proteomics, and metabolomics through systems biology approaches allows holistic modeling of soil microbial functions. Multi-omics datasets can be combined to construct regulatory networks that explain how microbial communities influence plant immunity, nutrient cycling, and pathogen suppression. Systems biology also facilitates predictive modeling of microbial inoculant efficacy under different environmental conditions, thereby improving reliability in field applications (Colarusso et al. 2021). For example, integrated omics studies have revealed that microbial inoculants not only suppress pathogens directly but also restructure soil microbiomes, enhancing beneficial microbial populations that contribute to long-term soil health (Mishra et al. 2019).

Microbial-driven soil functions play a pivotal role in IPDM by enhancing nutrient availability, promoting plant growth, and suppressing pathogens. Plant growth-promoting rhizobacteria (PGPR) such as *Azospirillum*, *Rhizobium*, and *Bacillus* improve nitrogen fixation and phosphorus solubilization, while mycorrhizal fungi enhance nutrient uptake and confer tolerance to abiotic stresses (Garciglia-Mercado et al. 2024). Biocontrol microbes such as *Trichoderma* and *Pseudomonas* produce antibiotics, lytic enzymes, and volatile compounds that inhibit pathogens. Omics approaches have deepened our understanding of these functions, enabling the design of microbial consortia that combine nutrient acquisition with pest suppression. Such consortia can be applied as biofertilizers or biopesticides, reducing dependence on synthetic inputs (Doni et al. 2022).

Soil microbial communities are highly diverse and dynamic, influenced by environmental factors, crop type, and management practices. This complexity makes it difficult to predict microbial behavior in field conditions. Moreover, many microbial metabolites remain structurally uncharacterized, limiting their

functional annotation. Standardisation of protocols for sample collection, sequencing, and data analysis is essential to improve reproducibility. Future research should focus on integrating omics data with precision agriculture technologies, such as remote sensing and AI-driven pest forecasting, to optimise microbial inoculant application timing and dosage. Synthetic biology offers opportunities to engineer microbial strains with enhanced biocontrol traits, guided by omics insights. Policy support and farmer training are also critical to promote the adoption of microbial-based IPDM strategies.

8. Promotes crop diversification and intercropping to disrupt pest cycles and enhance resilience

Among these strategies, crop diversification and intercropping have long been recognized as effective ecological tools to disrupt pest cycles, enhance resilience, and stabilize yields. By integrating omics insights with ecological practices such as diversification and intercropping, researchers and practitioners can design cropping systems that are both resilient and productive, while reducing reliance on chemical pesticides. Genomic sequencing of crops and associated microbes has revealed genes responsible for resistance, susceptibility, and stress tolerance. Comparative genomics of intercropped species shows how genetic diversity contributes to resilience by reducing uniform susceptibility to pests. For example, sequencing of legumes intercropped with cereals has identified resistance gene clusters that confer protection against soil-borne pathogens, while metagenomic profiling of rhizosphere soils has uncovered microbial consortia that suppress pest populations through competition and antibiosis (Mihrete & Mihretu 2025). Metagenomics also provides insights into microbial-driven soil functions that support diversification. By analyzing microbial communities in diversified cropping systems, researchers have identified beneficial taxa such as *Pseudomonas*, *Bacillus*, and mycorrhizal fungi that enhance nutrient cycling and suppress pathogens.

Transcriptomic profiling enables the study of gene expression changes in crops under intercropping conditions. RNA-seq analyses have shown that intercropped plants often upregulate defense-related genes, including pathogenesis-related proteins, jasmonic acid and salicylic acid pathways, and reactive oxygen species detoxification. These responses are triggered not only by pest pressure but also by beneficial microbial interactions facilitated by diversification (Chao et al. 2023). For instance, transcriptomic studies of maize intercropped with beans revealed enhanced expression of genes linked to systemic resistance, suggesting that intercropping primes crops for faster and stronger defense responses. Similarly, transcriptomic analyses of rice intercropped with pulses demonstrated activation of stress-responsive transcription factors that improved tolerance to both insect pests and fungal pathogens (Khan et al. 2025).

Proteomics complements transcriptomics by identifying proteins secreted by crops and microbes in

intercropping systems. Studies have shown that intercropped plants produce higher levels of defense-related proteins, including chitinases, glucanases, and proteases, which degrade pathogen cell walls. Proteomic analyses of beneficial microbes in diversified systems have revealed effector proteins that trigger induced systemic resistance in crops. For example, proteomic studies of *Trichoderma* spp. in intercropped soils identified enzymes that not only suppress pathogens but also enhance nutrient availability. Similarly, proteomic profiling of rhizobia in legume cereal intercropping systems revealed proteins involved in nitrogen fixation and stress tolerance, underscoring the dual benefits of diversification for pest suppression and soil fertility (Angelella et al. 2016).

Metabolomics provides insights into the chemical ecology of intercropping systems. By profiling metabolites produced by crops and microbes, researchers can identify compounds that contribute to pest suppression and resilience. For instance, metabolomic studies of intercropped wheat and chickpea revealed increased accumulation of flavonoids, phytoalexins, and hydroxycinnamate derivatives, which are known to deter pests and pathogens. Metabolomic analyses also highlight the role of microbial metabolites in diversified systems. Compounds such as surfactin, iturin, and fengycin (from *Bacillus subtilis*) and volatile terpenoids (from endophytic fungi) have been detected at higher levels in intercropped soils, suggesting that diversification enhances microbial activity and metabolite production. These metabolites not only suppress pests but also improve plant growth and resilience (Mihrete & Mihretu 2025). By combining multi-omics datasets, researchers can model how intercropping influences plant immunity, microbial community structure, and pest dynamics. Multi-omics integration has also revealed that diversified systems promote temporal regulation of defense responses, enabling crops to respond more effectively to pest attacks. These insights provide a scientific basis for designing intercropping strategies that maximize resilience and minimize pest outbreaks.

Crop diversification and intercropping offer multiple ecological benefits that align with IPDM goals: Diversification breaks monoculture-driven pest cycles by reducing host plant availability and increasing habitat complexity. Intercropping improves soil structure, nutrient cycling, and microbial diversity, which collectively suppress pests and pathogens. Diversified systems are more resilient to abiotic stresses such as drought and heat, reducing vulnerability to pest outbreaks. Intercropping provides habitat and resources for pollinators and natural enemies, enhancing biological control. These benefits are amplified when guided by omics insights, which enable precise selection of crop combinations and microbial inoculants for maximum impact.

Case studies of crop diversity

1. **Legume-Cereal intercropping:** Genomic and transcriptomic studies have shown that legumes

enhance nitrogen fixation and activate defense pathways in cereals, reducing susceptibility to soil-borne pathogens (Duchene et al. 20217).

2. **Rice-Pulse diversification:** Metabolomic profiling revealed increased accumulation of defense-related metabolites in rice intercropped with pulses, contributing to reduced pest incidence (Shen & Chu 2004).
3. **Maize-Bean systems:** Proteomic analyses demonstrated enhanced production of defense proteins in maize when intercropped with beans, improving resilience against insect pests (Xu et al. 2020).
4. **Wheat-Chickpea systems:** Multi-omics integration highlighted synergistic effects on soil microbial diversity and metabolite production, leading to improved pest suppression and yield stability (Lopes et al. 2016).

Omics technologies have transformed our understanding of crop diversification and intercropping as strategies for integrated pest and disease management. Genomics and metagenomics reveal genetic and microbial diversity, transcriptomics and proteomics elucidate functional mechanisms, metabolomics identifies bioactive compounds, and systems biology integrates these insights into predictive models. Together, these approaches provide a scientific foundation for designing diversified cropping systems that disrupt pest cycles, enhance resilience, and promote sustainability. By combining ecological practices with molecular insights, omics-guided diversification offers a pathway toward resilient agroecosystems capable of meeting the challenges of climate change, pest pressures, and food security.

Conclusion

The integration of omics technologies into Integrated Pest and Disease Management (IPDM) represents a paradigm shift in agricultural science and practice. Conventional pest control strategies, dominated by chemical pesticides, have provided short-term relief but are increasingly constrained by resistance development, ecological degradation, and human health concerns. Omics-driven approaches spanning genomics, transcriptomics, proteomics, metabolomics, microbiomics, and allied innovations such as RNA interference (RNAi), biopesticides, and microbial consortia offer a knowledge-intensive, eco-friendly alternative that aligns with the principles of sustainable and climate-smart agriculture. Genomics has enabled the identification of resistance (R) genes in crops and virulence factors in pests and pathogens, laying the foundation for marker-assisted breeding and precision crop improvement. Transcriptomics has revealed dynamic gene expression patterns during infection and stress, providing insights into how plants mobilize defense responses. Proteomics and metabolomics have uncovered functional proteins and metabolites central to plant immunity, nutrient cycling, and biochemical pathways that can be harnessed for crop protection. Microbiomics has highlighted the critical role of beneficial microbes in enhancing plant

resilience, suppressing pathogens, and restoring soil health. Together, these omics layers provide a holistic understanding of host–pathogen–pest interactions, enabling targeted interventions that go beyond reactive pesticide use.

The practical applications of omics in IPDM are diverse and transformative. Molecular diagnostics allow early detection of pests and pathogens, reducing the lag between infestation and intervention. RNAi-based strategies provide highly specific gene silencing tools to disrupt essential pest functions without harming non-target organisms. Biopesticides and microbial consortia, informed by omics insights, complement traditional IPM practices by offering bio-based alternatives that reduce chemical dependency. Moreover, omics-guided ecological practices such as crop diversification, intercropping, and microbial-driven soil functions disrupt pest cycles, enhance biodiversity, and strengthen agroecosystem resilience. These innovations collectively reduce pesticide reliance, safeguard pollinators, improve soil and water quality, and empower farmers with knowledge-driven, site-specific strategies.

Beyond pest control, omics-driven IPDM contributes to broader sustainability goals. By minimizing pesticide use, these approaches reduce greenhouse gas emissions associated with chemical production and application, while preserving soil organisms essential for nutrient cycling and carbon sequestration. They align with global biodiversity and climate frameworks, including the Kunming-Montreal Global Biodiversity Framework, which emphasizes sustainable agriculture and conservation. Importantly, omics-based strategies empower farmers by providing diagnostic tools, predictive models, and adaptive management practices that enhance resilience against both biotic and abiotic stresses. The complexity of multi-omics data integration, variability in field conditions, limited characterization of microbial metabolites, and adoption barriers among farmers highlight the need for continued research, capacity building, and policy support. Advances in computational biology, synthetic biology, and precision agriculture technologies such as IoT, AI, and machine learning will be critical to overcoming these challenges. Collaborative efforts among researchers, policymakers, and farmers are essential to translate omics insights into scalable, field-ready solutions.

In conclusion, omics technologies represent a transformative frontier in pest and disease management. They enable a transition from reactive, pesticide-dependent practices to proactive, knowledge-driven strategies that integrate molecular science with ecological principles. By promoting resilience, reducing ecological footprints, and ensuring food security, omics-driven IPDM offers a sustainable pathway for agriculture in the face of climate change, evolving pest pressures, and global population growth. The future of crop protection lies not in chemical intensification but in harnessing the molecular and microbial diversity of agroecosystems, an approach that is both scientifically robust and ecologically sound.

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Declarations of interests

All authors of this manuscript declare that they have no conflict of interest.

Data sharing

All relevant data are within the manuscript.

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