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Analysis of Genetic Variability, Heritability and Genetic Advance for Yield and Yield Associated traits in Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was conducted using 27-rice germplasm for the thirteen traits studied at the agriculture research farm, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during the *kharif* season 2022. A Randomized Block Design (RBD) with three replications were used to study genotypic and phenotypic variances, heritability, GCV, PCV, genetic advance, and genetic advance as a percentage of the mean (GAM %) for all the yield contributing traits. Harvest index recorded highest GCV (23.56) and PCV (25.06) respectively while Single plant yield had highest heritability h^2 (92.11 %). However, Number of spikelets per panicle (45.60), number of filled grains per panicle (32.65), plant height (20.81) had high genetic advance. Moreover, Harvest index (45.64) had highest genetic advance as percent mean (GAM).

Key words: Variability, Broad sense heritability, Genetic advance, Rice

Introduction

Rice (*Oryza sativa* L.) is a short-day, C3 plant that is cultivated primarily in Asian agroecosystems. It belongs to the family Poaceae (Graminae) and is an annual, semi-aquatic, and self-pollinating crop. There are two main domesticated species of rice: Asian rice (*Oryza sativa* L.) and African rice (*Oryza glaberrima* Steud.), both possessing the genome AA ($2n = 24$). According to data from the Punjab Agriculture Department, paddy cultivation covers approximately 87% of the total area dedicated to *kharif* crops (grown from June to October) in Punjab. The data for the current 2022-23 *kharif* season reveals that out of the total 3.59 million hectares under *kharif* crops, paddy was cultivated on 3.13 million hectares (Anonymous, 2023). In India, it accounts for

20-25% of agricultural production and ensures food security for over half of the population. Rice production in India constitutes 55% of the total cereal production, with 116.48 million tons of rice being produced in the year 2018-19 from approximately 44.16 million hectares of planted rice land (AGRISTAT, 2019).

Materials and Method

The current study was conducted at the agriculture research farm of the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during the 2022 season. A Randomized Block Design (RBD) with three replications was employed for various observations recorded, including 27 rice germplasm *viz.* Haldi

Chudi, Taiwan black, Java Pula, Siddha Sannalu, Kalajeera, Karikalave, HMT paddy, MTU 1061, MTU 1064, MTU 1318, PR 114, PR 122, Banspatri, Siddha Sanna, SannaJujulu, Gani, Nagara, RNR little, Radha 4, MTU 7029, MTU 1166, PR 118, PR 111, PR 126, PR 113, PR 121 and PR 128 for the thirteen traits studied including Days to 50% flowering, Plant height (cm), Panicle length (cm), Number of tillers per plant, Number of spikelets per panicle, Flag leaf length (cm), Flag leaf width (cm), Number of filled grains per panicle, Days to maturity, Single plant yield (g), Test weight (g), Biological yield (g) and Harvest Index.

The recorded observations were analyzed statistically using the procedure for analysis of variance to estimate the variability. The genotypic and phenotypic variances were calculated using the formula provided by Johnson *et al.* (1955). The genotypic and phenotypic coefficients of variation were estimated following the methods described by Burton (1952) and Singh and Chaudhary (1985). The broad-sense heritability (h^2b) was determined using the approach proposed by Hanson *et al.* (1956). The estimation of genetic advance was conducted using the formulae given by Johnson *et al.* (1955) and Allard (1960).

Results and Discussion

ANOVA of the thirteen traits tabulated in Table 1 exhibited significant variance at 1 percent level, indicating a substantial range of variability among the germplasm, except for the days to 50 % flowering,

which showed significance at the 5 percent level. These findings suggest that selection based on these traits can result in significant improvements, as there is a considerable degree of variability across all the characters as per Chaudhary *et al.* (2023).

Result tabulated in Table 2 presents the genotypic and phenotypic variances, heritability, GCV, PCV, genetic advance, and genetic advance as a percentage of the mean (GAM %) for all the yield contributing traits represented in Figure 1.

Genetic variability

The basic prerequisite for carrying out any crop enhancement effort is the presence of sufficient genetic heterogeneity. Generally, PCV values will be higher than their respective GCV values indicating that slight environmental influences.

Genotypic coefficient of variation (GCV)

Harvest index (23.56) recorded highest GCV followed by Single plant yield (21.86), 1000 grain weight (20.91). Number of tillers per plant (14.09), number of spikelets per panicle (12.57), flag leaf length (12.59), flag leaf width (14.11), number of filled grains per panicle (11.10) recorded moderate GCV. While, the traits like panicle length (8.84), plant height (9.86), days to maturity (5.68), biological yield (6.41) and days to 50 % flowering (3.96) recorded low GCV.

Phenotypic coefficient of variation (PCV)

Harvest index (25.06) recorded highest PCV followed by single plant yield (22.77), 1000 grain weight (22.10). Number of tillers per plant (15.83),

Table 1. Analysis of variance for 13 characters in rice

S. No.	Source Degrees of freedom	Mean Sum of Squares (MSS)		
		Replication 2	Treatment 26	Error 52
1	Days to 50% flowering	164.9750	95.488*	53.68
2	Plant height (cm)	18.8590	537.524**	77.186
3	Panicle length (cm)	0.9920	16.682**	2.321
4	Number of tillers plant ⁻¹	2.3380	13.612**	1.099
5	Number of spikelets panicle ⁻¹	63.2290	1893.162**	121.234
6	Flag leaf length (cm)	1.4460	48.358**	6.062
7	Flag leaf width (cm)	0.0110	0.183**	0.013
8	Number of filled grains panicle ⁻¹	22.9820	1202.643**	143.183
9	Days to maturity	11.2960	246.198**	79.716
10	Single plant yield (g)	6.9450	112.903**	3.136
11	1000 grain weight (g)	1.8750	64.643**	2.427
12	Biological yield (g)	1.9120	151.03**	62.353
13	Harvest Index	00	0.019**	0.001

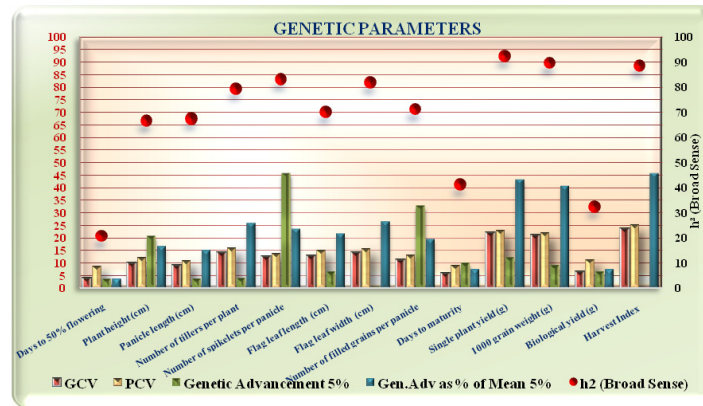


Fig. 1. Genotypic and Phenotypic variance, GCV, PCV, Heritability and Genetic Advance.

number of spikelets per panicle (13.80), flag leaf length (15.06), flag leaf width (15.61), number of filled grains per panicle (13.15) panicle length (10.77), plant height (12.09), biological yield (11.31) recorded moderate PCV. While, the traits like days to maturity (8.87) and days to 50 % flowering (8.72) recorded low PCV.

In the present study, the phenotypic coefficients of variation were slightly greater than the genotypic coefficients of variation indicated that environment had an impact on the expression of the character under study. High values for GCV and PCV were recorded for Harvest index, single plant yield and 1000-grain weight. This suggested the possibilities for making further improvement using these traits. Suman *et al.* (2020) observed highest magnitude of

GCV and PCV biological yield. Nithya *et al.* (2020) also report these findings for grain yield per plant and productive tillers per plant, Saha *et al.* (2019) for number of grains per panicle. Low GCV and PCV values of the traits indicated low variance and suggested that negligible influence of environment; hence phenotypic would be effective for these traits. These findings were in accordance with the result reported by Sandeep *et al.* (2018) and Amegan *et al.* (2020) for days to 50% flowering and days to maturity.

Heritability h² (Broad Sense)

Single plant yield had highest heritability h² (92.11 %) followed by 1000 grain weight (89.52 %), harvest index (88.43 %), number of spikelets per panicle

Table 2. Analysis of Genotypic and Phenotypic variance, GCV, PCV, Heritability and Genetic Advance.

S. No.	Characters	σ ² g	GCV	σ ² p	PCV	h2 (Broad Sense)	GA (5%)	GAM (5%)
1	Days to 50% flowering	13.94	3.96	67.62	8.72	20.61	3.49	3.70
2	Plant height (cm)	153.45	9.86	230.63	12.09	66.53	20.81	16.57
3	Panicle length (cm)	4.79	8.84	7.11	10.77	67.35	3.70	14.94
4	Number of tillers plant ⁻¹	4.17	14.09	5.27	15.83	79.14	3.74	25.81
5	Number of spikelets panicle ⁻¹	590.64	12.57	711.88	13.80	82.97	45.60	23.58
6	Flag leaf length (cm)	14.10	12.59	20.16	15.06	69.93	6.47	21.69
7	Flag leaf width (cm)	0.06	14.11	0.07	15.61	81.72	0.44	26.28
8	Number of filled grains panicle ⁻¹	353.15	11.10	496.34	13.15	71.15	32.65	19.28
9	Days to maturity	55.49	5.68	135.21	8.87	41.04	9.83	7.50
10	Single plant yield (g)	36.59	21.86	39.73	22.77	92.11	11.96	43.21
11	1000 grain weight (g)	20.74	20.91	23.17	22.10	89.52	8.88	40.76
12	Biological yield (g)	29.56	6.41	91.91	11.31	32.16	6.35	7.49
13	Harvest Index	0.01	23.56	0.01	25.06	88.43	0.15	45.64

*Significant at 1% and 5% level of significance respectively.

σ²g = Genotypic variance. σ²p = Phenotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, GA= Genetic advance, GAM (%) = Genetic advance as percent of mean.

(82.97 %), flag leaf width (81.72 %), Number of tillers per plant (79.14%), number of filled grains per panicle (71.15 %), flag leaf length (69.93 %), panicle length (67.35 %) and plant height (66.53 %). Biological yield had moderate heritability h^2 (32.16 %). Days to 50 % flowering (20.61%) had low GCV. This indicates that the trait is more influenced by environmental factors and governed by non-additive gene action. These results were in accordance with the results of Akshay *et al.* (2022).

Genetic Advance 5% (GA)

Number of spikelets per panicle (45.60), number of filled grains per panicle (32.65), plant height (20.81) had high genetic advancement 5%. Single plant yield (11.96) had moderate genetic advancement 5% (GA). While rest of the traits like days to 50 % flowering (3.49 %), panicle length (3.70), number of tillers per plant (3.74%), flag leaf length (6.47), flag leaf width (0.44), days to maturity (9.83), 1000 grain weight (8.88), biological yield (6.35) and harvest index (0.15) had low genetic advancement 5 % (GA).

Genetic Advance as Percent Mean (GAM)

Harvest index (45.64) had highest genetic advance as percent mean (GAM) followed by single plant yield (43.21 %), 1000 seed weight (40.76 %), flag leaf width (26.28 %), number of tillers per plant (25.81 %), number of spikelets per plant (23.58 %), flag leaf length (21.69 %). Plant height (16.57%), panicle length (14.94%), number of filled grains per panicle (19.28) had moderate genetic advance as percent mean (GAM). While, the traits like days to 50 % flowering (3.70), days to maturity (7.50) and biological yield (7.49) had low genetic advance as percent mean (GAM). These results are in agreement with the results of Kumar *et al.* (2020) and Naveen *et al.* (2022).

Conflict of interest

No conflict of interests directly or indirectly related to the work submitted for publication.

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