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ASSESSMENT OF PHENOTYPIC AND GENOTYPIC VARIABILITY IN RICE GENOTYPES FOR AGRONOMIC TRAITS

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ABSTRACT

The experiment was undertaken to determine the variability for phenotypic traits (qualitative and quantitative) of different parameters between rice genotypes. The experiments were laid out in a Randomized Complete Block Design (RCBD) with three replications. Analysis of variance reveled significant difference for all traits under study. Phenotypic variances for the traits under study were higher than genotypic variances in the seasons suggesting that the traits were more responsive to environmental influence. The character viz., grain yield exhibited high genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV). Highest heritability was observed in DFF, whereas for genetic advance highest values observe in plant height. During cluster analysis, the genotypes were grouped into eight different clusters, confirming the presence of genetic variability among genotypes. The genotypes with highest grain yield was obtained and included under cluster 1. Selection for these characters during selection programme will result in crop improvement.

***Keywords* :** Quantitative traits, Variance, Variability.

Introduction

More than half of the world's population depends on rice (*Oryza sativa* L.) as their primary staple, with over 3.5 billion people deriving at least 20% of their daily calories from it (Naomi & Ziska, 2019; Rezk *et al.*, 2023). Asia called as the powerhouse of rice production, contributing around 90% of global output across more than 100 countries (Bandumula, 2018). Individual consumption of rice, in certain African and Asian nations ranges between 100 and 140 kg per year (Rezk *et al.*, 2024). Globally, rice supplies over one-fifth of total caloric intake and in many developing regions like Southeast Asia, its contribution can reach up to 76% (Rezk *et al.*, 2024). This underscores the critical need for boosting rice productivity, either through expanding cultivation or increasing yields. However, expanding rice acreage faces considerable limitations including water scarcity, soil salinization, and climate change (Fahad *et al.*, 2019; Rezk *et al.*, 2024). Enhancing per-unit-area yield through the development of improved genotypes is thus the most promising approach. To enhance genetic traits, it's essential to first understand how genetic variation impacts the inheritance of quantitative traits such as yield and its component characteristics. Before launching any crop-improvement program, a comprehensive assessment of genetic diversity must be conducted to identify the most effective selection strategies. Although India is not only self-sufficient in food grain production, also it ranks as the world's second largest producer and exporter of high-quality rice (Sreedhar *et al.*, 2005). Rice is a staple for nearly half of the global population, providing over 50% of their daily calorie intake (Maclean *et al.*, 2002). Beyond calories, rice also supplies essential nutrients such as magnesium, thiamine, niacin, phosphorus, vitamin B6, zinc, and copper and in some varieties; iron, potassium, and folic acid are present. Although polished (white) rice is relatively low in protein, fortified type varieties can offer up to 12-14g of protein per 100g. With its blend of energy-rich carbohydrates, lipids, proteins, and modest levels of calcium and riboflavin, rice serves not only as a major global food source but also as feedstock for animals and industry. Analyzing trait correlations is highly effective for understanding associations between yield and other agronomic traits. The aim of this study is to search the variation between rice genotypes, and in addition of different parameters in rice genotypes.

Material and Methods

The Study was carried out at Research cum Instructional Agriculture, Indira farm, College of Agriculture, Indira Gandhi of Krishi Vishwavidyalaya, Raipur, Chhattisgarh. The material was comprised of Twenty-five genotypes were sown during 2021 *kharif* season. Seedling planted in a RCBD with three replications, were transplanted in 20X20cm. From all the genotypes three plants were randomly selected to record the observation on the quantitative characters studied were *viz.* Days to flowering (days), Plant height (cm), Panicle length (cm), leaf length (cm), Numbers of tillers, Grain length, grain width, Rice length, rice width, biological yield and grain yield were subjected to analysis of variance of mean value to test the significance for each character. The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952). The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952). The genotype was grouped into clusters according to Tocher's methods by Rao (1952).

Result and Discussion

Analysis of variance

Anova: Significant differences were exhibited among the twenty-five rice genotypes for the studied traits as shown in Table1. Data illustrate the presence of high amount of variability among these genotypes. For the pH, highest value was observed for Dubraj and Dhaksha (KMP-175), IWP, Thanu were found statistically at par with it, so the plant height was Significant at 1% level. Followed by for the PL for the PL, highest value was observed for IR13F167 and none of the treatments were at par with it, so the Panicle length was significant at 1% level. Similarly, for the LL, highest value was observed for Thanu and Dhaksha (KMP-175), Giza 178 were found statistically at par with it were significant at1% level. For the LW, highest value was observed for MINGHUI63 and none of the treatments were at par with it, the genotype was significant at 1% level. For NT the genotypes was significant at 1% level, hence for the NT, highest value was observed for ADPT-43 and Swarna, R-RHP-1K-120, IR13F167, MINGHUI6, Jaya, IWP were found statistically at par with it. For the DFF, highest value was observed for BPT-5204 and CBMAS-14065, Dubraj, Swarna were found statistically at par with it, The Genotypes was significant at 1%. For the GL, highest value was observed for MINGHUI63 and IRBB 66, R-RHZ-AS-45, IR-30864, R-RCM-ATN-47 were found statistically at par with it, The genotypes was significant at 1% level resulting in rejection the null hypothesis. For the GW, highest value was observed for M202 and Jaya, R-RHP-1K-120, MTU 1001, IR 93354, R-RCM-ATN-47, CK-35, MINGHUI63, Giza 178, IR13F167 were found statistically at par with it, The Treatment component was significant at 1% level. For the RL, highest value was observed for IRBB 66 and IR13F167 MINGHUI63, R-RCM-ATN-47, R-RHZ-AS-45, IR-30864 was found statistically at par with it, the treatment component was significant at 1% level. But for the RW the component was non-significant in ANOVA so the multiple mean comparison test was not performed. For the BY, highest value was observed for Dubraj and Thanu, IR13F167, CBMAS-14065, IWP, MTU 1001, BR-2655 was found statistically at par with it, and the genotypes was significant at 1% level. For the GY, highest value was observed for R-RHP-1K-120 and ADPT-4, IWP, R-RHZ-AS-45, IR13F167, R-RCM-ATN-47, Jaya, Thanu, CBMAS-14065 was found statistically at par with it, the treatment component was significant at 1% level, therefore the multiple mean comparison test is recommended to evaluate means of different levels of treatment.

Table 1 : Analysis of variance and Mean Sum of Square for morphological trait in rice genotypes.

Character	Mean sum of Square		
	Replication (d.f=2)	Treatment (d.f.=24)	Error
PH	50.6512	986.1374**	23.5613
PL	0.1646	12.0594**	1.7732
LL	17.7949**	55.2544**	1.4466
LW	0.0096*	0.0609**	0.002
NT	12.28	3.8772**	3.8772
DTF	0.6533	248.7422**	2.3756
GL	0.1456	2.0249**	0.1024
GW	0.0297	0.2062**	0.0363
RL	0.0641	1.3658**	0.1204
RW	4.3012	4.6391**	4.8241
BY	627740.04	1492433.5311**	331785.7
GY	63617.3333	331965.2222**	60235.39

**, * significant at 1% and 5% level, respectively, PH-Plant height, PL-panicle Length, LL-Leaf length, LW-leaf width, NT-numbers of tillers, DTF-Days to flowering,GL- grain length, GW-grain width, RL-Rice length, RW-Rice width, BY-Biological yield, GY-Grain yield

Variability

The analysis of variance indicated the existence of significant differences among all the genotypes for all the traits studied. The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. The result of analysis of variance is present in Table 2. The maximum genotypic and phenotypic variation were obtained for grain yield, biological yield, numbers of tillers, while moderate variation observed for plant height, lef length, days to 50% flowering (Priyanka *et al.*, 2010). The estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation for twenty-five rice genotype characteristics. For all of the characteristics, the magnitudes of the phenotypic coefficient of variability (PCV) were larger than the genotypic coefficient of variability (GCV). Grain Yield (22.9) had the highest phenotypic coefficient of variation, followed by number of tillers (21.8), biological yield (19.9), Plant height(15.4), Leaf Length (14.5), grain width (11.7), rice width (11.6),rice length (11.3), leaf width(10.5), grain length (10.0), panicle length (9.4), day of flowering (9.3) Similarly grain yield had highest genetic coefficient variance (18.0) followed by plant height (14.8), number of tillers (14.8), leaf length (14), rice length (10), leaf width (9.7), grain length (9.3), grain width(9.2), day of flowering (9.1), panicle length (7.7), rice width (7.6). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Similar results were observed by V. Ravindra Babu *et al.* (2012).

Heritability: The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. Estimation of heritability vary from 43.1percent to 97.2 percent. Days of flowering had highest value followed by leaf length, plant height, leaf width, grain length, rice length, panicle length, grain yield, grain width, biological yield, number of tillers, rice width respectively. Similar results were observed by V. Ravindra Babu *et al.* (2012), Khatun *et al.* (2015).

Genetic Advance: High estimate of heritability coupled with high genetic advance were observed for character viz., days to 50% flowering, plant height, leaf length, grain length. It indicates that it is due to additive gene effects and selection maybe effective (Thippannagari Radha *et al.,* 2019). Genetic advance serves as a valuable indicator of the potential improvement achievable through selection within a given population. When considered alongside heritability, it provides a more dependable measure of the effectiveness of selection. (Johnson *et al.,* 1955). Genetic advance was highest for plant height followed by grain yield, leaf length and the lowest for rice width character. Information regarding genetic variation, heritability, and genetic advance provides a basis for predicting the potential genetic gain in subsequent generations, should selection be applied to improve the trait of interest. Similar results were observed by Ravindra Babu *et al.* (2012).

Table 2 : Estimation of mean, range, GC, PCV, heritability and genetic advance and variability parameters for agronomic traits under study

Character	Mean	Range	GCV %	PCV %	Heritability	GA %
Plant Height	120.8	85.03	14.8	15.4	93.2	29.2
Panicle Length	24.2	11.03	7.7	9.4	66.3	12.7
Leaf Length	30.3	18	14.0	14.5	93.4	28.0
leaf Width	1.5	0.6	9.7	10.1	90.6	18.8
Number of tillers	11.8	13	14.8	21.8	46.5	21.1
DFF	99.1	31	9.1	9.3	97.2	18.3
Grain length	8.6	3.6	9.3	10.0	85.8	17.4
Grain Width	2.6	1.2	9.2	11.7	61.3	14.7
Rice Length	6.4	3	10.0	11.3	77.6	17.9
Rice Width	2.26	19.5	7.6	11.6	43.1	10.3
Biological Yield	4263.6	4900	14.5	19.9	53.1	21.7
Grain Yield	1655.2	2100	18.0	22.9	61.8	28.9

Association Analysis

Pearson Correlation: Pearson correlation analysis among traits, yield and its related traits shown in table 3. Pearson correlation is a statistical method used to measure the strength and direction of a linear relationship between two continuous variables in rice genotypes data. It helps determine how much two traits, like yield and plant height, tend to change together. The results revealed that panicle length, biological yield, and grain yield were highly positive significant with plant height (Sadimantara *et al.,* 2021). For genetic improvement in yield the mutual relationship between plant characters were measured by correlation coefficient analysis. It is also widely used to measure the degree and direction of relationship between various traits, including grain yield (Tiwari *et al.,* 2019; Rachana *et al.,* 2021).

Panicle length had positive and significant association with biological yield (0.317**), but in contrast the trait exhibits significant and negative correlation with leaf width (-0.23*). The trait grain width showed a positive and significant association with leaf length. In contrast, the trait exhibits significant and negative correlation with days to flowering (-0.265*). The trait leaf width exhibits significant and negative correlation with grain yield (-0.337**), numbers of tillers (-0.334**) and panicle length (-0.23*). The present investigation unveiled that trait number of tillers had a positive and significant association with grain yield (0.343**) and grain width (0.254*). But in contrast the trait exhibits significant and negative correlation with leaf width (0.334*). The trait biological yield (0.484**) showed a positive and significant association with days to flowering. In contrast, the trait exhibits significant and negative correlation with grain width (-0.349**), grain length (-0.307**), rice length (-0.276*) and leaf length (-0.265*).

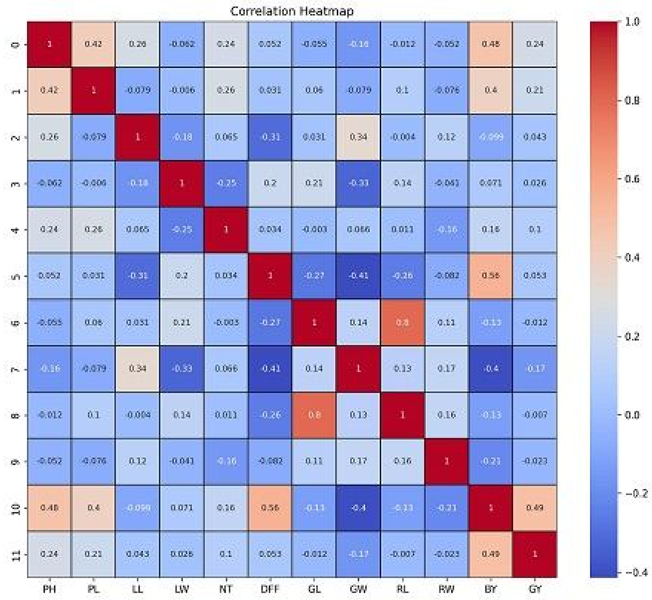
Table 3 : Pearson's Correlation coefficients analysis of twenty-five genotypes among twelve traits

Variables	PH	PL	LL	LW	NT	DFF	GL	GW	RL	RW	BY	GY
PH	1	0.385	0.208	-0.091	0.143	0.092	-0.104	-0.183	-0.076	-0.051	0.544	0.341
PL	0.385**	1	-0.08	-0.23*	0.222	-0.155	0.139	-0.027	0.198	-0.092	0.317**	0.223
LL	0.208	-0.08	1	-0.091	0.126	-0.265*	0.001	0.267*	-0.002	0.126	-0.119	0.092
LW	-0.091	-0.23*	-0.091	1	-0.334	0.05	0.203	-0.172	0.066	-0.049	-0.1	-0.337
NT	0.143	0.222	0.126	-0.334**	1	-0.045	-0.028	0.254*	-0.05	-0.185	0.17	0.343
DFF	0.092	-0.155	-0.265*	0.05	-0.045	1	-0.307**	-0.349**	-0.276*	-0.085	0.484**	0.018
GL	-0.104	0.139	0.001	0.203	-0.028	-0.307**	1	0.179	0.801	0.11	-0.12	-0.008
GW	-0.183	-0.027	0.267*	-0.172	0.254*	-0.349**	0.179	1	0.203	0.18	-0.355	-0.145
RL	-0.076	0.198	-0.002	0.066	-0.05	-0.276*	0.801**	0.203	1	0.166	-0.105	-0.022
RW	-0.051	-0.092	0.126	-0.049	-0.185	-0.085	0.11	0.18	0.166	1	-0.206	-0.037
BY	0.544**	0.317**	-0.119	-0.1	0.17	0.484**	-0.12	-0.355**	-0.105	-0.206	1	0.512
GY	0.341**	0.223	0.092	-0.337**	0.343**	0.018	-0.008	-0.145	-0.022	-0.037	0.512**	1

(**,* significant at 1% and 5% level, respectively)

The study revealed that trait grain length had a positive and significant relationship with rice/kernel length (0.801**). The trait exhibit significant and negative correlation with days to flowering (-0.307**). The traits grain width had a positive and significant association with leaf length (0.267*) and numbers of tillers (0.254*). Furthermore, a positive yet statistically non-significant correlation was observed with kernel length, kernel width and grain length. In contrast the trait exhibit significant and negative correlation with biological yield (-0.355**) and days to flowering (-0.349**). The trait biological yield had a positive and significant association with grain yield, days to flowering and panicle length, but the trait exhibit significant and negative correlation with grain width (-0.355**). The trait biological yield (0.512**) and number of tillers (0.343**) showed a positive and significant association with grain yield. Additionally, a positive correlation with PL (0.223 NS), LL (0.092 NS) and DFF (0.018 NS) was noted, albeit without statistical significance. The trait exhibit significant and negative correlation with leaf width (-0.337**) similar result found in (Tiwari *et al.*, 2019; Rachana *et al.*, 2021).

Cluster Analysis: The result of D^2 analysis is present in Table 4. The study cluster analysis depend on twelve traits was conducted using Tocher's method and Mahalanobis 'D2' statistics. The twenty five genotypes were divided into 8 clusters. Regarding inference of the distribution of genotypes in the clusters 1 had highest number of 15 genotypes, cluster 2 had number of genotypes 4 followed by cluster 3, cluster 4 cluster 5, cluster 6,cluster 7 and cluster 8 had the least number of genotypes 1.



Correlation Heatmap

	PH	PL	LL	LW	NT	DFF	GL	GW	RL	RW	BY	GY
0	1	0.42	0.26	-0.062	0.24	0.052	-0.055	-0.16	-0.012	-0.052	0.48	0.24
1	0.42	1	-0.079	-0.006	0.26	0.031	0.06	-0.079	0.1	-0.076	0.4	0.21
2	0.26	-0.079	1	-0.18	0.065	-0.31	0.031	0.34	-0.004	0.12	-0.099	0.043
3	-0.062	-0.006	-0.18	1	-0.25	0.2	0.21	-0.33	0.14	-0.041	0.071	0.026
4	0.24	0.26	0.065	-0.25	1	0.034	-0.003	0.066	0.011	-0.16	0.16	0.1
5	0.052	0.031	-0.31	0.2	0.034	1	-0.27	-0.41	-0.26	-0.082	0.56	0.053
6	-0.055	0.06	0.031	0.21	-0.003	-0.27	1	0.14	0.8	0.11	-0.13	-0.012
7	-0.16	-0.079	0.34	-0.33	0.066	-0.41	0.14	1	0.13	0.17	-0.4	-0.17
8	-0.012	0.1	-0.004	0.14	0.011	-0.26	0.8	0.13	1	0.16	-0.13	-0.007
9	-0.052	-0.076	0.12	-0.041	-0.16	-0.082	0.11	0.17	0.16	1	-0.21	-0.023
10	0.48	0.4	-0.099	0.071	0.16	0.56	-0.13	-0.4	-0.13	-0.21	1	0.49
11	0.24	0.21	0.043	0.026	0.1	0.053	-0.012	-0.17	-0.007	-0.023	0.49	1

Fig. 1 : Pearson's Correlation Coefficient among twelve quantitative traits across twenty five genotypes.

As per Singh (1981), the trait with highest contribution to genetic diversity was BY with contribution of 14842.3 % followed by PL with contribution of 177.3 % Inference regarding the means of the traits for clusters For the trait pH, the maximum value was observed for cluster 4 (154.67) while the minimum value was observed for cluster 3 (88.2233) The values for the trait PL, ranged from 26.45 (cluster 5) to 21.5767 (cluster 3) The trait LL exhibited its highest value in cluster 6 (37.31), whereas its lowest value was observed in cluster 8 (19.8867) For the trait LW, the maximum value was observed for cluster 5 (1.7433) while the minimum value was observed for cluster 1 (1.25) The values for the trait NT, ranged from 13.6667 (cluster 1) to 8.0 (cluster 7) The trait DFF exhibited its highest value in cluster 7 (111.3333), whereas its lowest value was observed in cluster 3 (82.6667) For the trait GL, the maximum value was observed for cluster 5 (10.3) while the minimum value was observed for cluster 6 (7.8) The values for the trait GW, ranged from 3.1 (cluster 3) to 2.3 (cluster 7) The trait RL exhibited its highest value in cluster 5 (7.5), whereas its lowest value was observed in cluster 6 (6.0333) For the trait RW, the maximum value was observed for cluster 3 (2.7333) while the minimum value was observed for cluster 7 and cluster 8 (2.1333) The values for the trait BY, ranged from 5333.3333 (cluster 6) to 2133.3333 (cluster 3) The trait GY exhibited its highest value in cluster 1 (1954.1667), whereas its lowest value was observed in cluster 3 (566.6667). Similar observation obtains in (El-Hadi *et al.*, 2017)

Table 4: Clustering pattern of twenty-five genotypes of Rice on the basis of Mahalanobis ‘D2’ statistics

Cluster	Total Genotypes	Genetic_Material
Cluster 1	15	BPT-5204, BR-2655, CK-35, IR13F167, IRBB 66, Jaya, JGL-1798, M202, MINGHUI63, MTU 1001, R-RCM-ATN-47, R-RCP-RH-122, R-RHP-1K-120, R-RHZ-AS-45, Swarna
Cluster 2	4	ADPT-43, CBMAS-14065, Dhaksha (KMP-175), IR 93354
Cluster 3	1	IR-30864
Cluster 4	1	Gaangavati Sona
Cluster 5	1	IWP
Cluster 6	1	Thanu
Cluster 7	1	Dubraj
Cluster 8	1	Giza 178

Conclusion

The observed variation among rice genotypes represents a step toward improving rice yield. This improvement is achieved through the expression of phenotypic traits, particularly when evaluated using genetic parameters such as broad-sense heritability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and genetic advance (GA). These parameters are essential for effective selection in breeding programs aimed at developing high-yielding varieties. The analysis of variance (ANOVA) revealed that the mean sum of squares due to treatments was highly significant for all traits among the twenty-five rice genotypes studied, indicating the presence of substantial genetic variability. For all traits, PCV values were higher than the corresponding GCV values, suggesting the influence of environmental factors on trait expression. Notably, grain yield per plant and biological yield per plant exhibited the highest phenotypic coefficients of variation, reflecting considerable variation among genotypes. High estimates of broad-sense heritability were recorded for traits such as days to 50% flowering, leaf length, plant height, leaf width, grain length, and rice length. In contrast, medium heritability estimates were observed for panicle length, grain yield, and biological yield, indicating a moderate genetic influence on these traits. The plant height, leaf width, number of tillers and biological yield were found significantly positive correlation with yield of genotypes. During cluster analysis, the genotypes were grouped into eight different clusters, confirming the presence of genetic variability among genotypes. The genotypes with highest grain yield was obtained and included under cluster 1.

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