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ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND YIELD COMPONENTS IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

To assess the magnitude of genetic variability and selection potential, 36 rice genotypes along with four check varieties (IR 64, MTU-1010, IGKV-R1, and IGKV-R2) were evaluated in a Randomized Block Design with two replications during *Kharif*-2023 at the Department of Genetics and Plant Breeding, IGKV, Raipur. Data were recorded on eleven quantitative traits and analyzed using ANOVA and genetic parameters including genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability and genetic advance. ANOVA revealed significant differences among genotypes for all traits except grain yield per plant, indicating substantial genetic variability. High mean square values for number of effective tillers (635.343) and number of filled grains per panicle (415.959) suggested strong genetic control, whereas grain yield exhibited only moderate significance (0.361), reflecting greater environmental influence. PCV values were consistently higher than GCV for all traits, though the differences were generally narrow, indicating limited environmental interference for most characters. The highest variability was observed for 100-seed weight (PCV 15.741%, GCV 13.986%) and number of filled grains per panicle (PCV 15.309%, GCV 11.699%), while days to maturity recorded the lowest variability (PCV 5.059%, GCV 3.709%). Overall, the presence of moderate to appreciable genetic variability for key yield components highlights strong prospects for effective selection and genetic improvement in rice breeding programs.

***Keywords* :** Rice, Variability assessment, Genetic Advance and Heritability.

Introduction

For half of the world's population rice (*Oryza sativa* L.) is one of the most consumed grains, Asia produces and consumes around 90% of the world's rice (Wennberg, 2014). It is the world's most significant staple food crop, farmed primarily in Asia. The top rice producing countries are China, India, Indonesia, Bangladesh, Vietnam, Myanmar and Thailand. China and India are the largest rice producers, Rice is produced in 114 nations throughout the world with an estimated production of 776.46 mt and a projection of 787 mt with a global rice acreage of 165.03mha (*FAO*, 2022). According to *FAO*, In India rice is planted in 46.40 million ha with production of 196.24 million tons and productivity of 4.32 t/ha. Among the rice-growing states in India, Uttar Pradesh is the biggest rice producing state with total rice output of 15.19 million tons (Agricultural Market Intelligence Centre, *PJTSAU* 2024) whereas Punjab has highest productivity of 4193kg/ha during the year 2022-2023.

Chhattisgarh the central-eastern state marks the prominent place and often referred to as the "Rice bowl of India." It occupies an area of around 3.77million ha with a production and productivity of 9.82 million tonnes and 2602 kg/ha, respectively, in 2022-23 (Anonymous, 2022-23). The production of rice accounts for more than 26% of all cereals (Anonymous, 2022).

Increasing rice production is essential to ensuring global food security as the worldwide population grows. Evans (1998) asserts that hunger might arise if the world's population grows faster than the amount of food available. Instead, then increasing arable area, productivity may be increased by choosing genotypes that are more nutrient-efficient and high yielding in order to feed an increasing population. Increasing yield is the primary goal of every crop enhancement effort.

High-yielding rice cultivars would require improved agronomic qualities and adaptability to different circumstances to meet increasing demand. Plant breeders face challenges in selecting yield due to its complicated polygenetic characteristic and intrinsic traits (Debsharma *et al.,* 2020). Rice improvement relies heavily on genetic variability, heritability, and the ability to transfer desired traits into new varieties. High variability in existing germplasm enhances breeding success and allows for faster generation of new varieties (Yared and Misteru, 2016).

A considerably more complicated characteristic, grain yield is influenced by a range of parameters, such as the weight of 100 grains, the length of the panicle, the number of grains per panicle, and the number of effective tillers per plant (Asante *et al.*, 2019). Parents selected for breeding programs should have a broad range of genetic diversity for the morphological and developmental qualities listed above, as these components also depend on a number of associated morphological and developmental features. Finding an appropriate selection process and creating a breeding plan both greatly benefit from the availability of the information mentioned earlier.

Variation is the foundation of selection; thereby lines are key components of base population in every crop and provide for a broad spectrum of variation. Knowledge of the nature and extent of genetic variation that governs the transmission of quantitative features such as yield, and its components is critical for efficient genetic improvement. A thorough investigation of genetic variation, as well as the use of proper selection strategies, is required before beginning any crop development effort. Genetics parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in detecting the amount of variability present in the genotype. The estimation of GCV was lower than the respective PCV, indicating the influence of environmental factor on the expression of the traits studied (Miller *et al.,* 1958). Heritability is a good index of the transmission of character from parents to their offspring (Falconer, 1981). Heritability estimates provide accurate information about a genetic trait that will be passed down to future generations. They can help breeders select parents for agricultural development programs (Rafi and Nath, 2004). However, extensive heritability may not be effective for phenotypic selection due to environmental influences. *Ogunbayo et al.,* (2014) found that estimating heritability and genetic advance together is more reliable in forecasting gain under selection than heritability alone.

This study aims to estimate genetic variability, heritability and advances in yield-related traits for rice genotypes. The findings could help develop salt-tolerant rice genotypes for future breeding programs (Rashid *et al.,* 2017).

Material and Methods

The present study was carried out during *Kharif* - 2023 at the Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, Chhattisgarh. The experimental site is located at 21.1°N latitude and 81.3°E longitude with an elevation of 289.60 m above mean sea level. The experimental material comprised 36 rice genotypes along with four standard check varieties, namely IR 64, MTU-1010, IGKV-R1 and IGKV-R2. The experiment was conducted using a Randomized Block Design (RBD) with two replications. Observations for plant height, panicle length, number of effective tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, harvest index and 100-seed weight were recorded from five randomly selected plants in each replication. In contrast, days to 50 per cent flowering, days to maturity, biological yield and grain yield were measured on a plot basis at the appropriate growth stage. Altogether, observations were collected for eleven quantitative characters associated with growth and yield of rice. The average values obtained from both replications were used for statistical analysis. The recorded data were subjected to analysis of variance (ANOVA) suitable for the Randomized Block Design using OPSTAT software as described by *Sheoran et al.,* (1998). Parameters related to variability such as range, mean, standard deviation, variance and coefficient of variation were estimated for each trait. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed according to the procedure suggested by Burton (1953). The magnitude of variability was classified as low (<10%), moderate (10–20%) and high (>20%) following the criteria proposed by Sivasubramanian and Madhavamenon (1973). Heritability in the broad sense (h^2) was estimated as the proportion of genotypic variance to phenotypic variance based on the method suggested by Hanson et al. (1956) and categorized as low (<30%), moderate (30–60%) and high (>60%) according to Johnson *et al.,* (1955). In addition, genetic advance and genetic advance expressed as percentage of mean were estimated to evaluate the expected improvement in traits through selection.

Table 1 : List of experimental material.

S. No.	Genotype
1	R 2483-RP5525-B-DRR-SPS-285-1
2	R 2404-362-1-178-1
3	R 2773-C8-2-4
4	R 2462-RP5530-DRR-SPS-47-1
5	R 2418-489-1-304-1
6	R 2299-146-1-120-1
7	R 2420-1418-1-743-1
8	R 2442-C1-11-445-1
9	R 2551-C10-6-510-1
10	R 2697-41-1
11	R 2699-4-1
12	R 2405-169-1-93-1
13	R 2404-151-2-73-1
14	R 2404-158-2-82-1
15	R 2404-166-1-90-1
16	R 2555-C16-5-551-1
17	R 2405-173-1-96-1
18	R 2404-1531-76-1
19	R 2547-C6-1-477-1
20	R 2698-101-1
21	R 2404-151-1-72-1
22	R 2754-11-1
23	R 2755-50-1
24	R 2748-4-1
25	R 2742-117-1
26	R 2743-93-1
27	R 2740-62-1
28	R 2754-51-1
29	R 2761-39-1
30	R 2754-12-1
31	R 2733-50-1
32	R 2741-21-1
33	R 2756-2-1
34	R 2749-35-1
35	R 2737-38-1
36	R 2740-98-1
37	IR 64 (Check)
38	MTU1010 (Check)
39	IGKV R1 (Check)
40	IGKV R2 (Check)

Results and Discussion

The analysis of variance (ANOVA) conducted for ten agronomic traits, except for grain yield among 40 rice genotypes revealed significant differences for all characters indicating the presence of substantial genetic variability. The traits analyzed included grain yield (GYP), days to 50% flowering (DF), days to maturity (DM), plant height (PH), panicle length (PL), number of effective tillers per plant (ET), number of filled grains per panicle (NFG), number of unfilled grains (NUFG),100 grain weight (HSW)), Biological yield (BY) and Harvest Index (HI). The presence of highly significant treatment means squares for most traits suggests ample scope for effective selection.

Among the traits, number of effective tillers (ENT) and number of filled grains exhibited exceptionally high mean square values of 635.343 and 415.959 respectively, suggesting a strong genetic component. Plant height (PH) also showed significant differences, indicating variability in phenological development which is critical for selecting varieties suited to specific ecological niches. Grain yield (GYP) is only moderately significant (0.361), suggesting weaker genetic differences or higher environmental influence. Genetic variability parameters for all the yield contributing traits are presented in the table 2.

Table 2: Analysis of variance of ten yield and yield attributing traits in rice

Character	Mean Squares		
	Replication	Treatments	Error
Degree of Freedom	1	39	39
GYP	0.903	0.361*	0.204
DFF	0.800	49.153**	12.928
DM	2.113	54.666**	16.446
PH	16.635	193.170**	3.744
PL	7.663	4.244**	0.241
ENT	70.312	635.343**	48.774
NFG	140.981	415.959**	110.230
BY	1.257	1.699**	0.557
HI	42.580	60.772**	16.189
100SW	0.009	0.288**	0.034

* and ** significant at 5% and 1% probability level
DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers; NFG = Number of filled grains per panicle; BY = Biological yield/plot (kg); HI = harvest index; HSW = Hundred seed weight (g); GYP = Grain yield per plot (kg).

The analysis of genetic variation revealed that the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits examined, suggesting that environmental factors obscured the expression of underlying genetic differences. The observed range of variation across all traits was substantial, confirming significant diversity. Furthermore, the high estimates of genetic variability parameters imply strong potential for selective breeding to enhance performance. A detailed discussion of these findings follows in the subsequent sections: -

Table 3 : Genetic parameters of eleven yield and yield attributing traits in rice

Genetic parameter	Grand mean	Range		GCV	PCV	Heritability	Gen-Adv % Means
		Min.	**Max.**				
GYP	4.242	3.09	5.6	6.609	12.531	27.813	7.180
DF	90.975	67	101	4.678	6.124	58.350	7.361
DM	117.8625	97	129	3.709	5.059	53.747	5.601
PH	111.5890	94.6	137.54	8.721	8.892	96.197	17.621
PL	24.5145	20.78	27.42	5.771	6.108	89.251	11.231
ENT	223.9625	167	261	7.647	8.258	85.741	14.586
NFG	105.9525	76.2	156	11.669	15.309	58.103	18.323
BY	7.4946	5.6977	10.8917	10.083	14.173	50.611	14.776
HI	56.9989	47.4234	72.3402	8.283	10.883	57.929	12.987
100SW	2.549	1.69	3.42	13.986	15.741	78.944	25.598

DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers/plant ; NFG = Number of filled grains per panicle; BY = Biological yield/plot (kg); HI = harvest index; 100SW= Hundred seed weight (g); GYP = Grain yield per plot (Kg)

The extent of phenotypic and genotypic coefficient variation is influenced by the genetic makeup of the source population. In this study, phenotypic coefficients of variation (PCV) consistently exceeded genotypic coefficients of variation (GCV) across all measured traits, highlighting the significant role of the all environmental factors in shaping trait expression (Tables-4).

The classification of variation was given by Sivasubramanian and Madhavamenon (1973) as low (<10%), moderate (10-20%) and high (>20%). Genotypic and phenotypic coefficient of variation was estimated which showed that values of phenotypic coefficient of variation was slightly greater than the corresponding genotypic coefficient of variation values for most of the traits studied indicating the negligible influence of extraneous factors. Except for Grain yield per plot only where the variation is double which indicates the impact of environment on those traits.

The highest value of PCV was recorded for 100 seed weight (15.741%) and number of filled grains per panicle (15.309%) while maximum GCV was recorded for 100 seed weight (13.986%) and number of filled grains per panicle (11.699%). The lowest amount of PCV and GCV was recorded for days to maturity (5.059% and 3.709% respectively). The high value (>20%) of genotypic coefficient of variation and phenotypic coefficient of variation was obtained for none of the character.

Table 4: PCV and PCV for different traits under study

Range	Low (<10%)	Moderate (10-20%)
Yield characters for PCV	Plant height, Days to 50 % flowering, Days to maturity, Panicle length, Number of effective tillers/plants.	100 seed weight, Grain yield/plot, Harvest index, Number of filled grain/ panicle, biological yield/plot.
Yield characters for GCV	Plant height, Days to 50 % flowering, Days to maturity, Panicle length, Grain yield/plot, Number of effective tillers/plants, Harvest index.	100 seed weight, Number of filled grain/panicle, biological yield/plot

Characters which showed moderate (10-20%) value of PCV and GCV were number of filled grain/ panicle (15.309%, 11.669%), biological yield/plot (14.173%, 10.083%) and Hundred Seed weight (15.741%, 13.986%). Characters which showed moderate (10-20%) value of PCV and low value of GCV were Grain yield/plot(12.531%, 6.609%), Harvest index (10.883%, 8.283%). Characters which showed low (<10%) value of GCV and PCV were days to maturity (3.709%, 5.059%), plant height (8.721%, 8.892%), panicle length (5.771%, 6.108%), Days to 50% flowering (4.678%, 6.124%) and number of effective tillers/plant (7.647%, 8.258%) Similar results were also obtained by Devi *et al.* (2016) for days to 50% flowering.

According to the current study's findings, maximum traits exhibited a relative resistance to environmental fluctuation, with the exception of only one character grain yield per plot, which shows impact of environment on these traits. Higher PCV than GCV values for a trait indicate that the environment plays a significant impact, and choosing such traits can occasionally be ambiguous. Therefore, under these conditions, selection is worthless. Characters whose estimated genotypic coefficient of variation is higher than their phenotypic coefficient of variation are those whose selection is beneficial or rewarding. This further elaborates why one should go for the selection of stable genotypes if characteristic yield is to be considered across environments.

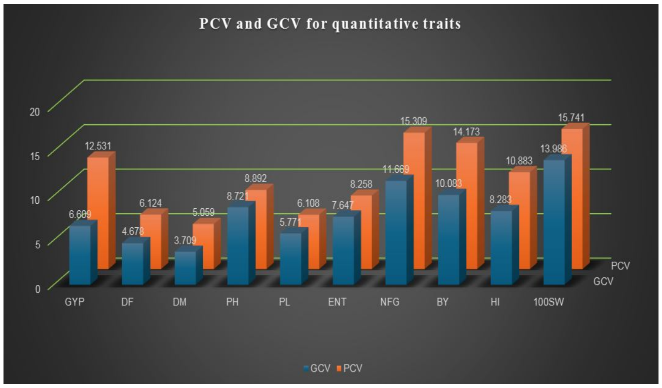
When predicting the potential improvement from selecting top-performing individuals, combining heritability estimates with genetic advancement proved more effective than relying solely on heredity. Heritability reflects both fixable and non-fixable genetic variations, so traits with high heritability are less affected by environmental factors and more likely to show consistent genetic progress.

In this study, broad-sense heritability was computed for various traits and classified as high (>60%), moderate (30-60%) or low (0-30%) following Robinson's (1955) guidelines. Among yield-related traits, plant height exhibited the highest heritability (96.197%), while grain yield per plot showed the lowest (27.813%).Traits with high heritability (>60%) included plant height (96.197%), panicle length (89.251%), number of effective tillers per plant (85.741%) and hundred-seed weight (78.944%). Such traits are less susceptible to environmental fluctuations and more responsive to genetic improvement through selection. These findings align with previous studies by Nath *et al.* (2021) and Akshay *et al.* (2022) for plant height as well as Pravallika *et al.,* (2023) for panicle length and plant height. Dhidhi *et al.* (2021) also reported similar results for plant height, filled and unfilled grains per panicle, hundred-seed weight and days to 50% flowering. Moderate heritability (30-60%) was observed in days to 50% flowering (58.350%), days to maturity (53.747%), number of filled grains per panicle (58.103%), number of unfilled grains per panicle (69.678%) and harvest index (57.929%). In contrast, grain yield per plot had low heritability (27.813%) indicating strong environmental influence on this trait.

The elite breeding lines exhibited varying degrees of genetic advance expressed as percentage of mean, ranging from low to high values following the classification system proposed by Johnson *et al.* (1955) that categorizes genetic advance as low (<10%), moderate (10-20%), or high (>20%). This parameter provides valuable insights into the effectiveness of selection for trait improvement in breeding programs. Among the yield-related traits analyzed, the number of unfilled grains per panicle showed the highest genetic advance (60.881%) while days to maturity displayed the lowest value (5.601%). Several traits demonstrated high genetic advance (>20%), including the number of unfilled grains per panicle (60.881%) and 100-seed weight (25.598%) indicating strong potential for improvement through direct selection due to their additive gene action. Moderate genetic advance (10-20%) was observed for multiple important agronomic traits such as number of filled grains per panicle (18.323%), plant height (17.621%), panicle length (11.231%), harvest index (12.987%), biological yield per plot (14.776%) and number of effective tillers (14.586%). In contrast, traits with low genetic advance (<10%) including days to maturity (5.601%), grain yield per plot (7.180%) and days to 50% flowering (7.361%) suggest predominant non-additive gene action, making them less responsive to conventional selection methods and more suitable for alternative breeding approaches like heterosis breeding to achieve genetic improvement. These findings provide crucial guidance for developing targeted breeding strategies based on the genetic architecture of different traits.

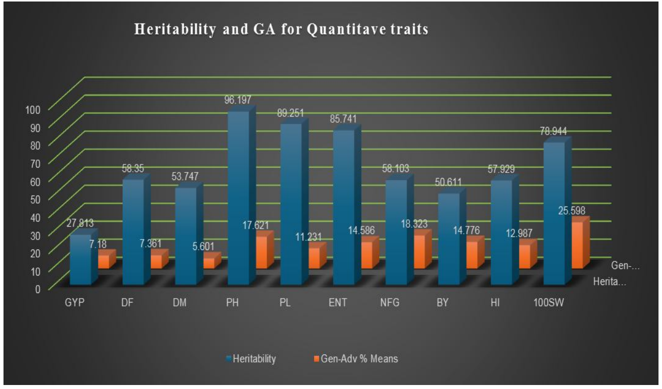
The high and moderate genetic advance (GA) estimates, expressed as a percentage of the mean, indicated additive gene action for certain traits implying that direct selection could be effective for improving these characteristics. Among the traits studied, the number of unfilled grains per panicle and hundred seed weight exhibited high heritability along with high genetic advance, suggesting stable inheritance governed by additive gene effects with minimal environmental influence. These findings align with Verma *et al.* (2024) who reported similar results for traits like 1000-seed weight.

For yield-related traits such as plant height, panicle length and the number of effective tillers, high heritability was accompanied by moderate genetic advance. This combination points to non-additive gene action, indicating that heterosis breeding could be a successful approach for enhancing these traits. Moderate heritability coupled with low genetic advance was observed in days to maturity, days to 50% flowering, number of filled grains per panicle, biological yield per plot and harvest index. In contrast, grain yield per plot displayed low heritability and low genetic advance, reflecting strong environmental influence and making selection for this trait ineffective.



DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers/plant ; NFG = Number of filled grains per panicle; BY = Biological yield/plot (kg); HI = harvest index; 100SW= Hundred seed weight (g), GYP= Grain yield per plot (Kg).

Fig. 1: Graphical representation of phenotypic and genotypic coefficient of variation for yield and its contributing traits



DF = Days to 50% flowering; DM = Days to maturity; PH = Plant height (cm); PL = Panicle length (cm); ET = Effective tillers/plant ; NFG = Number of filled grains per panicle; BY = Biological yield/plot (kg); HI = harvest index; 100SW= Hundred seed weight (g); GYP = Grain yield per plot (Kg)

Fig. 2: Graphical representation of heritability and GA for yield and its contributing traits

Conclusion

The present investigation revealed significant genetic variability among the evaluated rice genotypes for all yield and yield-attributing traits, as evidenced by ANOVA, indicating substantial scope for selection and genetic improvement. Phenotypic coefficients of variation were consistently higher than genotypic coefficients, reflecting environmental influence. However, the relatively narrow differences for most traits suggested predominant genetic control. High heritability estimates coupled with moderate to high genetic advance for traits such as hundred-seed weight, effective tillers per plant and panicle length indicated the predominance of additive gene action and their suitability for direct phenotypic selection. In contrast, grain yield per plot exhibited low heritability and low genetic advance, confirming its complex polygenic inheritance and strong environmental sensitivity, thereby limiting the effectiveness of simple selection methods. Overall, the findings suggest that improvement in rice productivity can be effectively achieved through selection for key yield-contributing traits with favorable genetic parameters, while grain yield per se may require alternative breeding strategies such as heterosis breeding and multi-environment evaluation for stable genetic gain.

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