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Analysis of genetic variability, heritability and genetic advance for yield and yield-associated traits for rice (*Oryza sativa L.*) improvement

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Abstract

Forty-six genotypes of rice were studied for genetic variability, heritability and genetic advance for thirteen economically important characters during *kharif* 2023-24 in SIF (Student's Instructional Farm), Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) India. Significant mean square values were observed across all traits. The estimates of phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for each trait, indicating a considerable environmental influence on these characteristics. The broad sense heritability were estimated high for days to maturity (93.46), plant height (92.38), days to 50 % flowering (90.55), grain yield/plant(85.05), number of spikelets per panicle (81.65), number of fertile spikelets per panicle (81.48), biological yield per plant (79.42), 1000 grain weight (75.90) whereas , productive tillers/plant (31.39), grain yield/plant (28.63), number of fertile spikelets per panicle (28.30), 1000-grain weight (22.45) and number of spikelets per panicle (21.90) revealed high genetic advance. The considerable heritability and genetic advance observed in numerous traits suggest the prevalence of additive genetic effects, indicating potential enhancement through targeted selection. Thus, the findings underscore ample variability across all genotypes, facilitating the development of superior rice varieties, with the identified traits serving as viable selection criteria.

Key words: Variability, broad sense heritability, genetic advance, rice

1. Introduction

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the family Poaceae with the chromosome number $2n = 24$ (Kumar *et al.*, 2020). The cultivated rice plant is an annual grass, leaves are long and flat and with hollow stems grows to about 1.2 metres in height. It stands as the predominant staple food for a significant portion of the global populace (Samal *et al.*, 2018). Over half of the world's inhabitants rely on rice for essential sustenance, with its cultivation spanning across Asia, parts of Africa, and Latin America, encompassing three main types: *japonica*, *indica*, and *javanica*. As the largest food crop worldwide, rice fulfills the daily caloric requirements of millions, playing a vital role in the Indian economy by serving as the primary food source for two-thirds of its population (Singh *et al.*, 2008). The adage "Rice is life" reflects its significance, being not only the staple diet for over 70% of Indians but also a livelihood source for approximately 120-150 million rural households. However, rapid population expansion poses a significant challenge in addressing hunger and malnutrition for sustainable development. Total production of rice in world is estimated at record 502.98 million metric tonnes. In India, estimated the area, production and productivity of rice was 46.38 million hectares (mha), 130.29 million tonnes (mt) and 2809 kg/ha, respectively, during 2021-22 (Anonymous, 2021-22, Dett. of Agriculture and Farmers Welfare, MoA & FW). Golden rice has been genetically modified to synthesize β -carotene within its grains, aiming to combat the widespread issue of vitamin A deficiency. Additionally, elevated levels of iron and zinc have been achieved through genetic engineering methods. The rice grain comprises significant proportions of starch, protein, fiber, lipids, minerals (such as potassium, phosphorus, magnesium, calcium, sodium, and iodine), and essential nutrients (including thiamine, riboflavin, niacin, pyridoxine, and folic acid), along with vitamins (Oko *et al.*, 2012).

Line \times tester technique is useful in deciding the relative ability of female and male lines to produce desirable hybrid combinations. Genotypic coefficient of variation (GCV) measures the extent of genetic variability within a population, providing insights into the inheritable traits' variation (Singh, 2019). Phenotypic coefficient of variation (PCV) assesses the overall variability in a population, encompassing both genetic and environmental influences on observed traits. GCV estimates genetic diversity, aiding in the selection of superior genotypes for breeding programs, while PCV reflects the total variation, guiding in trait selection across diverse environments (Bhardwaj *et al.*, 2018). Heritability estimates offer insights into the hereditary portion of variability passed on to

future generations (Kumar *et al.*, 2014). Genetic advance, on the other hand, informs about the anticipated genetic progress through the selection of superior individuals. These estimates hold considerable importance for plant breeders in formulating effective selection strategies. This gathered information will guide the selection of optimal parent plants and the adoption of suitable breeding techniques to cultivate high-yielding rice varieties or hybrids. Heritability estimates the proportion of phenotypic variation in a population that is due to genetic factors, providing insights into the degree to which traits are inherited. Broad-sense heritability (h^2) considers all genetic variation, including additive, dominance, and epistatic effects, offering a broader view of genetic influence on traits (Falconer & Mackay, 1996). Narrow-sense heritability (h^2) specifically measures the proportion of phenotypic variance attributed to additive genetic effects alone, indicating the potential response to selection in breeding programs. Genetic advance (GA) is a measure used in plant breeding to quantify the expected improvement in a trait due to selection. It is calculated as the difference between the mean of the selected individuals and the mean of the original population, scaled by the selection differential (Falconer & Mackay, 1996). Genetic advance can be expressed as a percentage of the population mean and is particularly useful in predicting the potential gain from selection for a specific trait. High genetic advance indicates that selection is likely to be effective for improving the trait, whereas low genetic advance suggests limited potential for improvement through selection (Johnson *et al.*, 1955).

2. Materials and Methods

The present investigation was carried out during *kharif*, 2023-2024 in SIF (Student's Instructional Farm), Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) India. A total of 46 genotypes were utilized in the study, comprising 10 parental lines, 3 testers, and their resulting 30 F1 crosses with 3 check varieties. The parental lines included Akhtahwa BBK, IET-6663, Bhadani-I, Bhadani-II, Tinpakhiya, IET-16605, Sorahi, Binni Deoria, Dhaniya, and Akhtahwa, while the testers consisted of NDR-6093, NDR-702, and HUR-1304, alongside the check varieties Sarju-52, NDR-97, and NDR-2065. Crosses were generated through a line \times tester mating scheme, resulting in a total of 30 crosses among the three testers and ten lines. The experimental setup involved 46 genotypes evaluated with three replications in a Randomized Block Design during the 2023 kharif, at SIF (Student's Instructional Farm). Seedlings aged 25 days were transplanted at a spacing of 20 cm between rows and 15 cm within rows, with meticulous attention to maintaining uniform

plant populations across treatments per replication. Various agronomic traits such as days to 50% flowering, days to maturity, plant height, flag leaf area (cm^2), number of spikelets per panicle, number of fertile spikelets per panicle, spikelet fertility (%), 1000 grain weight (g), biological yield per plant (g), harvest index (%), and grain yield per plant (g) were recorded and subjected to statistical analysis. Variability was estimated following the procedure outlined by Panse and Sukhatme (1957), while phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated using the formula proposed by Burton (1952). Broad-sense heritability (h^2) was determined according to Burton and De Vane (1953), and genetic advance, indicative of expected genetic gain, was computed using the method outlined by Johnson et al. (1955).

3. Results and Discussion

3.1 Variability Parameters

Significant variances were observed across all genotypes for various traits examined, indicating ample diversity among them. This diversity suggests that selective breeding could effectively yield desired crop plant varieties [Table 1]. Confirming the presence of adequate genetic variability is crucial, as it serves as a fundamental prerequisite for crop improvement efforts.

Table 1: Analysis of variance for RBD for 13 characters in rice genotype

S. No.	Characters	Source of variations		
		Replications	Treatments	Error
	Degree of freedom	2	32	64
1	Days to 50% flowering	1.83	116.37**	5.99
2	Days to maturity	24.77*	165.92**	5.26
3	Plant height (cm)	19.39	440.44**	12.35
4	Productive tillers per plant	2.43	17.12**	1.87
5	Panicle length (cm)	3.13	6.19**	3.46
6	Flag leaf area (cm^2)	7.47	28.05**	3.82
7	Number of spikelets per panicle	29.21	1394.87**	116.62
8	Number of fertile spikelets per panicle	203.58	1777.62**	141.59
9	Spikelet fertility (%)	45.97*	85.15**	11.45
10	1000-seed weight(g)	8.68*	25.25**	2.21
11	Biological yield per plant (g)	11.23	117.65**	7.83
12	Harvest index (%)	7.41	27.05**	6.87
13	Grain yield/plant(g)	9.24*	51.10**	2.65

** Significance at 1% level of probability, * Significance at 5% level of probability

Genotypic (GCV) and phenotypic (PCV) coefficient of variation were calculated for each character and presented in Table 2. The magnitude of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the

characters under study. The difference between genotypic and phenotypic coefficient of variation was less for all characters which was an indication of the more influence of the environment over characters. The characters studied in the present study exhibited low, moderate and high values of PCV and GCV. Among agronomical characters, the high estimates of phenotypic coefficient of variation (>20%) were recorded for productive tillers per plant (21.22), but its GCV recorded moderate level (17.98). The characters which exhibited moderate estimates (10-20%) of GCV and PCV were number of fertile spikelets per panicle (15.22 and 16.86), grain yield per plant (15.07 and 16.34), 1000-grain weight (12.51 and 14.36), number of spikelets per panicle (11.77 and 13.03), biological yield per plant (10.03 and 11.26). Moderate value of PCV was also recorded for plant height (10.10) and flag leaf area (10.08) but its GCV recorded low value. Rest traits viz., days to 50% flowering, days to maturity, panicle length, spikelet fertility and harvest index showed low estimates (<10%) of GCV and PCV. Acharya *et al.* (2019), Sirigadi *et al.* (2019), Singh *et al.* (2020), Shrestha *et al.* (2021) and Paramanik *et al.* (2024) also reported high PCV and GCV for most of the yield attributing traits. The high magnitude of phenotypic variation were composed of high GCV and less of the ECV, indicates the presence of high genetic variability with less environmental influence. Therefore, on the basis of phenotype alone selection can be effective for the improvement of these characters. Similar results for low to moderate values of PCV and GCV were also found by Rajpoot *et al.* (2017).

3.2 Heritability and Genetic advance

Heritability estimates offer insights into the transmission of traits from parents to offspring, aiding in the assessment of both genetic and environmental influences on phenotypic variation and facilitating selection processes. These estimates also enable breeders to anticipate the degree of improvement achievable through various selection intensities. According to Johnson *et al.* (1955), the combination of heritability estimates with genetic advance is more informative for selection than heritability alone. In this study, broad-sense heritability was calculated as a percentage for all traits examined in [Table 2]. The highest broad sense heritability belonged to days to maturity (93.46) while panicle length (27.12%) had the lowest. High estimates of broad sense heritability (>75%) were recorded for days to maturity (93.46), plant height (92.38), days to 50 % flowering (90.55) grain yield/plant (85.05), number of spikelets per panicle (81.65), number of fertile spikelets per panicle (81.48), biological yield per plant (79.42), 1000-g weight (75.90). The moderate estimates of heritability (50-75%) were recorded for productive tillers/plant (71.79), flag leaf area (71.73), and spikelet fertility (56.65). The trait possessed low

estimates of heritability (<50%) in broad sense for harvest index (43.27) and panicle length (27.12). The heritability of a trait significantly influences the strategies chosen for population enhancement, with hybridization and other selection methods proving effective for traits exhibiting high heritability (Robinson, 1966). The accuracy of phenotypic values relies heavily on heritability estimates, making traits with high heritability particularly conducive to effective selection. Consistent findings regarding heritability were also documented by Kishore *et al.* (2015), Singh *et al.* (2020), Parimala and Devi (2019) and Kujur *et al.* (2023).

Table 2: A summary illustrating the phenotypic and genotypic coefficients of variability (PCV and GCV), along with heritability (h² b) and genetic advance for various traits in rice

S. No.	Characters	Mean	Range		Coefficient of Variation		Heritability (%)	GA	GA % Mean
			Min	Max	GCV (%)	PCV (%)			
1	Days to 50% flowering	86.28	70.00	100.00	7.85	8.25	90.55	13.28	15.39
2	Days to Maturity	117.16	97.00	133.00	6.74	6.97	93.46	15.72	13.42
3	Plant height (cm)	120.90	85.16	146.37	9.71	10.10	92.38	23.24	19.22
4	Productive tillers per plant	11.75	6.37	18.34	17.98	21.22	71.79	3.69	31.39
5	Panicle length (cm)	26.13	19.34	30.76	3.99	7.66	27.12	1.12	4.28
6	Flag leaf area (cm ²)	33.60	24.26	41.26	8.53	10.08	71.73	5.00	14.89
7	Number of spikelets per panicle	175.13	119.34	229.34	11.77	13.03	81.65	38.37	21.91
8	Number of fertile spikelets per panicle	149.11	95.67	216.37	15.22	16.86	81.48	42.19	28.30
9	Spikelet fertility (%)	84.89	69.13	99.36	5.01	6.65	56.65	6.59	7.76
10	1000-seed weight (g)	20.89	13.26	26.34	12.51	14.36	75.90	4.69	22.45
11	Biological yield per plant (g)	56.01	42.26	71.26	10.03	11.26	79.42	10.32	18.42
12	Harvest index (%)	44.81	30.75	54.07	5.46	8.29	43.27	3.31	7.39
13	Grain yield/plant (g)	25.19	15.97	34.26	15.07	16.34	85.05	7.21	28.63

The traits under investigation were assessed for high, moderate, and low estimates of genetic advance as a percentage of the mean. The value of genetic advance as per cent of mean was highest for productive tillers/plant (31.39), whereas low for panicle length (4.28). High genetic advance in percent of mean (>20%) was recorded for productive tillers/plant (31.39), grain yield/plant (28.63), number of fertile spikelets per panicle (28.30), 1000-g weight (22.45) and number of spikelets per panicle (21.90) while, plant height (19.22), biological yield per plan (18.42), day to 50% flowering (15.39), flag leaf area (14.89), days to maturity (13.42) had moderate estimates (10-20%) of heritability. Rest traits i.e., Spikelet fertility (7.76), harvest index (7.39) and panicle length (4.28) were possessed low (<10%) estimates of heritability in the environment. Genetic advance estimates are depicted in Table 2. Genetic advance offers more dependable insights into the efficacy of selection for enhancing traits in the new population compared to the base or original population. Comparable findings were also documented by Kishore *et al.*, (2015), Singh (2020) and Saini *et al.* (2023). Broad-sense heritability encompasses both additive and epistatic gene effects, thus ensuring reliability primarily when coupled with a high genetic advance value. Therefore, the combination of heritability estimates with genetic advance, rather than heritability alone, proves more valuable in anticipating the effectiveness of selection, as emphasized by Johnson *et al.*, (1955).

In the present study the characters which showed high heritability coupled with high genetic advance was observed for the characters grain yield/plant, number of spikelets per panicle, number of fertile spikelets per panicle, and 1000-g weight. Traits exhibiting high heritability along with substantial genetic advance are governed by additive gene action (Panse and Sukhatme, 1957) and can be enhanced through straightforward or progeny selection techniques. Conversely, traits demonstrating high heritability combined with moderate or low genetic advance can be enhanced by interbreeding superior genotypes within segregating populations developed through combination breeding (Samadhia, 2005). In the present study high heritability associated with high genetic advance for yield attributing characters was in accordance with the Parimala and Devi (2019) and Saha *et al.* (2019).

4.

Conclusion

The analysis of variance revealed highly significant difference among the genotypes for all the characters under study. From the result, it was concluded that among the yield and its contributing characters days to maturity followed by plant height, days to 50 % flowering, grain yield/plant, number of spikelets per panicle, number of fertile spikelets per panicle, biological yield per plant and 1000-g weight could be easily inherited to their next generations due to high heritability, whereas the characters viz; harvest index and panicle length had low heritability which indicates that these characters are mainly influenced by environmental factors. Characters viz.; grain yield/plant, number of spikelets per panicle, number of fertile spikelets per panicle, and 1000-g weight showed maximum values of heritability and genetic advance, so for these characters direct selection can be adopted, whereas the characters viz; productive tillers per plant showed high values PCV, heritability and genetic advance. Thus, one should select these characters for direct selection.

5. References

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