Exploring the Dynamics of Genetic Parameters: Genetic Variability, Heritability and Character Association in Rice (*Oryza sativa* L.)

ABSTRACT

The present study was conducted to quantify the genetic variability present in a population and to assess the association among the traits at the Zonal Agricultural and Horticultural Research Station, Shivamogga, Karnataka, India. The experimental material comprised ninety rice germplasm evaluated in *Kharif* 2019 using augmented RCBD design with five blocks and five checks. Analysis of variance revealed that the mean sum of squares (MSS) attributed to genotypes is significant ($P <= 0.01$) for all the characters examined. The germplasm lines were highly variable for traits like numbers of tillers per plant, numbers of productive tillers per plant and decorticated grain length and breadth ratio whereas the trait days to heading recorded low genetic variability and remaining traits manifested moderate genetic variability. In the present study, all traits exhibited high heritability. Genetic advance as percent mean (GAM) spanned around 19.32 percent (days to heading) to 49.78 percent (number of tillers per plant). Grain yield in rice had a positive, significant correlation with the number of tillers per plant (0.31**) and the number of productive tillers per plant (0.35**), while other characters had non-significant correlations. Meanwhile, plant height had a negative correlation with the number of tillers per plant and the number of productive tillers per plant. The germplasm population exhibited adequate variation for studied traits. These variants can be effectively utilized in future breeding programs based on need but breeders should emphasize on attributing traits while dealing with dependent trait.

Keywords: Phenotypic coefficient of variation, Genotypic coefficient of variation, Heritability, Genetic advance as percent mean and Correlation coefficient.

INTRODUCTION

A starchy grain rice (*Oryza sativa* L.), botanically caryopsis, has been a predominant source of food and energy for human beings worldwide to the extent of 60 percent. Particularly in Asia, rice has been a major source of calorie and protein supplement (Vijay and Roy, 2013). India is the second largest rice producer in the world, with a total production of 135.76 million metric tonnes over 47.83 million hectares. Additionally, India is the top exporter of rice. (Anon., 2024a; Anon., 2024b).

Rice is cultivated around the world in various ecological regions with latitude ranging from 53^0 North to 40^0 South and altitude ranging from mean sea level to 3000 m above mean sea level. (Roy and Shil, 2020)This ability of rice to grow in different climate conditions, from wet to dry regions, indicates its greater adaptability. The greater adaptability of any species is the clear sign of the rich genetic variability and diversity. However, breeding goals are now focused on producing high-yielding varieties and hybrids to feed the ever-growing population. This has resulted in a narrow genetic base and lead to genetic erosion due to the use of common maternal parents with good GCA in the development of varieties and common parents with higher GCA and SCA in the development of hybrids.

Though breeding techniques such as hybridization, transgenic and mutation have been extensively used to generate genetic variability but utilizing the natural variation that is a result of structural variants in the genetic makeup of rice in response to selection pressure imposed by diverse ecological regions is a sensible choice. Hence, priorities have to be given for conservation and utilization of landraces (primitive cultivars) that are known to have greater genetic variability. One of the notable successful milestone examples is the identification of the *Sub1* QTL for submergence tolerance in the Indian landrace FR13A (Neeraja *et al*., 2007). Similarly, genetic variability in grain type in rice is the major area of concern; the basmati-type grain (known for its unique aroma and texture) is earning huge foreign exchange.

Even with desirable genetic variability for a character, direct selection would not be rewarding, as traits are governed by polygenes and may have interaction with other component traits. In such cases selection strategy based on correlation studies assists in increasing selection efficiency. The correlation coefficient can be defined as a statistical tool used to assess the strength of a linear relationship between two traits or characteristics (Dhavaleshvar *et al.* 2019). Association between traits may be due to the linkage between the loci or pleiotropic effect of candidate genes. Hence, assessment of genetic variability and correlation coefficient studies is a major area of concern to be successful in breeding.Present study was conducted with the objective of quantifying the genetic variability present in the germplasm population and assessing the trait association, so that germplasm with desirable traits can be selected for hybridization work or the entire population can be used as an association panel to identify the Quantitative trait loci (QTL) governing the trait. The trait association helps understand the direct or indirect influence of the component trait on the expression of the dependent trait.

2. MATERIAL AND METHODS

The experimental material comprised ninety rice germplasm collected from the Department of Genetics and Plant Breeding, College of Agriculture, Navile, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Iruvakki, Shivamogga. The study material comprised indigenous landraces, farmer's varieties, advanced breeding lines and released varieties. The experiment was conducted during the period of *Kharif* 2019 at the Zonal Agricultural and Horticultural Research Station (ZAHRS), Shivamogga, Karnataka, India.

The germplasm were sown to raise the nursery bed. Twenty-five-day-old seedlings were transplanted manually into the main field with a single seedling per hill following the augmented design with five blocks and each block having seventeen rice germplasm and five checks. The distance between row to row and plant to plant was 25 cm and 25 cm, respectively. The recommended operations and dose of fertilizers were applied accordingly to raise a healthy crop stand. Observations recorded on quantitative traits are presented in Table 1. Data analysis was carried out using R statistical tool version 4.4.1 by utilizing the augmented RCBD package. to estimate ANOVA and genetic parameters: Genotypic and phenotypic variances, Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV), Heritability (h^2) broad sense, Genetic advance as per cent mean (GAM) and Correlation coefficient.

Table1. List of quantitative traits studied

TRAITS	Trait abbreviation	units
Days to heading	DTH	Count
Plant height	PH	cm
Number of tillers per plant	TT	Count
Number of productive tillers per plant	PT	Count
Panicle length	PL	cm
Test weight	TW	g
Grain length	GL	mm
Grain breadth	GB	mm
Grain length and breadth ratio	GLB	ratio

Decorticated grain length	DGL	mm
Decorticated grain breadth	DGB	mm
Decorticated grain length and breadth ratio	DGLB	ratio
Grain yield	YLD	q/ha

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

Analysis of variance is a second-degree statistical tool that enables breeders to determine that variation observed among the germplasm is due to environment or genotype itself. In the study, the mean sum of squares (MSS) attributed to genotypes is significant (P <= 0.01) for all the characters examined (Table 2), suggesting a strong genetic influence on phenotypic trait variation. Hence, breeders can emphasize phenotypic selection. Similar results were reported by Gangadhar *et al.* (2023), Reddy *et al*. (2023).

3.2 Variability studies

Genetic variability in a crop species is a boon to plant breeders and ecosystems as a whole. The final outcome of a breeding program relies on the proportion of desired genetic variability (Khan *et al.*, 2023). and its heritability to the progeny. A keen utilization of available genetic variation in different gene pools has enabled us to meet the commercial requirements of today’s world. In the present study, the PCV was higher than the GCV and differences between the PCV and GCV were minimal for all the traits. Hence, selection would be effective as environmental influence on the expression of traits is less. Comparatively, grain yield manifested a higher difference, indicating the complexity of a trait.

The germplasm manifested a greater range for most of the traits studied. The detailed estimate of mean, range, GCV, PCV and GAM is presented in Table 3. The germplasm lines were highly variable for traits like numbers of tillers per plant, numbers of productive tillers per plant and decorticated grain length and breadth ratio, as indicated by the higher estimates of GCV and PCV (> 20%), while grain yield recorded moderate GCV (19.13 %) and high PCV (20.05%). The germplasm lines of the population were moderately variable (10.1% ≤ GCV & PCV ≤ 19.9%) for plant height at maturity, panicle length, test weight, grain length, grain breadth, grain length and breadth ratio, decorticated grain length and decorticated grain breadth. The trait days to heading recorded low GCV (9.41) & PCV (9.45).In the present study, GAM spanned around 19.32 to 49.78 (number of tillers per plant). The trait days to heading recorded moderate GAM (19.32), while remaining traits manifested higher GAM (> 20%). The traits, like grain or decorticated grain length and breadth and days to heading, are typically known to exhibit low to moderate PCV and GCV; this may be due to unidirectional selection pressure; in these situations, high or moderate GAM aids in selection and helps identify variants that deviate significantly from the mean.

All traits exhibited high broad-sense heritability of more than 60 percent, as rice germplasm are result of successive selfing; alleles are bound to be in a homozygous state. Higher heritability indicates that observed phenotypic variation is mainly governed by genetic factors. PCV and GCV quantify the proportion of genetic variability present in a population, and GAM indicates genetic gain of the progeny of the selected population over the base population and it is expressed in percent mean. Overall, the germplasm population exhibited moderate to high GAM with coefficients of variation ranging from low to high. These outcomes were closely aligned with the findings of Gour *et al*. (2017), Saha *et al* (2019); Sarif *et al*. (2020). Lakshmi *et al*. (2021); Akshay *et al*. (2022); Debsharma *et al.* (2022); Faysal *et al.* (2022), Nivedha *et al*. (2024).

High heritability coupled with high GAM clearly denotes that the trait is governed by additive gene action and phenotypic selection would be effective to improve the genetic gain. In present study, the majority of the traits expressed high heritability and GAM. Greater the difference between the GCV and PCV indicates higher environmental influence, but in our study we found minimal difference indicating the greater influence of genetic factor.

3.3 Correlation studies

The detailed estimation of the correlation coefficient among the traits is represented in Figure 1. Grain yield in rice germplasm had a positive significant correlation with the number of tillers (0.31**) and the number of productive tillers (0.35***), while positive non-significant correlation with days to heading (0.08), test weight (0.13), grain length (0.17), grain breadth (0.02), the grain length and breadth ratio (0.06), decorticated grain length (0.15), decorticated grain breadth (0.07), and the decorticated grain length and breadth ratio (0.03). The plant height (-0.18) and panicle length (-0.02) manifested negative non-significant correlation with grain yield. It is evident from the lesser magnitude of the correlation between yield and yield-attributing traits that grain yield is a complex trait; hence, precise selection is required in improving the grain yield. These findings were in accordance with Oladosu *et al*. (2018), Swapnil *et al*. (2020), Lakshmi *et al*. (2021) and Anusha *et al*. (2022).
In the study, germplasm with a higher number of tillers had a higher proportion of unproductive tillers, which could be attributable to the shadowing effect of too many leaves, resulting in decreased photosynthesis. These unproductive tillers not only reduce photosynthetic efficiency but also drain nutrients from the main stem. As per IRRI's new plant type concept, having the optimal number of tillers with few or no unproductive tillers is critical for increasing photosynthetic efficiency and production.

Test weight had a positive significant correlation with grain length (0.42***) and grain breadth (0.61***), but there was no significant correlation with the grain length and breadth ratio (-0.15), implying that grain length and grain breadth together contribute to the test weight. Plant height had a positive significant correlation with days to heading (0.24*), panicle length (0.50***), test weight (0.39***), and a negative significant association with the number of tillers per plant (-0.52***) and the number of productive tillers per plant (-0.52***). This depicts that germplasm with higher plant height spends its maximum energy in internode elongation rather than tillering and it is also well documented that the dwarfing gene enabled the improvement of the grain yield potential in rice by increasing the number of tillers. Similar results were reported by Dhavaleshvar *et al*. (2019) and Saleh *et al*. (2020).

Table 2. Analysis of variance

Source	Df	DTH	PH	TT	PT	PL	TW
Genotype	89	109.82**	577.79**	23.86**	18.34**	7.91**	29.47**
Check	4	532.1**	1852.94**	98.02**	70.83**	13.62**	215.6**
Genotype	84	83.44**	521.86**	19.65**	15.05**	7.72**	19.48**
Genotype vs. Check	1	636.75**	175.78**	80.77**	84.76**	0.52ns	124.29**
Block	4	0.8	10.84	1.33	1.31	0.6	0.7
Residuals	16	0.77	12.16	2.32	2.23	0.81	0.77

Source	Df	GL	GB	GLB	DGL	DGB	DGLB	YLD
Genotype	89	0.97**	0.14**	0.37**	0.58**	0.11**	0.29**	157.24**
Check	4	4.91**	0.46**	0.07**	2.41**	0.32**	0.13**	438.63**
Genotype	84	0.79**	0.11**	0.37**	0.5**	0.09**	0.3**	130.3**
Genotype vs. Check	1	0.12**	1.07**	1.33**	0.01ns	0.4**	0.66**	1295.23**

Block	4	0.0086	0.0027	0.0006	0.0064	0.0016	0.0004	20.9
Residuals	16	0.0114	0.0023	0.0019	0.0077	0.0018	0.0022	11.69

ns P > 0.05; * P <= 0.05; ** P <= 0.01

Table 3. Estimation of genetic variability parameters

TRAITS	**RANGE**		**MEAN**	**GCV (%)**	**PCV (%)**	**h^2 (%)**	**GAM (%)**
	MIN	**MAX**					
DTH	74.00	115.00	96.62	9.41	9.45	99.07	19.32
PH	79.00	165.00	128.79	17.53	17.74	97.67	35.74
TT	8.00	28.75	16.20	25.70	27.36	88.19	49.78
PT	7.50	25.75	14.95	23.95	25.95	85.20	45.61
PL	17.90	31.20	24.23	10.85	11.47	89.49	21.17
TW	12.30	36.69	25.95	16.67	17.01	96.03	33.70
GL	5.95	11.20	8.56	10.30	10.38	98.55	21.10
GB	1.85	3.45	2.86	11.64	11.76	97.94	23.76
GLB	2.30	5.31	3.05	19.89	19.94	99.48	40.93
DGL	4.35	8.15	6.23	11.22	11.31	98.44	22.97
DGB	1.40	3.10	2.47	12.13	12.25	97.99	24.76
DGLB	1.80	4.47	2.57	21.08	21.16	99.25	43.32
YLD	28.40	79.60	56.93	19.13	20.05	91.02	37.66

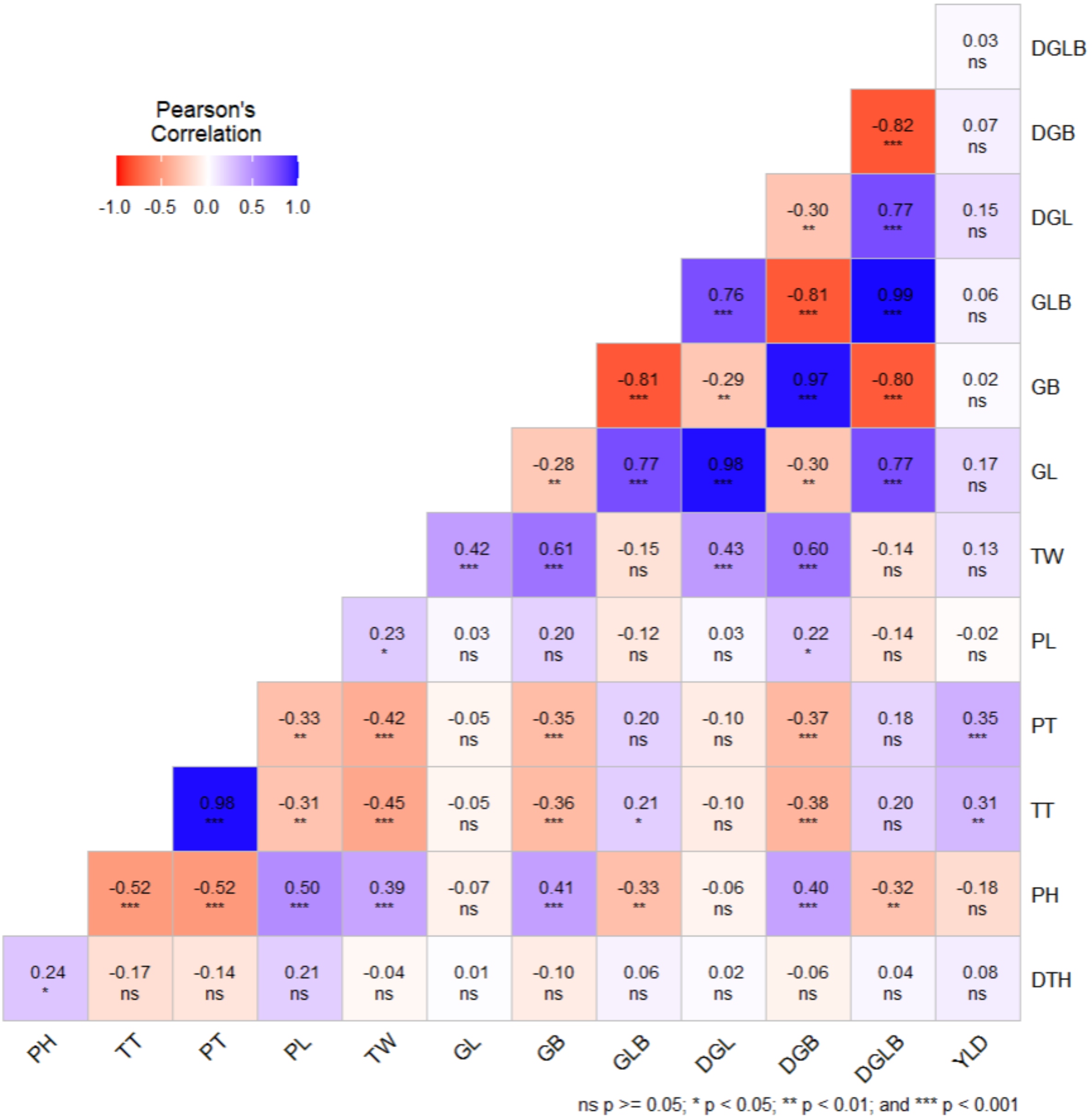

Figure 1. Estimation of correlation coefficient

4. CONCLUSION

The germplasm lines exhibited considerable genetic variation, providing scope for selection of desired variant in the studied traits or contrasting variants for a trait that can be effectively used as parents in breeding program. The trait days to heading exhibited low genetic variability, while rest traits exhibited moderate to high genetic variability. Additionally, GAM was high for all traits except days to heading (moderate). In general the population has adequate variation for studied traits and variants that deviate significantly from the mean. These variants can be effectively utilized in future breeding programs based on need but breeders should emphasize on attributing traits while dealing with dependent trait. For example, while improving grain yield, breeder should also focus on its attributing traits such as number of tillers per plant and number of productive tillers per plant.

Disclaimer (Artificial intelligence)

Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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