

ELITE RICE GERMPLASM RESOURCES: GENETIC VARIATION IN KEY AGRONOMIC TRAITS AND THEIR BREEDING UTILIZATION VALUE

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Abstract: The resources of rice germplasm are diverse in genetics and can provide the basis for new varieties. Systematically study the genetic diversity of yield, growth period and plant architecture traits in this paper to determine how distributed the phenotypic coefficient of variation, genetic diversity index and heritability are among various germplasm types and areas. Landraces have a relatively large number of different flag leaves and are generally taller than modern varieties, but they have fewer varieties of growth period and effective panicles. The coefficient of variation of empty grains is 89.75%, and the genetic diversity index for heading date is 2.069; thus, it is highly selected. More than 45% of the excellent haplotypes come from landraces, so traditional varieties need to be preserved and developed. There are three kinds of breeding and utilisation paths, in addition to direct application, parent selection and gene mining; in conjunction with pan-genomics and GWAS, a new model for precise characterisation and intelligent design breeding is being explored. This paper hopes to offer some references for the use and improvement of germplasm resources.

Keywords: Rice; Germplasm resources; Agronomic traits; Genetic variation; Breeding utilisation

1 INTRODUCTION

Rice (*Oryza sativa* L.) is the main food source for over half of the world's population, and continuous improvement of its varieties directly impacts food security and the sustainable development of agriculture. Germplasm resources are the raw materials for genetic improvement, and as such, they contain a large number of genes in different forms that can be used in rice breeding [1]. However, due to prolonged reliance on a small number of elite founder parents in breeding, the genetic foundation of modern varieties has gradually been narrowed down and cultivar homogeneity has increased. At the same time, although a large number of rice germplasm have been collected and conserved around the world, the genetic background and breeding value of most of these materials are not well understood, and superior alleles cannot be effectively incorporated into the breeding innovation chain [2]. Therefore, to address the existing breeding bottlenecks and promote more precise variety improvement, it is necessary to conduct systematic evaluations of genetic variation in key agricultural traits and analyse the breeding utilisation value of excellent germplasm resources to understand the genetic diversity status of current resources. Based on the main agronomic traits of yield, growth stage, plant structure and grain quality, this paper will employ a combination of phenotypic variation, genetic parameters and molecular data to investigate the genetic potential and application path of elite rice germplasm in modern breeding.

2 CHARACTERISTICS OF GENETIC VARIATION IN AGRONOMIC TRAITS OF RICE GERMPLASM RESOURCES

2.1 Genetic Variation of Yield Traits

Generally speaking, the first goals of yield-related traits in rice breeding are to increase the number of panicles, spikelets per panicle, seed-setting rate and thousand-grain weight. Analysis of the 20 agronomic traits in 1,775 rice germplasm accessions showed that the coefficient of variation for empty grains was as high as 89.75% and among all traits, it had the largest variation amplitude [3]. The genetic coefficient of variation for grain yield per plant was also about 29.51%, and it showed a considerable range of genetic variation and selection response [4]. Comparison of the phenotypic and genotypic coefficients of variation showed that for most yield-related traits, the phenotypic coefficient was higher than the genotypic coefficient; thus, it can be concluded that environmental factors have a non-trivial modifying effect on the expression of yield traits. The heritability estimates also showed that the number of spikelets per panicle (62.62%) and thousand-grain weight have relatively high broad-sense heritability, but the heritability of effective panicles per plant is relatively low [5]. According to the attribute, in the breeding plan, traits with high heritability can be chosen for in the early generations, and for other environmentally sensitive traits, the genetic potential needs to be determined after several years and at many different places. In addition, both the increase in spikelets per panicle (44.08%) and that of thousand-grain weight are relatively large; therefore, it can be seen that considerable genetic improvement is possible through selection.

2.2 Genetic Variation in the Growth Period and Plant Architecture Characteristics

The traits of the growth stage are directly related to the environmental conditions and crop-system organisation of the varieties [6]. The heading date showed the greatest number of varieties in the germplasm population and had a genetic diversity index of 2.069. The first heading date and the heading date are positively correlated with other agricultural characteristics, and all have a very small p -value ($p < 0.01$), among which the relationship between growth duration traits and yield traits is especially close. It can be seen from the above that restricting the growth time will also affect all parts of the yield trait, so we need to find a good balance between maturity period and yield in breeding programs. In terms of plant architecture traits, there were relatively rich diversities among 11 such traits in the landraces [7]. Germplasm from different areas has shown different types of plant structures; Among the seven attributes, Jilin Province's accessions are relatively diverse and perform well in many aspects, such as a high number of panicles and spikes per panicle; among the four attributes, Yunnan Province's accessions have been well-known for their early heading time and long panicles; and among the three attributes, Heilongjiang Province's accessions are relatively outstanding in the early heading time [8]. Different areas of the world have varying environments, so both natural selection and people's efforts to change them have produced many traits; therefore, trait stacking can be realised in different ecological zones.

2.3 Genetic Variation of Grain Traits

Grain traits affect not only the components of grain yield but also directly impact appearance quality and milling quality. Among the existing germplasm, the coefficient of variation for grain thickness was only 4.42%, and it was the smallest among all tested traits [9]. Thus, it can be concluded that grain thickness has been reduced by selection and breeding for a long time and is relatively uniform in terms of genes. Grain length had a relatively large number of types in the germplasm of Hebei, Shandong, Yunnan, Jiangsu and Xinjiang. Germplasm from South Asia has made some notable achievements in grain width and grain weight. OsGRW5.1 has been identified as a crucial gene regulating the width and weight of grains at the molecular level, and there are many alleles in the germplasm population; therefore, it can be precisely enhanced to improve grain characteristics [10]. In addition, meta-GWAS based on a graph of pan-genomes also found a new grain width gene GW10.2 and a new grain length gene GL11, which have been added to the collection of genes for grain trait improvement. Research on pan-tandem repeat variation has found that only about one-third of the tandem repeat variations are closely associated with bi-allelic variants, such as single nucleotide polymorphisms and insertions/deletions; thus, tandem repeats may be the main cause of multi-allelic variation that contains its own genetic information independent of common variants.

3 IDENTIFICATION AND ASSESSMENT OF ELITE GERmplasm RESOURCES

3.1 Precise Characterisation According to Phenotypic Data

Phenotypic characterisation is the first step of germplasm evaluation and can provide a general idea about the genotype for breeding. Systematic phenotypic characterisation of the large-scale germplasm population has made some good progress; genotyping has been conducted on 360,000 accessions, and multi-year, multi-location phenotypic evaluation has been carried out on 50,000 core accessions. As a result, about 2,943 accession varieties with good characteristics have been obtained that exhibit high yield, excellent quality, stress tolerance and disease resistance, etc. To simplify the number of dimensions, we use Principal Component Analysis to collect the extensive information of many correlated traits. The first six principal components explained a total of 79.309% of the variance in the analysis of 1,775 accessions, and traits related to growth duration were the main ones. After cluster analysis, the three groups of tested germplasm were divided as follows: Group I contained accession varieties from the three northeastern provinces as well as Beijing and Hangzhou, and had rich diversity in ten traits, such as initial heading date, tiller number and effective panicle number; Group II only had Ningxia accessions, which were genetically far from those in other provinces but had its own value of expanding the genetic base; and Group III covered germplasm from Hebei, Shandong, Yunnan, Jiangsu and Xinjiang, and had good diversity in grain length. Phenotype-based grouping can help us select a suitable parent for the child more easily.

3.2 Evaluation of Genetic Diversity Based on Molecular Markers

The development of molecular marker technology has made it possible to determine the genetic variation in germplasm at the DNA level. Simple sequence repeat markers have good co-dominance, high polymorphism and are easy to operate, so they have been used extensively in genetic similarity analysis and population structure dissection of germplasm. Research shows that the overall genetic diversity of Chinese rice varieties is relatively small, and this is mainly because the parents used in the breeding program are closely related genetically. Therefore, there is a problem of a narrow genetic base due to prolonged reliance on a few outstanding founders. Analysis of the 184 rice accessions based on 156 SSR markers showed that to improve crop genetics, it is necessary to know the population structure and range of genetic variation in germplasm. With the development of sequencing technology, in recent years many studies have been carried out on rice pan-genomes, and thus genome-wide genetic diversity assessment has gradually taken the place of traditional marker-assisted evaluation. Build a rice super-pangenome with the natural variation diversity of wild and cultivated rice populations to find superior natural variations in complex regions, such as transposon variants,

inversion variants, centromere regions, etc. According to the graph of the pan-genome for the 7,765 accessions, Meta-GWAS was built, and more than 6.6 million single nucleotide polymorphisms and more than 40,000 structural variations were discovered. With the progress of technology, marker-assisted selection and genomic selection have been applied to expand the scope of germplasm evaluation.

3.3 Main Selection Criteria for Elite Germplasm

Combine the phenotypic and molecular data to select the good germplasm in the following ways. The first is trait specialisation; that is to say, an excellent trait in only one essential characteristic of agricultural products, such as early maturity, large grain size or a high seed-setting rate. There are many rare favourable alleles and good breeding values in the material. The second is genetic distinctiveness; that is to say, germplasm that is genetically far from the main breeding materials and belongs to an independent branch in terms of population structure, such as the Ningxia group. This material is one of the good resources to expand the gene pool and introduce new genetic variation. The third is allelic superiority; that is to say, it carries excellent allelic variants of the already cloned or mapped genes, such as the yield-enhancing haplotype of OsGRW5.1 and the functional variants of GW10.2 and GL11. The fourth is the coordination of all-round traits, that is to say, reaching a high level of balance in many areas such as yield, quality, disease and drought resistance, etc. The four reasons are in agreement, and according to the breeding objectives, different weights can be given; taken together, they form a general selection system for outstanding germplasm.

4 UTILIZATION VALUE AND PATHWAYS OF GERMPLASM RESOURCES IN BREEDING

4.1 Direct Application of Elite Germplasm and Variety Improvement

Germplasm resources that have been regularly screened, show excellent characteristics, and have good genetic stability can be used in the following three ways: introduced as new varieties in the regional trial and release/commercialisation process; directly used as parents in crossing combinations; or the other way of using them in the crossing combination. It is simple to operate and practical for breeding; it is particularly good for materials with good coordination of all kinds of traits, broad adaptability and stable performance over many years in various areas. In fact, the successful development of many outstanding varieties in the history of Chinese rice breeding has been greatly aided by the ingenious use of specific germplasm resources, and even direct introduction has been employed. Through a general analysis of 2,088 rice accessions and the construction of crossing combinations based on 517 representative materials, it was found that more than 45% of the superior haplotypes are from landraces. The above results have some breeding applications; although the yield potential under modern intensive production conditions for landraces is lower than that of modern varieties, their genomes contain a large number of favourable alleles that have been lost or are very low in frequency in modern varieties. By using the traditional germplasm resources and introducing them into new breeding systems, it is hoped that new crop varieties with good traits will be obtained. South Asian rice germplasm has contributed significantly to the traits of grain width and grain weight; it is a typical case. It should be pointed out that the elite gene resources in landraces and wild relatives are also being re-examined and systematically evaluated. Yunnan Province is a typical case; due to its unique environment, a large number of local rice germplasm resources have been accumulated here, and many of them have excellent drought resistance, barren-ground ability, etc. Directly using or slightly improving these resources has already achieved some good results in raising production and income in some areas. Some of the imported materials have been adapted and cultivated in China; they have also served as breeding lines or important breeding parents in some places, and the first driving force to break the stagnation of variety homogeneity has been fully shown by elite germplasm. However, there are also practical problems in direct application, such as a long evaluation period and a large number of works that need to be screened for regional adaptation; therefore, standardisation of characterisation procedures and sharing mechanisms must be established to speed up the conversion of elite germplasm from resource banks to variety banks. In order to exceed the current ceiling of yield and quality, it is necessary to systematically collect, accurately identify and organise the elite genes of landraces and wild relatives.

4.2 Parent Selection Strategy According to Genetic Diversity

Parent selection is a key factor in the success of cross-breeding, and both parents should have good genetic differences to produce a large number of segregating offspring and desirable traits. The Magnitude of genetic variation is a selection marker. Generally speaking, if there is significant genetic distance between the parents, their offspring are more likely to be diverse and may show transgressive segregation. We divide the germplasm into several groups because inter-group crosses are likely to have higher genetic diversity than within-group crosses, and thus there will be more selection options for the offspring. Although the purpose of selecting parents is to increase genetic diversity, we also need to select parents that have good combined traits for the trait we are interested in and avoid those with harmful traits. Ability analysis is an indispensable aid to parental selection; generally speaking, the average transmission ability of parental traits is known as general combining ability, and specifically speaking, the non-additive genetic effect of a particular combination of traits is called specific combining ability. Together, they will improve the scientific basis and predictability of parent selection. The combination of parents' characteristics is also necessary to achieve trait pyramiding in the hybrid offspring. If the parents have obvious deficiencies in yield components or quality indicators, even a large genetic distance cannot ensure that the offspring will be superior to both parents in all aspects after a short

time. Recently, intelligent prediction models that have used a large number of cross-combination data have been able to accurately predict the traits of many crops. According to the phenotype and genotype data of the 770 hybrid combinations, a prediction model can be constructed to produce about 500,000 new combinations. Technology has moved us away from the traditional way of experiencing and trial-and-error; now, we use big data to make precise plans and improve both the efficiency and success rate of germplasm utilisation. In terms of optimisation of the selection strategy, one should also consider expanding the range of parental sources to prevent an increase in the genetic vulnerability of the breeding population due to too much use of a few core parents. Parent materials can be classified into several functional groups according to breeding objectives at the operating level, and then crosses among these groups can be carried out to achieve the goal of pyramiding desired traits. With the addition of genomic selection for parents, it is now possible to determine the breeding value of young plants and even seeds early in their life; thus, both the breeding cycle and the increase in genetic resources per unit of time will be reduced.

4.3 Elite Gene Mining and Molecular Design Breeding

Germplasm Resources have various uses, and they contain excellent genes. Traditional breeding is based on differences in phenotype; molecular design breeding can modify genes at the level of genes. With the rapid development of functional genomics in recent years, many genes that regulate all kinds of attributes of agriculture, such as grain output and quality, stress tolerance, etc., have been repeatedly cloned and functionally verified. Molecular Design Breeding starts with the desired traits of selected superior alleles, and through various means such as marker-assisted selection, gene pyramiding and gene editing, beneficial genes distributed in different germplasm resources can be efficiently introduced into a single genetic background. Therefore, the old way of breeding, which is based on phenotypic selection, has had some problems such as a long generation cycle and linkage drag of undesirable traits. Based on the graph of the pan-genome, Meta-GWAS found a total of 156 genetic loci associated with some important agricultural traits, but only 116 were confirmed after meta-analysis; therefore, it was found that by combining GWAS results from several independent populations, the power to detect QTLs and explain heritability has been enhanced, and it is now easier to discover minor-effect genes and low-frequency variants that are difficult to find in traditional single-population analyses. These new loci are distributed in all 12 chromosomes of rice and contain many beneficial traits for agriculture, such as grain shape, growth period, disease resistance, etc., so they have become rich resources in molecular design and breeding. Research on pan-tandem repeat variations has also found that multiple alleles can regulate gene expression and traits in different ways, so all kinds of genetic information need to be taken into account in the field of elite gene mining, such as traditional single nucleotide polymorphisms (SNPs) and insertions/deletions (indels), as well as structural variations and tandem repeats. Therefore, it can be seen that the resources of germplasm are not only about materials for variety improvement but also contain a wealth of outstanding genes. Discovery and cloning of genes, functional validation, marker-assisted selection and gene editing, etc., are all in the technology chain for the conservation of inheritance resources and new crop varieties. In order to avoid the negative effects of linkage drag and epistatic interference which can reduce the expression of the target trait in simple stacking, optimisation strategies for multi-gene pyramiding need to be used in practice. In the future, breeding will be conducted on the basis of genotypes rather than phenotype-dependent empirical breeding, and the main reason for this change is to use and systematically apply superior alleles in germplasm resources more accurately.

5 CONCLUSION

Genetic resources of rice can provide new materials for the development of new crop varieties. Existing research has found that the extent of genetic variation varies greatly among different traits; for example, the coefficient of variation of empty grains is nearly 90%, but that for grain thickness is only more than 5 per cent. Germplasm from various origins has its own characteristics; among them, accession Jilin Province is relatively good at a high number of panicles, and those from Yunnan Province are outstanding in the diversity of panicle length. The material has a different level of effect at different degrees of improvement; that is to say, although landraces possess rich traits of plant architecture, improved varieties are numerous in terms of many different characteristics, such as extended growth periods. The above results have formed the basic framework for the genetic variation of agronomic traits in rice germplasm and provided scientific guidance on "what to use and how to use it" in breeding practice; directly introducing germplasm, selecting parents, and then gene mining are all ways of using germplasm resources, which are continuously being expanded and increasingly precise. With the continuous development of leading technology, such as pan-genomics, genome-wide association studies and intelligent prediction, the concept of germplasm resources has moved from passive preservation to active application. In the future, detailed studies will be carried out to investigate the genetic basis of complex traits in germplasm, and systemic discovery of rare favourable alleles and the construction of accurate prediction systems linking genotype, phenotype and breeding value will be the main proposals to achieve a leapfrog improvement in rice varieties.

COMPETING INTERESTS

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REFERENCES

- [1] Jin J H, Li S F, Zhao Y D, et al. Genetic diversity of important agronomic traits in 1775 rice germplasm resources. *Journal of Plant Genetic Resources*, 2025, 26(3): 481-495.
- [2] Shang L, He W, Wang T, et al. A complete reference genome assembly and annotation of rice cultivar Nipponbare. *Molecular Plant*, 2023.
- [3] Shang L, Li X, He W, et al. A super pan-genome of rice. *Cell Research*, 2022.
- [4] Wang T, He W, Li X, et al. A rice variation map derived from 10 548 rice accessions reveals the importance of rare variants. *Nucleic Acids Research*, 2023, 51(20): 10924-10933. DOI: 10.1093/nar/gkad840.
- [5] He H, Leng Y, Cao X, et al. The pan-tandem repeat map highlights multiallelic variants underlying gene expression and agronomic traits in rice. *Nature Communications*, 2024, 15(1): 7291. DOI: 10.1038/s41467-024-51854-0.
- [6] Yang L, He W, Zhu Y, et al. GWAS meta-analysis using a graph-based pan-genome enhanced gene mining efficiency for agronomic traits in rice. *Nature Communications*, 2025, 16(1): 3171. DOI: 10.1038/s41467-025-58081-1.
- [7] Wang Y, Li Z, Wu B, et al. Dissection of the genetic basis of 1392 rice landraces and 770 hybrid combinations reveals great potential of rice landraces in hybrid rice improvement. *Molecular Plant*, 2026, 19(1): 66-80. DOI: 10.1016/j.molp.2025.10.004.
- [8] Sen A, Yasmin F, Sarkar M J, et al. Genetic and morphological traits diversity in germplasm of Aman rice (*Oryza sativa* L.). *Discover Plants*, 2026, 3(1): 43. DOI: 10.1007/s44372-026-00503-5.
- [9] Ali Z, Naeem M, Rafiq I, et al. Evaluation of Genetic Diversity, Yield, and Its Associated Traits in Rice (*Oryza sativa* L.) Genotypes. *Plant Molecular Biology Reporter*, 2026, 44(1): 11. DOI: 10.1007/s11105-025-01638-7.
- [10] Rama Sai M V, Sreelakshmi Ch, Shanthi Priya M, et al. Assessment of genetic variability and diversity for lodging resistance and yield related traits in rice germplasm (*Oryza sativa* L.). *Oryza-An International Journal on Rice*, 2025, 62(2): 105-116. DOI: 10.35709/ory.2025.62.2.1.