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ESTIMATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

The Present study was carried out to estimate the genetic variability, heritability and genetic advance for grain yield and its attributes in rice (*Oryza sativa* L.) under irrigated conditions during Kharif 2022 at Agricultural Research Farm, Institute of Agricultural & Natural Sciences, DDU Gorakhpur University, Gorakhpur (U.P.), India. Fifteen different rice genotypes were used in a randomized block design with three replications and data was recorded for grain yield per plant and twelve yield contributing characters. The results of analysis of variance revealed highly significant differences among genotypes for all characters, establishing the existence of high genetic variability. Grain yield per plant recorded a wide range from 22.00 to 38.67 g with very high heritability (95.9%) and genetic advance as percent of mean (40.59%), establishing a strong possibility for improvement through selection. Effective tillers per plant varied from 7.67 to 23.33, establishing high variability (GCV 32.02%, PCV 33.17%) and high genetic advance (63.66%), establishing the predominance of additive gene effects. Biological yield varied from 48.36 to 78.59 g, with very high heritability (98.7%), GCV 17.46% and genetic advance (35.58%). Plant height varied from 87.17 to 151.67 cm and recorded high heritability (97.7%) with GCV/PCV 16.48% and genetic advance as percent of mean 33.16%. Days to 50% flowering (97.00-133.67 days) and days to maturity (125.67-161.67 days) also recorded high heritability (96.6% and 94.1%, respectively). Grain breadth recorded comparatively low heritability (31.7%) and low genetic advance (6.69%), establishing a limited scope for improvement through selection. Overall, high heritability coupled with high genetic advance for grain yield per plant, effective tillers per plant, biological yield and plant height suggests that these traits can be effectively utilized as reliable selection criteria for improving rice productivity.

Keywords **:** Rice, Genetic variability, Heritability, Genetic advance.

Introduction

Rice (*Oryza sativa* L.) is one of the most widely grown cereals and continues to play an imperative role in the food security scenario. It is the staple diet for a significant portion of the global population, especially in the Asian region, where rice is an essential component that adds to the calorie intake (Muthayya *et al.*, 2014). Not only is it an essential source of carbohydrates, but it is also rich in other micronutrients and bioactive compounds, albeit the nutrient values change based on the processed nature and whether they are polished or not (Fukagawa and Ziska 2019). Due to the ever-growing population and the need to develop steady food security, advances in rice productivity and adaptability continue to receive due importance (FAO, 2022). Rice productivity can be made more efficient as grain production in crops like rice is a complex character whose generation is controlled by the

collective action of various component traits like tillering, panicle and grain weight, which are greatly affected by their environments (Allard, 1960). Therefore, crop improvement programmes must focus not only on increasing yield but also on stabilizing yield under variable conditions through selection of adaptive and efficiently partitioning genotypes. In any breeding programme, the fundamental prerequisite for genetic improvement is the presence of sufficient variability in the germplasm, because selection response depends on the magnitude of heritable genetic differences among genotypes (Allard, 1960). Consequently, quantifying genetic variability for yield and yield-attributing traits in rice is essential for identifying superior genotypes and formulating effective selection strategies. Genetic variability is commonly assessed through parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), which estimate the extent of variability present at genotypic and phenotypic levels, respectively (Burton, 1952). In most quantitative traits, PCV exceeds GCV due to environmental influence on trait expression and the magnitude of difference between PCV and GCV provides insight into the degree of environmental modulation and the reliability of phenotypic selection (Burton, 1952). Reliable estimation of variance components generally relies on appropriate experimental designs and statistical procedures for analysis of variance, which form the basis for partitioning total variation into genotypic and environmental components (Panse and Sukhatme 1967). Heritability is another important genetic parameter that indicates the proportion of phenotypic variance attributable to genetic causes. High heritability suggests that observed phenotypic differences among genotypes are largely genetic and that selection based on phenotype may be effective (Singh and Chaudhary 1985). However, heritability alone does not fully predict the expected gain from selection, because it does not account for the magnitude of genetic variance relative to the population mean. Therefore, genetic advance and genetic advance as percent of mean are widely used along with heritability to assess selection efficiency, as these parameters represent the expected improvement in population mean following selection under a given selection intensity (Allard, 1960; Singh and Chaudhary 1985). High heritability coupled with high genetic advance generally indicates predominance of additive gene action and better response to direct selection, whereas high heritability with low genetic advance may suggest non-additive gene effects and greater environmental influence (Allard, 1960).

Various studies conducted on rice have established that variation parameters, heritability and genetic advance can be useful for identifying those characters most decisive in propelling yields forward. This is crucial for plant breeders, allowing them to target characters that actually increase yields (Demeke *et al.* 2023). Established practice suggests that the characters associated with yield can be highly variable depending on their genetic background or environment in which they are tested, making it critical to consider such factors in local geographically associated materials (Sarker and Hasan-Ud-Daula 2020; Nithya *et al.*, 2020). of particular note is the consideration of the variation in important traits like effective tillers per plant, grains per panicle and thousand grain weight. These traits tend to result in increased yields and more efficient harvesting methods because of the direct relation to increased yields and efficient harvesting methods (Pandey *et al.*, 2018; Dhakal *et al.*, 2020). These findings indicate that identifying traits showing high heritability and high genetic advances would provide reliable criteria for their use in breeding programs for the development of high-yielding types. With this background, testing a set of rice genotypes for irrigated conditions can serve as a means to assess genetic variability and genetic gain for economically important traits. This can aid in their breeding and guide breeding programs for improvement in yield traits. This study was therefore planned to estimate genetic variability, broad sense heritability and genetic gain for grain yield per plant and yield contributing traits in order to identify traits and genotypes for their subsequent use in breeding programs.

Materials and Methods

The present investigation entitled "Correlation and path analysis studies in genotypes of rice (*Oryza sativa* L.)." was carried out during *Kharif* 2022 at Agricultural Research Farm, Institute of Agricultural & Natural Science, DDU Gorakhpur University Gorakhpur (U.P.). The experiment material comprised of 15 genotypes of rice (*Oryza sativa* L.) representing diversity for yield and yield contributing characters in irrigated conditions. The experiment material consisted of late maturing and tall genotypes was obtained from germplasm maintained at Department of Genetics and Plant Breeding, Institute of Agricultural & Natural Science, DDU Gorakhpur University Gorakhpur (U.P.). Five plants were randomly selected from each entry in all three replications. The plants are selected from the middle of plots, excluding border plants. Observations were recorded for grain yield per plant and 12 other component traits. Days to 50% flowering and days to maturity were computed on plot basis and

data was subjected to statistical analysis. The variability was estimated as per procedure for analysis of variance suggested by (Panse and Sukhatme 1967) PCV and GCV were calculated by the formula given by (Burton, 1952) heritability in broad sense (h^2) by Singh and (Chaudhary, 1985) and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Allard (1960).

Results and Discussion

Genetic variability and analysis of variance

The presence of adequate genetic variability in breeding material is a fundamental prerequisite for effective crop improvement, particularly for complex quantitative traits such as grain yield. ANOVA results revealed highly significant differences ($P \leq 0.01$) among the 15 rice genotypes among the 13 traits, indicating the existence of ample genetic variability in the breeding material (Table 2). The significance of the mean squares of flowering and maturation period, plant height, yield attributes and grain characteristics has already indicated the genetic variability existing in the rice genotypes, which would make a good source for future hybridization programs.

Phenotypic and genotypic coefficients of variation

The magnitude of phenotypic (PCV) and genotypic (GCV) coefficients of variation provides insight into the extent of variability available for selection and the influence of the environment on trait expression. Overall, at least for most traits, values of PCV are higher than values of GCV (Table 3 and Figure1), which indicated some effect of environmental factors on trait expression. However, for some traits, differences between PCV and GCV are not very large thus, for such traits, phenotypic selection may act effectively because masking by environment is not very strong in such cases.

Among the yield-related traits, the highest PCV and GCV value was found in effective tillers per plant, followed by grain yield per plant and biological yield. This trend was followed for PCV and GCV in descending order: effective tillers per plant > grain yield per plant > biological yield. PCV and GCV values for grain length > plant height > grain breadths. This indicates that there was sufficient variability in the characters related to the formation of yield, which in turn indicates that there was a good scope for their improvement. However, the lowest PCV and GCV values were found in harvest index, followed by days to maturity and grain breadths. This indicates that there was less variability in these characters, which in turn indicates higher stability and lower scope for their improvement. Similar findings on variability in related

yield and grain characteristics in rice are in agreement with (Anjaneyulu *et al.*, 2010), (Singh *et al.*, 2011), (Bhadru *et al.*, 2012), (Pandey *et al.*, 2018), and (Sarker and Hasan-Ud-Daula 2020).

Heritability and genetic advance

The broad-sense heritability (h²), indicated, estimates to what extent variation is programmed in the genetic makeup, while on the other hand, genetic advance (GA) and GA based on the mean provides an indicator regarding the scope of improvement that is to be anticipated under the influence of selection. The major traits had high estimates of heritability (Table 3 and Figure 1), indicating strong genetic control and suggesting that phenotypic selection could be reliable for these characters.

The highest heritability was recorded for biological yield (98.7%), followed by plant height (97.7%), days to 50% flowering (96.6%) and grain yield per plant (95.9%) (Table 3 and figure 1). High heritability coupled with moderate-to-high genetic advance as a percentage of mean for these traits indicates the predominance of additive gene effects and supports the effectiveness of direct selection. Such as, the trait grain yield per plant recorded a high value for heritability of 95.9% with a relatively high GA% of 40.59%, indicating the efficiency of the trait in improving the other trait, which is the yield. Similarly, the trait biological yield recorded a very high value for heritability of 98.7% with a GA% of 35.58%, indicating the efficiency of the trait in improving the other trait, which is the yield. Data showed that effective tillers per plant with 93.2% heritability and a GA value as a percent of mean of 63.66% is under stronger additive genetic control and has ample scope for improvement through selection. This is substantial, given that the number of functional tillers is an important yield-defining factor for rice and a prime breeding objective for rice improvement. These observations are not different from earlier literature, wherein a tendency for greater efficiency of selection for parameters having high heritability and a better association with yield has been indicated (Dhakal *et al.*, 2020; Nithya *et al.*, 2020; Pandey *et al.*, 2018; Sarker and Hasan-Ud-Daula, 2020).

In contrast, more moderate heritability estimates were obtained from grains per panicle at 72.3%, harvest index at 67.9%, and grain length at 65.4% (Table 3 and Figure 1). This is indicative that the latter three traits will be influenced by both genetic and environmental factors thus, gains via breeding will likely only be achieved through strict selection under replicated trials or over varying environments. on the

other hand, grain breadth was characterized by low heritability at 31.7% with a small GA% of 6.69%, revealing strong environmental influence and limited direct selection response. For such traits, indirect selection or testing over various environments may be prerequisite to relatively steady improvement.

Conclusion

This experiment indicates that there is actual dispersion of genetic variation among the fifteen rice genotypes regarding the yield per plant and the attributes that come with it. The variation in all traits is highly significant, emphasizing the diversity that is to be found. The greatest variability is to be found in effective tillers per plant, yield per plant, biological yield and plant height, emphasizing that there is great scope for enhancement via selection. The broad-sense heritability is found to be high in biological yield, plant height, days to 50% flowering and yield per plant, emphasizing that these traits are predominantly governed by genetic potential and can thus be safely selected based on observable traits. The traits that possess both high heritability and great values for genetic advance percentage mean values in effective tillers per plant, yield per plant and biological yield suggest additive gene effects and great potential to respond to selection. As such, these traits can thus be said to act as major indicators in the rice breeding scheme to develop superior-yielding strains under irrigated environments.

Table 1: List of 15 Rice Genotypes used in the present study

| S. No.	Genotype	Source of genotype
1.	Shambha Mahsuri	CRD, Gorakhpur
2.	Sarju – 52	ANDUAT, Ayodhya
3.	Bauna Kala namak (SL-03)	CRD, Gorakhpur
4.	Badshah Bogh	BHU, Varanasi
5.	CR DHAN 508	NRRI, Cuttak
6.	CR Dhan 206 (Gopinath)	NRRI, Cuttak
7.	Lunee Shree	NRRI, Cuttak
8.	HUR 917	BHU, Varanasi
9.	HUR 1309	BHU, Varanasi
10.	Varsha Dhan	NRRI, Cuttak
11.	HUBR 2-1	BHU, Varanasi
12.	Swarna	NRRI, Cuttak
13.	HUR 105	BHU, Varanasi
14.	CR Dhan 909	NRRI, Cuttak
15.	CR Dhan 801	NRRI, Cuttak

Table 2: Analysis of variance for yield and its attributing traits in rice genotypes

S.N	Source of Variations	df	Day of 50% flowering	Days to maturity	Plant Height (cm)	Grain Weight 1000(g)	Effective Tillers /Plant	Panicle Length (cm)	Grains per panicle	Grain Length (mm)	Grain Breadth (mm)	Length/ Breadth	Biological yield (gm)	Harvest index (%)	Grain yield per plant
1	Replication	2	2.29	27.36	21.8	4.70	4.02	1.63	113.76	1.60	0.051	0.0012	7.29	17.02	8.53
2	Treatments	14	299.6**	287.69**	1101.2**	27.43**	56.93**	18.71**	964.07**	3.51**	0.080**	0.29**	340.48**	19.61**	98.83**
3	Error	28	3.46	5.91	8.76	0.59	1.36	0.47164	108.97	0.53	0.033	0.012	1.89	2.47	1.379

*, ** = Significant at 5 and 1 per cent level, respectively.

Table 3: Genetic variability parameters for yield and its attributing traits in rice genotypes.

	Day of 50% flowering	Days to maturity	Plant Height (cm)	Grain Weight 1000(g)	Effective Tillers /Plant	Panicle Length (cm)	Grains per panicle	Grain Length (mm)	Grain Breadth (mm))	Length/ Breadth	Biological yield (gm)	Harvest index (%)	Grain yield per plant(gm)
GCV	9.007	6.667	16.483	32.249	32.015	9.938	10.338	19.798	5.768	11.851	17.46	5.167	20.117
PCV	9.163	6.874	16.483	13.675	33.166	10.317	12.154	24.486	10.239	13.034	17.561	6.179	20.539
h^2 (Broad Sense)	96.6	94.1	97.7	93.9	93.2	93.2	72.3	65.4	31.7	82.7	98.7	67.9	95.9
Genetic Advance 5%	20.118	19.362	38.846	5.971	8.559	8.559	29.581	1.661	0.145	0.558	21.70	4.121	11.5
Gen. Adv. As % of Mean 5%	18.237	13.321	33.158	26.442	63.664	63.664	18.113	32.976	6.693	22.197	35.581	8.902	40.589
Range Lower	97	125.667	87.1667	16	7.6667	19.3	142.333	2.37	1.86	2.0467	48.3633	42.8333	22
Range Higher	133.667	161.667	151.667	26.3333	23.3333	28.8333	205.333	6.6667	2.5367	3.2333	78.5867	49.6433	38.6667
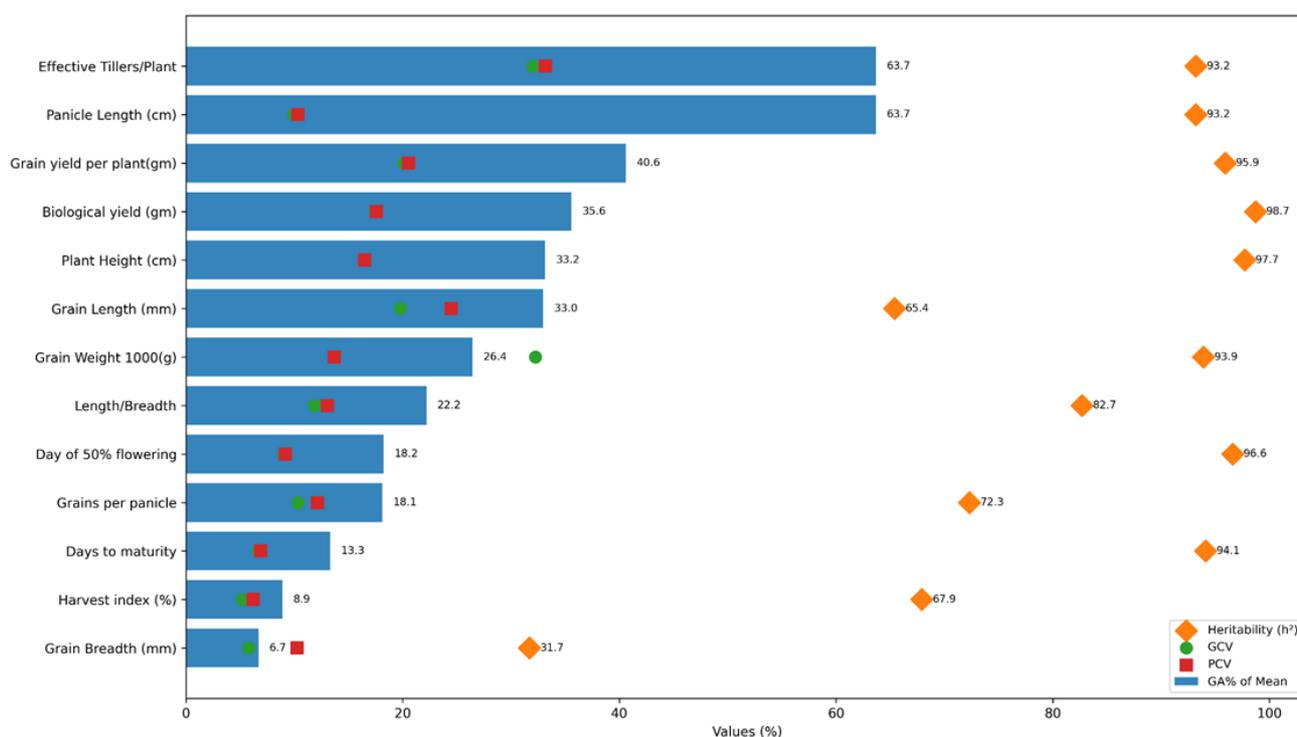
Fig. 1: Genetic variability parameters for yield and its attributing traits in rice genotypes.

Bars represent Genetic Advance as percent of mean (GA%). Diamond markers indicate broad-sense heritability (h^2). Green circles and red squares denote Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), respectively. Traits are arranged in descending order of GA% to highlight selection priority.

Acknowledgments

Conflict of Interest

The authors declare that there are no financial, personal or professional conflicts of interest that could have influenced the work reported in this manuscript.

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