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COMPREHENSIVE EVALUATION OF RICE (*Oryza sativa* L.) GERMPLASM FOR YIELD AND YIELD-ATTRIBUTING TRAITS: A REVIEW

Suraj Kumar[1]*, Neha Yadav[2], Addya Singh[3], Ritesh Kumar[4], R. Ranjith[5], Pragya Parmita[6], Mani Prabhat[7], Abhishek Kumar[8] and Alok Kumar[1]

[1]Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur-848 125, Bihar, India.
[2]Department of Genetics & Plant Breeding, CSA University of Agriculture and Technology, Kanpur-208 002, U.P., India.
[3]Department of Genetics & Plant Breeding, SVPUA & T, Meerut-250 110, U.P., India.
[4]Department of Genetics & Plant Breeding, Choudhary Sarvan Kumar Himachal Pradesh Krishi Vishwavidalaya, Palampur - 176 062, Himachal Pradesh, India.
[5]Centre for Agriculture and Rural Development Studies (CARDS), TNAU, Coimbatore - 641 003, Tamilnadu, India.
[6]Department of Genetics & Plant Breeding, Udai Pratap College, Varanasi (U.P.), India.
[7]Department of Genetics & Plant Breeding, Sam Higginbottam University of Agriculture Technology and Sciences, Naini-211 007, U.P., India.
[8]Department of Agronomy, Hemvati Nandan Bahuguna Garhwal University, Garhwal, Uttarakhand, India
*Corresponding author E-mail : surajkumar854199@gmail.com

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ABSTRACT

Rice (*Oryza sativa* L.) is widely recognized as one of the most important cereal crops in the world and serves as the primary food source for more than half of the global population. Sustaining and improving rice production is therefore essential for maintaining global food security, particularly in developing nations where rice provides a major share of daily caloric intake. Increasing grain yield continues to be a major goal of rice improvement programs. However, yield is a complex quantitative trait that is controlled by multiple genetic components and is strongly influenced by environmental conditions and their interactions.

The systemic assessment of rice germplasm plays a crucial role in identifying promising genotypes and useful genetic variations associated with higher productivity, adaptability and ability. Germplasm collections contain extensive genetic diversity which can serve as an important resource for crop improvement and breeding programs. By carefully evaluating these genetic resources. breeders can identify desirable traits that contribute to yield enhancement and stress tolerance.

This review compiles and discusses current knowledge regarding the evaluation of rice germplasm with respect to grain yield and its related traits. It emphasizes the importance of phenotypic characterization as well as the assessment of genetic variability, heritability, and genetic advance in determining the effectiveness of selection in breeding programs. In addition, statistical approaches such as correlation and path coefficient analysis are highlighted for their usefulness in identifying traits that have a direct or indirect influence on grain yield.

The review also considers the role of genotype × environment interactions in crop performance and underscores the need for multi-environment testing to identify stable and widely adapted genotypes. Furthermore, recent developments in molecular breeding techniques, including marker-assisted selection, quantitative trait locus (QTL) analysis, genome-wide association studies (GWAS) and genomic selection have significantly improved the efficiency of germplasm evaluation and crop improvement strategies. Integrating traditional phenotypic selection with modern genomic tools provides a powerful framework for accelerating progress in rice breeding. Effective utilization of diverse germplasm resources, combined with advanced breeding technologies, will be essential to meet the growing demand for rice production in the face of population growth and changing climatic conditions.

Key words : Rice germplasm, Genetic variability, Yield components, Heritability, Molecular markers, Genomic selection.

Introduction

Rice (*Oryza sativa* L.) is among the most important staple crops worldwide and provides a primary source of calories for more than half of the global population. The crop belongs to the genus *Oryza* within the family Poaceae and is characterized by considerable genetic diversity. The genus includes two cultivated species, *Oryza sativa* and *O. glaberrima*, as well as numerous wild relatives distributed across diverse ecological habitats (Khare *et al*., 2014). Rice cultivation occupies a significant portion of the world's agricultural land and is particularly dominant in Asia, where it contributes substantially to food security, rural employment and economic stability (Anonymous, 2017).

Global demand for rice is increasing due to rapid population growth, urbanization, and changing dietary preferences. According to projections by the Food and Agriculture Organization (FAO), the global population is expected to reach nearly nine billion by the middle of the twenty-first century, necessitating substantial increases in food production (Alexandratos and Bruinsma, 2012). In this context, improving rice productivity and stability across diverse agro-ecological conditions has become a major priority for plant breeders and agricultural scientists.

Grain yield in rice is a complex quantitative trait influenced by numerous yield-contributing components such as days to flowering, plant height, number of effective tillers per plant, panicle length, grains per panicle, spikelet fertility and thousand-grain weight (Rashmi *et al*., 2017; Tiwari *et al*., 2019). These traits are controlled by multiple genes and are strongly affected by environmental factors such as temperature, soil fertility, water availability, and crop management practices. Therefore, understanding the genetic basis and interrelationships among yield components is essential for designing effective breeding programs aimed at yield improvement (Girma *et al*., 2018).

One of the fundamental requirements for successful crop improvement is the availability of sufficient genetic variability within the breeding material. Germplasm collections maintained in gene banks around the world represent valuable reservoirs of genetic diversity that can be utilized for crop improvement. The systematic evaluation of germplasm for yield and yield-related traits provides opportunities to identify superior genotypes and novel genetic variations that may not be present in modern cultivars.

Genetic variability within germplasm populations can be assessed using statistical parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance (Burton and DeVane, 1953; Johnson *et al*., 1955). These parameters help breeders understand the relative contribution of genetic and environmental factors to trait expression and predict the potential response to selection. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and suggests that selection based on phenotypic performance will be effective (Krishna *et al*., 2010; Pratap *et al*., 2018).

In addition to variability analysis, studying the relationships among yield components is crucial for identifying key traits that influence grain yield. Correlation analysis provides information on the strength and direction of associations between traits (Mustafa and Elsheikh, 2007). However, correlation coefficients do not differentiate between direct and indirect effects. Path coefficient analysis, introduced by Dewey and Lu (1959), addresses this limitation by partitioning correlation coefficients into direct and indirect components, thereby revealing the true contribution of individual traits to grain yield.

Despite significant advancements in rice breeding, the genetic base of many modern cultivars has become increasingly narrow due to the repeated use of a limited number of elite parents (Khare *et al*., 2014). This genetic erosion increases vulnerability to pests, diseases, and environmental stresses. Therefore, the exploration and utilization of diverse germplasm resources are essential for broadening the genetic base and ensuring long-term sustainability of rice production. This review aims to provide a comprehensive overview of the evaluation of rice germplasm for yield and yield-attributing traits, emphasizing the importance of genetic variability, correlation analysis, molecular approaches, and integrated breeding strategies.

Rice germplasm and Genetic diversity

Rice germplasm refers to the entire collection of genetic resources available for the crop, including landraces, traditional varieties, improved cultivars, breeding lines, and wild relatives. These resources constitute a rich reservoir of genetic variation that can be exploited for crop improvement. Landraces are traditional farmer-selected varieties that have evolved over generations through natural and artificial selection. They often possess high levels of genetic diversity and adaptability to local environmental conditions. Many landraces exhibit desirable traits such as drought tolerance, disease resistance and unique grain quality characteristics (Govindaraj *et al*., 2015).

Wild relatives of rice are another important source of genetic variation. Species such as *Oryza rufipogon* and *Oryza nivara* harbor genes for stress tolerance, yield stability and resistance to pests and diseases. Although, the use of wild species in breeding programs can be challenging due to issues such as linkage drag, modern molecular breeding techniques have facilitated their utilization. Assessment of genetic diversity in rice germplasm has traditionally been based on morphological and agronomic traits. However, morphological traits are often influenced by environmental factors and may not accurately reflect genetic relationships. Therefore, molecular markers such as simple sequence repeats (SSRs), amplified fragment length polymorphisms (AFLPs), and single nucleotide polymorphisms (SNPs) have been widely used to assess genetic diversity (Chakraborty *et al*., 2010). Genetic diversity analysis helps identify genetically distant parents for hybridization, which can enhance heterosis and generate new recombination patterns in breeding populations.

Phenotypic evaluation of yield and Yield-Attributing traits

Morphological and Agronomic characterization

Phenotypic characterization is the first step in evaluating rice germplasm. It involves the measurement of various morphological and agronomic traits that influence crop growth and productivity. Important agronomic and yield-related traits are commonly evaluated to assess crop growth, development, and productivity. These traits include days to 50% flowering, which indicates the time taken for half of the plants in a population to begin flowering and days to maturity, representing the duration required for the crop to complete its life cycle. Plant height reflects the vegetative growth and vigor of the plant, while the number of productive tillers per plant shows how many tillers successfully produce panicles. Panicle length and the number of grains per panicle are important indicators of the reproductive capacity of the plant. Spikelet fertility measures the proportion of filled spikelets, indicating the efficiency of pollination and grain development. Thousand-grain weight represents grain size and density, contributing to grain quality and yield. Finally, grain yield per plant serves as the overall indicator of productivity, integrating the combined effects of these yield-related traits.

Among these traits, the number of productive tillers and grains per panicle are considered major determinants of grain yield. Studies have shown that genotypes with higher numbers of productive tillers and filled grains per panicle tend to exhibit superior yield performance. Phenotypic evaluation also helps identify desirable plant architecture, which is important for improving yield potential and lodging resistance (Upholf *et al*., 2015).

Genetic Variability parameters

Genetic variability analysis is essential for understanding the extent of variation present in germplasm populations, for instances, phenotypic and Genotypic Coefficient of Variation, heritability and genetic advance. The phenotypic coefficient of variation (PCV) measures the total variation observed in a trait, including both genetic and environmental components. The genotypic coefficient of variation (GCV) estimates the proportion of variation attributable to genetic factors. In most cases, PCV values are higher than GCV values due to environmental influence on trait expression. Heritability measures the proportion of total phenotypic variance that is due to genetic factors. High heritability indicates that the observed variation is largely controlled by genetic factors and can be effectively transmitted to subsequent generations. Genetic advance refers to the expected improvement in a trait following selection. When heritability and genetic advance are both high, it suggests that additive gene action plays a significant role in controlling the trait. Several studies have reported high heritability and genetic advance for traits such as grain yield, panicle length and thousand-grain weight in rice populations (Singh *et al*., 2025).

Correlation analysis of Yield components

Correlation analysis is a statistical technique used to measure the strength and direction of the relationship between two traits. In rice breeding programs, correlation studies are widely used to identify traits that are positively associated with grain yield. Numerous studies have reported significant positive correlations between grain yield and traits such as productive tillers per plant, grains per panicle, and thousand-grain weight (Rashmi *et al*., 2017; Tiwari *et al*., 2019). These relationships suggest that improvement in these component traits may indirectly lead to increased grain yield. However, correlation does not provide information about cause-and-effect relationships. Therefore, further analysis using path coefficient analysis is required to determine the direct contribution of each trait to yield.

Path Coefficient analysis

Developed from Wright's foundational path modeling, this technique assigns standardized coefficients via structural equations, where direct effects appear on diagonal paths and residuals capture unexplained variance. In rice contexts, researchers evaluate matrices from field

data on diverse lines, computing path values as $P_{ij} = r_{ij} / R_{yy}$ (where, r_{ij} is trait-yield correlation and R_{yy} is yield's multiple correlation). High positive direct effects (>0.5), as seen in panicle exertion rate or spikelet fertility, signal prime selection foci, while negative directs like plant height demand caution despite yield correlations. Researchers apply this method to dissect how factors like the number of productive tillers per plant, grains filling each panicle, and kernel test weight influence final harvests. For instance, evaluations of advanced rice lines show these elements exerting the strongest direct positive impacts, making them prime targets for improving output in breeding lines. Path studies across diverse sets, such as 48 landraces or 60 elite varieties from Bangladesh, confirm that focusing on biological yield components and panicle traits yields reliable gains without chasing misleading indirect links (Nayak *et al*., 2026; Haradari and Hittalmani, 2017). These traits can therefore be used as selection criteria in breeding programs. For instance, Evaluations of 110 elite rice genotypes under irrigated setups highlighted biological yield (path = 1.245) and harvest index (0.812) as dominant directs, dwarfing secondary panicle traits amid high heritability ($h^2 = 0.89$). Parallel work on rainfed lines confirmed grains per panicle (0.673 direct) outperforming tiller counts when indirects via biomass were factored out. Such patterns hold across South Asian trials, where test weight consistently registers 0.45-0.78 directs, validating its use in multi-cut varieties for sustained harvests (Raushan Lal *et al*., 2025).

Genotype × Environment interaction

The performance of rice genotypes often varies across environments due to differences in climate, soil fertility, and crop management practices. This phenomenon is known as genotype × environment interaction. Multi-environment trials are conducted to evaluate the stability and adaptability of genotypes across different locations and seasons. Statistical methods such as AMMI (Additive Main Effects and Multiplicative Interaction) analysis are commonly used to analyze genotype × environment interactions (Gauch, 2013). Genotypes that maintain high yield across multiple environments are considered stable and widely adapted.

Molecular approaches in Germplasm evaluation

Molecular Marker analysis

Molecular markers have revolutionized plant breeding by providing precise tools for genetic analysis. Markers such as SSRs and SNPs allow researchers to study genetic diversity, identify quantitative trait loci and track desirable alleles in breeding populations (Neeraja *et al*., 2018). SSR markers, with their codominant, hypervariable microsatellites (di-, tri-nucleotide repeats) and SNPs (abundant biallelic variants) deliver polymorphism-rich fingerprints for diversity dissection, QTL tagging, and foreground/background selection. SSR panels (*e.g.*, 50-plex RM markers) resolved 92% rice core collections into distinct clusters, tracing indica-japonica divergences.

QTL Mapping and GWAS

Quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS) are powerful approaches for identifying genomic regions associated with yield and its component traits. Numerous QTLs controlling grain number, grain size and panicle architecture have been identified in rice populations (Zhao *et al*., 2011). Biparental QTL linkage scans via composite interval mapping identify yield meta-QTLs like $gn1^{-1}$ (grain number) on chr1 and GS3 (grain size) on chr5, validated across 20+ mappings with 10-25% phenotypic variance. GWAS on 500+ diverse panels (*e.g.*, 44K SNP chips) uncovers novel associations, such as 12 panicle QTLs via mixed linear models correcting population structure, yielding peak SNPs at 0.05-0.12 effects (Huang *et al*., 2024).

Genomic selection

Genomic selection is a modern breeding strategy that predicts the genetic potential of individuals using genome-wide marker data. This approach accelerates breeding progress by reducing the time required for selection cycles (Crossa *et al*., 2017). GS deploys 73K GBS markers to train prediction models (Bayesian Lasso, rrBLUP), achieving 0.52-0.71 accuracies for yield in multi-environment IRRI sets, surpassing pedigree indices by 20-40%. Bangladesh deployments halved cycles from 4 to 2 years, pyramiding blast resistance with yield via polygenic scores (Spindel *et al*., 2015).

Integration of conventional and Molecular breeding

The integration of conventional phenotypic selection with molecular breeding techniques has significantly improved the efficiency of crop improvement programs. High-throughput phenotyping platforms combined with genomic data enable breeders to identify superior genotypes more accurately. The development of core and mini-core germplasm collections has also facilitated efficient evaluation of large germplasm collections while maintaining maximum genetic diversity (Singh and Upadhyaya, 2015).

Future Perspectives

Future rice breeding programs should place greater emphasis on broadening the genetic base of cultivated rice through the effective utilization of diverse germplasm

resources. Many traditional landraces, farmer-maintained varieties, and wild relatives of rice possess valuable genetic traits that have not yet been fully exploited in modern breeding programs. These genetic resources often contain alleles associated with tolerance to abiotic stresses such as drought, salinity, submergence, and high temperature, as well as resistance to important pests and diseases. Systematic collection, conservation and characterization of such germplasm using both morphological and molecular approaches can help identify novel genes and beneficial alleles. Incorporating these resources into breeding pipelines can significantly enhance genetic variability and provide new opportunities for improving yield stability and adaptability.

Along with germplasm utilization, the integration of modern genomic technologies is expected to transform rice improvement strategies. Advances in high-throughput sequencing and molecular marker technologies have enabled researchers to study the genetic architecture of complex traits in greater detail. Approaches such as genome-wide association studies, genomic selection, and marker-assisted breeding allow the identification of genomic regions controlling important agronomic characters, including yield components, grain quality, and stress tolerance. These tools help breeders select superior genotypes more efficiently and reduce the time required for variety development.

Recent developments in pangenomics have further expanded the understanding of rice genetic diversity. Unlike a single reference genome, a pangenome represents the collective genetic information present within a species, including both core and variable genes. This broader genomic framework makes it possible to detect genes that may be absent in standard reference genomes but present in specific cultivars or wild accessions. Such information can reveal new genetic factors responsible for important agronomic traits and can be strategically incorporated into breeding programs to improve crop performance.

Another promising advancement in crop improvement is genome editing, particularly the application of CRISPR-based technologies. Genome editing enables precise modification of target genes without introducing large segments of foreign DNA. Through targeted gene knockouts or allele modifications, researchers can enhance desirable traits such as grain yield, nutritional quality, and resistance to environmental stresses. Because these changes can be introduced directly into elite cultivars, genome editing has the potential to accelerate the development of improved rice varieties while maintaining their favorable agronomic characteristics.

In addition to molecular tools, data-driven approaches such as machine learning and artificial intelligence are becoming increasingly relevant in plant breeding. These computational methods can analyze large datasets derived from genomic, phenotypic and environmental sources to identify patterns and predict the performance of breeding lines. Predictive modeling can assist breeders in selecting promising genotypes at early stages of the breeding cycle, thereby improving selection accuracy and reducing the time and resources required for field evaluation.

Equally important is the advancement of high-throughput phenotyping technologies, which enable accurate measurement of plant traits under both field and controlled conditions. Techniques involving remote sensing, digital imaging, and automated phenotyping platforms allow researchers to monitor plant growth, physiological responses and stress adaptation more efficiently. Such technologies help bridge the gap between genotype and phenotype and provide more reliable data for selection decisions in breeding programs.

Finally, evaluating rice germplasm under diverse environmental and stress conditions will remain a critical component of future breeding strategies. Climate variability is expected to increase the frequency of abiotic stresses such as drought, salinity, and heat, which can significantly reduce crop productivity. Screening breeding materials under these conditions allows the identification of genotypes with stable performance and enhanced adaptability. The incorporation of these stress-tolerant traits into improved cultivars will be essential for sustaining rice production in changing climatic scenarios.

Overall, the combined use of diverse genetic resources, advanced genomic tools, innovative computational approaches, and improved phenotyping methods will play a central role in shaping the next generation of rice breeding programs. These integrated strategies will contribute to the development of high-yielding, climate-resilient and nutritionally improved rice varieties capable of meeting the growing global demand for food while supporting sustainable agricultural systems.

Conclusion

Comprehensive evaluation of rice germplasm for yield and yield-attributing traits is essential for sustainable crop improvement. The presence of significant genetic variability within germplasm collections provides opportunities for effective selection and breeding. Integration of phenotypic evaluation, genetic variability analysis, correlation and path coefficient studies and

molecular approaches offers a robust framework for improving rice productivity. Effective utilization of diverse germplasm resources combined with advanced breeding strategies will play a crucial role in developing high-yielding and stable rice cultivars capable of meeting future global food demands.

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