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META-TRANSCRIPTOMIC INTEGRATION IDENTIFIES CONSERVED DEFENSE MODULES AND POTENTIAL MOLECULAR MARKERS FOR *FUSARIUM* RESISTANCE ACROSS SOUTHEAST ASIAN CROPS

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SUMMARY

This study integrated 13 transcriptomic datasets, representing seven major Southeast Asian crops (banana, rice, wheat, garlic, chickpea, tomato, and common bean) challenged by six *Fusarium* lineages to identify conserved resistance mechanisms. Harmonizing gene expression profiles into six functional defense modules was successful before evaluation using a diversity-weighted recurrence approach. A conserved defense core's identification consisted of salicylic acid-jasmonic acid (SA-JA) signaling (score = 11.5), phenylpropanoid-lignin metabolism (10.0), and reactive oxygen species (ROS) detoxification (9.5), consistently enriched in resistant interactions. These modules coordinated key regulatory genes, including *WRKY*, *ERF*, *MYB*, and *NPR1*, together with downstream defense effectors involved in lignification, antioxidant activity, and pathogenesis-related responses. Additional contributions from RNA interference and cell wall-apoplast remodeling indicated adaptive, context-dependent defense layers operating across specific host-pathogen systems. Based on cross-system recurrence patterns, *NPR1*, *WRKY33/70*, *ERF071*, *PAL*, *SOD*, and *PR* genes emerged as promising candidate markers for resistance breeding. This study provides the first cross-crop meta-transcriptomic synthesis of *Fusarium* resistance in Southeast Asian cropping systems and establishes a conserved defense framework with potential applications in marker-assisted breeding and transcript-based diagnostics.

Keywords: *Fusarium* disease, crop improvement, plant resistance, defense modules, marker-assisted breeding, meta-transcriptomic

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Key findings: Meta-transcriptomic integration across the seven main crops revealed a conserved *Fusarium* resistance framework in Southeast Asia. A core triad—SA-JA signaling, phenylpropanoid-lignin metabolism, and ROS detoxification—dominates the resistant responses. Central gene families (*NPR1*, *WRKY*, *ERF*, *MYB*, *PAL*, and *PR*) act as key regulatory nodes. A robust candidate marker panel could support marker-assisted breeding and transcript-based diagnostics.

INTRODUCTION

Fusarium diseases are among the most destructive constraints to crop production in Southeast Asia (SEA). The humid tropical climate, combined with intensive monocropping systems, creates favorable conditions for pathogen proliferation, diversification, and evolution (Ferrigo *et al.*, 2016). Among the most damaging species, *Fusarium oxysporum* f. sp. *cubense* Tropical Race 4 (Foc TR4) threatens banana production throughout Indonesia, Malaysia, and the Philippines, while its rapid geographic expansion has elevated *Fusarium* wilt to a global phytosanitary concern (Dita *et al.*, 2018; Maryani *et al.*, 2019; Martínez *et al.*, 2023). Besides bananas, *Fusarium* pathogens affect numerous economically important crops in the region. *Fusarium fujikuroi* causes bakanae disease in rice, whereas *F. graminearum* and *F. proliferatum* reduce cereal productivity and contaminate grain with mycotoxins (Kolawole *et al.*, 2021). Likewise, *F. oxysporum* f. sp. *ciceris* remains a major constraint to chickpea production. Despite their taxonomic diversity, *Fusarium* species share common infection strategies, including vascular colonization, toxin production, and manipulation of host defense signaling (Dita *et al.*, 2018; Li *et al.*, 2019; Cheng *et al.*, 2020).

Advances in next-generation sequencing, particularly RNA sequencing (RNA-seq) and dual RNA-seq, have substantially improved understanding of plant-*Fusarium* interactions by enabling comprehensive analysis of host and pathogen transcriptomes (Naidoo *et al.*, 2018; Dinarvand *et al.*, 2022). Transcriptomic studies in bananas, rice, wheat, tomatoes, and other crops have revealed complex defense networks involving hormone signaling pathways; transcription factors such

as WRKY, MYB, and ERF; antioxidant systems; and pathogenesis-related proteins (Cheng *et al.*, 2018; Song *et al.*, 2018; Li *et al.*, 2019; Cheng *et al.*, 2020; Walker *et al.*, 2024). More recently, transcriptomic analyses have expanded beyond differential gene expression toward the reconstruction of regulatory networks and systems-level defense architectures (Tu *et al.*, 2022). However, most available studies remain restricted to individual crop-pathogen systems, limiting our ability to determine whether conserving resistance mechanisms occurs across diverse hosts and *Fusarium* lineages (Betin *et al.*, 2019; Ruan *et al.*, 2024).

The growing availability of transcriptomic datasets provides an opportunity to address this limitation through comparative synthesis. Integrating evidence across multiple host-pathogen systems can reveal conserved defense processes that have repeated associations with resistance and, therefore, possess greater biological relevance and translational value for breeding (Tu *et al.*, 2022). Nevertheless, no cross-crop meta-transcriptomic synthesis has systematically examined *Fusarium* resistance across major Southeast Asian cropping systems. Consequently, the extent to which resistance mechanisms are shared among crops and which candidate genes consistently contribute to resistance remains poorly understood. This knowledge gap constrains the development of broadly applicable molecular markers and limits the translation of transcriptomic discoveries into breeding programs.

The following study addressed this challenge by employing a diversity-weighted recurrence framework to integrate transcriptomic evidence from multiple crop-*Fusarium* systems. Unlike conventional narrative reviews that summarize findings

qualitatively or statistical meta-analyses that require comparable quantitative effect sizes, this approach evaluates the recurrence of biologically meaningful defense modules across diverse host species and pathogen lineages. By emphasizing cross-system consistency, the framework facilitates discrimination between conserved resistance mechanisms and species-specific responses.

The study aimed to identify recurrent defense modules and candidate gene families associated with *Fusarium* resistance across major Southeast Asian crops. Gene-expression responses reached classification into functional defense categories and evaluation for recurrence across independent transcriptomic datasets. Particular attention focused on regulatory and functional genes repeatedly detected across crop-*Fusarium* interactions, including *NPR1*, *WRKY33/70*, *ERF071*, *MYB108*, *PAL*, *SOD*, and pathogenesis-related genes. Through this systems-level synthesis, the study provides a conserved defense framework and prioritizes molecular candidates that may support future marker-assisted selection, genomic breeding, and functional validation for durable *Fusarium* resistance in Southeast Asian agroecosystems.

MATERIALS AND METHODS

Literature search strategy

A structured literature search commenced to assemble *Fusarium*-related transcriptomic datasets in major Southeast Asian (SEA) crops, performed across various databases. These were PubMed, Scopus, Web of Science, and Google Scholar, complemented by dataset repositories in NCBI Gene Expression Omnibus (GEO) and the European Nucleotide Archive (ENA). Search terms combined *Fusarium* species, transcriptomics, and crop-specific keywords (*Fusarium oxysporum* AND transcriptome AND banana; *Fusarium fujikuroi* AND rice AND RNA-seq; and *Fusarium graminearum* AND wheat). The search only included past studies published between 2013 and 2025 to capture recent advances in next-generation sequencing.

Study selection and eligibility criteria

The study selection process followed PRISMA-based principles. An initial identification of records totaled 162 through database and repository searches. After removing duplicate records and screening titles and abstracts, potentially relevant studies underwent full-text evaluation against predefined inclusion and exclusion criteria.

The included studies should have (i) reported transcriptomic datasets (RNA-seq, dual RNA-seq, small RNAs, or lncRNAs), (ii) compared resistant and susceptible host genotypes, and (iii) provided differential gene expression information suitable for comparative analysis. When available, small RNA- and lncRNA-associated defense components entailed incorporation into the RNA interference module and analysis at the level of functional defense categories rather than as separate transcriptomic classes. The selection excluded studies if they (i) focused on non-*Fusarium* pathogens, (ii) lacked usable expression data, or (iii) involved transgenic systems not directly associated with natural defense responses.

Following the selection process, the study retained 13 transcriptomic datasets representing seven crop species and six *Fusarium* lineages for synthesis. Although the number of eligible datasets was relatively modest, the selected studies encompassed substantial biological diversity, including multiple host species, pathogen lineages, experimental systems, and contrasting resistant-susceptible interactions. Given that the objective of this study was to identify recurrent defense modules and conserved molecular responses across diverse host-pathogen systems rather than estimate pooled effect sizes, dataset representativeness and biological coverage were the priorities over study abundance.

Data extraction, standardization, and analysis

Extracted data included gene expression profiles, functional annotations (GO/KEGG), and enrichment results. Gene identifiers'

standardization used UniProt/Pfam to synchronize conserved families (WRKY, ERF, NPR1, PAL, and PR). Expression values reached normalization as $\log_2$ FC, with infection stages classified into early (≤ 48 h) and late (≥ 72 h) solely for dataset harmonization purposes.

Assigning genes continued to six defense modules: SA-JA signaling, phenylpropanoid-lignin metabolism, ROS detoxification, PR/TLP response, RNA meddling, and cell wall-apoplast remodeling. Module occurrence scoring was binary presence/absence and integrated, using a diversity-weighted recurrence metric: $\text{Score} = f + 0.5Cd + 0.5Pd$, where f represents the frequency of module occurrence across all included datasets, Cd represents crop diversity (number of crop species in which the module was detected), and Pd represents pathogen diversity (number of *Fusarium* lineages associated with the module). The assignment of equal weighting coefficients (0.5) to crop and pathogen diversity sought to ensure balanced consideration of host and pathogen representation while maintaining frequency as the primary determinant of recurrence. This metric's design enabled prioritizing defense modules that occur repeatedly across biologically diverse host-pathogen systems rather than within a limited number of crop- or pathogen-specific datasets. The research intentionally kept the weighting scheme simple to facilitate reproducibility and interpretation across heterogeneous transcriptomic datasets.

Unlike conventional statistical meta-analysis, which requires comparable quantitative effect sizes across studies, this approach accommodates heterogeneous transcriptomic datasets generated from different crop species, *Fusarium* lineages, sequencing platforms, and experimental designs. Moreover, whereas constructing network analyses is typically within individual species or datasets, the diversity-weighted recurrence metric emphasizes cross-system reproducibility by prioritizing defense modules repeatedly detected across independent host-pathogen interactions. Consequently, the method enables identification of conserved resistance components that are more likely to

possess broad biological relevance and translational value for breeding applications.

Analyses proceeded in R (v4.3.2) using tidyverse, ggplot2, and heatmap. Evidence matrices (crop $\times$ module and pathogen $\times$ module) underwent construction to evaluate various patterns. Modules recurrent across ≥ 3 crops and ≥ 3 *Fusarium* taxa became priorities to define a core marker panel representing key regulatory, metabolic, and defense components. A simplified workflow diagram of the analytical framework appears in Figure 1.

RESULTS

Dataset integration and defense-module coverage

Transcriptomic datasets totaled 13, signifying seven primary crop species (banana, rice, wheat, garlic, chickpea, tomato, and common bean) and six *Fusarium* lineages (*F. oxysporum* f. sp. *cubense* TR4, *F. fujikuroi*, *F. graminearum*, *F. proliferatum*, *F. oxysporum* f. sp. *ciceris*, and *Fusarium* spp.), which were retained for synthesis. All datasets met the predefined enclosure criteria, including the accessibility of differential gene expression. The datasets also encompassed diverse pathosystems, including vascular wilt, root rot, crown rot, and head blight, as derived from resistant-susceptible genotype comparisons. Collectively, they captured substantial biological diversity across host species, pathogen lineages, tissues, and experimental conditions, providing a representative foundation for identifying conserved defense modules across crop-*Fusarium* interactions. With journal space limitations, the study did not present detailed dataset information. However, the authors can provide this upon reasonable request.

Consistency of gene annotations and classification into six defense modules enabled a cross-study comparison. Across all datasets, more than 72% of the identified resistance-associated gene families reached successful classification into one or more predefined defense modules, supporting its suitability for

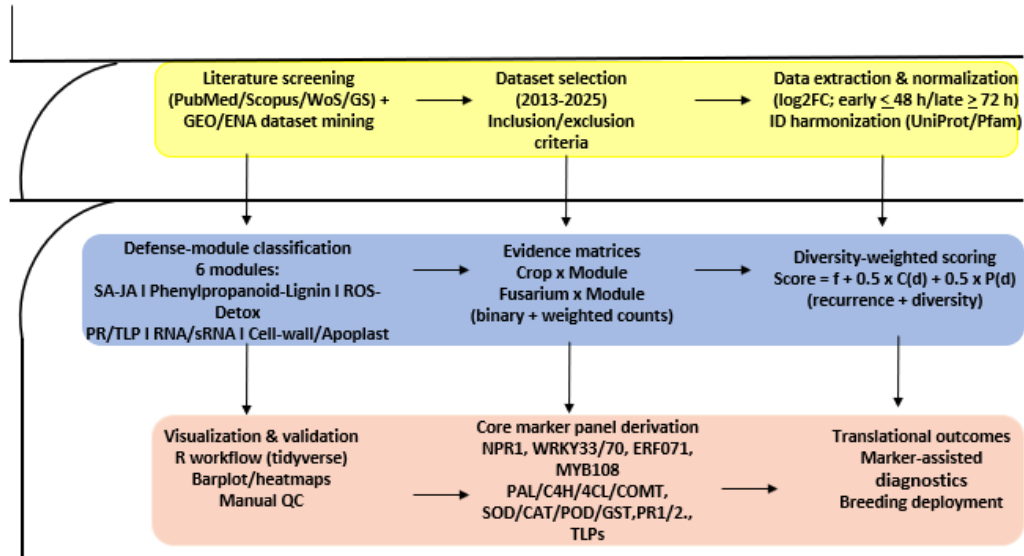


Figure 1. Workflow diagram summarizing the meta-transcriptomic synthesis.

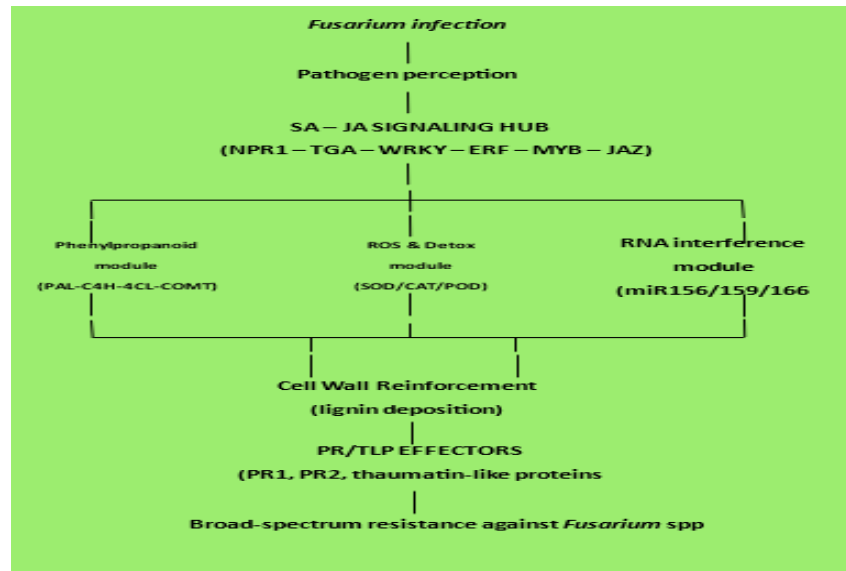


Figure 2. Conceptual model of molecular defense networks against *Fusarium* infection.

cross-system comparative analysis (Figure 2). This result indicates that the modular classification framework captured most of the defense-related transcriptional responses observed across the analyzed crop-*Fusarium* interactions, supporting its suitability for cross-system comparative analysis (Figure 2).

Frequency and diversity of defense modules

Quantitative synthesis of module occurrence revealed varied distribution across the datasets (Figure 3A). Three modules—SA-JA signaling, phenylpropanoid-lignin metabolism, and ROS

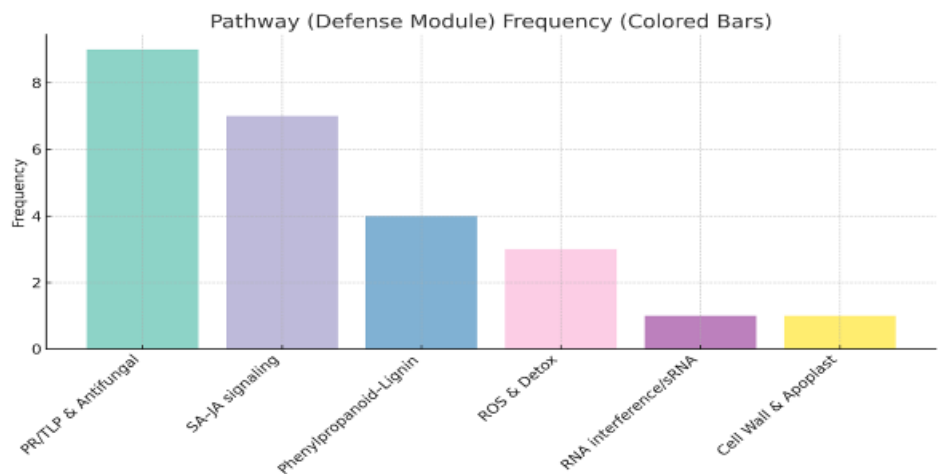


Figure 3A. Pathway (defense module) frequency across datasets.

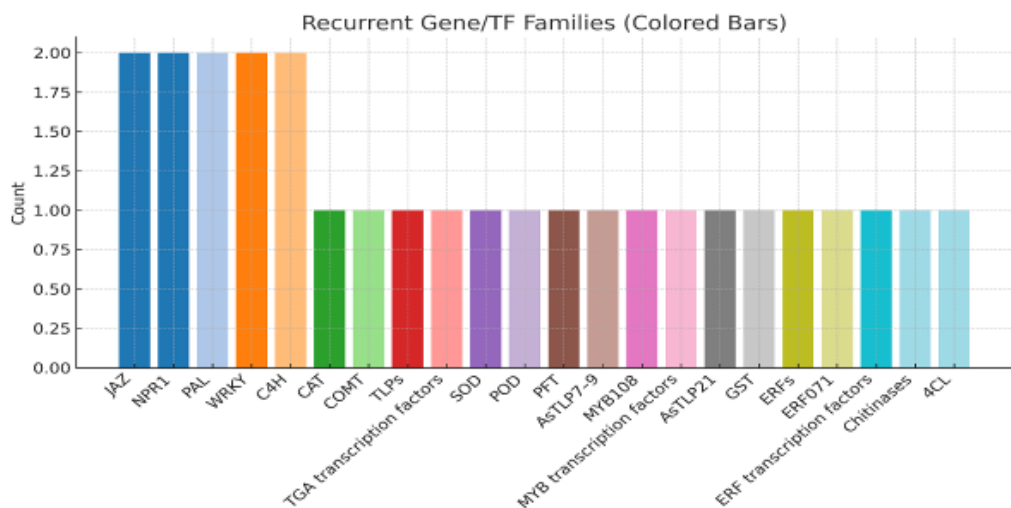


Figure 3B. Recurrent gene/transcription factor family frequency.

and detoxification—received constant identification across the seven crops and multiple *Fusarium* taxa.

The SA-JA signaling module disclosed the highest diversity-weighted recurrence score (Score = 11.5), followed by phenylpropanoid-lignin metabolism (Score = 10.0) and ROS and detoxification (Score = 9.5). The PR/TLP antifungal module and the cell wall-apoplast module were evident in multiple datasets; however, with lower frequencies. The RNA interference/sRNA module was notable in a subset of datasets,

with prominent demonstration in banana-associated studies.

Recurrent gene and transcription factor families

A total of 19 gene and transcription factor families entailed recurrent identification across datasets (Figure 3B). These factors included regulatory components (WRKY, ERF, MYB, NPR1, TGA, and JAZ) and functional effectors (PAL, C4H, 4CL, COMT, SOD, CAT, POD, GST, PR proteins, and TLPs) (Figure 3B).

The frequency distribution revealed the transcription factors WRKY, ERF, and MYB were among the most consistently reported regulators, while PAL and other phenylpropanoid pathway genes showed a wide representation across the crop systems. Antioxidant enzymes (SOD [superoxide dismutase], CAT [catalase], and POD [peroxidase]) and PR proteins also exhibited broad recurrence across multiple host-pathogen interactions. Following *Fusarium* recognition, plants commonly initiate an oxidative burst characterized by rapid ROS accumulation, which contributes to pathogen restriction and defense signaling. However, uncontrolled ROS production can promote cellular damage and tissue necrosis, potentially benefiting pathogen colonization. Consequently, antioxidant enzymes are essential to regulate ROS homeostasis, allowing effective defense activation while minimizing self-inflicted oxidative damage.

Cross-crop distribution of defense modules

The Crop × Module matrix enunciated the patterns of module occurrence across the host

species (Figure 4A). Consistent with the recurrence analysis (Figure 3A), SA-JA signaling, phenylpropanoid-lignin metabolism, and ROS-detoxification modules succeeded in their detection across all evaluated crops (Figure 4A). The PR/TLP antifungal responses and cell wall-apoplast remodelling resulted in the majority of the evaluated crops but showed variable representation.

The RNA interference/sRNA module displayed an irregular distribution, with higher representation in banana datasets and limited occurrence in other crops. Garlic and chickpea datasets also showed the relatively robust presentation of cell wall-apoplast-associated components compared with other species.

Fusarium-lineage associated module distribution

Analysis of the *Fusarium* × Module matrix revealed both conserved and lineage-associated patterns of defense module occurrence (Figure 4B). The SA-JA signaling, phenylpropanoid-lignin metabolism, and ROS and detoxification modules were distinct across all major pathogen groups included in the study.

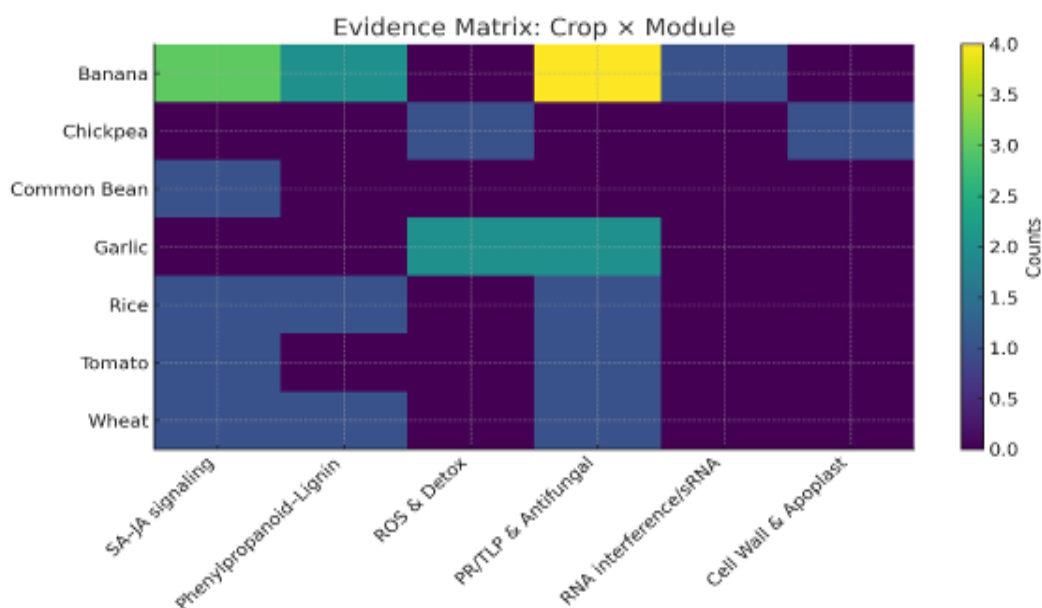


Figure 4A. Heatmap of crop × defense-module occurrence.

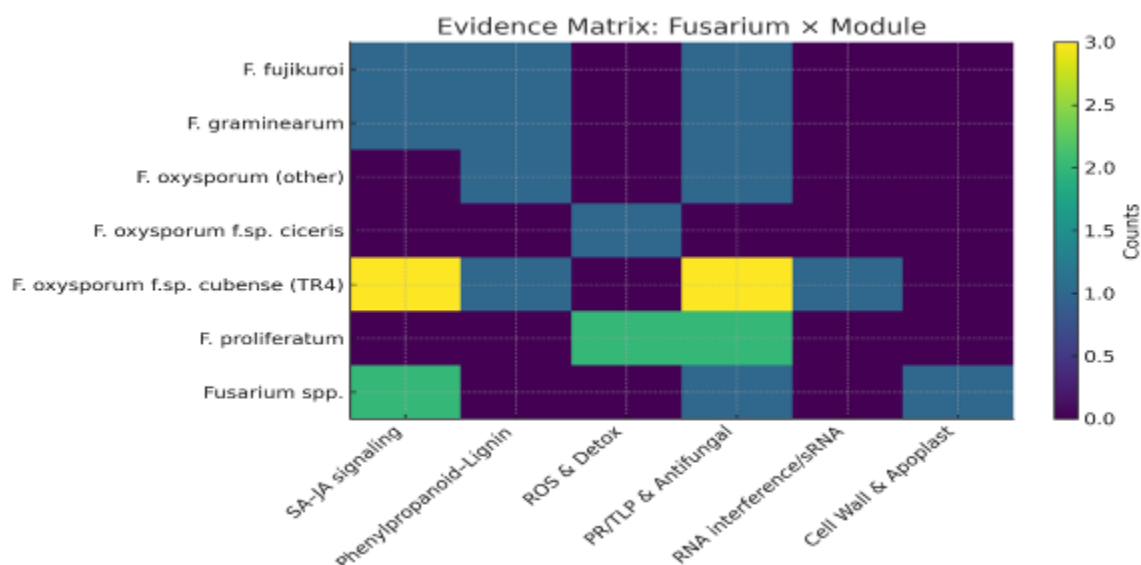


Figure 4B. Heatmap of *Fusarium* × defense-module distribution.

In the module representation, the variations were noteworthy among the specific pathogen-host combinations. For example, the datasets involving *F. oxysporum* f. sp. *cubense* TR4 revealed the frequent detection of transcription factor families (WRKY, ERF, and MYB) alongside phenylpropanoid and ROS-related genes. In contrast, the datasets associated with *F. fujikuroi* and *F. graminearum* also incorporated hormonal regulators and phenylpropanoid components; however, with variations in module frequency patterns. These quantitative patterns provide the basis for interpreting conserved and context-specific resistance mechanisms discussed in the following section.

DISCUSSION

The presented meta-transcriptomic synthesis revealed that *Fusarium* resistance has the governance of a conserved, multi-layered defense network, integrating hormonal signaling, metabolic reprogramming, and structural reinforcement. Across the analyzed datasets, salicylic acid (SA) and jasmonic acid (JA) signaling consistently emerged as central regulatory hubs, coordinating downstream

defense responses. Their dominance in the recurrence analysis (Figure 3A) and widespread distribution across crops and pathogen lineages (Figures 4A–B) support their role as a conserved defense backbone, consistent with previous transcriptomic studies in banana, rice, and wheat (Cheng *et al.*, 2018; Li *et al.*, 2019; Dong *et al.*, 2020).

The cross-crop comparison supports a two-tier model of *Fusarium* resistance. The first tier consists of universally recurrent modules—SA-JA signaling, phenylpropanoid metabolism, and ROS detoxification—that form a conserved immune backbone across host species, as evidenced by their high recurrence scores (Figure 3A) and widespread occurrence across crops and *Fusarium* lineages (Figures 4A–B). The second tier comprises context-dependent modules, including RNA interference and cell wall-apoplast remodelling, whose appearance varies according to crop species and pathogen lineage (Figures 4A–B). This distinction indicates that durable resistance is successful not only through activation of core defense pathways but also through recruitment of specialized responses adapted to the biological characteristics of individual host-pathogen systems.

The vital transcriptional regulators, including NPR1, WRKY, ERF, and MYB families,

attained identification persistently across datasets, revealing their conserved role in mediating hormone-dependent defense signaling. These transcription factors play a critical regulatory role as integrative nodes linking upstream hormonal signaling with downstream defense activation. Notably, the co-occurrence of SA- and JA-responsive pathways across the multiple systems suggested that the said resistance had the control of context-dependent crosstalk rather than strict antagonism, also getting critical support from previous observations in plant immune signaling networks (Cheng *et al.*, 2020; Zhao *et al.*, 2022).

Downstream of hormonal signaling, the phenylpropanoid-lignin module emerged as a major structural and biochemical defense component against *Fusarium*. Across the analyzed datasets, recurrent enrichment of *PAL*, *C4H*, *4CL*, and *COMT* genes was in a consistent association with resistant interactions, indicating activation of lignin biosynthesis and cell wall reinforcement pathways. These findings are consistent with the established role of phenylpropanoid metabolism in strengthening physical barriers and restricting pathogen invasion (Dong *et al.*, 2020; Li *et al.*, 2019). This mechanism is particularly relevant for vascular *Fusarium* pathogens, whose disease progression depends on successful colonization of root and vascular tissues. At the tissue level, the activation of phenylpropanoid-derived lignification strengthens cell walls in root cortical tissues and vascular bundles, creating physical barriers that restrict fungal ingress and impede longitudinal spread through the xylem.

Concurrently, ROS-related defenses generate antimicrobial conditions around infection sites and facilitate cell wall cross-linking, further limiting pathogen establishment. Together, these responses reduce tissue colonization, preserve vascular function and, ultimately, mitigate symptom development at the whole-plant level. Previous studies in wheat have demonstrated that activation of phenylpropanoid pathway genes proved to be in association with increased lignification and reduced disease progression in

Fusarium head blight and crown rot systems (Yang *et al.*, 2025).

Beyond structural reinforcement, phenylpropanoid-derived metabolites also contribute to antioxidant capacity and may exert direct antimicrobial effects against invading pathogens. Thus, the phenylpropanoid pathway functions not only as a source of lignin precursors but also as a multifaceted defense system integrating physical, biochemical, and redox-mediated resistance mechanisms (Qiao *et al.*, 2021).

The ROS and detoxification module represent an additional conserved layer of defense, reflecting the significance of redox regulation during pathogen attack. The ROS play a dual role as signaling molecules and antimicrobial agents; however, their accumulation must be securely controlled to prevent host damage. The recurrent upregulation of antioxidant enzymes, including SOD, CAT, POD, and GST (Glutathione S-Transferase), revealed a coordinated mechanism to uphold redox homeostasis. Studies on cotton and other crops considerably support the role of phenolic compounds and antioxidant pathways in balancing ROS dynamics during *Fusarium* infection (Walker *et al.*, 2024; Zhou *et al.*, 2025).

Additional defense layers, including PR/TLP antifungal responses and cell wall-apoplast remodeling, reached recurrent identification across the analyzed datasets, particularly during later stages of infection. Pathogenesis-related proteins, such as PR1, PR2, and thaumatin-like proteins, frequently appeared among resistant interactions, suggesting a conserved contribution to antifungal defense across diverse crop-*Fusarium* systems. Likewise, genes associated with cell wall-apoplast remodeling attained repeated detection, indicating that reinforcement of extracellular barriers constitutes an additional defense layer emerging from the present meta-transcriptomic synthesis. In legume systems, such as chickpea, the prominence of pectin-modifying enzymes and chitinases further signifies that apoplastic reinforcement plays an important role in limiting pathogen penetration and tissue colonization.

The RNA interference mechanisms, including small RNAs (miR156, miR159, and miR166) and long noncoding RNAs (lncRNAs), also incurred recognition in a subset of datasets, particularly in banana systems. These molecules were popular to manage the gene expression at the post-transcriptional level and have been concerned with stress and defense responses. Previous studies enunciated that sRNAs can adjust the JA signaling and other defense-related pathways, highlighting their prominent role as fine-tuning regulators of plant immunity (Fei *et al.*, 2019; Cheng *et al.*, 2021). The variation observed among *Fusarium* lineages and host systems suggests that resistance is in an organized hierarchy rather than uniform. Meanwhile, SA-JA signaling, phenylpropanoid metabolism, and ROS detoxification constituted a conserved immune backbone across most pathosystems; modules, such as RNA interference and cell wall-apoplast remodeling, exhibited more restricted distributions. These differences likely reflect both host-pathogen specificity and variation in infection strategies. For example, the greater representation of RNA interference-associated responses in banana-Foc TR4 interactions could reflect a greater contribution of RNA-mediated regulation to small RNA-mediated regulation during vascular colonization. In contrast, stronger cell wall-associated responses in other systems imply greater investment in structural defense barriers. Therefore, *Fusarium* resistance appears to emerge from the integration of universal defense mechanisms with context-dependent adaptive responses tailored to individual host-pathogen combinations.

Although the present synthesis was entirely according to transcriptomic datasets included in the analysis, additional supporting verification from other crop systems provides broader context for *Fusarium* resistance mechanisms. For example, single-cell transcriptomic analyses in maize have demonstrated the involvement of phenylpropanoid metabolism, lignification, and immune regulatory networks in restricting *Fusarium* invasion (Cao *et al.*, 2023). Similarly, resistance to fumonisin-producing *Fusarium* species in maize crops has appeared to be in

association with modulation of sphingolipid metabolism (Beccaccioli *et al.*, 2021). These plant resistance mechanisms, although not uniformly represented across the analyzed datasets, highlighted additional biochemical strategies that may harmonize the core defense modules identified in this study.

Cell wall-degrading enzymes (CWDEs), including pectin lyases and cellulases, emerged as pivotal virulence factors used by *Fusarium* species to facilitate the host colonization. Evidence from tomato-pathogen systems revealed that containment and modification of these enzymes can further reduce disease severity (Schwartz *et al.*, 2017). Although CWDE-associated responses were not among the most recurrent defense modules identified in this present synthesis, their involvement highlights the importance of host-pathogen interactions occurring within the apoplast and cell wall interface during *Fusarium* infection.

Although the selected datasets represented substantial biological diversity across seven crop species and six *Fusarium* lineages, the number of eligible transcriptomic studies remains limited for certain host-pathogen combinations. Therefore, the conserved defense modules identified here should undergo interpretation as recurrent patterns supported by the currently available evidence rather than as exhaustive representations of all *Fusarium* resistance mechanisms. Future transcriptomic studies encompassing additional crops, genotypes, and environmental conditions will further refine and validate the proposed resistance framework.

From a translational perspective, conserved gene families facilitate the prioritization of molecular markers in breeding programs. The proposed panel (*NPR1*, *WRKY33/70*, *ERF071*, *MYB108*, *PAL*, *COMT*, *SOD*, *CAT*, *POD*, and *PR* genes) represents key regulatory and functional nodes consistently detected across multiple crops and *Fusarium* lineages, supporting their potential utility in marker-assisted selection and transcript-based diagnostics. However, validation across diverse genetic backgrounds and environments remains essential before deployment in breeding programs. The identified resistance modules hold considerable promise for crop

improvement across Southeast Asia, where the conserved SA-JA-phenylpropanoid-ROS network could serve as a unifying framework for resistance breeding under endemic *Fusarium* pressure (Qiao *et al.*, 2021). Furthermore, miRNA-associated components (miR156, miR159, and miR166) identified in banana-TR4 interactions suggest opportunities for RNA-based resistance enhancement and functional genomic studies. Meanwhile, cross-crop transcriptomic benchmarking facilitates the transfer of molecular insights from model crops, such as rice, to regionally important species, including banana, garlic, and chickpea. Integration of hormonal, metabolic, and structural defense layers collectively supports a systems-level model in which coordinated module activation, rather than individual gene effects, underpins durable resistance (Yang *et al.*, 2025).

Integration of hormonal, metabolic, and structural layers revealed a systems-level defense model (Figure 2) where coordinated module activation determines disease resistance. The SA-JA signaling regulates the phenylpropanoid and ROS pathways, activating PR/TLP effectors and cell wall reinforcement, emphasizing pathway connectivity over single-gene effects (Yang *et al.*, 2025).

CONCLUSIONS

This study revealed that *Fusarium* resistance across Southeast Asian cropping systems has the governance of a conserved, multilayered defense network centered on SA-JA signaling, phenylpropanoid metabolism, and redox regulation. The recurrent occurrence of key regulatory and functional gene families suggests that resistance entailed mediation from coordinated pathway interactions rather than single-gene effects. Based on cross-system recurrence patterns, *NPR1*, *WRKY33/70*, *ERF071*, *PAL*, *SOD*, and *PR* genes emerged as promising candidate markers for resistance breeding and transcript-based screening. Although the synthesis encompassed seven crop species and six *Fusarium* lineages, it remains constrained by the availability and heterogeneity of published

transcriptomic datasets. Nevertheless, the findings provide a systems-level framework for developing durable *Fusarium* resistance in tropical agroecosystems. Future studies should focus on functional validation and breeding-oriented evaluation of the identified markers across diverse crop-*Fusarium* systems to support their integration into marker-assisted and genomic breeding programs.

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