

Genetic variability studies for yield and yield attributing traits in Rice (*Oryza Sativa* L.) genotypes.

ABSTRACT

Forty five rice genotypes were evaluated in a Randomized Block Design (RBD) at Regional Agricultural Research station, Polasa, during *kharif* 2023 to determine the genetic variability, heritability and genetic advance for ten traits. Analysis of variance showed significant variation for all the characters in the genotypes studied. Moderate level of Phenotypic Coefficient of variation Genotypic Coefficient of variation was recorded for plant height, number of productive tillers per plant, 1000 grain weight, grain yield and head rice recovery. Low level of Phenotypic Coefficient of variation Genotypic Coefficient of variation was recorded for days to 50% flowering, panicle length, hulling and milling percentage. Moderate Genotypic coefficient of variation and high Phenotypic Coefficient of variation was recorded for number of grains per panicle. Heritability was high for days to 50% flowering, plant height, panicle length, number of productive tillers per plant, 1000 grain weight, grain yield, milling and head rice recovery. Genetic Advance (%mean) was high for the traits plant height, number of productive tillers per plant, number of grains per panicle, 1000 grain weight, grain yield and head rice recovery. High heritability coupled with high genetic advance as percent of mean was recorded for plant height, number of productive tillers per plant, 1000 grain weight, grain yield and head rice recovery. It indicates that these characters are controlled by additive gene action. Low heritability coupled with low genetic advance as percent mean was recorded for hulling percentage which indicates that this character is governed by non additive gene action. It is vitally important to evaluate variability for yield and other characteristics in order to plan an appropriate breeding strategy for genetic improvement. For the purpose of a potential breeding program, the current study set out to ascertain the genetic variability and heritability of the necessary qualities among genotypes of rice.

Keywords: *Rice, genetic parameters, heritability, genetic advance.*

INTRODUCTION

Rice (*Oryza sativa* L.) is the most vital grain and a primary staple food for more than 100 countries world wide, which is why it is often referred to as the "global grain."It is the primary food source for nearly half of the world's population, significantly impacting global nutrition aand food security, particularly in Asian countries.Rice is cultivated on 165 million hectares worldwide, with an annual production of 508.9 million tonnes(INDIASTAT,2022-2023). Over 90% of rice is both produced and consumed in Asia. India leads in cultivation area, with 478.32 lakh hectares under rice, producing 1357.55 lakh tonnes and a productivity rate of 2838 kg ha⁻¹(INDIASTAT,2022-23). In India over 65% of the population depends on rice as their primary cereal food crop.Telangana, the eleventh largest state in India with a geographical area of 11.2 million hectares, grows rice on 46.62 lakh hectares, yielding 158.77 lakh tonnes with a productivity of 3406 kg ha⁻¹(INDIASTAT, 2022-2023). Recent studies indicate a 12% increase in the global population, necessitating a 13% rise in crop productivity and an additional 500 million metric tonnes of rice to meet the growing demand (Al-daejet *et al.*, 2023). Enhancing rice production through conventional breeding largely depends on diverse germplasm.

The success of any crop improvement program relies on the genetic variability present in the material. Relying solely on phenotypic selection based on performance might not always be effective, as these genotypes could underperform in future generations. Therefore, selecting genotypes based on their genetic potential, which includes factors like heritability and genetic advance, is crucial (Hamouda *et al.*,2016). Genetic variability combined with heritability estimates helps in predicting the expected genetic gains from selection (Burton, 1952; Swarup and Chaugle, 1962). Understanding variability and heritability is essential for developing effective selection criteria to enhance seed yield and its related traits. Heritability estimates, when paired with genetic advance, are typically more useful for predicting gains from selection than heritability estimates alone (Paul *et al.*,2006). Therefore, this study was conducted to assess the extent of genetic variability, heritability and genetic advance for seed yield and its component traits in rice.

MATERIALS AND METHODS.

All the 45 genotypes were sown separately in the nursery on raised beds. Twenty-five-day-old seedlings of each genotype were transplanted into two rows each in a 4 meter length plot, with 15 cm spacing between the rows and 15 cm between the plants in a Randomized Block Design, with two replications during *Kharif*, 2023 at Regional Agricultural Research Station, Polasa, Jagtial, Professor Jayashankar Telangana State Agricultural University. Standard agronomic practices were implemented throughout the crop growth period. The genotypes were assessed for the traits : days to 50% flowering, plant height(cm), panicle length(cm), number of productive tillers per plant, number of grains per panicle, 1000 seed weight(g), seed yield per plant(g), hulling percentage, milling percentage, and head rice recovery percentage. The traits plant height, panicle length, number of productive tillers per

plant, number of grains per panicle and grain yield per plant were recorded from 5 random plants from each genotype and each replication at the time of harvest. Days to 50% flowering was recorded from whole plot basis. Random seed sample was drawn from each genotype & replication to record 1000 grain weight and quality traits viz., hulling (%), mulling (%) and head rice recovery (%). The mean of recorded values was considered for statistical analysis. Analysis of variance was employed for partitioning the total variation caused by treatments and replications. Analysis of variance for the design of the experiment was carried out according to the procedure described by Panse and Sukhatme (1967). The phenotypic and genotypic coefficients of variation were estimated using the method proposed by Burton and de Vane (1953). The Phenotypic Coefficient of variation and Genotypic Coefficient of variation were categorized as low (0-10%), moderate (10-20%), and high (>20%) as per Johnson *et al.* (1955).

Heritability (h^2) is defined as the percentage of the ratio of genotypic variance (σ^2_g) to phenotypic variance (σ^2_p) or total variance. Heritability in broad sense (h^2_b) was estimated using the method outlined as per Johnson *et al.* (1955). Scale for heritability were classified as low (0 to 30%), moderate (30 to 60%) and high (> 60%) as per Robinson *et al.* (1949). Genetic advance is a measure of genetic improvement achieved through selection. The genetic advance as per cent mean was classified as low (< 10%), moderate (10-20%) and high (> 20%) as per Johnson *et al.* (1955).

Table 1 . Analysis of variance (ANOVA) for 10 yield and yield attributing characters for 45 genotypes of rice.

Source of Variations		Replication	Treatment	Error
		1	44	89
Mean Sum of Squares	DFF	3.211	61.519**	1.552
	PH	32.592	292.334**	8.739
	PL	1.067	8.411**	1.699
	PT	2.635	3.918**	0.758
	GPP	141.125	3203.354**	987.687
	TGW	0.613	29.272**	1.268
	SPY	3.516	32.162**	3.646
	H(%)	16.044	9.714*	5.567
	M(%)	9.344	13.734**	2.322
	HRR(%)	8.711	98.799**	2.757

*Significant at 5% level, **Significant at 1%

DFF- Days to 50% flowering, **PH** - Plant height (cm), **PL** - Panicle length (cm), **PT** - Number of productive tillers, **GPP** - Number of grains per panicle, **TGW** - 1000 grains weight (g), **SPY** - Grain yield per plant (g), **H (%)** - Hulling (%), **M (%)** - Milling (%), **HRR(%)** - Head rice recovery.

TABLE 2. Mean performance of yield and yield attributing characters and physical grain quality parameters.

SNO.	Entries	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No of productive tillers/plant	No of grains/panicle	1000 grain wt(g)	Grain yield/plot (g)	Hulling (%)	Milling (%)	Head rice recovery (%)
1	JGL 47682	89	102.9	27.3	8	175	20.6	15.7	77.50	66.0	55.5
2	JGL 47683	89	122.6	28.3	8	173	23.1	21.1	76.50	66.5	59.0
3	JGL 47684	88	128.5	26.9	7	186	23.5	25.9	79.50	67.5	62.0
4	JGL 47685	88	129.6	28.6	9	188	26.2	21.2	76.00	60.5	48.0
5	JGL 47686	107	114.1	27.7	8	173	23.9	24.5	79.00	71.5	60.0
6	JGL 47687	108	109.0	28.0	9	190	19.0	19.7	76.50	71.5	64.0
7	JGL 47688	88	134.5	27.6	9	115	26.3	26.2	75.00	64.0	43.5
8	JGL 47689	88	134.3	28.4	8	160	26.1	23.2	72.50	65.5	52.5
9	JGL 47690	89	135.8	27.8	9	158	28.0	28.3	77.00	69.0	54.5
10	JGL 47691	93	117.8	28.5	8	139	30.2	21.1	81.00	66.5	49.0
11	JGL 47692	102	114.9	27.0	8	151	29.2	25.3	78.50	66.0	59.5
12	JGL 47724	98	111.4	28.2	10	148	23.6	23.3	80.00	69.5	57.0
13	JGL 47765	102	121.6	29.4	7	190	22.5	27.6	73.50	68.0	63.0
14	JGL 47767	103	115.3	27.9	9	186	20.3	25.0	77.00	66.5	64.0
15	JGL 47768	103	122.8	33.8	7	217	24.7	27.7	77.00	65.5	60.0

SNO.	Entries	Days to 50% flowering	Plant height (cm)	Panicle length(cm)	No of productive tillers/Plant	No of grains/Panicle	1000 grain wt(g)	Grain yield/plant (g)	Hulling (%)	Milling (%)	Head rice recovery(%)
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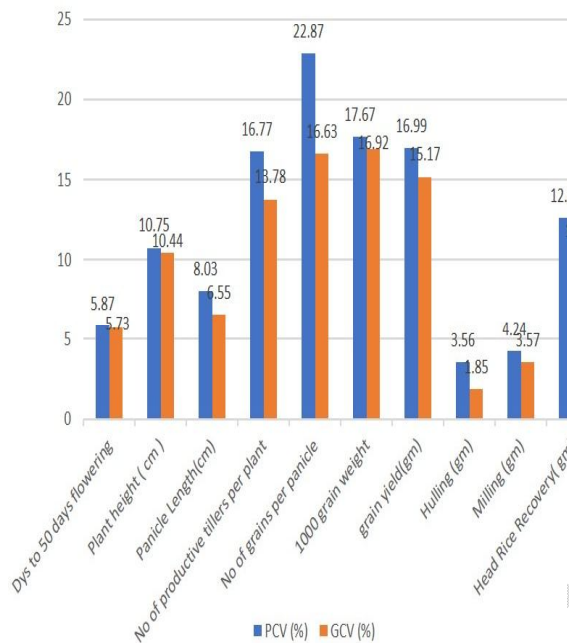
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16	JGL 47769	91	119.1	27.7	8	165	26.8	24.2	81.00	68.0	47.0
17	JGL 47771	105	120.5	30.1	8	296	20.1	24.0	76.00	68.5	61.5
18	JGL 47772	97	122.4	28	8	284	22.2	26.0	77.00	68.5	61.5
19	JGL 47773	102	112.7	31.1	7	306	18.0	18.4	76.00	61.0	55.5
20	JGL 47774	91	112.4	29.2	10	231	21.8	24.5	77.50	68.0	56.5
21	JGL 47775	92	119.1	29.4	7	234	22.4	31.8	80.00	68.0	59.5
22	JGL 47779	100	116.1	32.5	8	221	25.0	33.0	78.50	63.0	48.5
23	JGL 47780	98	137.8	30.6	8	258	22.5	20.7	71.50	60.5	58.5
24	JGL 47823	95	114.8	28.3	10	243	22.8	23.7	79.50	65.0	44.0
25	JGL 47824	88	121.1	32.8	8	269	25.3	26.9	78.50	68.0	39.0
26	JGL 47825	94	115.4	30.6	10	153	26.3	25.2	77.00	66.0	61.0
27	JGL 47826	88	114.4	28.3	11	216	25.6	26.5	79.50	68.5	51.5
28	JGL 47858	94	122.9	29.2	8	217	25.8	30.0	76.50	67.0	46.5
29	JGL 47859	97	125.9	28.0	9	205	25.8	34.1	77.00	64.0	39.0
30	JGL 47860	97	131.7	27.7	10	197	27.0	27.7	81.00	67.5	54.0
31	WGL 1940	93	104.1	27.5	9	184	20.4	19.6	78.50	67.0	62.0
32	WGL 1941	95	99.6	26.8	12	202	15.8	27.7	79.00	65.5	58.5
33	WGL 1943	94	98.7	26.3	11	216	18.3	22.9	78.50	66.5	56.0
34	WGL 1944	94	94.4	25.7	11	191	19.2	19.0	76.00	65.5	50.0

SNO.	Entries	Days to 50% flowering	Plant height (cm)	Panicle length(cm)	No of productive tillers/Plant	No of grains/Panicle	1000 grain wt(g)	Grain yield/plant (g)	Hulling (%)	Milling (%)	Head rice recovery(%)
35	WGL 1945	94	97.5	25.6	9	206	18.0	20.7	76.00	67.0	63.0
36	WGL 1947	96	99.3	27.1	10	177	18.6	26.5	79.00	71.5	65.5
37	WGL 1949	105	101.9	27.4	11	230	18.9	31.2	77.00	65.0	58.5
38	WGL 1950	94	93.8	24.5	10	180	18.6	21.1	76.50	69.0	63.0
39	WGL 1953	95	95.6	24.5	10	179	17.0	26.3	74.50	71.0	67.5
40	WGL 1954	94	106.0	26.3	9	191	18.9	24.8	74.50	64.5	59.0
41	WGL 1956	103	111.3	27.0	11	197	17.3	26.7	77.50	68.5	61.0
42	WGL 1959	94	106.3	26.9	13	197	16.6	31.9	80.50	70.5	64.5
43	WGL 1960	96	99.8	24.6	9.7	200	18.06	23.9	79.00	68	62
44	WGL 1962	96	98.6	25.2	11.7	227	16.6	23.8	79.00	66	57
45	WGL 1963	100	104.6	26.1	11.2	188	18.355	21.7	80.50	65.5	54.5
	Range Lowest	88	93.8	24.5	7	114.8	15.77	15.65	71.5	60.5	39
	Range Highest	108	137.8	33.8	13	305.5	30.22	34.1	81	71.5	67.5
	Mean	96	114.07	28.03	10	200.12	22.11	24.89	77.53	66.81	56.38
	C.V. (%)	1.30	2.59	4.65	9.55	15.71	5.09	7.67	3.04	2.28	2.95
	C.D. (at 5%)	2.51	5.96	2.63	1.75	63.34	2.27	3.85	4.76	3.07	3.35

TABLE 3. Estimates of variability, heritability and genetic advance for yield and quality parameters in rice

SNo.	Characters	Mean	Range		Phenotypic Variance	Genotypic Variance	PCV(%)	GCV(%)	Heritability inbroad sense(h^2)(%)	Genetic Advance %ofmean
			Min	Max						
1	Daysto50%flowering	95.54	87.50	107.50	31.53	29.98	5.87	5.73	95.1	11.51
2	Plantheight(cm)	114.06	93.80	137.80	150.53	141.79	10.75	10.44	94.2	20.87
3	Paniclelength(cm)	28.03	24.50	33.80	5.07	3.37	8.03	6.55	66.5	11.00
4	Numberofproductivetillers	9.12	6.90	12.60	2.33	1.58	16.77	13.78	67.6	23.35
5	Numberofgrainsperpanicle	200.12	114.80	305.50	2095.52	1107.83	22.87	16.63	52.9	24.91
6	1000grainsweight(g)	22.11	15.77	30.22	15.27	14.00	17.67	16.92	91.7	33.37
7	Grainyieldperplant(g)	24.89	15.65	34.10	17.90	14.25	16.99	15.17	79.6	27.88
8	Hulling(%)	77.53	71.50	81.00	7.64	2.07	3.56	1.85	27.1	1.99
9	Milling(%)	66.81	60.50	71.50	8.02	5.70	4.24	3.57	71.1	6.21
10	Headricerecovery(%)	56.37	39.00	67.50	50.77	48.02	12.63	12.29	94.6	24.62



Graph 1: Graphical representation of Phenotypic Coefficient of variation and Genotypic Coefficient of variation

Graph 2 : Graphical representation of heritability in broad sense and genetic advance as % of mean.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) showed that the treatments differ significantly for all the traits viz., days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000 grain weight, grain yield per plant, hulling percent, milling percent and head rice recovery indicating the presence of genetic variability among the genotypes. The findings pertaining to variability, heritability and genetic advance of each trait in the present study is represented in Table 3.

The mean performance of 45 rice genotypes for all the ten characters are presented in Table 2. The days to 50% flowering ranged from 88 to 108 days, with a general mean of 96 days. Among all genotypes JGL 47687 (108 days) recorded highest no of days to 50% flowering followed by JGL 47686 (107 days) and WGL 1949 (105 days). JGL 47684, JGL 47688 and JGL 47689 (88 days) recorded least no of days to 50% flowering. Identification of short duration

varieties with good yield potential is recommended as they save water and labor requirement. Plant height ranged from 93.8 cm to 137.8 cm with a general mean of 114.07 cm. The tallest genotype found was JGL 47780 (137.8 cm) followed by JGL 47690 (135.8 cm). The shortest genotype observed was WGL 1950 (93.8 cm) followed by WGL 1944 (94.4 cm). Even though biomass is positively correlated to

yield, identifying short genotypes with high biomass and high yield are benefits the farming community where lodging is main problem as these short genotypes are less prone to lodging. The longest panicle length was observed in JGL 47768 (33.8 cm) followed by JGL 47824 (32.8cm) and JGL 47779 (32.5 cm), whereas, the genotype WGL 1959 (13) recorded highest number of productive tillers per plant followed by WGL 1941 (12) , WGL 1962 (12) and WGL 1963 (12). The highest number of grains per panicle were found in JGL 47773 (306) followed by JGL 47771(296) and JGL 47772 (284). 1000 grain weight ranged from 15.8g to 30.22 g with a general mean of 22.11g. The highest test weight was recorded for the entry JGL 47691 (30.2 g) followed by JGL 47692 (29.2 g) and JGL 47690 (28 g). The entries WGL 1941 (15.8 g) exhibited lowest weight followed by WGL 1959 and WGL 1962 (16.6 g). These genotypes based on other desirable traits can be used as parents in the development of coarse and fine grain varieties respectively. JGL 47859 (34.1 g) recorded highest grain yield per plant followed by JGL 47779 (33.0 g) and WGL 1959 (31.9 g). These entries to be tested further in station and multi locations for their stability in yield performance. High head rice recovery is very important trait for any variety to possess for its release. The highest head rice recovery per cent was observed for WGL 1953 (68%) followed by WGL 1947 (65.5%) and WGL 1959 (64.5%).

The phenotypic coefficient of variation ranged from 3.56 (hulling %) to 22.87(number of grains per panicle)while, genotypic coefficient of variation ranged from 1.85 (hulling percentage) to 16.92 (1000 grain weight). ModeratePhenotypic Coefficient of variation and Genotypic Coefficient of variationwere observed for plant height (10.75,10.44), number of productive tillersper plant (16.77,13.78), 1000 grainweight (17.67,16.92),grain yield (16.99,15.17)and head rice recovery (12.63,12.89). It indicates that trait improvement through selection is predictable. The trait number of grains per panicle exhibited amoderateGCV (16.63) along with high PCV (22.87). Low Phenotypic Coefficient of variation and Genotypic Coefficient of variationwere observed for the traitsdays to 50% flowering (5.87,5.73), panicle length (8.03,6.55), hulling percentage (3.56,1.85) and milling percentage(4.24,3.57). It indicates that these traits are relatively stable and less subject to variation. In thisstudy, values of Phenotypic Coefficient of variation were higher for all the traits than Genotypic Coefficient of variationvalues and the small difference between Phenotypic Coefficient of variation and Genotypic Coefficient of variation suggests that the environment has a minimal impact on the expression of these traits. Similar reports of moderatePhenotypic Coefficient of variation and Genotypic Coefficient of variation for seed yield per plant was reported by Divya and Pandey (2020), Sudeepthi *et al.*

(2020) and Sadhana *et al.* (2022); similar results of high **Phenotypic Coefficient of variation** for number of grains per panicle was similar to that of Lakshmi *et al.* (2021), Mounika *et al.* (2022) and moderate **Genotypic Coefficient of variation** for number of grains per panicle was similar to Manjunatha and Kumara (2019). Further, low **Phenotypic Coefficient of variation** and **Genotypic Coefficient of variation** for Days for 50% flowering was reported by Devi *et al.* (2022), Faysal *et al.* (2022).

Heritability estimates ranged from 27.1% (Hulling percentage) to 95.1% (days to 50% flowering) while, genetic advance as percentage of mean ranged from 1.99 % (Hulling percentage) to 33.37% (1000 grain weight). Heritability and genetic advance are crucial selection parameters. Heritability estimates are more useful when combined with the genetic advance of corresponding trait. Hence, high heritability estimates along with high genetic advance are more effective in predicting genetic gain under selection than heritability estimates alone. High heritability along with high genetic advance as percent of mean was observed for the characters plant height (94.2 % ,20.87 %), number of productive tillers per plant (67.6 % ,23.35 %), 1000 grain weight (91.7% , 33.37 %), grain yield (79.6 % ,27.88 %) and head rice recovery (94.6 % ,24.62 %) indicating that these characters are controlled by additive gene action. Hence, good response to selection can be achieved for the improvement of these traits. Similar reports of high heritability along with high genetic advance for **plant height**, **1000 grain weight** and **grain yield per plant** was reported by Mounika *et al.* (2022), Chhodavadiya *et al.* (2023) and Tarunumet *et al.* (2023). High heritability estimates combined with moderate genetic advance was observed by the traits *viz.*, days to 50 % flowering (95.1%, 11.51%) and panicle length (66.5%, 11%) indicating non-additive gene action in the inheritance of these traits. Similar results were reported by Sadhana *et al.* (2022) for days to 50% flowering. Further, hulling (%) (27.1%, 1.99%) showed low heritability and low genetic advance indicating non-additive gene action plays a role in inheritance of this trait. Hence, this trait can be further improved through heterosis breeding.

CONCLUSION

Evaluating variability in grain yield and yield attributes is essential for achieving successful yield improvement through breeding. From the present study, it could be concluded that the traits plant height, number of productive tillers per plant, 1000 grain weight, grain yield per plant and head rice recovery exhibited moderate **Phenotypic Coefficient of variation** and **Genotypic Coefficient of variation** whereas number of grains per panicle showed high **Phenotypic Coefficient of variation** and **moderate Genotypic Coefficient of variation**. This indicates that direct selection could be practiced for improvement of these traits. The traits plant height, number of productive tillers per plant, 1000 grain weight, grain yield and head rice recovery are controlled by additive gene action suggesting that these traits can be improved through mass selection and progeny selection. The traits 50 % flowering, panicle length, hulling

(%) are under the influence of non-additive gene action and can be improved through heterosis breeding.

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