



Annotation of the Defence Genes in *Sorghum bicolor*: Current Insights and Future Prospects

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ABSTRACT

Sorghum bicolor is a climate-resilient C4 cereal crop widely cultivated in semi-arid and drought-prone regions. Despite its adaptability, sorghum productivity is substantially constrained by diverse biotic stresses, including fungal pathogens, insect pests and parasitic weeds. Recent advances in genomics, transcriptomics and bioinformatics have significantly enhanced the identification and annotation of defence-related genes in sorghum. This review consolidates current insights into key defence gene classes, including nucleotide-binding leucine-rich repeat (NLR) proteins, transcription factors and genes involved in secondary metabolite biosynthesis furthermore, emerging approaches such as pan-genomics, genome-wide association studies (GWAS), CRISPR/Cas-mediated genome editing and systems biology frameworks are critically examined for their role in improving annotation accuracy and functional validation. Future efforts should prioritize integrative multi-omics strategies and field-level validation to unravel complex defence networks and accelerate the development of resilient sorghum cultivars suited for changing agro-climatic conditions.

Key words: CRISPR/Cas, Defence genes, GWAS, NLR proteins, Pan-genomics, *Sorghum bicolor*.

Sorghum bicolor ranks among the most important cereal crops globally and serves as a primary dietary component for millions of people, particularly in Asia and Africa. Its exceptional tolerance to drought, high temperatures and marginal soils has positioned sorghum as a strategic crop under climate change scenarios. However, its yield potential remains vulnerable to a broad spectrum of biotic stresses, including anthracnose (*Colletotrichum sublineola*), downy mildew (*Peronosclerospora sorghi*), stalk rot (*Fusarium* spp.) and insect pests such as the sugarcane aphid (*Melanaphis sacchari*) (Kanaka, 2006; Sajjan *et al.*, 2011; Veerabadrhan and Deepalakshmi, 2003).

Plants have evolved sophisticated defence mechanisms involving constitutive barriers and inducible immune responses governed by complex gene networks. The annotation of defence genes is therefore a critical step in identifying resistance loci, understanding evolutionary dynamics and enabling genomics-assisted breeding. With the advent of high-throughput sequencing technologies and advanced computational tools, the resolution and accuracy of defence gene annotation in sorghum have improved considerably (Boyles *et al.*, 2021; Xu *et al.*, 2022). This review aims to synthesize recent developments and highlight future directions in this rapidly evolving field.

This review study was conducted at the School of Technology, Department of Bioinformatics, SRTM University Sub Campus, Latur, India, during the period 2023-2025.

A systematic literature survey was performed using major scientific databases, including Scopus, Web of Science, PubMed and Google Scholar. Relevant publications were identified using targeted keywords such as “sorghum defence genes”, “NLR proteins”, “pan-

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genomics”, “GWAS” and “CRISPR in cereals”. Only peer-reviewed articles published between 2015 and 2025 were considered, with priority given to high-impact and recent studies.

The collected literature was critically evaluated and synthesized using established review methodologies, with emphasis on integrating genomic, transcriptomic and functional data to provide a comprehensive understanding of defence gene annotation in sorghum (Kour *et al.*, 2022; Puri *et al.*, 2023).

Genomic resources and pan-genome landscape

The availability of high-quality reference genomes and pan-genomic assemblies has transformed sorghum genomics. These resources have revealed extensive structural variation, including presence/absence variations (PAVs), which play a pivotal role in shaping defence gene diversity. Pan-genome analyses have enabled the identification of novel resistance loci that are absent in single reference genomes, thereby offering a more comprehensive view of genetic variation underlying disease resistance (Xu *et al.*, 2022; Birhanu *et al.*, 2024).

Resistance genes and NLR protein architecture

Nucleotide-binding leucine-rich repeat (NLR) proteins constitute the central components of plant innate immunity. These proteins typically possess conserved NB-ARC domains coupled with variable leucine-rich repeats that facilitate pathogen recognition (Boyles *et al.*, 2021).

Recent studies have identified key resistance loci such as ARG2, ARG4 and ARG5 associated with anthracnose resistance (Mewa *et al.*, 2023; Habte *et al.*, 2024). Genome-wide analyses indicate the presence of a large repertoire of NLR genes in sorghum, many of which remain functionally uncharacterized. The expansion and diversification of NLR gene families through duplication events highlight their evolutionary significance in adaptive immunity (Lee *et al.*, 2022).

Transcriptomic reprogramming and regulatory networks

Transcriptomic analyses have provided valuable insights into the dynamic reprogramming of gene expression during pathogen challenge. Defence responses are characterized by the activation of key metabolic pathways, including phenylpropanoid and flavonoid biosynthesis (Kour *et al.*, 2022; Puri *et al.*, 2023).

Transcription factors such as WRKY, MYB and NAC families play crucial roles in regulating these responses. Additionally, hormonal signaling pathways involving salicylic acid, jasmonic acid and ethylene orchestrate coordinated defence responses through intricate cross-talk mechanisms (Yu *et al.*, 2021; Zhang *et al.*, 2021).

Insect resistance and adaptive challenges

The sugarcane aphid has emerged as a major constraint in sorghum cultivation. Resistance loci such as RMES1 and RMES2 have been successfully identified and utilized in breeding programs (VanGessel *et al.*, 2024). However, the rapid evolution of new aphid biotypes poses a significant challenge to the durability of resistance. This underscores the need for continuous exploration and incorporation of novel resistance genes.

Role of secondary metabolites in defence

Sorghum synthesizes a diverse array of secondary metabolites, including dhurrin, tannins, flavonoids and 3-deoxyanthocyanidins, which function as chemical deterrents against biotic stressors (Satish *et al.*, 2020).

The biosynthesis of these compounds is tightly regulated and often induced under stress conditions. Recent studies have demonstrated coordinated upregulation of these pathways in resistant genotypes, highlighting their importance in plant defence (Zhang *et al.*, 2021).

Epigenetic regulation of defence responses

Epigenetic modifications, including DNA methylation and histone modifications, are increasingly recognized as key regulators of defence gene expression. These mechanisms

enable plants to rapidly respond to environmental stimuli and may contribute to stress memory and transgenerational resistance. Understanding epigenetic regulation offers new avenues for crop improvement (Yu *et al.*, 2021).

Emerging technologies and future directions

Recent technological advancements are reshaping defence gene annotation and functional validation:

- Pan-genomics provides insights into gene presence/absence variation and structural diversity (Xu *et al.*, 2022).
- GWAS and QTL mapping facilitate identification of resistance-associated loci (Nida *et al.*, 2020; Upadhyaya *et al.*, 2021).
- CRISPR/Cas genome editing enables precise functional validation and targeted improvement of defence genes (Liu *et al.*, 2022).
- Systems biology and machine learning approaches allow integration of multi-omics datasets to identify key regulatory networks (Meng *et al.*, 2023; Yu *et al.*, 2021).

Collectively, these tools are accelerating the development of next-generation sorghum cultivars with enhanced resistance and adaptability.

CONCLUSION

The annotation of defence genes in *Sorghum bicolor* has progressed remarkably through advances in genomics, transcriptomics and bioinformatics. Identification of resistance-related genes and molecular pathways provides a strong foundation for developing disease-resistant and climate-resilient sorghum cultivars. Emerging technologies such as pan-genomics, GWAS, CRISPR/Cas genome editing and systems biology are improving the precision of functional gene characterization and crop improvement strategies. These developments are highly important for sustainable agriculture and food security, especially in drought-prone regions where sorghum supports farming communities and rural livelihoods. Future research should emphasize field-level validation, conservation of genetic diversity and farmer-oriented breeding programs to ensure environmentally sustainable and nutritionally secure agricultural systems for future generations.

Conflict of interest

There is no any conflict of interest as per my understanding.

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