www.journalworlds.com
AGRI JOURNAL WORLD
VOL. 5 ISSUE 2 APRIL-JUNE, 2025

BREEDING STRATEGIES OF BASMATI RICE (*Oryza Sativa* L.) FOR MULTIPLE DISEASE RESISTANCE

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ABSTRACT

Dwarfism (sd-1) from Pusa-1121 was combined with Khalsa-7's scent and disease resistance into a Type-3 basmati background. Plants devoid of common rice illnesses were chosen by screening the dwarf segregants of the cross (Khalsa 7 × Pusa 1121) with Type-3 under artificially produced epiphytotic conditions. All India Coordinated Research Project (AICRP) trials were utilized to demonstrate yield and physical requirements of quality traits that are acceptable in world trade. Although breeders have been using biotechnology tools to increase their breeding capacity, many programs are still having trouble integrating them and balancing the distribution of resources between traditional and new technologies.

KEYWORDS: Backcrossing, Basmati rice, BLB, Marker-assisted breeding, Resistance

INTRODUCTION

The entire traditional basmati growing area under India's Geographical Indication (GI) has been designated as an Agri-Export Zone for Basmati rice by the Indian government in order to promote production of the commodity and improve the socioeconomic conditions of the local farmers due to the high demand for basmati rice on the domestic and international markets at premium prices. Traditional basmati rice cultivars are resilient, photosensitive, and vulnerable to all local rice diseases (Singh *et al.*, 2000). Due to their thin stems and height, these types also fall under high input agriculture, which lowers yield and degrades quality. Thus, extra attention must be paid to the development of dwarf, short-duration, photo-insensitive, and disease-resistant kinds of basmati rice. In light of this, the review involves various breeding strategies for multiple diseases resistance.

MAJOR DISEASES AFFECTED BASMATI RICE

Various diseases affected Basmati rice include:

1. Bacterial leaf blight
2. Rice blast
3. Rice tungro disease

4. Sheath blight

BREEDING APPROACHES FOR MULTIPLE DISEASE RESISTANCE

1. MOLECULAR MARKER-ASSISTED BREEDING

From one varietal background to another, a large number of genes for resistance to disease and insects are frequently transferred. Transferring most genes takes time and requires dominant or recessive behaviour. Occasionally, the screening processes are costly, time-consuming, and space-intensive. Transferring these genes from one varietal background to another can save time and money if they can be identified by close association with molecular markers. Rice blast, which is caused by the fungus *Pyricularia oryzae*, and bacterial blight, which is caused by *Xanthomonas oryzae pv. oryzae* are two of the most dangerous and pervasive diseases in rice cultivation. International Rice Research Institute (IRRI) is working together to use molecular marker technologies to develop long-term resistance to certain illnesses.

The backcrossing of a gene or QTL from exotic cultivars or wild relatives into an elite cultivar or breeding line was accelerated using molecular markers. Backcrossing to elite cultivars of rice has revealed the presence of favoured genes or alleles from wild species (Moncada, 2001). Likewise, this method could detect genes from foreign cultivars that provide a better phenotype, even if the parent may not have a worse phenotype for this characteristic. This strategy seems to be promising in the rice industry as some cultivars are widely cultivated due to their adaptability, consistent performance, and good grain quality.

2. GENETIC ENGINEERING

The simplicity, ease of use, and versatility of the CRISPR-Cas9 system have made it the preferred approach for genome editing. By using DNA's complementary base pairing mechanism, this technique directs site-specific Cas9 endonuclease to the intended location. Following template screening, the guide RNA (gRNA) identifies the precise complementary target sequence and instructs Cas9 to create a double strand break (DSB) at the target location. It is necessary for Cas9 to introduce a double strand break (DSB) 3-bp upstream of the protospacer-associated motif (PAM), which is a triplet of nucleotides (NGG) at the 3′ end of the target site. According to (Barrangou *et al.*, 2007), these DSBs are fixed by either template-guided precise homology directed repair (HDR) or imprecise non-homologous end joining (NHEJ). As of right now, this method has shown effectiveness in enhancing agronomic traits and engineering resistance against a variety of diseases.

3. POLYMERASE CHAIN REACTION

Blast resistance was found in the genotype Vallabh Basmati-21 using PCR products employing random amplified polymorphic DNA (RAPD) and sequence characterized amplified regions (SCAR) markers.

The genealogy with historic types of basmati rice was evaluated for the Basmati type, disease-resistant, and promising selections.

4. CONVENTIONAL BREEDING

Disease-resistant Basmati rice cultivars are created using traditional breeding techniques such as recurrent selection, backcrossing, and pedigree selection. By means of repeated crosses and selections, these techniques aim to introduce resistance genes from donor plants into Basmati rice. The use of marker-assisted selection (MAS) to lessen linkage drag and promote the transmission of resistance genes is also growing.

A. Pedigree method

Pedigree choice is the method most frequently used to breed for disease resistance. Using this method, the individual plant life from the F_2 generation is selected for resistance by crossing parents (one with the resistance trait and some with specific agronomic qualities). These options are permitted to provide seed for the next generation. With each new technology, the selection process is repeated, and until homozygosity is achieved, a higher proportion of resistant plant life is obtained. The majority population choice technique bulks early separating generations typically F_2 to F_5 collectively without giving them a choice. In subsequent generations, when the majority of plant life is homozygous, male or female plants are selected for resistance, and their offspring are assessed for resistance using the pedigree technique.

B. Backcrossing

Another popular method for interrogating or replacing the desired gene from donor parent to the recipient parent in rice breeding is backcrossing. The primary purpose of the backcrossing procedure is to reduce the amount of donor genetic material in the offspring. Recurrent selection is another well-established breeding technique for disease management in rice, in addition to backcross breeding (Fujimaki, 1979). In addition to offering the chance to create a wide variety of genetic diversity in breeding lines, it permits shorter breeding cycles and more focused monitoring of genetic improvements. Recurrent selection is used to create many blast-resistant cultivars, including the upland variety CG-91.

5. TRANSGENICS

A highly effective strategy for increasing the gene pool of commercial cultivars is the genetic transformation approach, which can transfer particular genes from chosen sources to cultivated species. For *R* genes in rice, the transgenic method has proven to be highly effective in avoiding time-consuming and laborious backcrossing. Given its tiny genome, enriched genetic map, and accessibility to the complete genome sequence, rice is arguably the monocot most suitable for genetic transformation (Kathuria *et al.*, 2007).

In plants, antimicrobial peptide genes have also been demonstrated to act as resistance genes. In multiple studies, transgenic plants that carry genes for antimicrobial traits have a markedly increased resistance to bacterial and fungal infections. The main problems with transgenic techniques for disease resistance breeding include transgene silencing, instability, and rearrangements, which are frequently seen in transgenic plants; as a result, thorough evaluations are required because these are deemed to be extremely undesirable. The ultimate goal of transgenic techniques is to locate and modify plant genes that increase disease resistance without materially compromising production.

ACHIEVEMENTS

1. Using genes like *Pi1*, *Pi2*, and *Pi54*, rice lines resistant to blast disease are developed.
2. Multiple disease resistance genes in peak Basmati cultivars are efficiently pyramided.
3. Basmati varieties with better yield stability under disease pressure.
4. Increased potential for exports and farmer income as a result of consistent quality and yield.
5. Utilizing genomic selection and QTL mapping, disease resistance characteristics are found and monitored.
6. India's leadership in Basmati rice breeding is recognized through global collaborations (e.g., IRRI).
7. Decreased reliance on fungicides and insecticides as a result of inherent resistance

FUTURE PROSPECTS

1. Pan-genomics and transcriptomics are used to find new genes.
2. Combining phenomics with artificial intelligence for high-throughput screening.
3. Breeding techniques that adapt to the climate.
4. To guarantee adoption, farmers participate in breeding.
5. Machine learning models are used to forecast disease outbreaks and direct breeding decisions.
6. To guarantee local acceptability and adaptability, farmers should be involved in variety selection.
7. Persistent application of various resistance genes (e.g., *Xa*, *Pi*, *qSBR*) in conjunction using marker-assisted selection (MAS).

CONCLUSION

Through the integration of conventional breeding, molecular tools, and biotechnological approaches, breeding tactics for producing Basmati rice (*Oryza sativa* L.) with various disease resistance have evolved dramatically over the past few decades. While maintaining the distinctive quality characteristics of

Basmati rice, researchers have made significant strides in improving resistance against important rice diseases like bacterial blight, blast, and sheath blight through the use of marker-assisted selection, gene pyramiding, and genomic selection. The formation of novel pathogen races and the intricate inheritance of resistance traits are two obstacles that still exist in spite of these advancements. Prospects for the future include using state-of-the-art technologies such as pan-genomics, high-throughput phenotyping, and CRISPR/Cas9 to create long-lasting, broad-spectrum disease-resistant Basmati cultivars. Maintaining sustainable rice production and food security will need ongoing co-operation between breeders, pathologists, and biotechnologists.

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How to cite:

Sadhu S. and Nandi R. (2025). Breeding Strategies of Basmati Rice (*Oryza sativa* L.) for Multiple Disease Resistance. Leaves and Dew Publication, New Delhi 110059. *Agri Journal World* 5 (2): 55-59.

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