

REVIEW

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Plant immune and defense responses to microorganisms and insects: molecular signaling, crosstalk, and adaptive plasticity

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Abstract

Plants encounter a diverse array of pathogens and herbivorous insects, necessitating a well-coordinated response for survival and growth. Recent research has elucidated a complex network of molecular processes, including signal perception, hormonal interactions, transcriptional changes, and metabolic modifications, that govern plant responses to these biotic challenges. Plants recognize microbial and insect-derived signals through specific receptor systems that trigger cascades of signal transduction, which ultimately converge on shared defense mechanisms. Additionally, plant hormones such as salicylic acid, jasmonic acid, and ethylene play a critical role in regulating these responses, enabling plants to defend against multiple pathogens and pests while maintaining overall fitness. The initiation of defense responses results in extensive alterations in gene expression and epigenetic regulation, as well as a redirection of primary metabolism toward the synthesis of specific secondary metabolites, including phenolics, terpenoids, and alkaloids, which are essential for defense against both pathogens and insects. Notably, the findings indicate considerable overlap between defense mechanisms activated by microbial and insect threats, underscoring the importance of integrated signaling over distinct defense pathways. This review aims to synthesize current knowledge of the molecular and metabolic foundations of plant responses to biotic stressors, with an emphasis on common regulatory components and adaptable defense strategies that enable effective, sustainable plant defense.

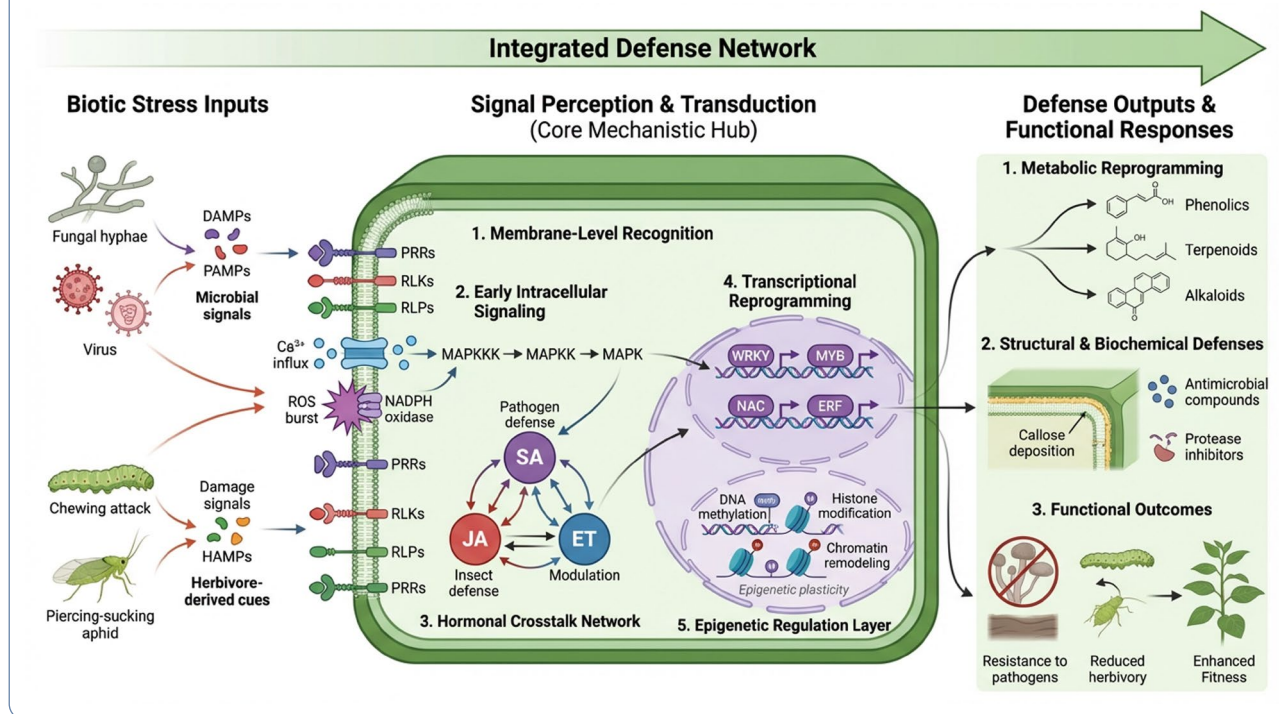
Keywords Plant immunity, Insect herbivory, Microbial interactions, Hormonal crosstalk, Defense signaling, Metabolic reprogramming

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Graphical Abstract



Introduction: convergent and divergent plant responses to microorganisms and insects

Plants exist within environments rich in dynamic ecological matrices, constantly interacting with microorganisms and insects. Consequently, they have evolved defense mechanisms capable of detecting a wide range of biotic cues related to microbial pathogens, mutualistic microbes, and insect herbivores [1, 2]. While plant responses to biotic stresses are often perceived as sequential, they involve a complex network of regulatory mechanisms, including signal detection, intracellular transduction, hormonal modulation, transcriptional regulation, and metabolic reprogramming [3]. For decades, biotic stresses have been studied as two separate entities: those caused by microorganisms and those caused by insects. However, recent research reveals significant overlap in the molecular frameworks that govern plant responses to both stress types [4]. Therefore, a unified conceptual model that transcends traditional disciplinary boundaries and recognizes both convergent and divergent aspects of plant defense is necessary [5]. Microorganisms such as bacteria, fungi, oomycetes, and viruses interact with plants via diverse mechanisms, ranging from pathogenic invasion to mutualism [6]. Herbivorous insects cause physical damage and introduce oral secretions on plant surfaces to facilitate feeding [7]. Despite fundamental differences in their modes of interaction, both microorganisms and insects trigger similar defense

signaling events within comparable timeframes and at shared molecular sites [7]. Plants contain pattern recognition receptors (PRRs) that detect conserved molecular patterns produced by microorganisms, as well as signature and damage-associated molecular patterns emitted by insect herbivores [8]. The activation of PRRs initiates overlapping downstream signaling cascades, indicating that plants rely on signal integration rather than isolated pathways to mount defenses [9]. This integration enables plants to dynamically adjust their responses based on the type of attacker and environmental conditions [10]. A key characteristic of plant defenses is their reliance on converging signaling pathways rather than separate response modules [6]. Detection of either microbes or insects triggers rapid activation of calcium influxes, reactive oxygen species (ROS) bursts, mitogen-activated protein kinase (MAPK) cascades, and phytohormone signaling networks [11]. These early events serve as foundational platforms for downstream transcriptional and metabolic adjustments [12]. Although the qualitative and quantitative aspects of these signals influence response specificity, the same signaling molecules can produce different outcomes depending on timing and location [13]. This versatility in signaling underpins the plasticity observed in plant immune responses. Phytohormones play a central role in balancing convergence and divergence within these defenses [10]. Salicylic acid typically mediates resistance to biotrophic and hemi-biotrophic pathogens,

whereas jasmonic acid and ethylene are mainly involved in defenses against necrotrophic pathogens and insect herbivores [14]. However, the traditional view of these pathways as largely separate is increasingly challenged, as extensive crosstalk among phytohormonal signals allows plants to fine-tune their defenses to suit prevailing biotic threats [15]. This hormonal interplay enables plants to prioritize defenses effectively while conserving energy, reducing the costs of unnecessary responses [10]. Such integration is particularly vital in natural environments, where microorganisms and insects often attack simultaneously. At the transcriptional level, plant defense involves widespread changes in gene expression networks [14]. Families of transcription factors such as WRKY, MYB, bHLH, NAC, and AP2/ERF serve as regulatory hubs, integrating upstream signals to control defense gene expression [9, 16–19]. Many of these regulators are activated by elicitors from both microbes and insects, reinforcing the concept of shared regulatory architectures [14]. Genome-wide expression studies show considerable overlap in transcriptomic responses to microbial and herbivore stimuli, notably in genes related to signaling, secondary metabolism, and cell wall reinforcement [14, 20]. While this overlap does not imply redundancy, it indicates a modular regulatory logic in which conserved frameworks are selectively employed and adapted to produce context-dependent defenses [9]. Beyond transcriptional regulation, epigenetic mechanisms such as chromatin remodeling, histone modifications, DNA methylation, and small RNA-mediated regulation have emerged as vital for defense integration. These epigenetic changes facilitate immediate responses and establish long-term stress memory [21, 22]. Repeated exposure to elicitors can epigenetically prime defenses, enabling faster, stronger responses to subsequent challenges [23]. Many priming effects are non-stressor specific, highlighting the interconnectedness of plant defense pathways [23]. The molecular memory of past attacks confers adaptive advantages in variable environments, underscoring the role of epigenetic plasticity in durable defenses [24]. Metabolic reprogramming adds another dimension: defense activation often reroutes primary metabolism to produce specialized metabolites with antimicrobial and anti-herbivore activities. Compounds such as phenylpropanoids, terpenoids, alkaloids, and glucosinolates contribute directly to defense and indirectly by attracting natural enemies of herbivores [26]. These metabolites often have broad-spectrum activities, inhibiting microbes and deterring insects. The regulation of these metabolic pathways is tightly coordinated with hormonal and transcriptional networks, underscoring that defense metabolism arises from complex, multilayered signaling rather than being a passive outcome [10].

Importantly, the timing and location of immune signals within tissues significantly influence how metabolism functions in specialized pathways. Variations in the duration or intensity of hormone signals, along with changes in ROS levels and kinase activity, can modify the production of defense-related chemicals. This regulation helps shape context-dependent chemical defense patterns during interactions with microbes and insects. While microbial pathogens and insect herbivores often trigger overlapping early signaling events—such as Ca^{2+} influxes, ROS bursts, and MAPK cascades—the resulting metabolic outputs vary considerably depending on the specific biotic stimulus. Differences in hormonal balance, tissue-specific signaling, signal duration, and transcriptional activation direct metabolic flux toward classes of defense compounds, leading to context-specific chemical defense profiles optimized for distinct ecological interactions [10].

Although the convergence of signaling and regulatory mechanisms in plant defense has become increasingly apparent, divergence remains equally important for effective defense. Plants must differentiate among attackers to avoid producing ineffective defense responses that reduce plant fitness [27]. Divergence occurs through the selective activation of different receptors, modulation of signal amplitudes, tissue-specific responses, and differential regulation of defense programs [4]. Additionally, the ecological context, including nutritional status, abiotic stress, plant microbiome composition, and developmental stage, significantly impacts the effectiveness of defense responses [28]. Therefore, understanding how plants coordinate common defense mechanisms with specialized responses is crucial for elucidating the underlying principles of plant immunity and adaptive plasticity [29]. Further justification for developing a unified approach to analyzing plant responses to microorganisms and insects is provided by recent developments in systems biology and multi-omics technologies [30]. Multi-omics approaches have combined data from transcriptomics, proteomics, metabolomics, and phosphoproteomics to reveal interconnected networks of plant defense responses that cannot be fully appreciated using single-stressor or single-pathway approaches [31, 32]. Network modeling and data-driven analyses have shown that plant defense operates as an adaptive system, dynamically influenced by signal integration, feedback regulation, and resource competition [33]. These findings contradict reductionist paradigms and highlight the need for comprehensive frameworks that accurately depict the complexities of real-world plant–biotic interactions [34]. In the context of sustainable agriculture and crop resilience, understanding the convergence and divergence in plant responses to microorganisms and insects has significant practical applications [35, 36]. Strategies for breeding

and engineering crops that target shared defense nodes have the potential to enhance broad-spectrum resistance without compromising plant fitness [36]. However, these approaches require a detailed understanding of the relationships between defense and signaling crosstalk to avoid unintended consequences. Therefore, the development of a unified conceptual model of plant defense is required not only to advance our fundamental knowledge but also to translate molecular information into resilient agricultural strategies [33, 37].

Together, the reviews support the concept that plant defense mechanisms against pathogens and insect pests operate through interconnected systems rather than isolated pathways. Key shared control points include danger detection, calcium signaling, reactive oxygen species bursts, MAPK activation, hormone-signaling interactions, transcription factor cooperation, and changes in gene regulation. These components work collectively to translate external threat signals into an immune response. Although signaling pathways often overlap, plants still tailor specific defenses to situations. Variations in pathogen lifestyles, insect feeding behaviors,

attack locations, signal intensity, plant developmental stages, beneficial microbes, and environmental factors influence the strength, speed, and precision of plant defenses. Consequently, plant immunity is a flexible, adaptable process that allows plants to balance protection, energy expenditure, and environmental adaptation. A diagram illustrating the multilayered architecture linking biotic stress perception to the downstream immune response is shown in Fig. 1. This review also synthesizes current knowledge regarding plant immune responses to microorganisms and insects, emphasizing molecular signaling integration, regulatory crosstalk, and plasticity. By highlighting common regulatory nodes alongside context-dependent divergence, we aim to offer a coherent framework capturing the complexity of plant–biotic interactions. Such an integrative approach is timely and essential for addressing emerging challenges in plant health, ecological resilience, and sustainable food production.

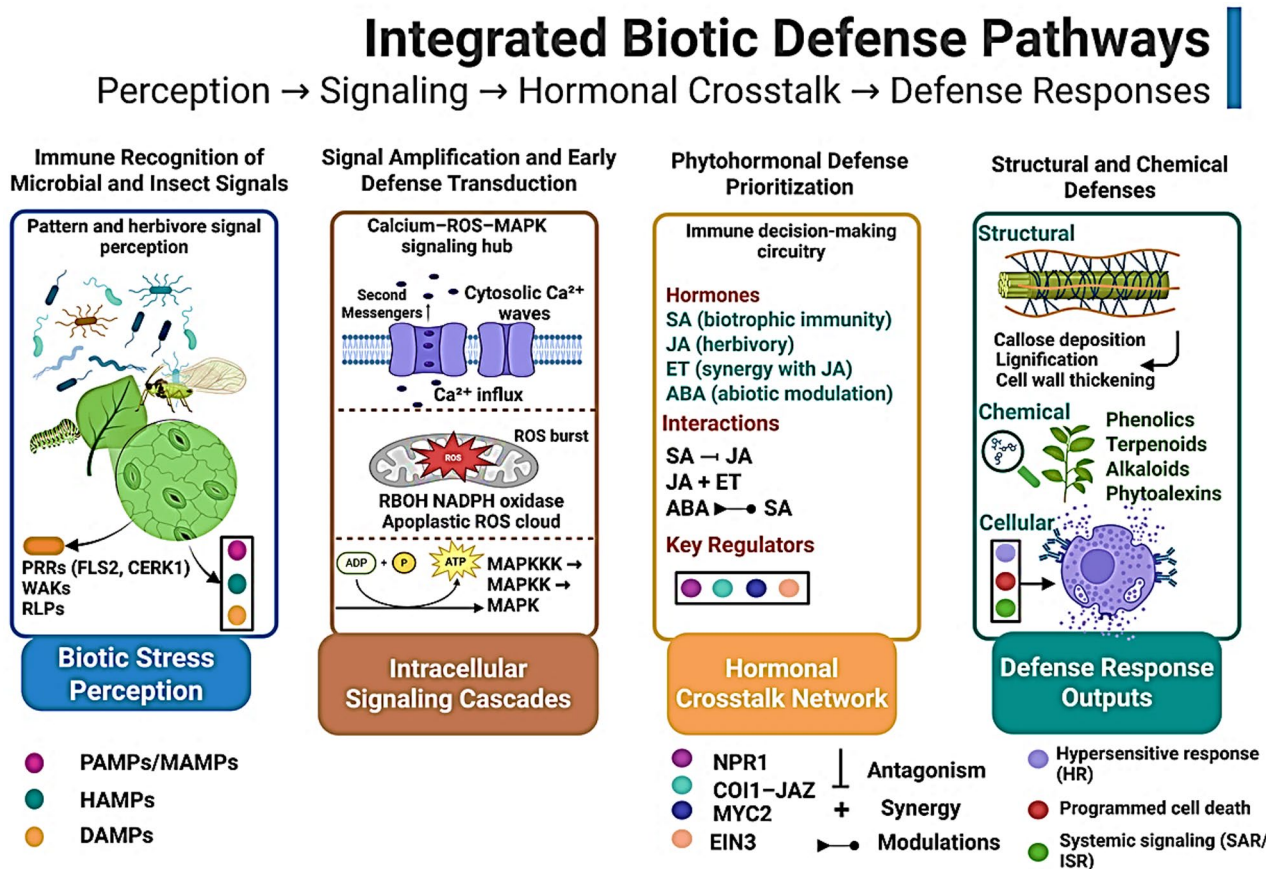


Fig. 1 Integrated plant biotic defense signaling network. Recognition of microbial and insect cues via PRRs activates Ca^{2+} signaling, ROS bursts, and MAPK cascades, which converge on SA–JA–ET–ABA hormonal crosstalk networks. These regulatory hubs coordinate transcriptional reprogramming through key immune regulators to drive structural, chemical, and cellular defense outputs, including cell wall reinforcement, specialized metabolite biosynthesis, hyper-sensitive response, and systemic resistance. Image created using the Biorender program

Early perception of biotic signals: from microbial patterns to herbivore-derived cues

The first level of plant defense is initiated at the plasma membrane, where a variety of cell-surface receptors act as “molecular sentinels” to recognize external biotic signals. Upon recognition of biotically produced cues from microbes or insects by one of the many pattern recognition receptors, the receptor rapidly activates downstream signaling through receptor complex formation and kinase activation. As a result of this rapid signaling process, the initial recognition event triggers early immune responses, including changes in ion flux across the plasma membrane, activation of phosphokinase cascades, and changes in the redox state. These changes are necessary to establish the fundamental basis for downstream defense programming. Therefore, the cellular interface can be considered the key regulatory checkpoint where biotic information is converted into the plant immune signaling network [8, 38]. Unlike mammalian immune systems, which use roaming immune cells to survey the body, plant immunity is inherently cell-autonomous and contains plasma-membrane anchored surveillance machinery in every cell type. This surveillance machinery comprises pattern recognition receptors (PRRs) and co-receptors that associate with PRRs to form dynamic receptor complexes that continuously scan the extracellular environment for conserved microbial- and herbivore-derived molecular patterns, due to the stationary nature of these receptors but their organized spatial distribution they allow for very rapid signal generation upon detection of potential threats, a high degree of sensitivity to ligands and fine temporal regulation of immune response activation. The decentralized architecture of this type provides an immediate local response to invading organisms at the site of invasion. It ensures that the intensity of the immune response is tightly controlled upon invasion [39, 40]. In plant immunity, early perception represents a dynamic layer of active signal interpretation rather than a static layer of passive recognition. Plant cells interpret biochemical elicitors, mechanically induced damage cues, and context-dependent information within the cellular environment to discriminate threat identity, intensity, and duration by quantitatively modulating early signaling outputs [41, 42]. Importantly, the perception layer already embodies the duality of plant defense; at the receptor level, specificities converge onto common downstream signaling modules [4]. An organization such as this enables plants to produce rapid, synchronized immune responses while providing the plasticity needed to develop appropriate defenses against diverse biotic challengers [3]. Microbial pathogens and insect herbivores interact with plant tissues using fundamentally different biological approaches, which impose distinct recognition demands [42]. For example,

microbial pathogens tend to invade plant tissues through direct contact (surface colonization), apoplastic growth, or direct entry into plant cells. In contrast, herbivorous insects inflict mechanical damage and deposit a range of biochemically complex substances via oral secretions and regurgitation during feeding. Despite differences in the modes of interaction among microorganisms, insects, and plant tissue, plants have developed partially overlapping sets of receptors and early signaling mechanisms to recognize both microbial- and herbivore-derived signals. This shared logic of perception reflects an evolutionary bias towards integrating signals and building a robust network, thereby allowing plants to mount reliable immune responses without maintaining energetically expensive, entirely separate recognition pathways. The early perception of microbial-, herbivore-derived- and damage-associated molecular signals occurs at the plasma membrane through pattern recognition receptors that aggregate into dynamic signaling complexes to generate rapid intracellular defense signaling (See Fig. 2).

Pattern recognition receptors and damage-associated molecular signals

The innate immune response in plants does not involve an animal-type adaptive immune system with specialized cells; rather, it is based on an ancient, universal innate immune system. Plants utilize this innate immune response system to identify and respond to molecular patterns associated with invading pathogens and cellular damage. Plants use pattern recognition receptors (PRRs) to recognize molecular patterns produced by pathogens, known as pathogen-associated molecular patterns (PAMPs), and molecules produced by damaged plant cells, known as damage-associated molecular patterns (DAMPs). This enables an appropriate defensive response to protect the plant from pathogen infection. Unlike animals, whose cells can move throughout the body to perform immune functions, plants are stationary and have therefore developed mechanisms to recognize danger in their environment and respond appropriately. Plants employ PRRs to recognize both PAMPs and DAMPs, and to activate downstream signaling pathways that lead to an immune response. Plant PRRs are primarily located on the plasma membrane, where they continually monitor the surrounding environment for pathogens and damaged tissues. PRRs include receptor-like kinases (RLKs) and receptor-like proteins (RLPs). Because PRRs are located on the plasma membrane, they can quickly detect invasion-related cues and immediately activate downstream signaling pathways [43, 44]. Once PRRs recognize a ligand, they initiate various early defense responses, such as changes in the plasma membrane's electrical charge, transient increases in intracellular Ca^{2+} concentrations, rapid bursts of reactive oxygen

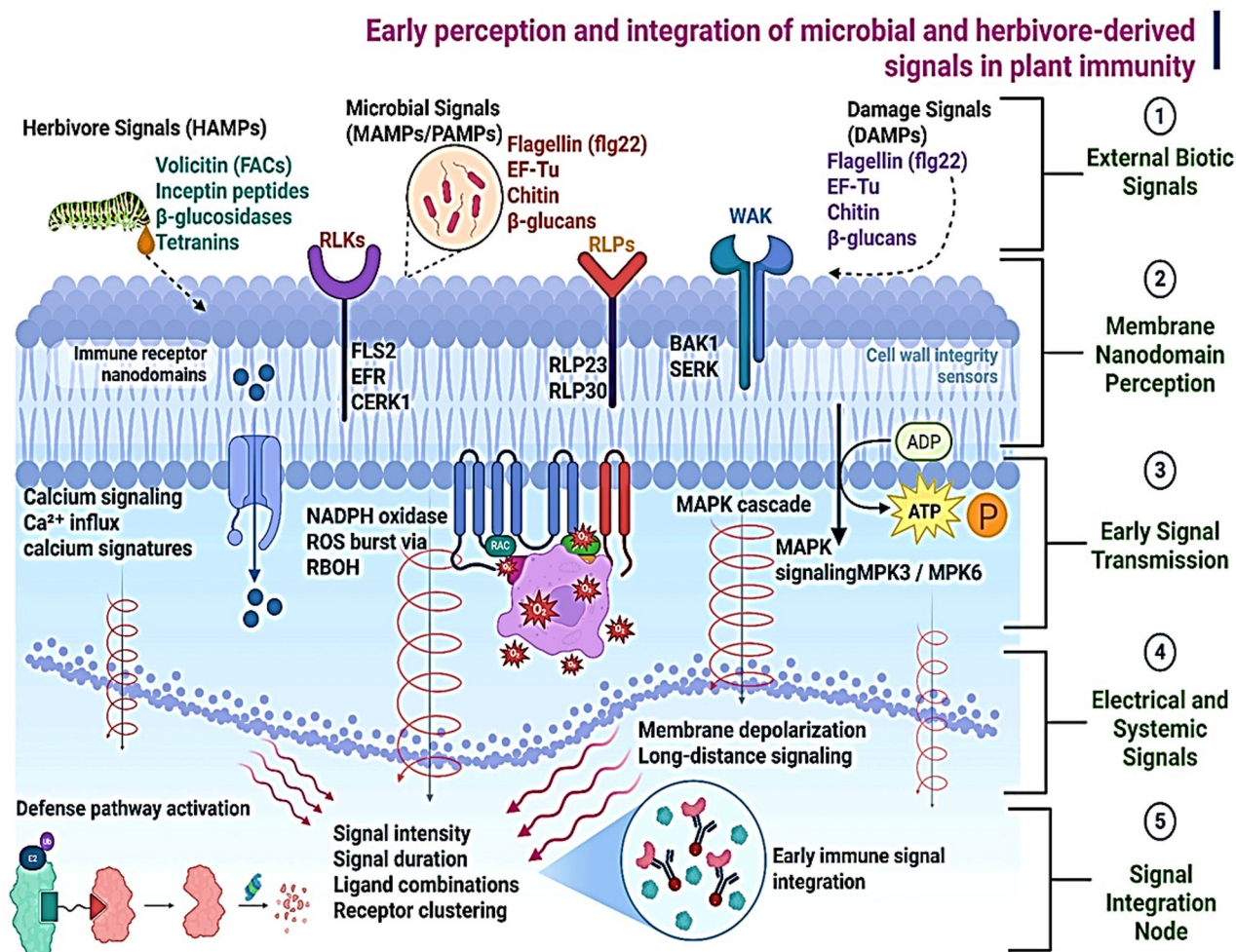


Fig. 2 Early perception and signal integration of microbial, damage-associated, and herbivore-derived cues at the plant cell surface. Microbial patterns, herbivore elicitors, and cell wall-derived damage signals are perceived by plasma membrane pattern recognition receptors (PRRs), including RLKs, RLPs, and WAKs that assemble with co-receptors such as BAK1/SERK within membrane nanodomains. Ligand perception activates early signaling events, including Ca^{2+} influx, ROS production, MAPK activation, and membrane depolarization. Integration of these signals generates systemic electrical and biochemical waves that coordinate the activation of downstream defense pathways. Image created using the Biorender program

species (ROS), and activation of mitogen-activated protein kinase (MAPK) pathways. All of these initial events eventually lead to a dramatic alteration in plant gene expression and metabolism [45]. Since plants cannot move to avoid pathogens, they have evolved numerous types of receptor kinases and receptor-like proteins to form a “border control” system on their cell surfaces. They can distinguish between self and non-self, and between intact and damaged tissue [46]. However, plant surveillance is not limited to identifying pathogens; it also detects endogenously produced signals resulting from cell wall disruption. Specifically, PRRs can identify both conserved microbe-associated molecular patterns (MAMPs) and DAMPs produced or synthesized after the pathogen attacks or mechanically damages plant tissue. This allows plants to integrate the extent of invasion and tissue damage [47, 48]. The plant cell wall is a key

component of this process. It serves as both a structural component providing mechanical support and a signaling platform that communicates with the rest of the plant cell. Embedded in the cell wall are cell wall-associated kinases (WAKs) that detect structural disruptions and degradation products generated by pathogen-derived cell wall-modifying enzymes, thereby linking cell wall integrity to immune activation [43]. When a PRR binds a ligand, it recruits a co-receptor, such as a somatic embryogenesis receptor kinase (SERK), to form an activated receptor complex that phosphorylates receptor-like cytoplasmic kinases and amplifies downstream signaling [49]. This network of PRR-mediated signaling activates a variety of defense responses, including transcriptional reprogramming, phytohormone synthesis, callose formation, and, in some cases, programmed cell death, all of which limit pathogen growth and spread [44, 49].

Calcium-dependent signaling modules interact closely with RLK-mediated pathways, underscoring the necessity of integrating signals to execute immune responses [43] effectively. Different sub-families of PRRs recognize different ligands. For example, leucine-rich repeat (LRR) RLKs such as FLAGELLIN SENSING 2 (FLS2) and ELONGATION FACTOR TU RECEPTOR (EFR) detect bacterial flagellin and elongation factor Tu, respectively. On the other hand, LRR RLPs, such as RLP23 and RLP30, recognize fungal elicitors and bacterial cold-shock proteins, respectively [50, 51]. Similarly, WAKs detect oligogalacturonides (OGs), pectin-derived fragments released during cell wall damage, which serve as strong DAMPs that rapidly induce Ca^{2+} fluxes and immune signaling [51, 52]. OGs are among the well-studied DAMPs and demonstrate the close relationship between cell wall remodeling and immune activation. Perception of OGs by WAKs not only initiates signaling to activate defenses but also affects cell expansion and development, demonstrating their pleiotropic roles [53]. In addition to OGs, there are several other oligosaccharides derived from plant cell walls, including β -1,3-glucans, β -1,2-glucans, cellodextrins, xyloglucan, mannan, and arabinoxylan fragments, that have been identified as potent immune elicitors, expanding the repertoire of DAMPs recognized by plants [54, 55]. Recent studies have demonstrated that a mixture of β -1,3/1,4-glucans and other hemicellulose-derived oligosaccharides induces characteristic features of pattern-triggered immunity, including cytosolic Ca^{2+} transients, ROS generation, and MAPK activation in multiple plant species [56, 57]. Partially-hydrolyzed pectin products were shown to increase resistance of *Arabidopsis thaliana* to *Pseudomonas syringae* pv. tomato DC3000 by increasing ROS levels, nitric oxide levels, and levels of PR1, PR2, and PR5 mRNAs [58]. Cell wall-derived oligosaccharides are perceived by unique receptor complexes in monocotyledons, such as rice, including OsCERK1 and OsCEBiP, which specifically bind certain β -glucan and cellulose-derived fragments. Activation of these receptor complexes triggers a series of immune responses, including ROS production, MAPK activation, and increased expression of defense genes, thereby increasing resistance to fungal pathogens [51, 59]. Importantly, OsCERK1 plays a major role in activating local immune responses and ROS production, whereas OsCEBiP plays a greater role in triggering systemic signaling, demonstrating that receptor complexes have specialized functions [60]. Overall, these results indicate the complexity of plants' ability to perceive disturbances to their structural integrity and microbial invasion through an interconnected network of PRRs and cell-wall structural-integrity sensors. Simultaneous perception of DAMPs and PAMPs allows plants to obtain context-specific information about both damage severity and pathogen

presence, thereby enabling them to modulate their immune response to achieve an optimal balance between defense efficacy and metabolic costs [61, 62]. Identifying how a wide array of molecular cues is integrated at the cell surface and transduced into coherent defense programs represents a major area of study in plant immunity, with important implications for the development of durable and sustainable crop protection methods [59].

Herbivore-associated molecular patterns and oral secretion signaling

Early detection of herbivory, based on HAMP perception, and subsequent development of defense responses requires an understanding of how plants perceive these elicitors, how they process them, and what type of responses they elicit. This includes understanding the chemical nature of these elicitors and how they interact with plant receptors to trigger downstream signaling processes. As discussed previously, research has identified several types of elicitors that trigger plant defense responses, including fatty acid–amino acid conjugates, β -glucosidases, and other compounds found in insect oral secretions and oviposition fluids. These elicitors interact with plant receptors, primarily located on cell surfaces, to activate a signaling cascade that ultimately leads to the expression of defense-related genes [63, 64]. While this process provides a general mechanism for how plants respond to insect feeding, many questions remain about how different elicitors influence plant defense responses and how these responses vary depending on the type of insect causing the damage. For example, it is known that certain elicitors induce higher levels of gene expression than others, and that some may induce more defense-related genes than others [65]. Furthermore, research has also shown that some elicitors can suppress or redirect plant immunity, allowing for sustained feeding by the insect [65]. Plants have evolved mechanisms to detect insect attacks and mount effective defense responses. However, it is equally apparent that the effectiveness of these defenses varies widely among plants and that insects have evolved mechanisms to counteract many of them. Further research is needed to understand better the mechanisms by which plants recognize insect attacks and to develop new strategies to improve the effectiveness of plant defense responses. Insect oral secretions are rich in bioactive molecules that play crucial roles in facilitating successful herbivory and plant-pathogen interactions. For example, volatile organic compounds (VOCs) emitted by aphids can activate systemic defense responses in host plants, leading to the production of toxic secondary metabolites that negatively affect aphid populations [66]. Additionally, several insect-secreted proteins, including those from the cotton bollworm, *Helicoverpa armigera*, have been identified as potential

effectors that interact with plant cellular machinery to modulate host responses during herbivory [66]. Thus, understanding the biochemistry and molecular biology of insect oral secretions is essential for developing novel strategies to control agricultural pests and mitigate plant disease. Plants have evolved sophisticated mechanisms to recognize and respond to a wide variety of environmental stimuli, including insect herbivory. Upon detection of insect feeding, plants initiate a complex signaling network that triggers a range of defense responses, including the production of secondary metabolites and the activation of defense-related genes [67]. This defense response is typically accompanied by changes in plant physiology, such as alterations in stomatal density, root architecture, and photosynthetic activity [68]. These physiological changes reflect the plant's ability to allocate resources away from growth and towards defense. They are thought to be critical for limiting the impact of insect herbivory on plant fitness. Studies examining the effects of insect herbivory on plant physiology have employed a range of methodologies, including electrophysiology, imaging techniques, and biochemical assays [69]. One area of particular interest in recent years is the use of electrophysiology to examine the effects of insect herbivory on plant membranes and electrical properties [70, 71]. Electrophysiology has provided valuable insights into short-term changes in plant physiology following insect feeding. For example, researchers have used patch-clamp technology to demonstrate that insect herbivory causes significant depolarization of guard cells in *Arabidopsis thaliana*, which results in increased stomatal conductance and altered gas exchange [70]. Additionally, researchers have used techniques such as voltage-sensitive dye imaging (VSDI) and fluorescence microscopy to demonstrate that insect herbivory induces rapid changes in plant electrical activity, including depolarization of epidermal cells and generation of action potentials [69, 71]. The use of electrophysiology to study the effects of insect herbivory on plant physiology has provided a unique window into the rapid and dynamic changes that occur following insect feeding. Future studies using these technologies should continue to explore the relationships between plant physiology and various insect elicitors.

Intracellular signaling cascades orchestrating defense activation

Plant innate immunity begins when pattern recognition receptors (PRRs) recognize conserved microbe-associated molecular patterns (MAMPs) and trigger an initial defense response [72]. Most plant PRRs are receptors, such as kinases or other proteins. They are localized to the plasma membrane, where, upon binding to their respective ligands (such as bacterial flagellin or fungal chitin), they rapidly elicit intracellular signaling

via phosphorylation [73]. Upon recognition of microbial elicitors, such as bacterial flagellin or fungal chitin, receptor complexes form and receptor-like cytoplasmic kinases are recruited, thereby translating the detection of extracellular signals into intracellular biochemical signals [49]. Immune signaling in plants is coordinated via the interaction of the surface-localized PRRs and the intracellular Nucleotide Binding Leucine Rich Repeats (NLRs) [49, 74]. Activation of PRRs induces Pattern-Triggered Immunity (PTI), whereas activation of NLRs that recognize pathogen effectors induces Effector-Triggered Immunity (ETI). While PTI and ETI utilize different recognition mechanisms, they result in identical signaling outputs, such as increased levels of cytosolic Ca^{2+} , production of reactive oxygen species (ROS), activation of mitogen-activated protein kinase (MAPK) cascades, and widespread changes in transcription [73, 75]. The convergence of PTI and ETI increases the strength of the immune response and enables a versatile response to various pathogens. Initial immune activation is characterized by rapid ion fluxes across the plasma membrane, specifically, an increase in Ca^{2+} influx, which serves as a universal second messenger in plant defense [43]. Different pathogens elicit stimulus-specific Ca^{2+} signatures that define their amplitudes and durations, enabling discrimination among immune stimuli [76]. These Ca^{2+} signals are interpreted by specific sensor proteins, such as calcium-dependent protein kinases (CDPKs), calmodulins (CaMs), calmodulin-like proteins (CMLs), and calcineurin B-like proteins (CBLs) [77]. These sensor proteins decode Ca^{2+} signals into phosphorylation cascades and transcriptional responses [78, 79]. CDPKs serve as sensor-kinases that link Ca^{2+} perception to phosphorylation cascades. For example, CPK5 responds to small Ca^{2+} fluctuation and controls PTI responses, whereas CPK4, CPK6, and CPK11 regulate early transcriptional activation and ROS production [43, 80]. CMLs further regulate immune specificity and can function either positively or negatively, depending on the pathogen context [81, 82]. Calcium signals can be transmitted from infected to uninfected cells, coordinating systemic acquired resistance (SAR) throughout the organism [83]. Beyond this long-distance coordination of SAR, Ca^{2+} waves facilitate defense priming in distant tissues [83]. Moreover, Ca^{2+} fluxes among the cytosol and organelles (vacuole, chloroplasts, mitochondria, and endoplasmic reticulum) determine the magnitude and the duration of immune signaling [76]. In addition to their roles in how things work, the amounts and patterns of immune signals are now seen as key to defense specificity. Changes in how strong, how long, where, and how signals like Ca^{2+} surges, ROS bursts, and MAPK activity spread can strongly shape which genes are turned on and which metabolic pathways are triggered. Different types of

threats can produce unique signal patterns that influence the strength and direction of defenses by changing signal flow and linking messages between parts of the cell and different tissues.

Mitogen-activated protein kinase networks and phosphorylation dynamics

Mitogen-activated protein kinase (MAPK) cascades represent the central signaling networks that convert Ca^{2+} and ROS signals into transcriptional responses during plant immunity [77]. These cascades are composed of three sequentially activated kinases—MAPKKKs, MAPKKs, and MAPKs—that convey signals through phosphorylation cascades to transcription factors and defense regulators [84, 85]. Following the activation of PRRs, receptor-like cytoplasmic kinases such as Botrytis-induced kinase 1 (BIK1) transduce signals to MAPK pathways, linking extracellular perception with intracellular signaling [49, 86]. The Flg22-induced FLS2–BAK1 receptor complex, for example, activates MAPK pathways including MPK3 and MPK6. These kinases phosphorylate transcription factors such as WRKY22 and WRKY29, thereby inducing defense-related gene expression [75, 87]. There are two primary MAPK cascades involved in the activation of PTI in Arabidopsis: MEKK1–MKK1/2–MPK4 and MAPKKK3/5–MKK4/5–MPK3/6 [88, 82]. The latter cascade plays a role in stomatal immunity, phytoalexin biosynthesis, and the regulation of the hypersensitive response [89, 90]. In addition to regulating the intensity and duration of MAPK signaling, MAPK phosphatases prevent overactivation of the immune response [47]. Furthermore, MAPK signaling intersects with hormone pathways regulating salicylic acid, ethylene, and jasmonic acid biosynthesis [91]. Additionally, MAPK-mediated phosphorylation modifies auxin signaling by altering the activities of AUX/IAA repressor proteins, ARF transcription factors, and PIN transporters, thereby coordinating growth and defense responses [92]. The kinase hubs, including SnRK2s, CDPKs, and MAPKs, combine Ca^{2+} and ROS signals with abiotic stress responses to ensure the optimal utilization of cellular resources under environmental and pathogenic stresses [92].

Hormonal crosstalk as a central regulatory hub in biotic stress responses

The plant's use of phytohormones as part of an integrated signaling language converts pathogen perception to a coordinated defense response. The four hormones involved, salicylic acid (SA), jasmonic acid (JA), ethylene (ET), and abscisic acid (ABA), form a highly interdependent signaling network [93]. This network functions through coordinated regulation of hormone biosynthesis, hormone receptor function, transcriptional and

posttranscriptional regulation, enabling plants to deploy their immune response based on the type of pathogen they encounter and to minimize the growth costs associated with their immune responses [94, 95]. One of the most well-studied features of this network is the SA-JA antagonism, which determines whether the plant will prioritize resistance to biotrophic pathogens, necrotrophic pathogens, or herbivorous insects [96]. Beyond regulating the intensity of immune signaling, phytohormonal networks also exert major control over the qualitative composition of defense-associated metabolites. SA-dominated responses are frequently associated with the accumulation of phenolics, phytoalexins, and antimicrobial pathogenesis-related compounds. In contrast, JA/ET-associated pathways preferentially induce terpenoids, alkaloids, protease inhibitors, and volatile organic compounds involved in anti-herbivore defense and indirect ecological interactions. Consequently, hormonal crosstalk functions not only as a signaling coordination mechanism but also as a major determinant of downstream metabolic specialization during biotic stress adaptation.

While there is considerable antagonism between these two pathways, it is not absolute and can be influenced by factors such as developmental stage, tissue identity, and environmental conditions. ABA plays a critical role in connecting abiotic stress to immune signaling. For example, ABA signaling can inhibit SA-dependent immunity by down-regulating ISOCHORISMATE SYNTHASE1 (ISOCHORISMATE SYNTHASE1) expression, thus providing a link between pathogen defense and responses to drought or salt stress [97]. Additionally, age-dependent regulation adds further complexity to how ABA affects SA signaling; ABA can suppress SA signaling in older rosette leaves under abiotic stress, but can also enable younger tissues to retain SA signaling competence through PBS3-mediated buffering [93]. As such, crosstalk among the various phytohormones serves as a central regulatory node controlling the magnitude, timing, and quality of biotic stress responses.

Salicylic acid-mediated immunity against microbial pathogens

Salicylic acid (SA) regulates defense against biotrophic and hemibiotrophic pathogens and initiates local antimicrobial gene expression and systemic acquired resistance (SAR) [98]. The temporal pattern of SA accumulation varies among different stress types. Early ROS bursts typically precede SA accumulation under various stress conditions. Simultaneous ROS and SA accumulation can also be triggered in some abiotic stresses (heat/light) [99]. These observations provide evidence for a model in which ROS serves as the initial warning signal. At the same time, SA is involved in long-term transcriptional programming and the establishment of immune

memory. SA signaling is centered upon regulatory hubs containing NONEXPRESSOR OF PATHOGENESIS-RELATED GENES1 (NPR1) and ENHANCED DISEASE SUSCEPTIBILITY1 (EDS1), which orchestrate the activation of pathogenesis-related (PR) genes and antimicrobial programs [100]. SA biosynthesis is subject to lineage-dependent plasticity via two distinct biochemical pathways, namely the isochorismate synthase (ICS) pathway and the phenylalanine ammonia-lyase (PAL) pathway [99, 101]. The plastidial ICS pathway is responsible for the bulk of SA produced in response to pathogens in *Arabidopsis thaliana*. ICS mutants exhibit greatly reduced levels of both basal and pathogen-induced SA [76, 102]. PAL-derived pathways contribute significantly to SA biosynthesis in several crops, especially monocots, where ICS mutations do not completely abolish SA accumulation [85]. More recent studies have identified a conserved phenylalanine-derived metabolic module that produces SA from benzoyl-CoA intermediates, including benzylated derivatives, through sequential conversions of these compounds [99, 85]. As such, SA formation involves enzymatic actions across peroxisomal, endoplasmic reticulum, and cytosolic compartments in a variety of crop systems. This illustrates the evolution of diverse SA biosynthetic strategies [103]. Redox-regulation of NPR1 controls its ability to perceive SA. Under uninduced conditions, NPR1 exists as an oligomer; however, redox changes associated with SA lead to monomerization, nuclear translocation, and transcriptional coactivation with TGA transcription factors, thereby activating PR gene expression [76]. NPR1 activity is further regulated by NPR3 and NPR4, which control NPR1 turnover via proteasome-dependent pathways, providing mechanisms to tune the intensity of the immune response based on NPR1 levels [46, 104]. Independent branches of SA signaling exist outside of NPR1, including transcriptional regulators such as WHIRLY and MYB30 that mediate PR gene expression and control of the hypersensitive response, ensuring redundancy within SA-mediated immune signaling [73].

Jasmonic acid and ethylene signaling in herbivore defense

JA and ET are the primary hormones involved in defense against necrotrophic pathogens and herbivorous insects [105]. JA perception occurs through the SCF^{COI1}-JAZ receptor complex, in which the active conjugate JA-Ile promotes ubiquitin-mediated degradation of JAZ repressors, thereby enabling transcription factors such as MYC2 to induce defense gene expression [106, 107]. The responses generated include the synthesis of proteinase inhibitors, secondary metabolites, and structural barriers that inhibit herbivory. JA biosynthesis arises from α -linolenic acid via the plastidial octadecanoid pathway,

resulting in the production of 12-oxophytodienoic acid (OPDA); OPDA is then converted into JA in peroxisomes through a series of reduction and β -oxidation reactions, followed by the conversion to JA-Ile by JAR1 [108, 109]. MYC2 cooperates with the transcriptional co-regulator MED25 to coordinate defense gene expression and promote, thereby limiting excessive defense investment [110]. The extensive interaction networks formed by multiple JAZ proteins enable JA signaling to connect developmental processes with stress responses, rather than function as a single-purpose defense pathway [110]. ET signaling generally synergizes with JA-mediated defenses. ET perception occurs through receptors localized to the endoplasmic reticulum and regulates downstream signaling through EIN2 and the stabilization of EIN3/EIL1 transcription factors [111]. These regulators activate AP2/ERF transcription factors that regulate defense genes such as chitinases and defensins [105]. The synergy between JA and ET signaling is mediated by ERF transcription factors, such as ERF1 and ORA59, which bind GCC-box elements in the PDF1.2 promoter to activate antimicrobial responses [18]. MAPK-dependent phosphorylation of selected ERF proteins stabilizes them and strengthens transcriptional outputs during infection or herbivory [18]. In crops such as rice, rapid induction of JA biosynthesis and MYC-dependent transcriptional programs following herbivore attack leads to the accumulation of protease inhibitors and enhanced resistance [67].

Antagonism, synergy, and context-dependent hormonal trade-offs

The interplay among plant hormones imposes a resource-allocation framework on immune responses. Antagonism between SA- and JA-dominated pathways frequently biases the defense response toward either biotrophic or necrotrophic threats by suppressing the respective pathway regulators and transcriptional hubs [107, 112, 113]. NPR1 often mediates SA-dependent repression of JA signaling, enhancing biotroph-specific immunity [114]. Increasingly, SA-JA interactions are context-dependent rather than strictly antagonistic. Under combined stress or specific pathogen encounters, simultaneous activation of both pathways can enhance PR gene expression, phytoalexin accumulation, and cell wall fortification [115, 116]. In certain cases of effector-triggered immunity, SA-regulated components, including NPR3/4, can facilitate JA-associated signaling, resulting in programmed cell death [96, 117]. Environmental conditions also affect hormone integration. Several factors, including temperature, light regimes, and abiotic stresses, can alter hormone biosynthesis and receptor sensitivity, thereby producing varied immune responses and climate resilience [118]. Crosstalk among hormones often occurs through multifunctional regulatory proteins; for example, JAZ proteins

interact with transcription factors from the JA, ET, and ABA pathways to integrate hormone signals to varying degrees rather than simply producing binary outcomes [110]. Therefore, hormone trade-offs should be viewed as dynamic equilibria determined by the timing, signal intensity, and cellular environment of the plant, allowing plants to continuously adjust their growth-defense balance in response to changing environmental and pathogenic stresses [119].

Transcriptional reprogramming and regulatory network architecture

The plant's ability to mount an appropriate immune response is directly linked to its capacity to reprogram its transcriptional profile in response to perceived threats rapidly. This is achieved through pattern recognition receptors, which are activated upon perception of microbial or damage-associated molecular patterns. Once activated, these receptors initiate signaling cascades that rapidly redirect cellular priorities to support the mobilization of immune functions in response to variable environmental conditions. Frequently, these signaling cascades result in the redeployment of basic metabolic processes to support the mobilization of immune resources. As a result, the resulting transcriptional response is controlled by a wide array of transcription factor families, including WRKY, TGA, NAC, CBP60/SARD1, AP2/ERF, bZIP, bHLH, MYB, CAMTA, and TCP regulators, each controlling the temporal, spatial, and quantitative characteristics of the transcriptional activation of defense-related genes, and thus representing common targets of pathogen interference. Rather than functioning independently as isolated switches, these regulators act in concert with one another within integrated signaling frameworks. Nucleocytoplasmic immune receptors, kinases, and co-regulatory complexes modulate the stability and activity of transcription factors via phosphorylation, protein-protein interactions, and regulated turnover [120]. Immune transcription is thus the result of the coordinated interaction among DNA-binding regulators, Mediator complexes, transcriptional co-activators or repressors, and chromatin remodeling enzymes, all of which ultimately determine promoter accessibility to the transcription machinery and the level of transcriptional output [121]. Pathogens exploit this architecture by using effectors that inhibit transcription factor activity, disrupt regulatory complexes, or redirect host proteins to ubiquitin-proteasome degradation to suppress the host's immune response [122]. Hormone-responsive regulators further modulate the transcriptional amplitude of immune transcription. WRKY proteins are often found at the center of immune coordination, while MYB and bHLH modules are often responsible for regulating the hypersensitive response

and hormone-linked metabolic regulation [123]. WRKY proteins bind to W-box promoter elements to regulate defense genes. In contrast, bZIP proteins recognize TGACG motifs and interact with MYB, bHLH, and AP2/ERF regulators to form combinatorial promoter logic that enables context-dependent transcription of defense genes [124]. Due to their role as central regulators of immune transcription, many pathogen effectors target transcription factors or their associated co-regulators, such as NPR1 and the TOPLESS (TPL) corepressor complex, to destabilize the transcriptional competence of immune transcription [125]. WRKY proteins play a critical role in providing broad-spectrum resistance against fungi, bacteria, oomycetes, and viruses by integrating downstream immune signaling networks [85]. An example of this is WRKY33, which regulates hormone-associated metabolic defense mechanisms during infection by *Botrytis cinerea*. At the same time, AP2/ERF factors such as ERF1 and ORA59 integrate jasmonate-ethylene signaling to activate necrotroph-effective defense programs [89]. Thus, hormonal signals such as SA, JA, ET, and ABA serve as system-level inputs to immune transcription. In contrast, transcription factor families act as the executive regulatory layer, translating these inputs into promoter-specific outputs [105]. The AP2/ERF family illustrates this integration particularly well: while some members of the family (e.g., ERF5 and ERF6) increase the expression of JA/ET-responsive genes, other members decrease the expression of the same promoter targets, showing antagonistic regulation within the same transcription factor family [18]. The stability and transcriptional activity of AP2/ERF proteins are also modulated by MAPK-dependent phosphorylation during immune escalation [18]. The evolutionary diversification of AP2/ERF subfamilies has enabled them to selectively recognize distinct promoter motifs and stress conditions, with ERF-type regulators frequently involved in the transcriptional responses to pathogens [92].

The convergence of early immune signaling pathways ultimately reshapes plant defense metabolism through extensive transcriptional reprogramming. Shared signaling components, including Ca^{2+} signaling, ROS accumulation, MAPK activation, and phytohormonal integration, regulate large transcription factor networks that selectively activate biosynthetic pathways associated with specialized metabolite production. The differential regulation of these transcriptional modules enables plants to generate distinct chemical defense repertoires despite utilizing partially conserved upstream signaling architectures.

Defense gene clusters and co-expression modules

Immune transcription is organized at both genomic and network levels. Many defense genes reside in physical

clusters formed through duplication events, allowing for the simultaneous induction and diversification of resistance gene analogs and pathogenesis-related loci [126]. Shared promoter grammar and epigenetic environments allow for the synchronized activation of these clusters during infection, facilitating defense deployment [127]. Large-scale co-expression analysis reveals that co-expression modules are enriched in regulatory hubs, including ERF, MYB, bHLH, bZIP, and C2H2 zinc-finger transcription factors [128]. WRKY, NAC, and AP2/ERF proteins often serve as anchors of these modules by binding to conserved promoter motifs and coordinating the sequential activation of groups of defense genes [129]. However, network topology differs significantly between resistant and susceptible genotypes. Typically, resistant cultivars have densely connected, modular regulatory architectures that stabilize the host's immune outputs, whereas susceptible cultivars have disrupted connectivity consistent with decreased transcriptional coordination [130]. Hub genes within these modules often regulate ubiquitination pathways, receptor signaling, cell wall modification, RNA metabolism, redox homeostasis, and hormone responses [128, 131]. Large-scale co-expression analysis, such as WGCNA, also partitions immune transcription into early signaling modules and late reinforcement modules that support metabolic defense and structural barriers. The delayed activation of early defense modules in susceptible genotypes results in kinetic mismatches between perception and response. It ultimately leads to attenuated resistance despite the presence of key immune components [133].

Integration of microbial and insect-induced transcriptional signatures

Diverse biotic cues often quickly converge on a generalized danger response during early transcriptional stages, which significantly overlaps with abiotic stress signaling [134]. In subsequent transcriptional phases, responses become highly specialized, adjusting regulatory modules according to the pathogen's lifestyle and the specific tissue type of the infected plant [121]. Generally, incompatible interactions lead to faster and more robust activation of defense regulators compared to compatible interactions, supporting the idea that rapid transcriptional responses help limit pathogen proliferation [120]. Comparative studies have also revealed distinct transcriptional signatures linked to different insect feeding guilds. Chewing insects tend to induce jasmonate (JA)-dominated transcriptional programs, whereas piercing-sucking insects usually activate salicylate-biased responses, reflecting biotrophic-like interactions with the host [135]. Although there is considerable overlap in the pathways activated by chewing and cell-content feeding insects—allowing plants to adapt their transcriptional responses

to multiple attack strategies [134]—cross-guild comparisons show that cell-content feeders more severely disrupt circadian and light-related regulatory networks [135]. Systemic signaling further enhances transcriptional coordination, with localized infections or herbivory potentially triggering systemic defense priming through mobile signals like jasmonate waves and hydraulic cues, thus preparing distant tissues with anticipatory transcriptional states [136]. Root responses also display guild-specific transcriptional profiles; for instance, roots respond to chewing herbivores with JA/ABA-associated signatures, while responses to piercing-sucking insects are characterized by sustained SA-associated responses [136]. Attackers may manipulate plant transcriptional trade-offs by altering hormonal balances—salivary effectors, for example, can shift signaling toward SA dominance, thereby diminishing the effectiveness of JA-mediated defenses [137]. Plants counter these manipulations by diversifying receptor systems and compartmentalizing JA signaling into distinct branches—such as ERF-driven JA/ethylene responses against necrotrophs and MYC-dependent JA/ABA responses to extensive tissue damage [138]. A conceptual model illustrating the hierarchical organization of transcription factors, co-regulatory complexes, and defense gene modules that orchestrate immune transcriptional reprogramming is depicted in Fig. 3.

Epigenetic regulation and stress memory in plant defense

Stress memory in plants enables them to develop faster, stronger responses to future stress events based on prior stress experiences. Stress memory is primarily regulated by epigenetic mechanisms (DNA methylation, histone modifications, chromatin remodeling, and small RNA-directed pathways), which lead to a more responsive transcriptional state in response to future stress without altering the plant's genomic sequence [139, 140]. Plants have developed three types of memory: somatic memory (memory within an organism), intergenerational memory (memory transmitted from one generation to the next), and transgenerational memory (memory transmitted across generations). The combination of these memory types allows plants to retain a stress-induced transcriptional state throughout their life cycle and even pass it on to their offspring [140]. An example of this type of memory is defense priming, in which a plant previously exposed to stress produces a transcriptionally poised chromatin structure that enables it to respond quickly to future stress by rapidly inducing defense-associated genes [141, 142]. Loci that are primed for defense tend to acquire permissive histone modifications, such as H3K4me2/3, which facilitate the rapid recruitment of transcriptional machinery when the plant responds to a pathogen [143, 144]. Chromatin remodeling complexes, which include components of the SWI/SNF and ISWI

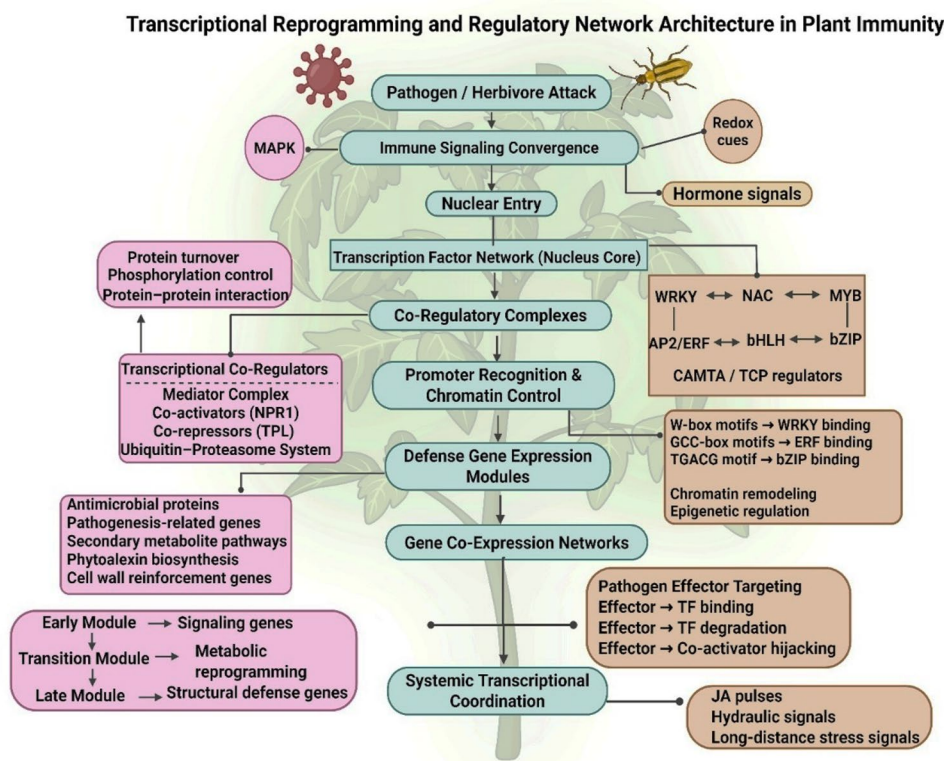


Fig. 3 Transcriptional reprogramming and regulatory network architecture underlying plant immune responses. Perception of a pathogen or herbivore initiates the convergence of several different immune signal transduction pathways and relays information from these to the nucleus regarding hormone, MAPK, and redox status. The nuclear signals converge on an interconnected network of transcription factors that activate one another, including bHLH, bZIP, AP2/ERF, NAC, MYB, WRKY, CAMTA, and TCP, which regulate the expression of all defense-associated genes. These transcriptional outputs are regulated by multiple complexes that modulate transcription factor activity and/or stability, including co-activators such as NPR1, co-repressors such as TPL, the ubiquitin-proteasome system, and the Mediator complex. Recognition of specific promoters by specific cis-regulatory motifs (such as W-box, GCC-box, and TGACG), and/or chromatin remodeling events, modulate the accessibility and specificity of transcriptional regulation. Coordinated activation of defense-related gene modules, involving antimicrobial proteins, pathogenesis-related responses, secondary metabolites, phytoalexins, and cell wall fortification, occurs as a result of these processes. In addition, at the network level, the transcriptional response is organized into early, intermediate, and late co-expression modules that progressively regulate signaling competency, metabolic reprogramming, and structural reinforcement of defenses. Additionally, the regulatory architecture of the immune system can be compromised by effector molecules produced by pathogens that target transcription factors and/or co-regulatory components, and by systemic signals (such as pulses of jasmonate and long-distance stress signals) that coordinate transcriptional priming across distant tissues. Image created using the Biorender program

families, regulate the position of nucleosomes on memory loci and can regulate the transcriptional competence of those loci [145]. Regulators of chromatin remodeling complexes, such as FORGETTER1 (FGT1), interact with chromatin remodelers, including BRAHMA, CHR11, and CHR17, to regulate the transcriptional competence of stress-responsive genes, such as HSP21 and HSA32 [145]. Histone variants such as H2A.Z and H3.3 confer chromatin plasticity, stabilize permissive chromatin states, and reduce nucleosome turnover [146, 147]. DNA methylation in the CG, CHG, and CHH contexts also regulates transcription by limiting transcription factors' binding to promoters or by recruiting chromatin compaction proteins, and environmental stress can alter DNA methylation landscapes through mechanisms such as RNA-directed DNA methylation (RdDM) mediated by small interfering RNAs [140, 148]. Small RNAs also

regulate transcripts involved in hormone signaling, reactive oxygen species balance, and metabolic adjustment [149]. The epigenetic memory that develops in plants in response to stress can extend beyond the lifespan of an individual plant, as the progeny of a previously stressed plant often exhibit increased salicylic acid-dependent defense gene expression and greater resistance to pathogens, along with the persistence of chromatin modifications associated with defense [143]. Similarly beneficial microbes, such as *Trichoderma* spp. and plant growth-promoting rhizobacteria, induce long-lasting epigenomic changes that enable durable priming across generations [150]. Importantly, these epigenetically influenced states are reversible in the absence of stress, providing the plant with continued adaptive flexibility. In contrast, recent advances in epigenome editing technology demonstrate that direct modification of specific chromatin marks can

significantly affect the inheritance of resistance traits, thereby providing a promising avenue for developing genetically engineered crops with durable resistance to pathogens [151].

Shared defense nodes and signaling convergence between microorganism and insect responses

Despite significant differences in their biology and physiology, both insects and microorganisms utilize a subset of highly connected, broadly used signaling components to coordinate their defense responses to infections. Examples of such signaling components in insects include the Toll and IMD signaling pathways, which are extensively linked to other signaling networks, including MAPK/JNK cascades, JAK-STAT signaling, autophagy pathways, RNA interference mechanisms, oxidative stress responses, and proteostasis-related processes such as the integrated stress response and unfolded protein response [152]. As in insect defense responses, many microorganisms employ similar signaling architectures to integrate environmental stress sensing with the regulation of survival, competition, and virulence. Therefore, the concept of defense convergence between organisms of different kingdoms can be understood based on the presence of shared regulatory nodes and signaling interfaces, including NF- κ B-like transcriptional regulation, programmed cell death pathways, redox signaling networks, ubiquitin-mediated protein degradation, and endoplasmic reticulum stress responses [68]. These conserved modules serve as modular, reusable regulatory frameworks that guide resistance, tolerance, and fitness tradeoffs during infection (Suppl. Table 1). This system-level convergence can explain why diverse biological threats can trigger overlapping response programs and why the disruption of a single signaling node, such as TAK1, TRAF adaptor proteins, or JNK signaling, can affect multiple branches of an organism's immunity [153].

Systems biology and multi-omics insights into plant biotic stress responses

Plant pathologists, previously focused on individual genes, now view plant immunity as an emergent property of connected molecular networks and physiological tradeoffs. While this integrated approach is useful for studying the trade-off between growth and defense, it also emphasizes the importance of regulatory proteins (e.g., AVRPPHB SUSCEPTIBLE 3 and XYLEM NAC DOMAIN 1) that coordinate signaling across multiple hormone pathways and respond to both biotic and abiotic stresses [154, 155]. For example, in *Arabidopsis*, phosphate starvation signaling via PHR1 activates jasmonate- and salicylate-associated defense pathways, demonstrating that plant immune responses are part of the larger stress response physiology [156]. Another example

of spatial regulation of ROS involves NADPH oxidases such as RbohA and RbohC, which generate developmental and defensive trade-offs and require the coordinated regulation of gene expression that controls ROS localization, cell wall dynamics, and immune signaling [93]. Together, these advances have fostered the use of holo-omics approaches that combine plant molecular data with microbiome profiles to study how cross-kingdom interactions shape plant immunity and microbial community structure [156]. However, holo-omics studies also pose analytical challenges (such as integrating heterogeneous datasets and the need for robust statistical frameworks), so there is growing interest in developing new computational tools and experimental designs to support multi-omics analysis [156]. Metabolomics plays a key role in multi-omics research because metabolites are the end products of gene expression and protein activity, providing information about the biochemical states of organisms under different conditions [157]. Small metabolites (typically < 1.5 kDa) play a significant role in plant-microbiome communication and can alter microbial community composition in response to stress [158]. However, metabolomics is still in its infancy in terms of technological capabilities, and several limitations exist, including incomplete metabolite identification, ambiguous spectral data, and limited experimental replication [159]. Additionally, very few metabolite reference libraries are available, particularly for fungal metabolites and compounds produced by non-model organisms [159]. Therefore, expanding standardized protocols and creating more comprehensive metabolite databases will be necessary to translate holo-omics data from descriptive maps into functional insights. Recent advances in AI, machine learning, and predictive computational biology are transforming plant immunity research. These advances enable large-scale integration and interpretation of transcriptomic, proteomic, metabolomic, and microbiome-associated datasets. AI-assisted analytical systems can expose hidden regulatory relationships, prioritize immune-associated hub genes, and predict key signaling interactions in complex plant-microbe-insect responses. Researchers use network-based modeling to reconstruct immune regulatory architectures and forecast defense outcomes under combined biotic and abiotic stresses. Meanwhile, digital phenotyping, image-based diagnostics, and analytics-based tools support the development of precision crop protection strategies and climate-adaptive agriculture. Combining systems biology with AI frameworks constitutes a new frontier for translating molecular immune findings into expandable, eco-friendly agricultural applications. As illustrated in Fig. 4, integrating transcriptomics, proteomics, metabolomics, and computational modeling allow researchers to reconstruct regulatory frameworks that describe the

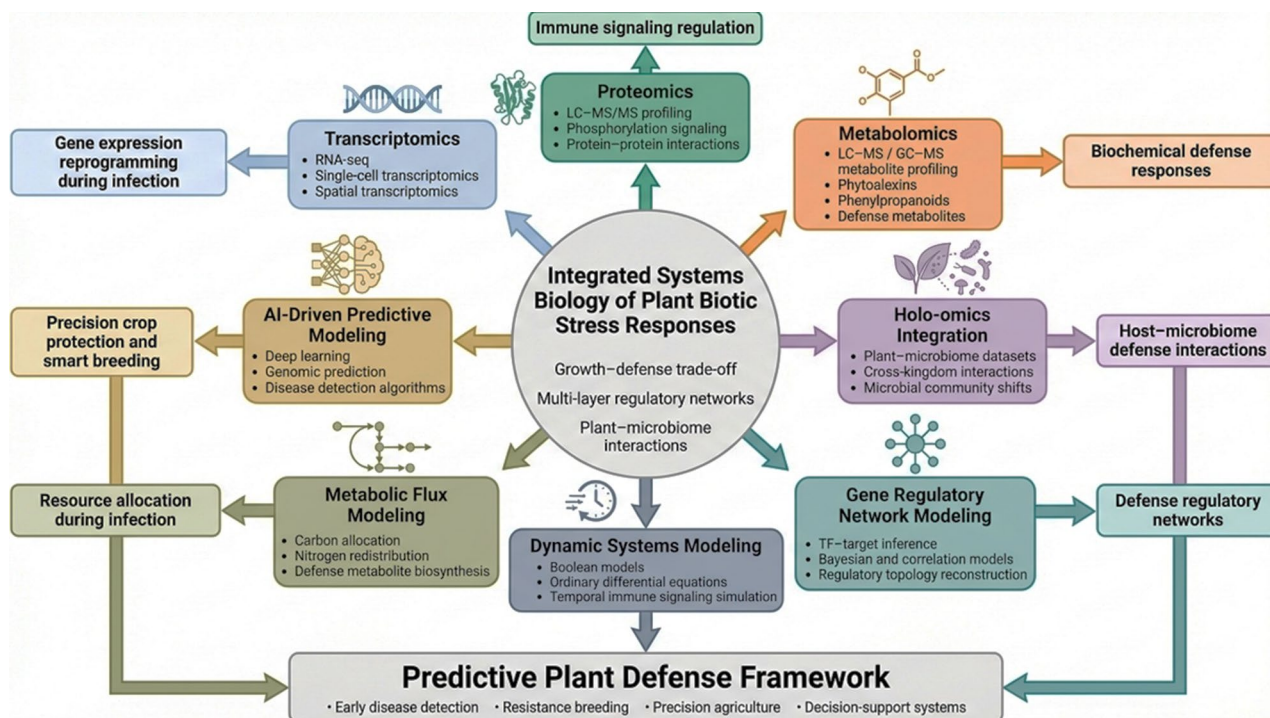


Fig. 4 System-level integration of multi-omics datasets for understanding plant responses to biotic stress. This conceptual figure was generated using the AI-assisted scientific illustration platform FigureLabs (figurelabs.ai) and the Bio render program and was manually curated and edited by the authors

relationships between signaling networks and physiological outcomes.

Transcriptomics, proteomics, and metabolomics approaches

Transcriptomics has been particularly important for identifying plant responses to biotic stress, especially through RNA sequencing technologies that measure the entire plant transcriptome during pathogen attack [76, 160]. When a plant recognizes microbial signals or undergoes cellular damage, it responds rapidly by activating pattern-triggered immunity, leading to widespread transcriptional reprogramming that upregulates defense genes while downregulating growth-related metabolic pathways [134, 159]. The interactions between hormones, especially the antagonism between salicylic acid and jasmonic acid, further define which defense mechanisms are used and when developmental processes are temporarily halted [156, 161]. Newer single-cell and spatial transcriptomics methods have demonstrated that immune responses vary by cell type and tissue location in the plant and have uncovered specific subpopulations of immune-active cells [162]. However, isolating single plant cells can cause stress, complicating the interpretation of rapid immune responses [163]. Spatial transcriptomics preserves tissue context and mitigates some of the issues associated with single-cell studies, but achieving complete transcriptome coverage at single-cell resolution

remains a technical challenge [164]. Despite these limitations, single-cell studies in *Arabidopsis* leaves have identified clusters of immune-active, transitionally active, and susceptible cells during infection, and have shown, using pseudotime analyses, that progression occurs from the initial activation of defense to pathogen colonization [165]. Reporter imaging has localized immune-active cells near the stomata and at the site of bacterial colonization, indicating that early invasion leads to localized transcriptional specialization [165]. Droplet-based sequencing technologies, such as Drop-seq and Chromium 10x, have enabled cell-type classification across diverse plant tissues and species [109, 166] and have validated the spatial gene expression patterns observed in infected plants [166, 167]. Proteomics complements the information provided by transcriptomics by directly quantifying proteins involved in pathogen recognition, signaling, transport of antimicrobial compounds, and antimicrobial activities [134]. High-resolution liquid chromatography-mass spectrometry (LC-MS/MS) methods can detect thousands of proteins during infection and reveal discrepancies between transcript and protein abundances, often due to post-transcriptional regulation, protein turnover, and post-translational modifications [134]. Important regulatory processes in plant proteomes include receptor-like kinases and MAPKs, which mediate phosphorylation and ubiquitination, regulating protein degradation and signaling intensity [168, 169]. Targeted

proteomics approaches, such as selected reaction monitoring and parallel reaction monitoring, provide higher sensitivity and specificity for detecting low-abundance immune regulators [170]. Spatial proteomics further enhances these analyses by determining how cell-to-cell interactions affect tissue-level immune responses. Proximity labeling techniques, such as TurboID, enable the capture of transient protein–protein interactions and signaling complexes in live tissues [171]. These studies have identified kinase-associated protein networks that influence transcription, RNA processing, and intracellular trafficking [171, 172]. For example, in rice, proximity-dependent labeling was used to identify protein–protein interactions of OsPUX8B.2 linked to immune suppression [173]; and in *Arabidopsis*, host proteins interacting with the HopF2b effector of *Pseudomonas syringae* were mapped [172]. Also, large-scale phosphoproteomic analyses of *Arabidopsis* have identified tens of thousands of phosphorylation sites, supporting the concept of “phosphocodes” that determine signaling specificity in biological contexts [92]. The ubiquitin-proteasome system is crucial in limiting the effectiveness of immune responses while preventing excessive inflammation [173]. Metabolomics provides additional insights into the biochemical outcomes of defense induction. Typically, infections lead to increased levels of phytoalexins, alkaloids, phenylpropanoids, and structural metabolites that either reinforce plant barriers or inhibit pathogens [128, 174]. These compounds arise from reprogrammed primary metabolism and represent the dynamic metabolic changes needed for immune responses [128]. Secondary metabolites can function as antimicrobial compounds, signaling molecules, or metal transporters involved in stress adaptation [175]. The recent advances in NMR and mass spectrometry-based platforms (GC-MS and LC-MS) have enabled sensitive, comprehensive metabolite profiling. LC-MS/MS is particularly effective for detecting complex and labile metabolites, whereas GC-MS is well-suited for volatile and stable compounds involved in central metabolism [176, 157]. Since plants can produce over 200,000 metabolites, high-resolution chromatographic and mass-spectrometric methods are necessary to achieve broad metabolomic coverage [177]. However, the vast chemical diversity of plant metabolites introduces technical challenges in extracting, identifying, and quantitatively comparing them, and requires optimized protocols capable of extracting both primary and secondary metabolites [178].

Network modeling and predictive defense frameworks

By integrating multi-omics datasets into regulatory networks and predictive models, mechanistic relationships among genes, proteins, metabolites, and phenotypic outcomes become more apparent. Therefore, systems

biology approaches attempt to create signaling pathways and interaction networks that describe how individual molecules contribute to the collective response of plants to stress [179]. Gene regulatory network inference is one of the primary approaches for reconstructing such networks. Gene regulatory network inference analyzes gene expression patterns to identify relationships between transcription factors and their targets and to develop hierarchical regulatory structures that control plant immunity [180]. The construction of networks typically occurs through statistical methods, including correlation analysis, mutual information, and Bayesian inference. Additionally, prior biological knowledge is often used to increase the accuracy and interpretability of the network [180]. To distinguish direct regulatory relationships from indirect co-expression relationships, transcription factor binding information, chromatin accessibility profiles, and promoter motif analysis are added. However, static association networks do not effectively represent dynamic and nonlinear biological interactions. As a result, dynamic modeling approaches, such as Boolean networks and ODE models, have been developed to simulate the temporal transitions in signaling states during pathogen infection [179, 181]. These models enable researchers to understand how regulatory cascades evolve and to test hypotheses regarding signal transmission and defense activation [182]. Platforms such as NetAct enhance regulatory inference by estimating transcription factor activity from transcriptomic data and developing compact regulatory core representations that more accurately capture dynamic behavior [182]. Additionally, machine-learning-based regression approaches, including Elastic-Net, enable researchers to quantify regulatory influence and compare interaction networks across different environmental conditions or pathogen pressures [183].

Metabolic flux analysis is a method that quantifies the flow of carbon and nitrogen through cellular networks. During an infection, this type of analysis reveals how metabolic resources are redistributed towards the biosynthesis of defense compounds [184, 185]. The integration of flux analysis with transcriptomic and proteomic data enables researchers to develop predictive genotype-to-phenotype frameworks to identify regulatory bottlenecks and key signaling nodes that govern stress adaptation [76, 186]. Increasingly, predictive modeling also uses machine learning algorithms to predict disease progression based on molecular signatures and environmental variables, enabling early detection and precision crop management strategies [186, 187]. Evolutionarily informed modeling can also be used to simplify network complexity by focusing on conserved stress-responsive modules across plant species, improving gene-to-trait inference, and providing a basis for translating defense mechanisms across species [188]. These predictive frameworks are currently

being evaluated for use in crop improvement, in which simulation models predict the performance of untested genotypes under various pathogen pressures and environmental conditions [189]. The successful deployment of such models will require standardized datasets, validatable metrics, and assessments of predictive robustness across varying environmental and pathogen populations [190].

Emerging role of artificial intelligence and data-driven discovery

AI is transforming plant systems biology by enabling the discovery of complex patterns in high-dimensional omics and phenotyping data that cannot be interpreted with traditional statistical methods. Machine learning algorithms can detect molecular signatures of early-stage plant disease and predict infection before symptoms appear [191, 192]. Machine learning supports several applications in plant pathology, including resistance classification in germplasm collections, pathogen identification, and early stress detection, ultimately enhancing the speed of breeding and crop protection strategies [128, 188, 193]. When combined with high-throughput phenotyping platforms and remote sensing technologies, AI can transform molecular and imaging data into real-time surveillance systems that monitor crop health at scale across large agricultural areas [194]. Convolutional Neural Networks have shown exceptional performance in image-based disease diagnosis and enable automated detection and classification of plant diseases without manual feature extraction [195–197]. Furthermore, integrative AI frameworks that combine genomic, transcriptomic, metabolomic, and environmental data are increasingly being used to predict disease susceptibility and resistance phenotypes under different field conditions [198, 199]. Principal Component Analysis and LASSO regression are commonly employed to reduce dimensionality and improve the interpretability of high-dimensional data [188]. Automated machine learning platforms and ensemble algorithms, including LightGBM, Random Forest, and XGBoost, have proven effective for genomic prediction and trait selection in breeding programs due to their ability to process large genomic datasets and maintain predictive stability [200, 201]. Similarly, models have been applied to predict plant disease outbreaks in climate-driven pathosystems, such as coffee rust, where environmental variables play a significant role in pathogen development [202, 203]. These approaches are increasingly integrated into genomic-environmental prediction frameworks that extend traditional genomic selection by modeling genotype-by-environment interactions using multi-omics data and environmental covariates [193, 204]. Such frameworks show the greatest potential for orphan crops, where the transfer of

predictive knowledge from major crop species and application of machine learning to conserved genetic elements can significantly accelerate breeding progress [205]. However, the effective utilization of AI in plant science requires proper governance. Large-scale genomic and environmental datasets raise concerns about data ownership and privacy, and algorithmic bias can arise when models are trained on non-representative datasets [128]. Maintaining the interpretability and transparency of predictive models is critical for biological validation and scientific trust, especially when predictive models influence decisions made in agriculture or breeding [206]. The regulatory framework for AI adoption often lags behind technological advances, creating gaps in ethical oversight and safety standards [207]. Emerging solutions such as blockchain-based data management and federated learning provide promising avenues for secure data sharing and decentralized model training, while maintaining data ownership and traceability [176, 208]. Collectively, these emerging developments demonstrate the transformative capabilities of AI-driven analytical tools to accelerate the discovery of plant defense mechanisms and develop predictive, data-informed crop management systems, as displayed in Fig. 4.

Adaptive plasticity and context-dependent defense outcomes

The trade-off between how much you spend on defense and how much you spend on other parts of your life (like growing) is a key part of plant defense theory, and it helps explain why different species (and even individual plants) use different strategies to resist pests and diseases. Many researchers think defense and growth are completely opposed. Still, in reality, many plants will grow and defend themselves simultaneously, especially in long-lived plants like trees, which can use chemical and structural defenses to protect themselves from harm, and these two types of defense can work together depending on the conditions around the plant [93, 209]. Conifers are a good example of this. While there is a growth–oleoresin trade-off in pines, and we see this trade-off clearly when plants are stressed, it appears that the genetic correlation between growth and resistance is expressed only when environmental constraints limit a plant's ability to allocate its limited resources [93, 210]. As such, abiotic factors (e.g., drought, nutrient limitation, temperature stress) can shape plant resistance both directly (by altering host physiology and defense allocation) and indirectly (by altering pest/pathogen pressure) [210]. Induced defense mechanisms, used by plants to conserve resources when no threats are present, come with a cost: activating them imposes a metabolic burden, so their adaptive value will depend heavily on the environmental conditions a plant experiences and the likelihood of

encountering a threat [93, 209]. Epigenetic mechanisms, including DNA methylation, may enable longer-lasting induced resistance [210], as seen in conifers such as Norway spruce. At all ecological scales, constitutive and induced defense strategies are generally negatively correlated due to shifts in allocation strategies in response to biotic pressures and habitat quality, which can affect population divergence [93, 209]. For example, environments that experience high levels of competition may favor rapid growth at the expense of resistance and, over time, alter a population's genetic composition [93, 210]. The Resource Availability Hypothesis provides a theoretical basis for this idea, stating that under resource-limited environments, plants will invest more in defense than in growth. Conversely, under resource-rich environments, plants will invest less in defense and more in growth. Data collected from *Pinus pinaster* demonstrate that this is true, with fast-growing families being more susceptible to *Hylobius abietis*, and populations from favorable habitats being more susceptible to *Matsucoccus feytaudi* than those from more extreme environments [93]. Carbon-based defensive metabolites, produced through biosynthetic pathways, require carbon and energy and can be constrained by resource limitations from drought or intraspecific competition, thereby increasing a tree's risk of bark beetle attacks and demonstrating that defense capability depends on the availability of carbon and energy [211]. Sustained defense investment can also divert resources away from growth and reproduction [93, 212]. Additionally, defense activation is also subject to signaling thresholds. Weak signals may fail to elicit a response, and abiotic stress can disrupt the hormone crosstalk necessary for proper defense induction, thereby weakening resistance when the plant is physiologically stressed [213, 214]. Shade avoidance strategies can also affect defense outcomes by redirecting resources toward growth-related traits (such as rapid stem elongation), which can decrease structural resistance and chemical defenses [215]. These relationships have important implications for forest management and breeding programs, as selecting for growth may indirectly select for resistance if a trade-off exists between the two [93, 209]. Furthermore, ecological factors (such as pheromone-mediated mass attacks by bark beetles) can overwhelm even resistant trees when they surround highly susceptible individuals, reinforcing the need to combine genetic improvement with landscape-scale management strategies [93, 210]. Plant defense is increasingly viewed as an ecosystem property shaped by interactions among plants, insects, and associated microbiomes. The phyllosphere and rhizosphere microbiomes can directly suppress pathogens/herbivores and indirectly modify host chemistry/inducible defenses [216]. Fungal endophytes, for example, can reduce herbivory through entomopathogenic activity or

secondary metabolite production, suggesting that forest management strategies that affect microbial communities could enhance resistance [216]. This perspective is consistent with the phytobiome concept, which views plants, pests, and their microbiomes as interconnected ecological units whose health can be modified through breeding, ecosystem management, or microbial inoculations [216]. However, most studies continue to investigate simple host–insect systems, indicating a need for experimental investigations that include the dynamic nature of microbial community structure across ecological scales. To maintain defense effectiveness without excessive fitness costs, constitutive and inducible defense mechanisms must be carefully regulated, particularly in long-lived conifers experiencing rapid climate change and evolving pest pressures [210, 217]. Microbiome engineering may provide a scalable means of improving plant resilience, but additional challenges related to establishing, maintaining, and predicting microbial behavior in perennial systems must be addressed [218]. Understanding microbial transmission dynamics (including horizontal transmission via insects and air, as well as vertical transmission through seeds) may provide the information needed to develop microbiome-informed management strategies from seed orchards to plantation systems [216]. Therefore, future research should emphasize community-level approaches examining microbial assemblages rather than beneficial microbial strains alone, to identify network properties that confer robust protection while minimizing trade-offs with forest productivity [216, 219].

Knowledge gaps, experimental challenges, and future research directions

Many plants are exposed to an array of biotic and abiotic factors simultaneously throughout their development and lifespan. These include the presence of pathogens and herbivorous insects, as well as various environmental changes. The combination of these stressors dictates the ultimate level of immune response, energy allocated to survival versus reproduction, and ultimately fitness. Although plants have been extensively studied in both natural and agricultural ecosystems, many studies continue to rely on a single biotic or abiotic factor, resulting in an inadequate representation of the complex interactions among genotype, environment, and management [212, 220, 221]. Furthermore, because plants often respond to multiple stimuli simultaneously, many researchers do not understand how plants decide which response pathway to use when faced with competing DAMPs, MAPK cascades, and jasmonic acid-dependent pathways [93]. In addition, abiotic stresses such as drought and salinity add another layer of complexity to the hierarchy of immune response by altering the ability of plants to mount an effective immune response

through hormonal antagonisms and limitations on available resources, thereby obscuring the full range of resistance capacity of the genotypes tested under less complex conditions [97]. Finally, current models of plant defense cannot adequately describe the emergent properties of co-infected plants with microbes and insects fed upon concurrently, since the regulation of plant hormone networks, including salicylic acid, jasmonic acid, auxins, gibberellins, and cytokinin, occurs in a dynamic regulatory network whose directionality changes depending on the multi-stress regime [212]. For example, vector-borne pathogens, such as those transmitted by Hemiptera, exemplify this complexity. Hemiptera feeding can increase salicylic acid levels in the plant, but viruses can also modulate the same hormonal circuitry to down-regulate the plant's immune system and upregulate transmission efficiency; however, the molecular basis of these three-way interactions remains poorly understood [46]. Another limitation of current studies is that controlled experiments lack the temporal ordering and environmental heterogeneity found in field environments, where the sequence, magnitude, and duration of stress events determine whether plants prime, antagonize, or become metabolically exhausted after each stress event [93, 222]. This is particularly important for long-lived tree species, where breeding cycles can take decades, and pest complexes and climate variability can change in just a few years. For example, in *Pinus pinaster*, breeding lines selected for growth rate were more susceptible to herbivores and scale insects than slower-growing lines, indicating that selective pressure on growth can alter multi-pest resistance architectures [93]. Therefore, understanding the genetic basis of plant multi-stress resilience is a major next frontier, particularly to determine whether plant tolerance to multiple stresses is due to a small number of high-effect regulators or to distributed polygenic networks that interact with environmental variance [222]. Additionally, epigenetic memory mechanisms may enable some degree of acclimation in plants subjected to repeated or overlapping stresses. Still, the causal relationships between specific chromatin states and durable field resistance in perennial systems remain poorly characterized [212]. Overcoming these challenges will require ecologically valid experimental designs that incorporate spatial heterogeneity, community interactions, and time-course phenotyping combined with longitudinal molecular profiling [36, 223]. Systems-based multi-omics approaches that integrate transcriptomics, proteomics, and metabolomics are powerful methods for identifying regulatory nodes controlling cross-tolerance responses, particularly when combined with predictive modeling and environmental parameterization [212, 224]. Ultimately, developing models of plant defense that bridge laboratory reductionism and field realism will

require systems-driven approaches that use ecological niche modeling, process-based simulation, and advanced sensing technologies to predict plant performance under climate variability [160,225,226]. The use of systems-based modeling of plant defense, coupled with emerging tools for modifying plant genomes such as genome editing, multigene engineering, and synthetic regulatory circuits, offers new and unparalleled opportunities for reconfiguring defense networks into climate-resilient crops, provided that standard evaluation pipelines and coordinated breeding strategies are developed across all agroecological environments [190]. The development of integrated systems-based models of multi-stress defense biology will be essential to providing the framework needed to improve the climate resilience of crops (Fig. 5).

Concluding remarks: toward durable and sustainable plant defense strategies

Plants function within ecological environments in which various types of stresses (such as infection by a pathogen, herbivory, and environmental variations) interact and force the plant's immune system to make decisions constantly regarding whether to activate an immune response, allocate resources to growth and development, and support an appropriate level of metabolism. Although there has been significant progress in understanding the mechanisms underlying plant immune responses, much of our current knowledge was derived from studies using reductionist, single-stressor models. These single-stressor models do not adequately capture the converging signals that occur in the real world, leading to a major unresolved question: How do plants prioritize their defense responses when competing cues are directed at shared regulatory networks that involve damage perception, kinase cascades, and hormone-mediated transcriptional regulation? The difficulty of making prioritization-based decisions is further compounded under abiotic stress conditions such as drought or salinity; these conditions have been shown to alter the plant's hormonal equilibrium and limit resource availability, which may mask the plant's intrinsic resistance capacity. In addition, the study of interactions among microbial pathogens, insect herbivores, and host physiology shows that defense signaling occurs in a networked rather than linear manner. Hormonal circuits, including those involving salicylic acid, jasmonate, and auxin, form a dynamic regulatory lattice that reconfigures its structure in response to multiple stresses. Vector-borne pathosystems serve as a paradigmatic example of the complexity of defense signaling in networked systems. As insect feeding can stimulate the plant's immune response, which pathogens can then exploit to enhance their ability to infect and transmit via the vector, this raises fundamental questions about the molecular logic governing these tripartite relationships.

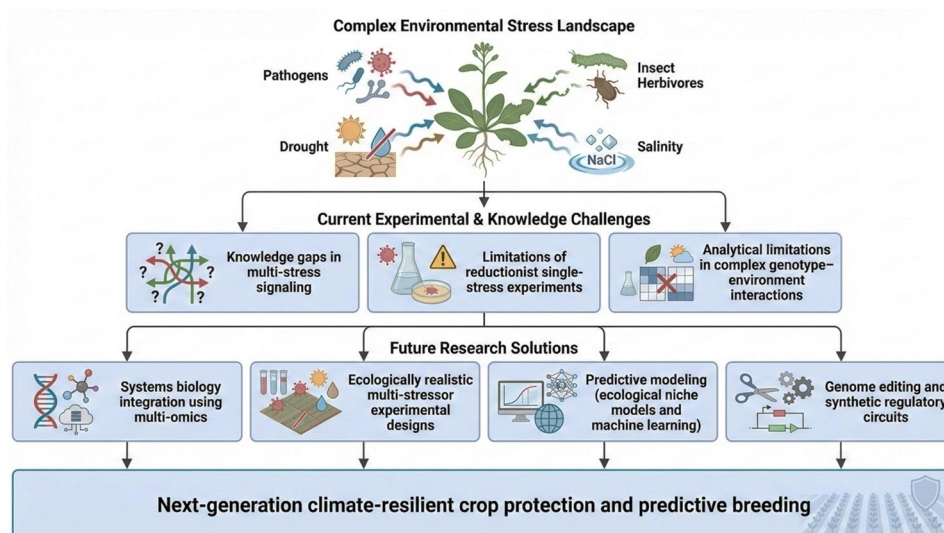


Fig. 5 Conceptual overview of major knowledge gaps and experimental limitations in multi-stress plant immunity research and emerging integrative strategies, including systems biology, predictive modeling, and genome engineering to advance climate-resilient crop protection. This conceptual figure was generated using the AI-assisted scientific illustration platform FigureLabs (figurelabs.ai) and the Bio render program and was manually curated and edited by the authors

Answers to these questions will likely be determined by developing experimental systems that capture the temporal sequencing of events, the heterogeneity of environmental factors, and the interactions among members of plant communities in natural ecosystems. However, these conditions are difficult to reproduce in controlled laboratory settings. The challenges of studying perennial crops are exacerbated by long generation times, the rapid evolution of pest pressure, climate instability, and the potential for selection for growth traits that can reduce resistance. Equally unresolved is the genetic basis of plant resistance to multiple stresses: does adaptive robustness arise from a few regulatory centers, from many polygenes, or from environmentally responsive epigenetic memory? The answers to these questions will depend on the use of methodological advancements, including time-resolved phenotyping, longitudinal molecular profiling, and multi-omics analyses, to identify regulatory nodes that govern cross-tolerance and stress memory. From a forward-looking perspective, the convergence of systems biology, predictive modeling, and molecular engineering provides a pathway toward anticipatory plant defense science. Using computational frameworks to simulate environmental complexity enables ideotype prediction, while genome editing and synthetic regulatory circuits enable the directed reorganization of defense networks. When used in conjunction with high-throughput phenotyping and coordinated breeding programs, these approaches may allow for the transformation of crop protection from reactive management to predictive design. Ultimately, resilient plants will not be developed by maximizing individual resistance traits, but by balancing immunity with

growth, metabolism, and ecological adaptation. From an applied agricultural perspective, understanding the interconnected regulatory architecture underlying plant immune signaling offers significant opportunities. These opportunities support the development of resilient and sustainable crop protection strategies. Identifying shared defense regulatory nodes—such as PRR-associated signaling components, MAPK cascades, hormone integration hubs, and transcriptional regulators—may help engineer or breed crops with broad-spectrum resistance against multiple biotic stressors. Advances in immune priming, microbiome-assisted crop protection, RNA-based technologies, and precision biocontrol offer promising alternatives to conventional, chemical-dependent pest management. Integrating multi-omics platforms, predictive modeling, and AI-assisted decision-support systems could speed up climate-resilient crop improvement programs. These programs can optimize defense activation while minimizing growth penalties. Altogether, these emerging strategies underscore the translational potential of integrated plant immunity research. They can support agricultural sustainability, ecological resilience, and long-term food security under rapidly changing environmental conditions. Future advances in plant immunity research will increasingly depend on quantitative and spatiotemporal approaches capable of experimentally resolving dynamic immune signaling processes. Integrating live-cell imaging, spatial metabolomics, isotope tracing, time-resolved multi-omics, and computational flux modeling may provide deeper insight into how signal amplitude, localization, and pathway kinetics collectively determine downstream metabolic specialization

and defense outcomes under complex biotic stress conditions. Developing this balance requires a systems-based approach that combines molecular genetics, ecology, and computational biology to build predictive frameworks that sustain crop productivity amid increasing rates of climatic and biotic change.

Supplementary Information

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Supplementary Material 1

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During the preparation of this manuscript, the authors used BioRender (BioRender.com) and Figures Lab (<https://www.figurelabs.ai/>) to create schematic illustrations and graphical representations of conceptual frameworks. In addition, Grammarly (Grammarly Inc.) was used exclusively for grammar checking and minor language editing. All scientific concepts, interpretations, data analysis, and the final intellectual content of the manuscript were independently developed, verified, and revised by the authors.

Author contributions

Conceptualization, P.V., A.J., and S.S.; methodology, P.V.; validation, P.V., R.S., and S.K.; formal analysis, P.V., R.S., Y.S.H., S.K., and K.B.P.; investigation, P.V., R.S., A.J., S.S., Y.S.H., S.K., and K.B.P.; resources, A.J. and S.S.; data curation, P.V., R.S., Y.S.H., S.K., and K.B.P.; writing—original draft preparation, P.V.; writing—review and editing, R.S., A.J., S.S., Y.S.H., S.K., and K.B.P.; visualization, R.S., A.J., S.S., Y.S.H., S.K., and K.B.P.; supervision, A.J., S.S., and Y.S.H.; project administration, A.J. and S.S.; funding acquisition, A.J. and S.S. All authors have read and agreed to the published version of the manuscript.

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Declarations

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