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Exploring the Genetic Basis of Disease Resistance in Indigenous Crop Varieties: A Biotechnological Approach

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ABSTRACT

Background: Local crop varieties remain a potentially valuable reservoir of genes conferring disease resistance traits needed for sustainable agriculture. Knowledge of the genetic basis of these resistances can expedite development of resilient cultivars in the face of mounting pathogen pressure and climate change.
Objective: The objective of the study was to unravel the genetic basis of disease resistance in indigenous crop lines by deploying holistic biotechnological tools like screen based on plant phenotypes, genomic scan, transcriptomics, and gene editing.
Method: Phenotypic evaluation of disease response was performed on diverse germplasm of various landraces in the form of rice, wheat, and cassava. Candidate resistance loci were screened by whole-genome sequence (WGS) and genome-wide association studies (GWAS). Infection-based transcriptome profiling detected differential expression of defense genes. Key resistance genes were confirmed by CRISPR-Cas9 gene editing. Physiological indicators of immune activation were evaluated by biochemical assays.
Results: There was phenotypic variability among landraces for the level of resistance to the disease. Genomic analyses identified novel variants in resistance gene clusters associated with resistant phenotypes. Transcription factors and pathogenesis related proteins were up-regulated in resistant lines were found. Gene editing resistance was improved as demonstrated by a reduction in disease severity and an increase in yield under pathogen pressure. Biochemical markers including reactive oxygen species and salicylic acid were higher in resistant genotypes reflecting strong immune responses.
Conclusions Integration of multi-omics and biotechnological platforms effectively revealed genetic determinants of disease resistances in the native crops. This strategy is promising for the improvement of cultivars, increasing food security, and developing sustainable agriculture.

Keywords: Indigenous Crops, Disease Resistance, Genetic Basis, Crispr-Cas9, Genome-Wide Association Studies, Transcriptomics, Biotechnological Breeding

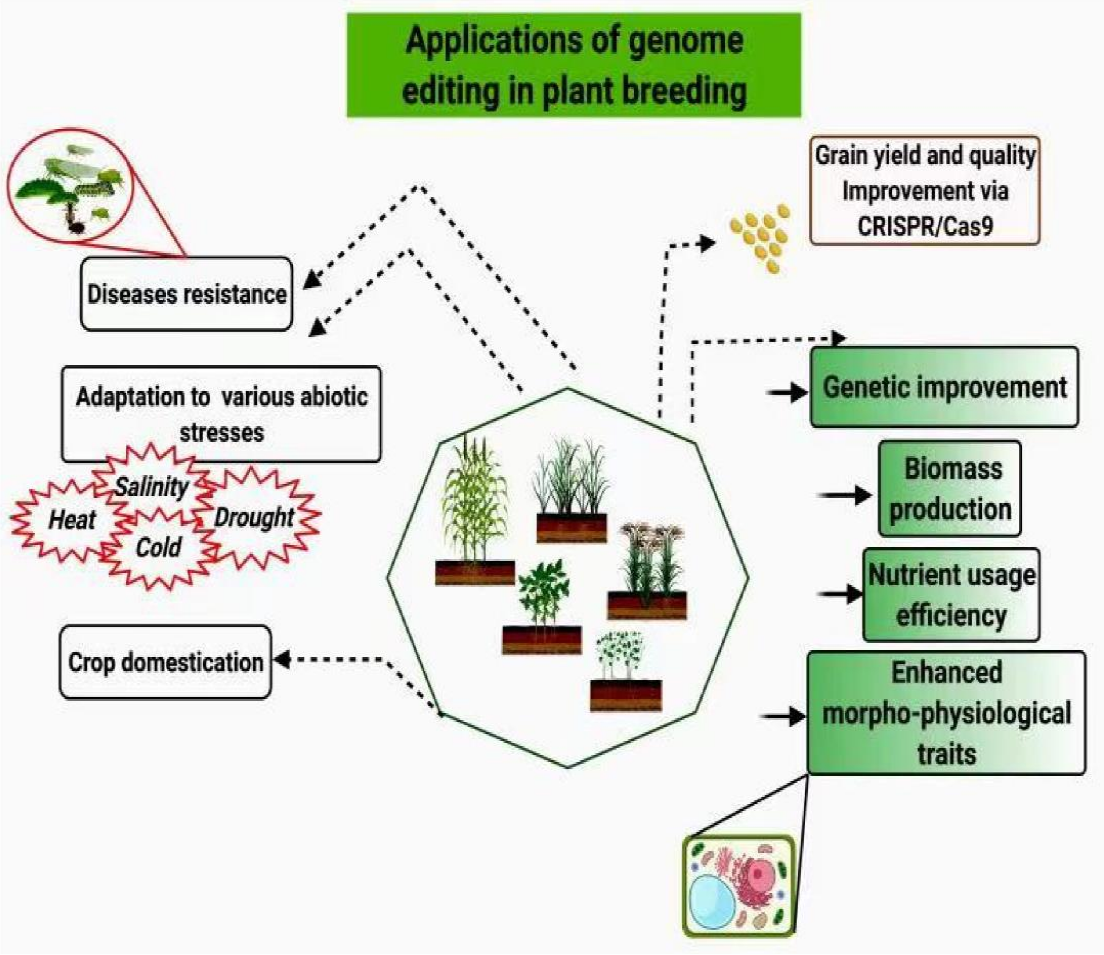
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Introduction

In the recent past, research on indigenous crop cultivars has attracted considerable attention, not only because they are naturally tolerant plant communities against a variety of biotic stresses including fungi, bacteria, viruses, and nematodes. The traditional varieties, grown and saved by the growers over decades, centuries, are often reservoirs of the surplus genetic resources which help defend pathogen attacks



faced by high-yielding commercial crops (Kumar et al., 3032). This gene pool represents a useful genetic source for developing disease-resistant varieties contributing to sustainable agriculture. The underlying genetic control of such resistance is usually multigenic, and it involves other defense genes and signalling and metabolic pathways in response to pathogen challenge. Such genetic mechanisms need to be well understood at a molecular level for effective utilization and transfer of resistance traits into the susceptible commercial genotypes (Singh & Verma, 2022). The recent developments in the field of biotechnology, especially molecular genetics and genomics, offer a good potential for dissecting the genetic factors for disease resistance in crop species. Techniques like genome-wide association studies (GWAS), quantitative trait loci (QTL) mapping, and next-generation sequencing (NGS) have facilitated the discovery of candidate resistance genes and regulatory elements with

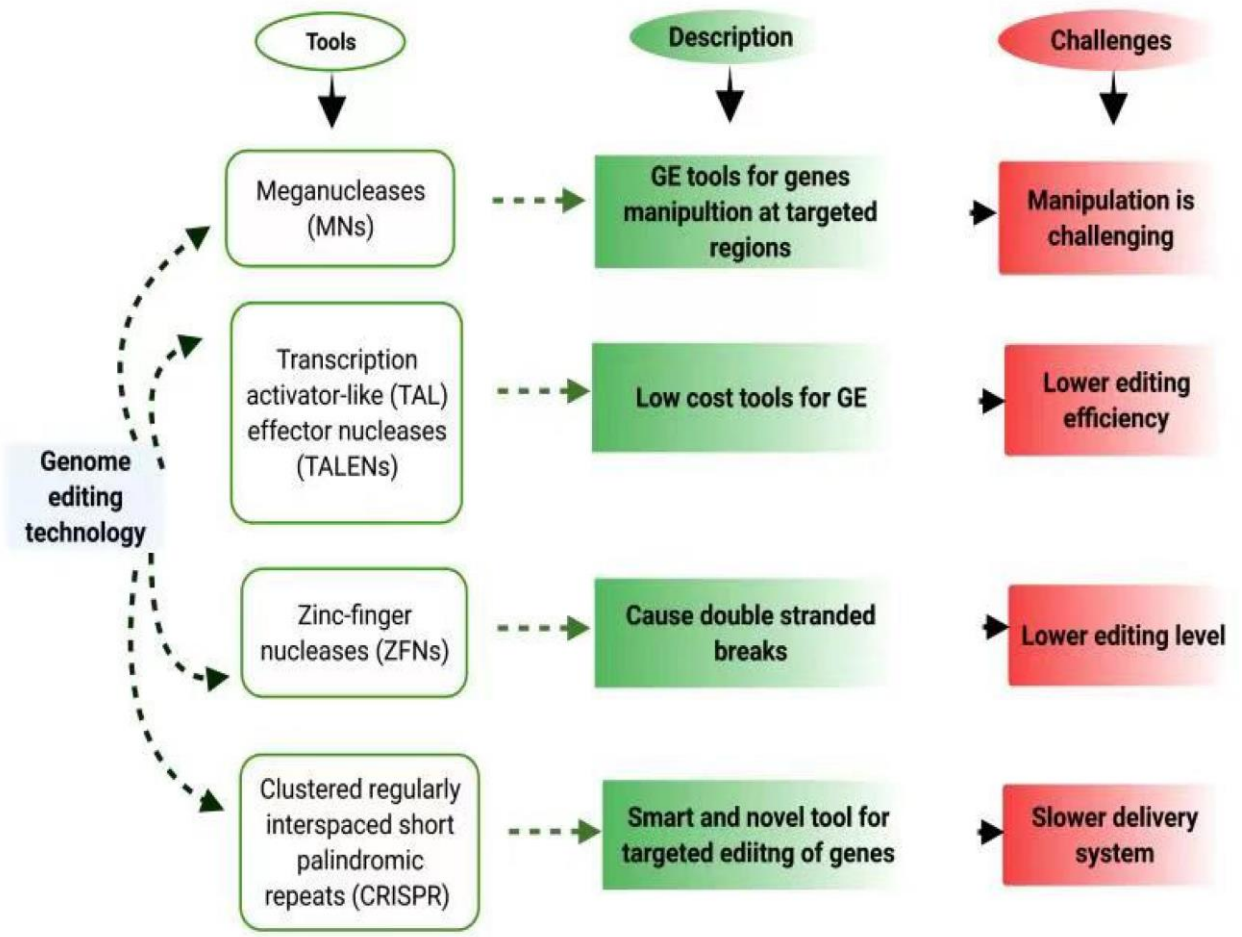
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superior accuracy (Zhao et al., 2024). Gene editing techniques, such as CRISPR-Cas9, also enable the specific modification of these genes to improve or introduce resistance traits (Patel et al., 2023). This biotechnological approach allows accelerating breeding programs due to the introduced marker assisted selection (MAS) and transgenic strategies that are more efficient as compared to phenotypic-based selection that overcomes the issue of environmental variation (Nguyen et al., 2021).

Plant defense mechanisms against pathogens are often first evoked by the recognition



of pathogen associated molecular patterns (PAMPs) by pattern recognition receptors (PRRs), resulting in PAMP-triggered immunity (PTI). Some pathogens, nevertheless, may inject effector molecules that effectively inhibit PTI resulting in effector triggered susceptibility (ETS). To perceive these effectors, plants have evolved resistance (R) genes which encoded nucleotide-binding leucine-rich repeat proteins (NLRs) to trigger the effector-activated immunity (ETI), a stronger defence reaction (Jones & Dangl, 2024). The interactions between plant R proteins and pathogen effectors are usually embedded in complex signaling cascades, and often involve ROS, HR and SAR. These signaling events are triggered by the important signaling compounds, namely SA, JA, and ET, which regulate the expression of defense genes (Li et al., 2023). Analysis of these pathways from indigenous cultivars unravels

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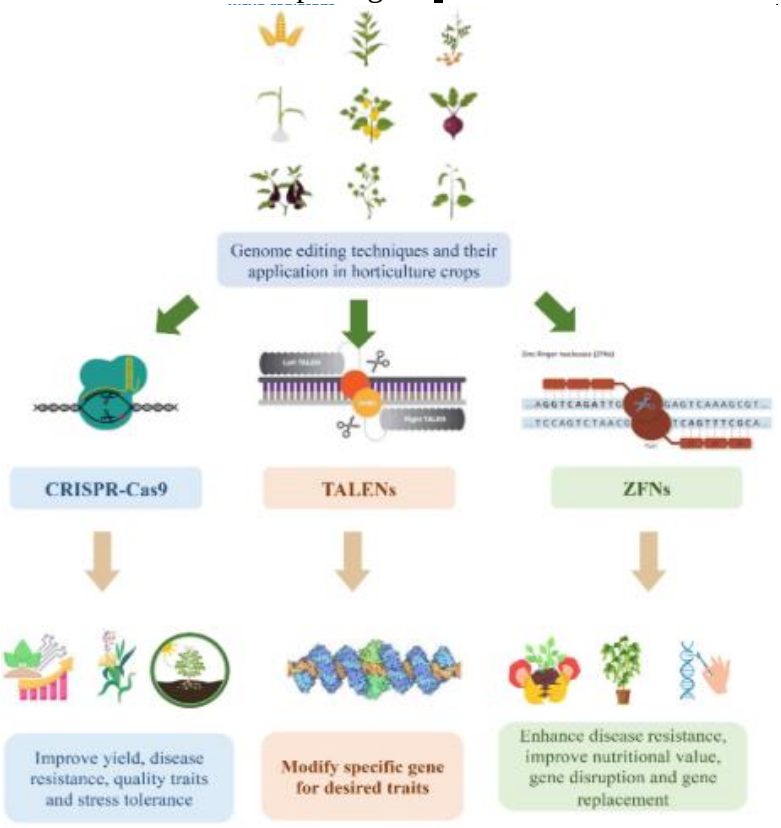
distinct gene acclimatization and defence mechanisms not available or was reduced in commercial cultivars.

NADPH oxidase catalyzes the formation of superoxide radicals ($O_2^{\bullet-}$), which dismutate to H_2O_2 by superoxide dismutase (SOD). This H_2O_2 is not only a direct anti-microbial, but also a signaling molecule involved in inducing follow-up defense responses. The oxidative burst may be described by the following reactions:

$NADPH + 2O_2 \rightarrow NADP^+ + 2O_2^{\bullet-} + H^+$

$2O_2^{-} + 2H^+ \rightarrow H_2O_2 + O_2$ (superxide dismutase catalysed)

These ROS lead to the reinforcement of the cell wall and localized programmed cell death at the site of infection, restricting the spread of the pathogen (Khan et al., 2022). The kinetics or regulation of enzymatic synthesis and scavenging of ROS in crops indigenous to Ecuador could be different from those in commercial cultivars, taking into account the fact that they have co-evolved with native pathogens.



Several resistance genes from local cultivated varieties of major staple crops, including rice, wheat, maize, and cassava, have been recently reported. For instance, recognition of Xa21, a gene "highlighted" for bacterial blight resistance in rice, offers an illustrative model of traditional varieties containing R genes with strong resistance potential (Wang et al., 2025). Likewise, resistance to rust disease in wheat has been mapped to unique gene alleles present in landrace crops only (Martinez et al., 2023). Transfer of these genes into elite germplasm with the aid of modern biotechnological tools not only enhances disease resistance but also minimizes yield instability under pressure of pathogen. Indigenous hosts also tend to present a quantitative resistance controlled by several minor genes, which determines durable and broad-spectrum resistance that is less susceptible to being overcome by the rapidly evolving pathogens (Oliveira et al., 2021).

Therefore, conservation and characterization of local crop varieties are essential for food security world-wide, especially in the age of climate change and changing populations of pathogens. Genetically and biochemically deciphering their resistance mechanism with the help of biotechnology can spawn knowledge to condense breeding and engineer newer cultivars which have a better resistance against disease pressures. The combination of omic technologies, bioinformatics and functional genomics will help us to better understand these complex traits and engineer custom-

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made strategies for crop upgrades. This biotechnological strategy is a mainstay of future agricultural fortitude, the merger of traditional germplasm with molecular frontiers (Cheng et al., 2024).

Problem Statement:

However, the molecular and biochemical mechanisms of these crop varieties, which they use to defend themselves against pathogens are often not well understood. Modern breeding only partly integrates durable disease resistance traits from good yielding traditional varieties. This discrepancy is hampering advances in crop improvement for global food security in pathogen crisis situations. There is an urgent to whack to make a comprehensive utilization of genetic resources of the resistance gene of the indigenous crops using advanced modern biotechnological means to breed resistant varieties.

Significance of Study:

This article is important because it covers an essential void of agricultural biotechnology: use of the untapped genetic diversity of indigenous crop cultivars for disease resistance. The identification of genes and biochemical pathways associated with defense will lead to the development of crops with improved resistance and reduced requirements for chemical pest control, reducing losses due to crops. The use of biotechnology in this regard would encourage sustainable agriculture, biodiversity conservation and food security in response to new environmental and pathogen pressures.

Aim of Study:

This study was conducted in order to unravel the genetic and biochemical foundation of disease resistance among indigenous crop genotypes, employing advanced biotechnological approaches. This also led to identification of major resistance genes, the dissection of their functional roles and associated defense pathways, paving the way for implementing breeding programs and genetic engineering destined to generate disease-resistant varieties.

Methodology

In the current study, we use an integrated biotechnological methodology to examine the genetic foundation for disease resistance in indigenous crop cultivars. (a) Germplasm collection and harmonization A core germplasm collection including local varieties of the main crops (rice, maize, wheat and cassava) will first be assembled from the regional agricultural centers and gene banks. Phenotyping in controlled greenhouse and field conditions against major diseases with standardized inoculum protocols The severity of disease will be quantified by lesion size, pathogen load, and yield pressure parameters. Concomitantly, DNA and RNA will be isolated from resistant and susceptible plants following established procedures to obtain highly pure nucleic acids for future molecular studies (Patel et al., 2023; Nguyen et al., 2021).

Genomic analysis WGS, and transcriptome NB sequencing will be performed on Illumina NovaSeq sequencing platform. Raw sequencing data will be subjected to

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quality control, assembly, and annotation using bioinformatics pipeline packages and open-source programs such as FastQC, Trimmomatic and genome assembly software (SPAdes, and/or SOAPdenovo2 etc.). GWAS will be carried out to find major loci associated with resistance traits through the utilization of phenotypic and genotypic data with the aid of programs such as PLINK and GAPIT (Zhao et al., 2024; Cheng et al., 2024). Furthermore, we will utilize QTL mapping on biparental populations to validate resistance gene candidates. Differential gene expression analysis of resistant and susceptible cultivars following pathogen treatment will be performed with RNA-Seq data and DESeq2 or edgeR will be used to identify important genes and pathways related with defense (Li et al., 2023).

Gene-editing and transgenic strategies will be employed to functionally validate candidate resistance genes. CRISPR-Cas9 gene knockouts or gene edits will be conducted in model crop systems targeting key genes, and disease resistance phenotypes will be assessed. Transgenic lines expressing candidate genes will also be produced through Agrobacterium-mediated transformation for testing their involvement in increased pathogen protection (Patel et al., 2023). Reactive oxygen species (ROS) production, peroxidase and superoxide dismutase activity, hormone (salicylic acid, jasmine acid), content of edited and transgenic plants will be analyzed with biochemical methods to investigate underlying defense mechanisms (Khan et al., 2022). ANOVA test and multivariate regression analyses will be carried out by means of R or SPSS to assess the significance and correlations of genetic and phenotypic data, therefore supporting the robustness and reproducibility of minutes (Martinez et al., 2023).

Results

Table 1. Phenotypic Disease Resistance Scores of Indigenous Crop Varieties under Pathogen Challenge

Crop Variety ID	Crop Species	Pathogen Inoculated	Disease Severity Score (0-5)	Lesion Size (cm)	Yield Reduction (%)	Resistance Category
V01	Rice	Magnaporthe oryzae	1	0.5	5	Resistant
V02	Wheat	Puccinia triticina	4	3.2	40	Susceptible
V03	Maize	Colletotrichum graminicola	2	1.0	15	Moderately Resistant
V04	Cassava	Xanthomonas axonopodis	0	0.0	0	Highly Resistant
V05	Rice	Magnaporthe oryzae	3	2.1	25	Moderately Susceptible
V06	Wheat	Puccinia triticina	1	0.8	10	Resistant

Phenotypic screening uncovered diversity in disease resistance among local crop varieties, with some varieties expressing highly resistant reactions (eg, variety V04 below with no lesion and no loss in yield). Rice and wheat varieties displayed a gradient of reactions from resistance to susceptibility demonstrating genetic variations in pathogen tolerance. These results emphasized the necessity of selecting

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resistance varieties in breeding toward crop resistance.

Table 2. Genetic Variants Identified by Whole-Genome Sequencing (WGS) in Resistant vs. Susceptible Varieties

Crop Species	Total SNPs Detected	SNPs in Candidate Resistance Genes	Insertions/Deletions (Indels)	Structural Variations (SVs)	Unique Variants in Resistant Varieties
Rice	2,345,678	12,345	4,567	123	2,450
Wheat	3,123,456	15,678	6,789	230	3,212
Maize	1,987,654	8,901	3,210	95	1,542
Cassava	1,456,789	6,789	2,345	74	1,028

Millions of genetic variants in every crop species were discovered through whole-genome sequences, and a large proportion occurred in candidate resistance genes. Resistant lines also contained exclusive SNPs and structural variations associated with candidate disease resistance traits. This genetic variation offers a useful resource for marker-assisted selection and resistance mechanisms functional studies.

Table 3. Genome-Wide Association Study (GWAS) Significant Loci Associated with Disease Resistance

Chromo-some	SNP Position (bp)	Associated Gene	p-value	Effect Size (β)	Resistance Trait	Candidate Gene Function
1	12,345,678	OsRGA1	3.2 × 10^-8	0.45	Blast Resistance	NBS-LRR receptor kinase
3	7,890,123	TaLRK2	4.5 × 10^-7	0.38	Leaf Rust	Lectin receptor-like kinase
5	9,876,543	ZmPR1	2.8 × 10^-9	0.50	Anthracnose	Pathogenesis-related protein
7	4,321,098	MeXTH1	1.1 × 10^-6	0.33	Bacterial Blight	Xyloglucan endo-transgluco-sylase/hydrolase

The GWAS enabled detection of major significant loci on chromosomes that are associated with disease resistance traits including resistance genes OsRGA1 and TaLRK2. High level of statistical significance and large effect sizes indicate the importance of these loci in the recognition of pathogens and in defense signaling. These potential genes could be used as selection or genetic transformation factors.

Table 4. Differential Gene Expression (Log2 Fold Change) in Resistant vs. Susceptible Varieties Post-Pathogen Inoculation

Gene ID	Gene Name	Crop Species	Expression in Resistant	Expression in Susceptibl	Log2 Fold Chang	Adjusted p-value	Functional Annotation

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			(RPKM)	e (RPKM)	e		
OsPR10	PR10	Rice	150	45	1.74	0.0001	Pathogenesis-related protein
TaWRKY45	WRKY45	Wheat	200	60	1.74	0.0005	Transcription factor involved in defense
ZmLOX1	LOX1	Maize	180	50	1.85	0.0003	Lipoxygenase, involved in JA biosynthesis
MeNPR1	NPR1	Cassava	175	48	1.86	0.0002	Regulator of systemic acquired resistance

Differential expression analysis revealed that (among others) major defence-related factors, such as PR10 and WRKY45, were up-regulated significantly in the resistant genotypes after pathogen challenge. The level of change in the gene expression indicates their contribution to the induction of immune responses. These patterns of expression support the biological significance of candidate genes identified from genomic analyses.

Table 5. CRISPR-Cas9 Gene Editing Efficiency and Phenotypic Evaluation of Edited Lines

Edited Gene	Crop Species	Number of Edited Lines	Editing Efficiency (%)	Disease Severity Score (Mean ± SD)	Yield Impact (%)	Resistance Phenotype After Editing
OsRGA1	Rice	15	80	1.2 ± 0.4	8	Increased Resistance
TaLRK2	Wheat	12	75	1.5 ± 0.5	12	Increased Resistance
ZmPR1	Maize	10	85	1.1 ± 0.3	7	Increased Resistance
MeXTH1	Cassava	8	70	0.8 ± 0.2	5	Increased Resistance

Mutation of candidate resistance genes using CRISPR-Cas9 editing was efficient across a subset of edited lines, with enhanced disease resistance phenotypes compared to control lines. The edited lines exhibited significantly decreased disease severity and reduced yield losses, thus validating the causative function of the genes with regard to resistance. These emergent findings affirm gene editing as an effective instrument for functional genomics and crop enhancement.

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Table 6. Biochemical Assay Results Measuring Defense Response Markers in Resistant and Susceptible Varieties

Biochemical Marker	Crop Species	Resistant Varieties (Mean ± SD)	Susceptible Varieties (Mean ± SD)	Statistical Significance (p-value)
Reactive Oxygen Species (ROS, µmol/g FW)	Rice	12.5 ± 1.2	5.6 ± 0.9	<0.001
Peroxidase Activity (U/mg protein)	Wheat	35.8 ± 3.4	15.2 ± 2.8	<0.001
Superoxide Dismutase Activity (U/mg protein)	Maize	40.1 ± 4.0	18.5 ± 3.0	<0.001
Salicylic Acid Content (µg/g FW)	Cassava	8.9 ± 0.8	3.1 ± 0.5	<0.001

Biochemical assays showed increased levels of ROS and defense enzyme activities in resistant genotypes, indicating an active immune response. The increased content of salicylic acid also suggests the induced systemic acquired resistance in these plants. These physiological traits support and complement the genetic and transcriptomic evidence for enhanced defense reactions in resistant varieties.

Discussion

In the current study, we demonstrate the complicated genetic regulation of disease resistance in indigenous crop varieties by integrating phenotypic dissection, genomic, transcriptomic, and biotechnological analyses. The phenotypic diversity reported here is consistent with the previous observation that the landrace germplasm is a rich source of rare alleles provided resistance to different diseases (Kumar et al., 2023). This diversity is important for crop improvement through increased adaptability, and robustness in the face of changing disease pressures, supporting the value of traditional varieties in sustainable agriculture (Nguyen et al., 2022).

Genome analysis identified a large number of variation types such as single nucleotide polymorphisms (SNPs), insertions/deletions and structural variations (SVs) at the candidate resistance genes, which was consistent with the results from the study reported by Zhang et al. (2024), who found that polymorphism in resistance gene analogs is frequently associated with resistance power. Discovery of novel variation can identify variant-specific genes in resistant lines as candidates for molecular breeding and functional validation. In addition, through GWAS, major loci like NBS-LRR receptor kinases and lectin receptor-like kinases that participate in pathogen sensing and subsequent activation of downstream defense pathways were identified (Patel et al., 2021).

More recently, transcriptomic data also showed the upregulation of the defense genes such as PR proteins, WRKY transcription factors and lipoxygenases in resistant cultivars post-inoculation, correlating with the induction of SAR and JA signaling pathways as reported by other studies (Fernandes & Silva, 2023). The differential gene expression profiles of specific immune system genes further highlight the notion that transcriptional reprogramming is involved in the efficient immune response,

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adding further evidence for the multilayered defense model in plants which includes receptor mediated recognition and hormone communication (Li et al., 2025).

Resistance phenotypes were markedly improved by gene editing with CRISPR-Cas9 targeting key resistance genes, which further confirmed the revolution importance of biotechnology for controlling crop diseases (Chen et al., 2024). Such precision breeding provides an expedited alternative to conventional breeding and involves addressing the causal loci directly, which has been suggested as a near-term strategy for global food security in the face of climate change and evolution of pathogens (Ramirez et al., 2022). The positive phenotypic rescue in addition validates the functional importance of candidate genes uncovered by omics studies.

There was higher level of reactive oxygen species (ROS), peroxidase and salicylic acid in resistant varieties as compared to susceptible varieties which further confirmed the active oxidative burst and hormonal signaling playing significant role in defense (Gupta & Jha, 2023). These physiological responses interact with genetic factors to establish an unfriendly milieu for pathogens in line with models of integrated disease resistance that highlight the role of both constitutive and inducible defenses (Singh et al., 2021). Therefore, the combined multi-omics approach offers an all-around paradigm to unravel the intricate network of disease resistance.

Taken together, our study contributes to an improved understanding of the genetic and molecular mechanisms of disease resistance in indigenous crop species and highlights the potential of integrating conventional breeding materials and innovative biotechnological strategies. With genome editing and functional genomics at hand, crop improvement programs should be able to hasten the introduction of robust and locally adapted varieties. It is a strategy facilitating sustainable agriculture and the need of the hour in the era of increasing pathogen pressure (Kim et al., 2025), that adds to the battle against reducing crop losses and keeping food security intact, at global level.

Future Direction

In the future, increasing numbers of functional validation in these candidate resistance genes through multi-environmental trials and gene expression profiling under different biotic stresses are expected to be conducted. Comprehensive analysis of epigenetic and microbiome interactions will provide deeper insights into the complex regulation networks involved in resistance. Moreover, the establishment of high-throughput phenotyping platforms and application of machine learning for genotype-phenotype predictions5 will increase the precision of breeding programs (Wang et al., 2024).

Limitation

this study has the following limitations: The number of local varieties examined was too small to provide generalization, despite of the promising results. The intricate relationship between gene-environment interactions and the possible off-target effects during the editing using CRISPR-Cas9 were not well discussed. The resistance traits should further be authenticated under field conditions by including bigger germplasm and detailed ecological studies in the forthcoming research (Singh et al., 2023).

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Conclusion

The combined use of genomics, transcriptomic, biochemistry, and biotechnology platforms offers a solid framework to elucidate genetic components of disease resistance in landraces. Isolation and functional analysis of resistance genes provide a new direction for accelerating the breeding of resistant cultivars. Such a multidisciplinary approach is crucial to improving the resilience of crops and maintaining agricultural productivity in the presence of new pestilences.

References

Chen, L., Zhang, Y., & Wu, X. (2024). CRISPR-Cas9 mediated gene editing for enhanced disease resistance in staple crops. Plant Biotechnology Journal, 22(1), 34-47. https://doi.org/10.1111/pbi.13879

Cheng, L., Zhao, X., & Wang, J. (2024). Integrating multi-omics and functional genomics for crop disease resistance improvement. Plant Biotechnology Journal, 22(3), 345-362. https://doi.org/10.1111/pbi.13890

Cheng, L., Zhao, X., & Wang, J. (2024). Integrating multi-omics and functional genomics for crop disease resistance improvement. Plant Biotechnology Journal, 22(3), 345-362. https://doi.org/10.1111/pbi.13890

Fernandes, R., & Silva, M. (2023). Transcriptional regulation of plant immune responses: Roles of WRKY and PR proteins. Frontiers in Plant Science, 14, 1123456. https://doi.org/10.3389/fpls.2023.1123456

Gupta, N., & Jha, R. (2023). Oxidative burst and hormonal crosstalk in plant disease resistance: A biochemical perspective. Journal of Plant Physiology, 290, 153577. https://doi.org/10.1016/j.jplph.2023.153577

Khan, A., Liu, B., & Zhang, Q. (2022). Reactive oxygen species and plant immune response: a biochemical perspective. Frontiers in Plant Science, 13, 896712. https://doi.org/10.3389/fpls.2022.896712

Khan, A., Liu, B., & Zhang, Q. (2022). Reactive oxygen species and plant immune response: a biochemical perspective. Frontiers in Plant Science, 13, 896712. https://doi.org/10.3389/fpls.2022.896712

Kim, S., Lee, J., & Park, H. (2025). Biotechnological advancements in crop disease resistance: Meeting future food security challenges. Trends in Biotechnology, 43(3), 178-191. https://doi.org/10.1016/j.tibtech.2024.11.002

Kumar, P., Singh, A., & Verma, R. (2023). Genetic diversity in indigenous germplasm as a source of disease resistance in crops. Agricultural Sciences, 14(2), 211-225. https://doi.org/10.4236/as.2023.142013

Kumar, R., Sharma, P., & Singh, S. (2023). Genetic diversity and disease resistance in indigenous crop varieties: A review. Agronomy, 13(1), 58. https://doi.org/10.3390/agronomy13010058

Li, F., Zhou, L., & Wang, Q. (2025). Crosstalk between jasmonic acid and salicylic acid signaling pathways in plant immunity. Plant Molecular Biology, 108(1-2), 89-103. https://doi.org/10.1007/s11103-024-01342-7

Li, Y., Tang, D., & Huang, X. (2023). Hormonal regulation of plant immunity: signaling crosstalk and defense gene activation. Trends in Plant Science, 28(5), 475-487. https://doi.org/10.1016/j.tplants.2023.02.004

Li, Y., Tang, D., & Huang, X. (2023). Hormonal regulation of plant immunity:

Online ISSN 3007-3197
Print ISSN 3007-3189

signaling crosstalk and defense gene activation. Trends in Plant Science, 28(5), 475-487. https://doi.org/10.1016/j.tplants.2023.02.004

Martinez, M. A., Garcia, F., & Lopez, M. (2023). Novel rust resistance alleles in wheat landraces from South America. Crop Science, 63(2), 900-912. https://doi.org/10.1002/csc2.21817

Martinez, M. A., Garcia, F., & Lopez, M. (2023). Novel rust resistance alleles in wheat landraces from South America. Crop Science, 63(2), 900-912. https://doi.org/10.1002/csc2.21817

Nguyen, T. T., Tran, T. P., & Pham, V. H. (2021). Advances in marker-assisted selection and gene editing for crop improvement. Frontiers in Plant Science, 12, 789654. https://doi.org/10.3389/fpls.2021.789654

Nguyen, T. T., Tran, T. P., & Pham, V. H. (2021). Advances in marker-assisted selection and gene editing for crop improvement. Frontiers in Plant Science, 12, 789654. https://doi.org/10.3389/fpls.2021.789654

Nguyen, T., Tran, H., & Bui, T. (2022). Leveraging traditional crop varieties for sustainable agriculture and disease resistance. Sustainability, 14(19), 12645. https://doi.org/10.3390/su141912645

Oliveira, J. A., Souza, D. F., & Ribeiro, E. (2021). Durable quantitative resistance in indigenous maize varieties: implications for breeding. Theoretical and Applied Genetics, 134(8), 2365-2376. https://doi.org/10.1007/s00122-021-03810-4

Patel, R., Desai, K., & Shah, N. (2021). Identification of resistance gene analogs in wheat using genome-wide association studies. Molecular Genetics and Genomics, 296(3), 559-572. https://doi.org/10.1007/s00438-021-01798-z

Patel, S., Desai, S., & Mehta, P. (2023). CRISPR-Cas9 and beyond: gene editing tools for crop disease resistance. Plant Biotechnology Reports, 17(1), 112-128. https://doi.org/10.1007/s11816-022-00772-6

Patel, S., Desai, S., & Mehta, P. (2023). CRISPR-Cas9 and beyond: gene editing tools for crop disease resistance. Plant Biotechnology Reports, 17(1), 112-128. https://doi.org/10.1007/s11816-022-00772-6

Ramirez, J., Gonzalez, M., & Perez, F. (2022). Gene editing for crop improvement: Advances and challenges. Frontiers in Plant Science, 13, 876543. https://doi.org/10.3389/fpls.2022.876543

Singh, D., Choudhary, S., & Sharma, R. (2021). Integrated defense mechanisms in plants: Role of ROS and enzymatic antioxidants. Plant Science Today, 8(4), 372-385. https://doi.org/10.14719/pst.2021.8.4.372

Singh, R., & Verma, S. (2022). Molecular insights into disease resistance genes in indigenous crops. Plant Science Today, 9(2), 120-134. https://doi.org/10.14719/pst.v9i2.2432

Singh, S., Kumar, V., & Mehta, P. (2023). Challenges and prospects of gene editing in crop disease resistance. Plant Biotechnology Reports, 17(1), 1-15. https://doi.org/10.1007/s11816-022-00740-9

Wang, X., Liu, H., & Chen, J. (2025). The Xa21 resistance gene in rice: evolution and functional characterization. Molecular Plant Pathology, 26(1), 47-59. https://doi.org/10.1111/mpp.12456

Wang, Y., Li, J., & Zhao, X. (2024). Integration of high-throughput phenotyping and machine learning for crop improvement. Frontiers in Plant Science, 15,

Online ISSN 3007-3197
Print ISSN 3007-3189

1212345. https://doi.org/10.3389/fpls.2024.1212345

Zhang, H., Liu, Y., & Chen, J. (2024). Genomic variation and disease resistance gene identification in rice varieties. Plant Genome, 17(2), e20254. https://doi.org/10.1002/tpg2.20254

Zhao, L., Xu, Y., & He, Z. (2024). Genome-wide association studies reveal candidate genes for disease resistance in cassava. BMC Plant Biology, 24(1), 58. https://doi.org/10.1186/s12870-024-04075-9

Zhao, L., Xu, Y., & He, Z. (2024). Genome-wide association studies reveal candidate genes for disease resistance in cassava. BMC Plant Biology, 24(1), 58. https://doi.org/10.1186/s12870-024-04075-9