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**Research Article**

# Estimation of Different Genetic Parameters for Efficient Selection of Hybrids in Rice (*Oryza sativa* L.)

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## Abstract

The comprehension of genetic parameters like variability, heritability and genetic advance in any crop is most crucial to detect different quantitative traits under improvement and thereby follow an efficient selection of desirable plants in breeding program. Here genetic parameters for fourteen yield and yield-related traits of rice hybrids were estimated from an experiment conducted at the rice research center, agricultural research institute, Rajendranagar, Hyderabad during Kharif 2017. Estimates showed that the Phenotypic Coefficient of Variation (PCV) was slightly higher than those of the Genotypic Coefficient of Variation (GCV) for all the traits studied. The GCV ranged from 2.457 for hulling percent to 25.359 for grain yield, whereas PCV ranged from 3.106 for Hulling percent to 27.059-grain yield. In the estimates of narrow-sense heritability were varied from 63.806 (kernel breadth) to 6.708 (head rice recovery). In the present study, the value of genetic advance as a percentage of mean ranged from 3.552% to 48.957%. High heritability coupled with high genetic gain (>20%) as a percentage of mean was observed for 1000 grain weight (29.88%) and plant height (21.966%).

**Keywords:** Genetic parameters, *Oryza sativa* L, HPTLC analysis, Mangiferin

## INTRODUCTION

Rice (*Oryza sativa* L.) is the most consumed cereal of the world and about 75 percent of the people of Asia consume rice as a staple food. In India rice is cultivated in an area of 43.8 million hectares with the production of 102.13 million tonnes. Despite the age-old human concerns about balancing population and food supplies.

The world population is expected to continue to grow, possibly reaching 9-11 billion times during 2030-2050. To meet the growing population demand we need to increase rice production through the development of high yielding varieties, which requires the knowledge of existing genetic variability (Akinwal e et al., 2011).

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The large spectrum of genetic variability in the segregating population depends on the amount of the genetic variability present in the genotypes and offer better scope for efficient selection. The magnitude of heritable variation in the traits studied has immense value in understanding the worth of the genotype for a further breeding program. Assessment of variability for yield and its related characters become important before planning of an appropriate breeding strategy for genetic improvement. Genetic parameters such as the Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are useful in detecting the amount of variability present in the germplasm (Burton, 1952).

The genotypic coefficient of variation does not offer full scope to estimate the variation that is heritable or environmental and therefore the estimation of heritability becomes necessary to fulfill our selection efficiently. While estimating heritability, we always remember that narrow sense heritability is more effective than broad sense heritability because it considers an additive portion of the genotypes and hence more accurate towards selection (Falconer, 1981). Crop improvement could be studied on the magnitude of genetic variability transfer to progeny and the extent to which the desirable characters are heritable.

High heritability alone is not enough to make an efficient selection in segregating generation unless the required information is accompanied by a substantial amount of genetic advance. The information on heritability alone may be misleading when used in combination with genetic gain the utility of heritability estimate increases (Hasan, et al., 2015). The present investigation was undertaken to study the genetic parameters among the 48 rice genotypes for grain yield and yield contributing traits.

## MATERIALS AND METHODS

A field trial was conducted with four CMS lines having the WA cytoplasmic background *viz.*, CMS 23A, CMS 59A, CMS 64A and JMS 13A used as females and eight promising rice varieties as males and thirty-two hybrids generated adopting line x tester mating design in Rabi, 2016-17. We used four local commercial checks to compare the performance of our hybrid (Table 1). All the forty-eight genotypes were sown in Randomized Block Design (RBD) with two replications at Rice Research Centre, Agricultural Research Institute, PJTSAU, Hyderabad during Kharif, 2017. Standard spacing of 30 cm x 15 cm was adopted for planting with a plot size of 1.2 m<sup>2</sup> each. Recommended packages of practices were followed during the crop growth period (Kole et al., 2008).

**Table 1.** List of successful lines, testers and checks (*i.e.*, 2 varietal checks and 2 hybrid checks) used in the present study.

S.No	Lines	Source	Characters
1	RNR 26060	Rice research centre, Hyderabad	135-140 days duration, medium bold, high yielding culture
2	WGL 14	RARS, Warangal	135-140 days duration, medium slender, straw glume variety with high head rice recovery and good cooking quality
3	JGL 18047	RARS, Jagtial	125 days duration, LS slender, high yielding variety. Moderate resistant to leaf blast
4	JGL 11118	RARS, Jagtial	125 days duration, medium slender grain type
5	RDR 1140	RS and RRS, Rudrur	120 days duration, LS grain type
6	RNR 11450	Rice research centre, Hyderabad	125 days duration, medium slender grain type
7	IET 26264	IIRR, Hyderabad	135 days duration, medium slender grain type
8	IET 26274	IIRR, Hyderabad	130 days duration, medium slender grain type. Resistant to leaf blast
<b>Testers</b>			
1	CMS 23B	IIRR, Hyderabad	120 days duration, LB grain type
2	CMS 59B	IIRR, Hyderabad	135 days duration, LS grain type
3	CMS 64B	IIRR, Hyderabad	130 days duration, LS grain type
4	JMS 13B	RARS, Jagtial	135 days duration, MS grain type. Resistant to leaf blast
<b>Checks</b>			
1	JGL 11470	Rice research centre, Hyderabad	135-140 days duration, medium slender grain type
2	MTU 1010	Rice research centre, Hyderabad	135 days duration, medium bold and high yielding blast and BPH resistant variety

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3	US 312	Private company	130 days duration, MS grain type
4	HRI 174	Private company	135 days duration, LB grain type

Observations were recorded for fourteen characters viz., days to 50% flowering, plant height (cm), panicle length (cm), number of productive tillers per plant, panicle weight (g), spikelet fertility%, 1000 grain weight (g), hulling percent, milling percent, head rice recovery (%), kernel length (mm), kernel breadth (mm), L/B ratio and grain yield per plant (g). Data on days to 50% flowering recorded on a plot basis at the flowering stage. Five representative plants for each genotype were randomly selected to record observations on the quantitative characters under study. Data on plant height, panicle length, number of productive tillers per plant were recorded at physiological maturity and number of grains per panicle, spikelet fertility, 100-grain weight, hulling percent, milling percent, head rice recovery, kernel length, kernel breadth, L/B ratio and grain yield per plant were post-harvest estimates. Genotypic and phenotypic coefficients of variance, heritability and genetic advance were estimated for all fourteen characters by following standard procedures. The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer. Heritability in the narrow sense refers to the proportion of additive variance to the total observed variance in the total population. Heritability ( $h^2$ ) in the narrow sense was calculated according to the formula given by Lush. Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under a certain amount of selection pressure. From the heritability estimates the genetic advance was

estimated by the formula given by Burton (Lush, 1945).

## RESULTS AND DISCUSSION

Variability is a pre-requisite for the selection of superior genotypes from the population over the existing cultivars. To study the variation, a statistical component called analysis of variance is used. Here analysis of variance for different characters is presented in Table 2. The analysis of variance for grain yield and yield contributing characters revealed a significant difference between the treatments for all the characters viz., days to 50% flowering, plant height, panicle length, number of productive tillers per plant, panicle weight, spikelet fertility, 1000 grain weight, hulling percent, milling percent, head rice recovery, kernel length, kernel breadth, L/B ratio and grain yield per plant shown presence of sufficient genetic variability for these traits. In the case of replications, there was no significant difference in genotypes for all the characters). The significance of difference indicates that there was sufficient variability among the genotypes tested. The immensity of variation between genotypes was reflected by high values of mean and range for genotype traits studied (Table 3). The highest range variation was found in the case of plant height (48.50) followed by grain yield per plant (39.60), spikelet fertility (29.58) and days to 50% flowering (29.0) shown that simple selection was effective for these characters (Kencharahut et al., 2018).

**Table 2.** Analysis of variance for 14 different characters of 32 hybrids, parents and standard checks in rice.

Source of variation	Degrees of freedom	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers per plant	Panicle weight (g)	Spikelet fertility (%)	1000-grain weight (g)
Replicates	1	2.91	2.32	0.45	0.27	0.01	2.42	0.03
Treatments	43	93.00**	344.27**	10.80**	7.02**	0.29**	76.76**	18.17**
Parents	11	59.01	259.38	6.75	7.31	0.15	46.41	22
Lines	7	90.29	368.02	8.98	6.79	0.09	52.42	25.76
Testers	3	3.46	66.83	3.03	8.95	0.23	31.75	19.97
L x T	1	6.75	76.51	2.25	6.02	0.37	48.3	1.75
Crosses	31	72.72**	382.38**	11.11**	7.06**	0.29**	79.68**	17.37**
Lines	7	156.14*	998.52**	15.35	14.61**	0.73**	92.82	37.35**
Testers	3	79.64	310.48	1.52	2.68	0.04	32.15	34.83*
L x T	21	43.93**	187.28**	11.07**	5.17**	0.18**	82.09**	8.21**
Parents vs. crosses	1	1095.38	96.78	45.62	2.82	1.81	320.11	0.91
Error	43	1.05	7.68	1.04	1.76	0.03	1.09	0.87
Total	87	46.52	173.98	5.85	4.34	0.16	38.51	9.41

### Coefficients of variation

The extent of variability present in the genotypes was measured in terms of the Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), it is shown in Table 3. The results revealed that the estimates of the Phenotypic Coefficient of Variation (PCV) were slightly higher than those of the Genotypic Coefficient of Variation

(GCV) for all the traits studied. Large differences between GCV and PCV values reflect the high environmental influence on the expression of traits. In this study, slight differences indicated minimum environmental influence and consequently greater role of genetic factors on the expression of traits. Similar observations were also noted earlier in rice (Srinivas et al., 2016).

**Table 3.** Analysis of variance for 14 different characters of 32 hybrids.

Source of variation	Degrees of freedom	Hulling percent	Milling percent	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)
Replicates	1	2.53	0.33	2.54	0	0	0.01	4.18
Treatments	43	10.77 <sup>**</sup>	12.30 <sup>**</sup>	15.68 <sup>**</sup>	0.53 <sup>**</sup>	0.03 <sup>**</sup>	0.19 <sup>**</sup>	169.33 <sup>**</sup>
Parents	11	3.87	11.73	7.49	0.59	0.04	0.28	44.42
Lines	7	1.6	2.1	2.19	0.66	0.05	0.33	53.24
Testers	3	10.14	32.64	5.61	0.61	0.01	0.11	21.22
L x T	1	0.9	16.4	50.25	0.04	0.15	0.41	52.25
Crosses	31	13.48 <sup>**</sup>	12.85 <sup>**</sup>	16.98 <sup>**</sup>	0.48 <sup>**</sup>	0.03 <sup>**</sup>	0.13 <sup>**</sup>	178.03 <sup>**</sup>
Lines	7	22.89	22.14	15.3	0.6	0.08 <sup>**</sup>	0.24 <sup>*</sup>	279.89
Testers	3	6.26	6.67	2.89	0.73	0.02	0.07	95.83
L x T	21	11.38 <sup>**</sup>	10.63 <sup>**</sup>	19.56 <sup>**</sup>	0.41 <sup>**</sup>	0.01	0.10 <sup>*</sup>	155.82 <sup>**</sup>
Parents vs. crosses	1	2.77	1.79	65.46	1.41	0.12	1.13	1273.67
Error	43	1.87	4.33	4.88	0.07	0.01	0.04	10.94
Total	87	6.28	8.23	10.19	0.3	0.02	0.11	89.15

**Note:** <sup>\*\*</sup>Significant at 1% level of significance; <sup>\*</sup>Significant at 5% level of significance

In contrary to the present study which showed close values between GCV and PCV recorded wide differences (Seyoum et al., 2012). The GCV ranged from 2.457 for hulling percent to 25.359 for grain yield whereas PCV ranged from 3.106 for Hulling percent to 27.059 for grain yield. Next to grain yield per plant, characters of thousand grains weight (15.136, 15.790), number of productive tillers (12.135, 16.524), panicle weight (12.410, 14.071) and plant height (10.916, 11.175) also showed high GCV and PCV respectively.

The lowest GCV and PCV were observed on hulling percent (2.457, 3.106), milling percent (2.634, 1.023) and head rice recovery (3.607, 5.131). Similarly low GCV and PCV results found by Manjunath et al., 2018. Whereas Akinwake et al., 2011 and Ullah et al., 2011 reported moderate to low GCV and PCV estimates for different quantitative traits in rice.

### Heritability

High heritability is not enough to make an efficient selection in segregating generation unless the information is accompanied by a substantial amount of genetic advance. Heritability and genetic advance, when calculated together, would prove more useful in predicting the resultant effect of selection on phenotypic expression, without genetic advance the estimation of heritability will not be of practical value and emphasized the concurrent use of genetic advance along with heritability (Mustafa et al., 2007).

High narrow sense heritability with high genetic advance shows a better selection of hybrids leading to the substantial improvement of the character (Rahman et al., 2014). In the present study, high heritability coupled with high genetic gain (>20%) as a percentage of mean was observed for 1000 grain weight (29.88%) and plant height (21.966%) (Table 4).

**Table 4.** Variability, heritability and genetic advance as percent mean on the performance of hybrids.

Character	Range lowest	Range highest	Range variation	Coefficient of variation		Heritability (%) (Narrow sense)	Genetic advance as percent mean at 5%
				Genotypic	Phenotypic		
Days to 50% flowering	75.5	104.5	29	7.959	8.042	46.996	16.227
Plant height (cm)	92.5	141	48.5	10.916	11.175	53.516	21.966
Panicle length (cm)	22.9	30.85	7.95	8.132	9.189	18.222	14.823
Number of productive tillers	9.5	17	7.5	12.135	16.524	30.762	18.359
Panicle weight (gm)	2.02	3.87	1.85	12.41	14.071	38.619	22.549
Spikelet fertility (%)	66.17	95.75	29.58	7.051	7.177	19.955	14.272
Test weight (gm)	14.47	25.82	11.35	15.136	15.79	58.831	29.888
Hulling (%)	69	84.15	15.15	2.457	3.106	27.124	4.003
Milling (%)	62.45	75.4	12.95	2.634	4.023	23.996	3.552
Head rice recovery (%)	52	65.7	13.7	3.607	5.131	6.708	5.224
Kernel length (mm)	5.46	7.58	2.12	6.844	7.918	32.613	12.185
Kernel breadth (mm)	1.76	2.61	0.85	7.246	8.839	63.806	12.238
Length/Breadth ratio	2.54	3.8	1.26	8.782	10.552	28.992	15.056
Grain yield per plant (gm)	17.4	57	39.6	25.359	27.059	27.455	48.957

Whereas got the same results in the case of days to heading which gave a better response to selection. In the estimates of narrow-sense heritability were varied from 63.806 (kernel breadth) to 6.708 (head rice recovery). Low heritability was observed for traits of head rice recovery (6.708) (Tiwari et al., 2011). Panicle length (18.222), spikelet fertility (19.955), milling percent (23.996) and hulling percent (27.124). Lowest narrow-sense heritability (17.54%) was recorded for panicle length by Ganapathi et al., 2020 reported moderate heritability and high genetic advance for kernel length and grain yield per plant, which attributes that genetic advance is due to additive gene action and heritability was influenced by environmental factors thus the selection may be effective (Sadeghi, 2011). These results are in accordance with hulling percent and milling percent had low heritability and low genetic advance (<10%). Reported similar results for low heritability coupled with low genetic advance as percent of mean for hulling percent and milling percent (Shekhawat et al., 2015). Selection would be ineffective due to low expected gain or improvement in the next generation by these traits. Therefore, priority should be given to those traits which showed higher estimates of genetic advance as percent mean while deciding selection strategies and selection based on these characters may be useful in realizing better gain by selection (Shinde et al., 2015).

High heritability percent was observed for the characters like kernel breadth (63.806), test weight (58.831), plant height (53.516), days to 50% flowering (46.996), panicle weight (38.619) and kernel length (32.613) (Shivakumar et al., 2014). Similar results of high heritabilities were found for plant height, days to 50% flowering and test weight by Ganapathi et al.; Manjunath et al. and Seyoum et al.

## CONCLUSION

Based on the present results it may be concluded that high heritability coupled with high genetic advance was recorded for plant height and 1000 grain weight indicating the major role of additive gene action in the inheritance of these characters. Thus, these characters could be improved through simple selection methods. The characters showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence selection could be postponed for these characters or these characters could be improved by intermating of superior genotypes of segregation population from recombination breeding.

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