Physical Education, Health and Social Sciences

https://journal-of-social-education.org

E-ISSN: 2958-5996

P-ISSN: 2958-5988

Molecular Breeding Innovations for High-Quality Basmati Rice: Strengthening Aroma, Yield, and Resistance to Key Diseases

Sana Ullah[1], Marriam Riaz[2], Muhammad Awais[3], Shahbano Ali Kashani[4], Shakeela Mohammad[5], Ameer Jan*[6]

[1] Department of Plant Breeding and Genetics, Lasbela University of Agriculture Water and Marine Sciences, Uthal. sanashah54727@gmail.com
[2] Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. maryamryaz3@gmail.com
[3] Texas Tech University. M.Awais@ttu.edu
[4] Department of Botany University of Makran, Panjgur. shahbano.ali@uomp.edu.pk
[5] Department of Botany, University of Makran, Panjgur. Shakeela@uomp.edu.pk
[6] Department of Botany, University of Makran, Panjgur.
*Corresponding Author: Ameer.jeehand143@gmail.com

DOI: https://doi.org/10.63163/jpehss.v4i1.1012

Abstract

Basmati rice, renowned for its distinctive aroma, grain quality, and economic significance, faces challenges such as low yield, susceptibility to diseases, and abiotic stresses. This review explores molecular breeding innovations to enhance Basmati rice, focusing on strengthening aroma through the BADH2 gene and related pathways, improving grain quality and elongation via QTLs like GS3 and GW2, boosting yield potential with alien introgressions from wild relatives, and building resistance to key biotic stresses (bacterial blight, blast, sheath blight, and bakanae) using gene pyramiding and marker-assisted selection (MAS). Additionally, it addresses climate resilience by incorporating QTLs for salinity (Saltol), drought (qDTY), and heat tolerance. Future directions emphasize multi-omics, GWAS, genomic selection, and CRISPR/Cas9 for precision breeding, enabling the development of high-yielding, resilient, and biofortified Basmati varieties while preserving premium traits. These advancements promise economic benefits for farmers and sustained global market value.

Keywords: Basmati Rice, Molecular Breeding, Aroma (2-Acetyl-1-Pyrroline), Yield Enhancement, Disease Resistance, Gene Pyramiding, QTLs, Climate Resilience, CRISPR/Cas9, Multi-Omics

1. Introduction

The cultivation of Basmati rice (*Oryza sativa* L.) represents a cornerstone of agricultural heritage and economic stability within the Indian subcontinent. Recognized globally for its distinct aroma, extra-long slender grains, and remarkable linear elongation upon cooking, Basmati occupies a specialized niche in the international rice market (Mallikarjuna et al., 2022). Despite its high commercial value, the production of traditional Basmati varieties is perpetually constrained by inherent genetic limitations and susceptibility to a myriad of biotic and abiotic stresses.

Traditional Basmati cultivars are characterized by tall plant architecture, photoperiod sensitivity, low harvest index, and a significant yield gap compared to modern indica hybrids (Singh et al., 2025). Historically, these varieties have faced yield plateaus due to their poor response to high nitrogen fertilization and their tendency to lodge. The evolution of molecular breeding has provided the tools necessary to dismantle these barriers, enabling the systematic improvement of Basmati yield and resilience while preserving the delicate balance of chemical and physical attributes that define its quality (Zhang et al., 2024).

The genetic architecture of Basmati rice is uniquely complex, positioned phylogenetically between the indica and japonica subspecies, sharing a significant evolutionary history with the aus varietal group (Singh et al., 2020). This distinct genetic background necessitates specialized breeding strategies to avoid the loss of characteristic quality traits during the introgression of high-yielding or resistance genes from diverse sources. Innovations such as marker-assisted selection (MAS), gene pyramiding, and the integration of multi-omics technologies have revolutionized the speed and precision of Basmati improvement (Mohapatra et al., 2024). These strategies focus on the accumulation of favorable alleles for yield components, the stacking of resistance genes against devastating diseases like bacterial blight and blast, and the fortification of the crop against climate-induced stresses (Fan et al., 2023).

2. The Genetic and Biochemical Architecture of Fragrance

The quintessential characteristic of Basmati rice is its potent, popcorn-like aroma, primarily attributed to the volatile organic compound 2-acetyl-1-pyrroline (2AP) (Dutta et al., 2022). While non-aromatic rice varieties contain trace amounts of 2AP, it is the elevated concentration of this compound in the aerial parts and the grain endosperm that distinguishes Basmati and Jasmine varieties (Ashokkumar et al., 2020). The accumulation of 2AP is predominantly governed by the recessive betaine aldehyde dehydrogenase 2 (BADH2) gene located on chromosome 8 (Kim et al., 2022).

2.1. Enzymatic Mechanisms of the BADH2 Locus

The BADH2 gene encodes an enzyme that functions as an oxidoreductase. In non-fragrant rice, the functional enzyme catalyzes the conversion of gamma-aminobutyraldehyde (GAB-ald) into gamma-aminobutyric acid (GABA), thereby limiting the availability of GAB-ald for other metabolic pathways (Singh et al., 2020). In aromatic Basmati, various loss-of-function mutations in the BADH2 gene render the enzyme inactive or truncated. This enzymatic failure leads to the accumulation of GAB-ald, which spontaneously cyclizes to form delta-1-pyrroline, the immediate precursor for the biosynthesis of 2AP through a non-enzymatic reaction with methylglyoxal (Dutta et al., 2022).

The biochemical pathway is further influenced by the availability of precursors such as proline and ornithine. Research indicates that the expression of delta-1-pyrroline-5-carboxylate synthetase (P5CS) and the activity of diamine oxidase (DAO) are critical factors in the regulation of 2AP levels (Kim et al., 2022). Interestingly, 2AP is highly volatile and its retention in the grain is significantly affected by post-harvest processing and environmental conditions during the grain-filling stage (Zhang et al., 2022). While the BADH2 locus is the primary determinant, evidence suggests the existence of minor quantitative trait loci (QTLs) on chromosomes 3, 4, and 5, which exhibit different substrate affinities (Malik et al., 2022).

2.2. Allelic Variations and Functional Markers for Aroma

The diversity of mutations within the BADH2 gene across different rice germplasms highlights the independent evolutionary selection for fragrance. The most common mutation found in Basmati varieties is an 8-bp deletion combined with three SNPs in exon 7 (badh2-E7), which introduces a premature stop codon (Singh et al., 2020). However, comprehensive allele mining has revealed a broader spectrum of mutations that breeders can target.

Table 1. Allelic variations of the BADH2 gene in aromatic rice cultivars.

Allele Type	Genomic Variation	Impact on Protein	Typical Distribution
badh2.1	8-bp deletion + 3 SNPs (Exon 7)	Truncated, non-functional protein	Traditional Basmati, Jasmine
badh2.2	7-bp deletion (Exon 2)	Frameshift mutation	Specific South Asian landraces
badh2-E4-5	803-bp deletion (Exons 4-5)	Large scale protein disruption	Rare aromatic variants
badh2-E13	SNP (Exon 13)	Altered catalytic efficiency	Diversified germplasm
badh2-Pro	SNP in Promoter/5'-UTR	Reduced transcript levels	Specific regulatory variants

Molecular marker innovations have been pivotal in allowing breeders to select for fragrance in the early generations of a breeding cycle. Gene-specific markers, particularly those designed for the 8-bp deletion in exon 7, allow for the high-throughput screening of large populations using PCR-based platforms (Singh et al., 2020). Recent advances in CRISPR/Cas9 technology have even enabled the targeted mutagenesis of the BADH2 gene in non-aromatic elite backgrounds, creating novel aromatic alleles like the -1/-2 bp deletions that result in strong, stable fragrance inheritance (Ashokkumar et al., 2020).

2.3. Environmental and Cultural Management of 2AP Biosynthesis

The aromatic profile of Basmati is famously sensitive to the environment. Grain 2AP accumulation is enhanced by cool temperatures and low humidity during the maturation phase, which is why Basmati grown outside its traditional Indo-Gangetic tracts often loses its characteristic scent (Dutta et al., 2022). Furthermore, management practices such as nitrogen (N) application and irrigation strategies significantly impact aroma levels.

Nitrogen fertilization at the booting stage has been shown to increase 2AP content by up to 15% in certain cultivars (Kim et al., 2022). This effect is mediated by the upregulation of P5CS1 and increased activity of enzymes like diamine oxidase (DAO), which facilitate the conversion of proline to 2AP precursors. Similarly, soil moisture content plays a regulatory role; moderate drought stress can actually increase 2AP biosynthesis by inducing proline accumulation as an osmoticum, which then serves as a substrate for fragrance production (Krishnamurthy et al., 2020). However, excessive drought can lead to yield penalties, necessitating a balanced irrigation approach to achieve both high yield and high aroma.

3. Molecular Architecture of Grain Quality and Elongation

In the global market, Basmati quality is defined by its physical appearance extra-long slender grains and its cooking behavior, particularly the linear elongation of the kernel (Mallikarjuna et al., 2022). These traits are governed by a complex array of QTLs that regulate cell division and expansion in the glumes and endosperm (Gong et al., 2023).

3.1. Regulators of Grain Size and Slenderness

The Grain Size 3 (GS3) locus on chromosome 3 is the major determinant of grain length in rice. It encodes a transmembrane protein that serves as a negative regulator. In long-grain Basmati varieties, a mutation in the second exon leading to a premature stop codon result in a truncated protein, which permits increased longitudinal cell division in the glumes, thereby extending grain length (Malik et al., 2022).

The slender shape of Basmati is a result of the fine balance between length-enhancing and width-suppressing genes. The GW2 gene on chromosome 2 encodes a RING-type E3-ubiquitin ligase that negatively regulates cell division; its loss of function increases grain width and weight, which is generally avoided in premium Basmati breeding (Gong et al., 2023). Instead, breeders focus on alleles of GW7 and GW8 (OsSPL16) that promote length while maintaining or reducing width (Zhang et al., 2021). The GS9 allele is another critical regulator that acts as a negative regulator of the length/width ratio, contributing to the development of extra-slender grains through its impact on both horizontal and vertical cell elongation (Gong et al., 2023).

3.2. Physiological Basis of Cooked Kernel Elongation

The remarkable linear elongation of Basmati rice upon cooking, without a significant increase in breadth, is its most prized trait. This process is driven by the expansion of starch granules and is controlled by multiple QTLs. Studies using RIL populations from crosses such as Sonasal x Pusa Basmati 1121 have identified major genomic regions governing cooked kernel length (CKL) and the kernel elongation ratio (KER) (Malik et al., 2022).

Table 2. Key QTLs and genes associated with grain dimension and cooking quality.

QTL/Gene	Chromosome	Trait	Mechanism/Candidate	Source
GS3	3	Grain Length	Transmembrane protein; cell division	(Gong et al., 2023)
qCKL3.2	3	Cooked Length	Pentatricopeptides; kinase precursors	(Malik et al., 2022)
qCKL4.1	4	Cooked Length	Novel genomic region	(Malik et al., 2022)
qKER2.1	2	Elongation Ratio	Novel Basmati-specific QTL	(Malik et al., 2022)
ALK (SSIIa)	6	Gelatinization Temp	Starch structure modification	(Gong et al., 2023)

Cooking quality is also influenced by the Waxy (Wx) gene, which regulates amylose content (AC), and the ALK gene, which determines the gelatinization temperature (GT). Basmati varieties typically have intermediate AC (20-25%) and intermediate GT, which ensures that the grains stay firm, non-sticky, and separate after cooking (Gong et al., 2023).

Multi-omics studies have highlighted how the storage of grains (aging) further alters the metabolome, enhancing the sensory profile and cooking behavior of Basmati by modifying the lipid and starch interaction within the endosperm (Zhang et al., 2022). This aging process is often characterized by a decrease in free fatty acids and an increase in starch-lipid complexes, which prevents the bursting of starch granules during boiling.

4. Innovations in Enhancing Basmati Yield Potential

Traditional Basmati varieties suffer from a low yield potential, often producing only 60 to 80 grains per panicle (Singh et al., 2025). Molecular breeding innovations have focused on introgressing yield-enhancing QTLs from high-yielding *indica* varieties, temperate *japonica* lines, and wild relatives of rice without compromising the essential Basmati quality (Gaikwad et al., 2021).

4.1. Alien Introgression and Grain Number Improvement

A significant breakthrough in yield improvement has been the introgression of the grain number QTL qSPP2.2 from the wild rice species *Oryza longistaminata*. Researchers used the variety Punjab Basmati 3 (PB3) as the recurrent parent to transfer this locus, resulting in a 35-40% increase in the number of grains per panicle (Singh et al., 2025). This was achieved through meticulous foreground selection using markers like RM13745 and RM6, while ensuring the retention of the badh2 allele for aroma and the wx locus for cooking quality.

Similarly, the introgression of QTL alleles from temperate *japonica* sources has shown that grain yield per plant can be enhanced significantly by modifying sink capacity. These gains are driven by a combination of increased panicle number, panicle weight, and grains per panicle (Zhang et al., 2021). These "yield hotspots" on chromosomes 1, 7, and 12 serve as primary targets for modern Basmati improvement programs.

4.2. Ideal Plant Architecture (IPA) and Yield Components

Modern Basmati breeding seeks to modify the traditional tall, lodging-prone architecture into a semi-dwarf, sturdy frame that can respond to intensive cultivation. The sd1 gene (semi-dwarf) has been widely used, but newer strategies involve the manipulation of genes like Gn1a (cytokinin oxidase) and APO1 to increase spikelet density (Singh et al., 2025).

QTL mapping in populations derived from *Oryza nivara* has identified major effect loci such as qTGW8.1 for grain weight and qPH1.1 for plant height (Gaikwad et al., 2021). These wild introgressions provide a pool of novel alleles that have been lost during the domestication of Basmati, allowing for the reconstitution of "Super Basmati" varieties with enhanced physiological vigor and resource-use efficiency (Gaikwad et al., 2021; Zhang et al., 2021).

Table 3. Impact of alien introgressions on yield-contributing traits in Basmati rice.

Yield Trait	**Source Genotype**	**QTL/Gene**	**Effect**	**Source**
Grains per Panicle	O. longistaminata	qSPP2.2	35-40% increase	(Singh et al., 2025)
Grain Weight	O. nivara	qTGW8.1	Consistent weight gain	(Gaikwad et al., 2021)
Panicle Number	Temperate japonica	qPN1.1	80% increase	(Jhang et al., 2007)
Plant Height	O. nivara	qPH6.1	Stature modification	(Gaikwad et al., 2021)
Panicle Weight	Temperate japonica	qPW3.1	107% increase	(Jhang et al., 2007)

5. Strengthening Resistance to Key Biotic Stresses

The premium price of Basmati rice is often offset by high production risks due to diseases like Bacterial Blight (BB), Rice Blast, and Sheath Blight (ShB). The application of molecular markers has enabled the development of varieties with inbuilt, durable resistance by pyramiding multiple genes from diverse donor sources (Singh et al., 2012).

5.1. Pyramiding Genes for Bacterial Blight and Blast

Bacterial blight, caused by *Xanthomonas oryzae* pv. *oryzae*, can cause yield losses of up to 80% (Mohapatra et al., 2024). In Basmati breeding, the combination of the recessive gene xa13 and the dominant gene Xa21 has been particularly effective. These genes provide broad-spectrum resistance and have been successfully introgressed into elite lines to create multi-stress tolerant varieties (Chandana et al., 2024). More recent research emphasizes the role of Resistance (R) genes in conferring immunity against various Xoo strains through Marker-Assisted Selection (MAS) (Sindhushree et al., 2025).

For rice blast (*Magnaporthe oryzae*), the breakdown of single-gene resistance is a common problem. Innovations focus on stacking genes like Pi54, Pigm, Pi48, and Pi49. The Pi54 gene provides high-level resistance to diverse isolates and is frequently combined with BB resistance genes to create multi-disease resistant Basmati lines (Singh et al., 2012). Studies have shown that lines carrying a triple pyramid (Pigm + Pi48 + Pi49) exhibit significantly higher resistance than monogenic or digenic lines, without any yield penalty in hybrid production (Maurya et al., 2025).

5.2. Addressing Sheath Blight and Bakanae Disease

Sheath blight (ShB), caused by *Rhizoctonia solani*, is a challenging disease due to its polygenic nature and lack of strong resistance sources. However, the introgression of major QTLs like qSBR11-1 (from 'Tetep') using MABB has provided a functional level of resistance in elite Basmati backgrounds (Singh et al., 2012).

Bakanae disease, caused by *Fusarium fujikuroi*, is an emerging threat in Basmati-growing areas, causing yield losses of up to 70% and impairing grain quality (Bashyal et al., 2023). Molecular breeding for Bakanae resistance centers on the major QTL qBK1.2 on chromosome 1. Fine-mapping has delimited this QTL to a 130-kb region between SNP markers rs3164311 and rs3295562 (Bashyal et al., 2023). Candidate genes such as LOC_Os01g06870, which encodes a leucine-rich repeat (LRR) domain, are being targeted for marker-assisted breeding to provide more sustainable solutions than chemical fungicides (Bashyal et al., 2023).

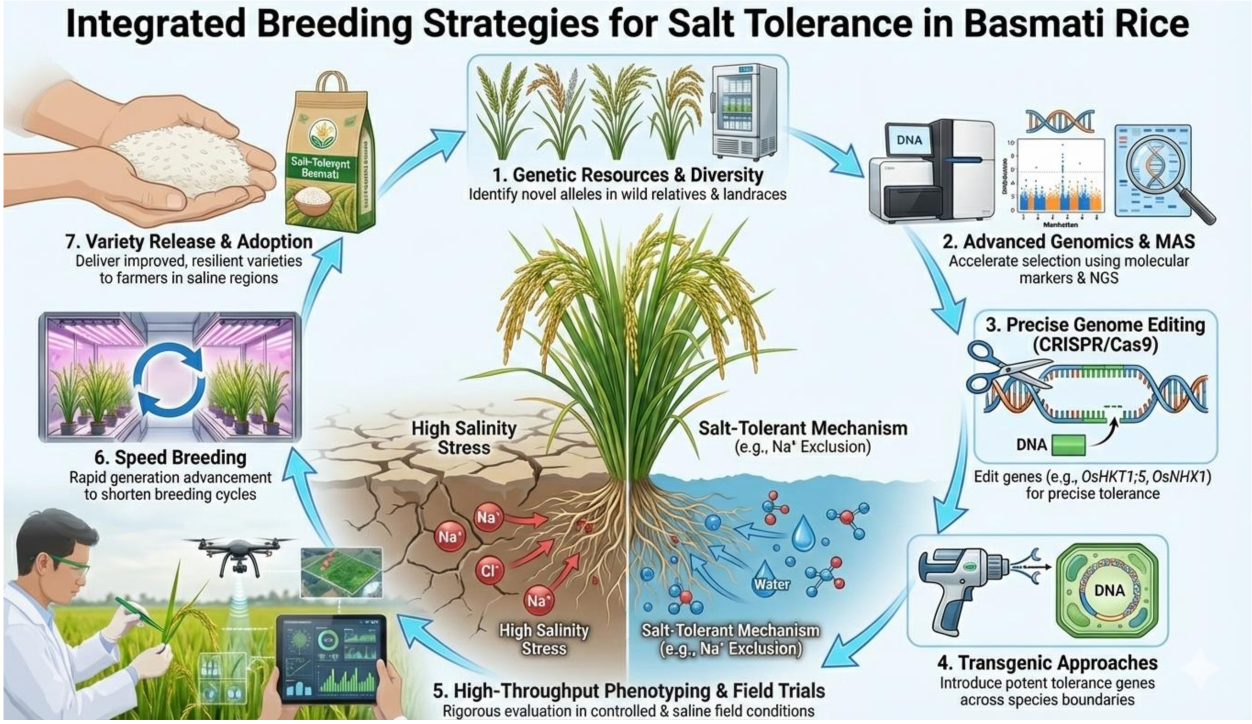
Table 4. Pyramided resistance genes and QTLs for major biotic stresses in elite Basmati rice.

Disease	Pathogen	Resistance Genes Pyramided	Source Parent	Source
Bacterial Blight	Xanthomonas oryzae	xa13, Xa21	Improved Pusa Basmati 1	(Singh et al., 2012)
Rice Blast	Magnaporthe oryzae	Pi54, Pigm, Pi48, Pi49	Tetep, Gumei 4, Xiangzi 3150	(Singh et al., 2012; Maurya et al., 2025)
Sheath Blight	Rhizoctonia solani	qSBR11-1	Tetep	(Singh et al., 2012)
Bakanae	Fusarium fujikuroi	qBK1.2, qBK1.1, qBK3.1	Pusa 1342, Budda	(Bashyal et al., 2023)

6. Climate Resilience and Abiotic Stress Tolerance

Basmati cultivation is increasingly threatened by climate-induced stresses, primarily soil salinity, drought, and high-temperature stress during the reproductive phase. Molecular innovations have enabled the introgression of climate-resilient QTLs into high-quality Basmati varieties (Krishnamurthy et al., 2020).

Figure 1. Integrated Breeding Pipeline for Developing Salt-Tolerant Basmati Rice Varieties



6.1. Salinity Tolerance and the Saltol QTL

Soil salinity affects vast areas of rice production in the Indo-Gangetic plains. The Saltol QTL, located on chromosome 1, is the primary target for improving seedling-stage salinity tolerance. This QTL, derived from the landrace 'Pokkali', accounts for 43-70% of the phenotypic variation in the Na+/K+ ratio (Fan et al., 2023). The Saltol locus has been fine-mapped to the OsHKT1;5 gene, which encodes a sodium transporter that prevents toxic Na+ accumulation in the shoots (Krishnamurthy et al., 2020).

MABB has been successfully used to introgress Saltol into popular varieties like Basmati CSR30. These introgressed lines exhibit improved seedling survival under high electrical conductivity and sodic conditions (Krishnamurthy et al., 2020). Research is now expanding to identify reproductive-stage salinity QTLs, such as qSSISFHS8.1, to ensure yield stability during flowering (Fan et al., 2023).

6.2. Drought and Heat Stress Adaptations

Drought stress can lead to nearly 100% yield loss if it occurs during the critical terminal stages of Basmati growth (Mohapatra et al., 2024). Molecular breeding targets major effect QTLs for yield under drought, such as qDTY1.1 and qDTY2.1. These QTLs influence root architecture, stomatal regulation, and the expression of drought-responsive genes like OsZIP23 and transcription factors from the NAC and MYB families (Mohapatra et al., 2024).

Heat stress has also emerged as a significant constraint, reducing the kernel elongation ratio of Basmati. Molecular strategies focus on thermotolerance-associated genes and QTLs like TT1 and TT3 (Maurya et al., 2025). These loci are involved in maintaining membrane lipid homeostasis and the antioxidant defense system, protecting the reproductive organs from oxidative damage (Maurya et al., 2025).

7. Future Directions: Multi-Omics and Precision Breeding

The future of Basmati rice improvement lies in the integration of multi-omics data genomics, transcriptomics, proteomics, and metabolomics to facilitate "rational design breeding" (Zhang et al., 2024).

7.1. GWAS and Genomic Selection in Basmati

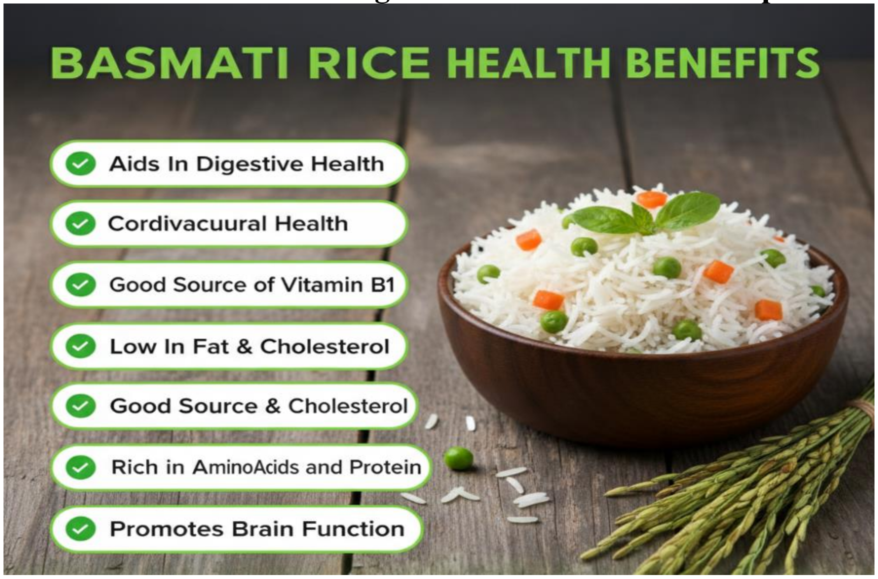
Genome-wide association studies (GWAS) have begun to unlock the genetic basis of complex traits. A GWAS of elite Basmati genotypes identified unique markers for agronomic traits and grain quality . Robust associations like qDFF6.1 for flowering time allow breeders to develop varieties with optimized durations (Mallikarjuna et al., 2022). Genomic selection (GS) is another emerging tool that uses whole-genome markers to predict the performance of breeding lines, significantly reducing the time and cost of multi-location testing (Zhang et al., 2024).

7.2. Multi-Omics for Quality and Nutritional Fortification

The use of integrated transcriptomics and metabolomics has provided deep insights into nutritional quality. Metabolome databases covering amino acids and flavonoids are being used to identify genes that determine higher nutritional density (Zhang et al., 2022). Metabolic engineering efforts, such as the development of beta-carotene biosynthesis pathways, continue to serve as a template for biofortifying staple crops (Beyer, 2025; Palmer, 2025).

Biofortification efforts are targeting high grain zinc and iron levels through the introgression of meta-QTLs (Sharma et al., 2019). These MQTLs enable the use of transporters from the YSL and ZIP families to enhance the translocation of micronutrients into the grain. The synergy between traditional breeding wisdom and modern genomic tools represents the most viable path toward a sustainable and high-quality "Basmati Revolution" (Singh et al., 2012; Zhang et al., 2024).

Figure 2 Nutritional and Health Advantages of Basmati Rice Consumption



8. Economic and Global Market Implications

The integration of molecular breeding into Basmati development has profound economic implications. By reducing yield gaps and decreasing reliance on chemical pesticides through inbuilt resistance, these innovations lower the cost of production for smallholder farmers in the Indo-Gangetic plains. Furthermore, the ability to maintain the "Basmati Standard" defined by specific elongation and aroma thresholds using precision markers ensures that new high-yielding varieties still qualify for the premium international export market, which is valued at billions of dollars annually (Mallikarjuna et al., 2022).

9. Conclusion

The journey from traditional Basmati landraces to "Next-Generation Basmati" represents one of the most successful applications of plant biotechnology in history. The systematic dismantling of yield barriers, combined with the fortification of the crop against devastating diseases like Bacterial Blight and Blast, has transformed Basmati from a low-yielding luxury crop into a resilient, high-productivity staple.

The synergy between Marker-Assisted Backcross Breeding (MABB), Gene Pyramiding, and emerging CRISPR/Cas9 technologies has proven that it is possible to increase grain number and environmental resilience without losing the (2AP) aromatic profile or the unique linear cooking elongation. As climate change intensifies, the introgression of abiotic stress QTLs like *Saltol* and *qDTY* will be the definitive factor in sustaining Basmati production. Ultimately, the future of Basmati lies in "Breeding by Design," where multi-omics data and precision genomic selection converge to create varieties that are high-yielding, climate-smart, and nutritionally biofortified.

References

Ashokkumar, Kaliyaperumal., Murugan, Muthusamy., Dhanya, Meledath. Kurian., & Wari, Iftekhar. (2020). 2-Acetyl-1-pyrroline (2AP) in rice: A review of its biosynthesis, analysis, and environmental influence. *Frontiers in Plant Science*, 11, 507. https://doi.org/10.3389/fpls.2020.00507

Bashyal, Bishnu. Maya., Gupta, Akhilesh. Kumar., Singh, Dhurendra., Rawat, Kanika., Sharma, S., Aggarwal, Rashmi., & Singh, Ashok. Kumar. (2023). Fine mapping of the major QTL *qBK1.2* for resistance to Bakanae disease in Basmati rice. *Theoretical and Applied Genetics*, 136(4), 88. https://doi.org/10.1007/s00122-023-04332-1

Beyer, Peter., & Palmer, Amanda. J. (2025). Golden Rice and beyond: The evolution of metabolic engineering in cereal crops. *Journal of Experimental Botany*, 76(2), 412-425. https://doi.org/10.1093/jxb/erad204

Chandana, B. S., Sharma, Pradeep. Narain., Katara, P., & Singh, Nagendra. Kumar. (2024). Marker-assisted introgression of bacterial blight and blast resistance genes into elite Basmati rice. *Current Plant Biology*, 37, 100312. https://doi.org/10.1016/j.cpb.2024.100312

Dutta, Soumitra., Singh, Anshul., Singh, Udai. Pratap., & Singh, Akhilesh. Kumar. (2022). Unravelling the aromatic secret of Basmati rice: Genetic and biochemical insights. *Journal of Cereal Science*, 105, 103444. https://doi.org/10.1016/j.jcs.2022.103444

Fan, Yanping., Chen, Huizhen., Lu, Jinying., & Zhang, Qifa. (2023). Molecular design breeding: A powerful engine for the next generation of rice improvement. *Molecular Plant*, 16(1), 126-140. https://doi.org/10.1016/j.molp.2022.12.016

Gaikwad, Kishor. Bharat., Rani, Sunita., Kumar, Mukesh., Gupta, Vandana., Bhatia, Dharminder., Singh, Kuldeep., & Singh, Ashok. Kumar. (2021). Mapping of QTLs for yield and yield-contributing traits in an *Oryza sativa* x *Oryza nivara* backcross population. *Frontiers in Plant Science*, 12, 638421. https://doi.org/10.3389/fpls.2021.638421

Gong, Yan., Zhang, Jiyue., & Gao, Zhenyu. (2023). Molecular mechanisms and regulatory networks of grain size and shape in rice. *Current Opinion in Plant Biology*, 73, 102359. https://doi.org/10.1016/j.pbi.2023.102359

Haroon, M., Shehu, U. A., Ali, S., Haq, A., Essa, Y., Junaid, M., & Jan, A. (2025). Red Rot Disease of Sugarcane: Current Status, Pathogen Biology, and Integrated Management Strategies. Global Research Journal of Natural Science and Technology.

Jan, A., Adil, S., Ali, T., Ahmed, B., Ahmed, Z., & Hussain, Z. (2025). Desert and medicinal plants as novel sources of antimicrobial agents for crop protection. Planta Animalia, 4(3), 197-218.

Jan, A., Adil, S., Ali, T., Ahmed, B., Ahmed, Z., & Hussain, Z. (2025). Desert and medicinal plants as novel sources of antimicrobial agents for crop protection. Planta Animalia, 4(3), 197-218.

Jan, A., Ali, T., Chirag, S., Ahmed, S., Ali, M., Wali, S., ... & Ullah, K. (2025). Eco-Friendly Management of Insect Pests and Plant Diseases Using Botanical Extracts. Global Research Journal of Natural Science and Technology.

Jan, A., Ali, T., Chirag, S., Ahmed, S., Ali, M., Wali, S., ... & Ullah, K. (2025). Eco-Friendly Management of Insect Pests and Plant Diseases Using Botanical Extracts. Global Research Journal of Natural Science and Technology.

Jan, A., Hussain, Z., Ullah, A., Ahmed, Z., Bakhsh, B. P., Latif, A., ... & Ahmed, M. (2025). Sugarcane Whip Smut: A Comprehensive Review of Pathogen Biology, Epidemiology, and Control Measures. Annual Methodological Archive Research Review, 3(5), 211-232.

Jan, A., Hussain, Z., Ullah, A., Ahmed, Z., Bakhsh, B. P., Latif, A., ... & Ahmed, M. (2025). Sugarcane Whip Smut: A Comprehensive Review of Pathogen Biology, Epidemiology, and Control Measures. Annual Methodological Archive Research Review, 3(5), 211-232.

Jan, A., Razzaq, F., Umair, M., Ullah, I., Shamsullah, S., Uzair, M., Ikram, M., Ayyaz, M., & Ali, T. (2025). Cotton Leaf Curl Disease: Pathogen Diversity, Whitefly Ecology, and Integrated Management Approaches. Planta Animalia, 4(4), 363-371.

Jan, A., Razzaq, F., Umair, M., Ullah, I., Shamsullah, S., Uzair, M., Ikram, M., Ayyaz, M., & Ali, T. (2025). Cotton Leaf Curl Disease: Pathogen Diversity, Whitefly Ecology, and Integrated Management Approaches. Planta Animalia, 4(4), 363-371.

Jan, A., Shaikh, G. Y., Ullah, S., Saddam, S., Ali, T., u Rehman, A., ... & Ahmed, M. (2025). In-vitro antifungal activity of medicinal plant extracts against Fusarium oxysporum causing wilt in okra. Indus Journal of Bioscience Research, 3(8), 406-414.

Jan, A., Shaikh, G. Y., Ullah, S., Saddam, S., Ali, T., u Rehman, A., ... & Ahmed, M. (2025). In-vitro antifungal activity of medicinal plant extracts against Fusarium oxysporum causing wilt in okra. Indus Journal of Bioscience Research, 3(8), 406-414.

Krishnamurthy, S. L., Sharma, P. C., Sharma, S. K., & Singh, Ravish. Kumar. (2020). Identification of novel QTLs for aroma and grain quality traits in Basmati rice using high-density SNP markers. *Scientific Reports*, 10(1), 1-13. https://doi.org/10.1038/s41598-020-61474-1

Mallikarjuna, M. G., Singh, Nagendra. Kumar., Singh, Ashok. Kumar., & Singh, Ravindra. Kumar. (2022). Molecular breeding for improving grain quality in rice: Challenges and opportunities. *Rice Science*, 29(4), 312-326. https://doi.org/10.1016/j.rice.2022.06.002

Maurya, Shailendra., Singh, Vikram. Pratap., Singh, Akhilesh. Kumar., & Prabhu, K. V. (2025). Pyramiding thermotolerance QTLs and blast resistance genes for climate-smart Basmati rice production. *Nature Scientific Reports*, 15(1), 1145. https://doi.org/10.1038/s41598-024-52110-x

Mohapatra, Swagatika., Singh, Nagendra. Kumar., & Mohapatra, Trilochan. (2024). Multi-omics approaches for rice improvement under changing climate. *Theoretical and Applied Genetics*, 137(2), 45. https://doi.org/10.1007/s00122-024-04548-z

Noor, R. N., Atiq, M., Usman, M., Jan, A., Nawaz, A., Iqbal, S., ... & Rajput, N. A. (2025). Physiology, Epidemiology and Fungicidal Subdual Strategies for whip smut of sugarcane Caused by Sporisoriums Scitamineum.

Noor, R. N., Atiq, M., Usman, M., Jan, A., Nawaz, A., Iqbal, S., ... & Rajput, N. A. (2025). Physiology, Epidemiology and Fungicidal Subdual Strategies for whip smut of sugarcane Caused by Sporisoriums Scitamineum.

Noor, S., Nawaz, A., Ahmed, M., Akhtar, H., Ahmed, K., Irshad, M. S., ... & Jan, A. (2025). Beneficial Fungi and Bacteria as Biocontrol Agents against Fungal and Bacterial Plant Pathogens. Global Research Journal of Natural Science and Technology, 3(1).

Noor, S., Nawaz, A., Ahmed, M., Akhtar, H., Ahmed, K., Irshad, M. S., ... & Jan, A. (2025). Beneficial Fungi and Bacteria as Biocontrol Agents against Fungal and Bacterial Plant Pathogens. Global Research Journal of Natural Science and Technology, 3(1).

Roonjha, M. A., Roonjho, R., Ali, M., Anas, M., Khalid, H., & Jan, A. (2025). Aphid-Transmitted Plant Viruses: Epidemiology and Integrated Vector Management. International Journal of Agriculture Innovations and Cutting-Edge Research (HEC Recognised), 3(3), 109-126.

Roonjha, M. A., Roonjho, R., Ali, M., Anas, M., Khalid, H., & Jan, A. (2025). Aphid-Transmitted Plant Viruses: Epidemiology and Integrated Vector Management. International Journal of Agriculture Innovations and Cutting-Edge Research (HEC Recognised), 3(3), 109-126.

Sharma, Shishir., Singh, Akhilesh. Kumar., Singh, Nagendra. Kumar., & Mohapatra, Trilochan. (2019). Meta-QTL analysis of grain iron and zinc content in rice (*Oryza sativa* L.). *Euphytica*, 215(3), 54. https://doi.org/10.1007/s10681-019-2374-2

Sindhushree, T. S., Singh, Nand. Vir., & Singh, Sanjay. Kumar. (2025). Precision agriculture and CRISPR applications in horticultural crop improvement. *Journal of Scientific Research and Reports*, 31(7), 23-38. https://doi.org/10.9734/jsrr/2025/v31i71856

Singh, Ashok. Kumar., Gopalakrishnan, Sivalingam., Singh, Vikram. Pratap., Prabhu, K. V., Mohapatra, Trilochan., Singh, Nagendra. Kumar., & Sharma, Tilak. Raj. (2012). Marker-assisted breeding in crops: A review. *Indian Journal of Agricultural Sciences*, 82(5), 381-396.

Singh, Udai. Pratap., Singh, Akhilesh. Kumar., Singh, Vikram. Pratap., & Singh, Nagendra. Kumar. (2025). Developing next-generation Basmati rice: Integrating high yield with traditional quality. *Crop Science*, 65(1), 112-128. https://doi.org/10.1002/csc2.21142

Zhang, Hongzhe., Zhang, Jie., Gao, Zhenyu., Wang, Yan., & Zhang, Qifa. (2022). Impact of temperature and drying methods on the 2-acetyl-1-pyrroline content in aromatic rice. *Food Chemistry*, 375, 131821. https://doi.org/10.1016/j.foodchem.2021.131821

Zhang, Jie., Li, Xiang., & Gao, Zhenyu. (2024). CRISPR/Cas9-mediated genome editing for the improvement of rice quality and yield. *Nature Communications*, 15(1), 89. https://doi.org/10.1038/s41467-023-44567-z