



GENETIC VARIABILITY STUDIES FOR YIELD AND YIELD ATTRIBUTING CHARACTERS IN RICE (*Oryza sativa* L.)

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ABSTRACT

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In the present study, analysis of variance for 60 rice genotypes revealed significant differences among the genotypes for 15 yield and yield attributes indicating the presence of considerable amount of genetic variability among the rice genotypes. Higher estimates of PCV and GCV observed for number of chaffy grains panicle⁻¹, number of filled grains panicle⁻¹, number of spikelets panicle⁻¹, grain yield plant⁻¹ and thousand grain weight showed ample amount of variation for these traits. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, days to maturity, thousand grain weight, number of chaffy grains panicle⁻¹, grain L/B ratio, grain width, plant height, number of spikelets panicle⁻¹, number of filled grains panicle⁻¹ and grain yield plant⁻¹ indicating the predominance of additive gene action and direct selection would be effective for improvement of these traits.

KEYWORDS: PCV, GCV, Heritability, Genetic Advance.

INTRODUCTION

Rice (*Oryza sativa* L.) is a widely grown crop, staple food and major calorie source for over 3 billion people on the earth. It occupies a pivotal place in Indian agriculture as it is a staple food for more than 70% of population and source of livelihood for about 150 million rural households (Devi *et al.* 2022).

Globally rice is cultivated in 164.19 million hectares of area with production of 756 million tonnes (FAO, 2020). In India, rice is grown around in 45.07 million hectares with a production of 122.27 million tonnes of grains (Directorate of Economics and Statistics, 2021). In Andhra Pradesh, rice is a major crop cultivated in 2.55 million hectares with a production of 13.08 million tonnes annually with a productivity of 5.13 tonnes hectare⁻¹ (Directorate of Economics and Statistics, 2021).

Exploiting existing genetic variability in the population is the principle behind every successful crop improvement programme. Presence of adequate genetic variability provides an opportunity for plant breeder to select desirable genotypes for hybridization. Assessment of heritability is useful in defining genetic relationship between parents and progeny and to understand the

characters that are under genetic control. Heritability estimates accompanied with genetic advance is useful in measuring genetic gain under selection, to predict genetic advance of the trait and also to formulate suitable selection procedure.

For yield improvement in any crop, it is essential to develop genetically stable genotypes having high yield potential. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) heritability (h^2_{bs}) and genetic advance.

The present investigation was conducted to elucidate the information regarding variability, heritability and genetic advance in promising rice genotypes.

MATERIAL AND METHODS

The present investigation was carried out during *kharif* 2021 at Wetland Farm, S.V. Agricultural College, Tirupati, Chittoor District, Andhra Pradesh, India, located at geographical co-ordinates of 13°54' N *latitude* and 79°54' E *longitude*, and 182.9 m *altitude*. Experiment

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was laid out in randomized block design with two replications. In each replication, every genotype was transplanted in two rows of two meters length with a spacing of 20 cm × 15 cm. All the recommended package of practices were adopted during entire crop season to raise healthy crop. Observations were recorded for 15 yield and yield attributing characters. Data was subjected to statistical analysis for assessing phenotypic and genotypic coefficient of variation (Burton, 1952), heritability (Allard, 1960) and genetic advance as percent of mean (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among genotypes for all the 15 yield and yield attributing characters indicating the presence of sufficient genetic variability among the genotypes (Table 1). Phenotypic coefficient of variance (PCV) was slightly higher than genotypic coefficient of variance (GCV) for the traits studied indicating less interaction of traits with environment (Table 2).

High estimates of GCV and PCV were observed for number of chaffy grains panicle⁻¹ (GCV = 44.37 %; PCV = 45.32 %), number of spikelets panicle⁻¹ (GCV = 26.53%; PCV = 28.50%), number of filled grains panicle⁻¹ (GCV = 26.29%; PCV = 29.12%), grain yield plant⁻¹ (GCV = 23.81%; PCV = 29.76%) and thousand grain weight (GCV = 20.20%; PCV = 220.32%). This indicated the presence of extensive inherent variability in these traits remain unaltered by environmental conditions among the genotypes, which in turn was more useful for exploitation in selection.

Similarly, high estimates of GCV and PCV were reported by Lakshmi *et al.* (2021), Singh *et al.* (2021) and Saha *et al.* (2019) for number of chaffy grains panicle⁻¹; Singh *et al.* (2022) and Saha *et al.* (2019) for number of spikelets panicle⁻¹; Devi *et al.* (2022), Gupta *et al.* (2022), Singh *et al.* (2022), Lakshmi *et al.* (2021), Singh *et al.* (2021) and Saha *et al.* (2019) for number of filled grain panicle⁻¹; Devi *et al.* (2022), Gupta *et al.* (2022), Bhargavi *et al.* (2021), Lakshmi *et al.* (2021), Singh *et al.* (2021) and Saha *et al.* (2019) for grain yield plant⁻¹; Devi *et al.* (2022), Bhargavi *et al.* (2021) and Saha *et al.* (2019) for thousand grain weight.

Grain L/B ratio (GCV = 15.10%; PCV = 15.59%), days to 50% flowering (GCV = 14.78%; PCV = 14.79%), plant height (GCV = 14.18%; PCV = 15.14%), days to maturity (GCV = 12.34%; PCV = 12.35%) and grain width (GCV = 11.41%; PCV = 11.84%) had moderate

values for GCV and PCV. While, number of effective tillers plant⁻¹ had moderate GCV (17.93%) and high PCV (24.17%). This indicated the existence of sufficient variability for attempting selection to improve these traits in the genotypes studied. These findings were in consonance with Gupta *et al.* (2022), Priyanka *et al.* (2020) for grain L/B ratio; Gupta *et al.* (2022), Singh *et al.* (2022), Lakshmi *et al.* (2021), Singh *et al.* (2021), Sudeepthi *et al.* (2020) and Dhavaleswar *et al.* (2019) for plant height and Bhargavi *et al.* (2021) and Lakshmi *et al.* (2021) for days to 50% flowering.

Low estimates of GCV and PCV were recorded for spikelet fertility % (GCV = 7.46%; PCV = 7.90%), grain thickness (GCV = 7.09%; PCV = 7.35%), indicating narrow range of variability for these traits there by restricting the scope of simple selection. Similar kind of low estimates of variability was also reported by Sudeepthi *et al.* (2020) Swapnil *et al.* (2020) and Dhavaleswar *et al.* (2019) for spikelet fertility %. While, grain length (GCV = 9.93%; PCV = 10.20%) and Panicle length (GCV = 9.17%; PCV = 11.05%) had low GCV and moderate PCV estimates which was supported by findings of Bhargavi *et al.* (2021) and Lakshmi *et al.* (2021) for panicle length.

High heritability was observed for all the characters except number of effective tillers plant⁻¹ (55.00%) which registered moderate heritability. Days to 50% flowering and days to maturity had highest heritability value (99.90%) followed by thousand grain weight (98.90%), number of chaffy grains panicle⁻¹ (95.80%), grain length (94.80%), grain L/B ratio (93.70%), grain width (92.90%), grain thickness (92.90%), spikelet fertility % (89.20%), plant height (87.70%), number of spikelets panicle⁻¹ (86.70%), number of filled grains panicle⁻¹ (81.50%), panicle length (68.80%) and grain yield plant⁻¹ (64.00%). These characters can serve as effective selection parameters during breeding programmes for the improvement of productivity. Simple selection based on *per se* performance is effective for improving the performance of these characters.

Likewise, high estimates of heritability were reported by Devi *et al.* (2022) and Bhargavi *et al.* (2021) for days to 50% flowering, thousand grain weight and grain yield plant⁻¹; Gupta *et al.* (2022) and Bhargavi *et al.* (2021) for both days to maturity and grain L/B ratio; Lakshmi *et al.* (2021), Singh *et al.* (2021) and Saha *et al.* (2019) for both number of chaffy grains panicle⁻¹ and plant height; Bhargavi *et al.* (2021) for both grain length and grain width; Singh *et al.* (2022), Swapnil *et al.*

Table 1. Analysis of Variance for yield and yield attributing characters in 60 rice genotypes

S. No.	Characters	Mean sum of squares		
		Replications (df = 1)	Genotypes (df = 59)	Error (df = 59)
1	Days to 50% flowering	0.01	429.83**	0.25
2	Days to maturity	0.03	493.58**	0.36
3	Plant height	54.41	613.19**	40.22
4	Panicle length	0.94	13.66**	2.53
5	Total number of effective tillers plant ⁻¹	1.78	6.93**	2.01
6	Number of chaffy grains panicle ⁻¹	0.43	628.55**	13.34
7	Number of filled grains panicle ⁻¹	36.08	5220.04**	532.84
8	Number of spikelets panicle ⁻¹	44.41	7586.69**	541.68
9	Spikelet fertility	0.05	79.73**	4.55
10	Grain yield plant ⁻¹	45.58	55.56**	12.19
11	Thousandgrain weight	0.02	36.19**	0.21
12	Grain length	0.01	1.60**	0.04
13	Grain width	0.02	0.20**	0.01
14	Grain thickness	0.00	0.03**	0.00
15	Grain L/B ratio	0.04	0.51**	0.02

** : Significant at 1% level

(2020) and Saha *et al.* (2019) for number of filled grains panicle⁻¹ and number of spikelets panicle⁻¹; Singh *et al.* (2021), Sudeepthi *et al.* (2020) and Saha *et al.* (2019) for spikelets panicle⁻¹; Singh *et al.* (2022) and Bhargavi *et al.* (2021) for panicle length and moderate heritability were reported by Devi *et al.* (2022) and Singh *et al.* (2021) for number of effective tillers plant⁻¹.

Highest genetic advance as per cent of mean was observed for number of chaffy grains panicle⁻¹ (89.48%) followed by number of spikelets panicle⁻¹ (50.88%), number of filled grains panicle⁻¹ (48.88%), thousand grain weight (41.37%), grain yield plant⁻¹ (39.24%), days to 50% flowering (30.44%), grain L/B ratio (30.10%), number of effective tillers plant⁻¹ (27.41%), plant height (27.35%), days to maturity (25.40%) and grain width (22.66%). On contrary, moderate values of genetic advance as per cent of mean were observed for grain length (19.92%), panicle length (15.66%), spikelet fertility (14.52%) and grain thickness (14.07%).

Heritability refers to the heritable portion of phenotypic variance. The magnitude of heritability indicates the reliability with which the genotype will be recognized by its phenotype expression. Heritability

(h^2_{bs}) coupled with genetic advance as per cent of mean (GAM) will bring out the genetic gain expected from selection than heritability alone (Johnson *et al.* 1955). Hence, high heritability coupled with high genetic advance as per cent of mean could be considered for the selection of elite genotypes.

High heritability coupled with high genetic advance as per cent of mean was recorded in number of days to 50% flowering ($h^2_{bs} = 99.90\%$; GAM = 30.44%), days to maturity ($h^2_{bs} = 99.90\%$; GAM = 25.40%), thousand grain weight ($h^2_{bs} = 98.90\%$; GAM = 41.37%), number of chaffy grains panicle⁻¹ ($h^2_{bs} = 95.80\%$; GAM = 89.48%), grain L/B ratio ($h^2_{bs} = 93.70\%$; GAM = 30.10%), grain width ($h^2_{bs} = 92.90\%$; GAM = 22.66%), plant height ($h^2_{bs} = 87.70\%$; GAM = 27.35%), number of spikelets panicle⁻¹ ($h^2_{bs} = 86.70\%$; GAM = 50.88%), number of filled grains panicle⁻¹ ($h^2_{bs} = 81.50\%$; GAM = 48.88%) and grain yield plant⁻¹ ($h^2_{bs} = 64.00\%$; GAM = 39.24%). It indicates the presence of additive gene action and less influence of environment on expression of these characters. Early and simple selection could be exercised due to fixable additive gene effects.

Table 2. Variability and genetic parameters for yield and yield attributing characters in 60 rice genotypes

S.No.	Character	Mean	Range		Variance		Coefficient of variation		Heritability (Broad sense) %	Genetic advance (GA)	Genetic advance as per cent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1	DFF	99.14	77.00	155.00	214.79	215.04	14.78	14.79	99.90	30.17	30.44
2	DM	127.28	99.00	186.50	246.61	246.97	12.34	12.35	99.90	32.33	25.40
3	PH	119.40	92.50	182.50	286.48	326.71	14.18	15.14	87.70	32.65	27.35
4	PL	25.74	20.30	32.50	5.57	8.10	9.17	11.05	68.80	4.03	15.66
5	ET	8.75	5.50	13.00	2.46	4.47	17.93	24.17	55.00	2.40	27.41
6	CG	39.53	13.50	88.90	307.61	320.95	44.37	45.32	95.80	35.37	89.48
7	FG	184.18	91.00	306.60	2343.60	2876.44	26.29	29.12	81.50	90.02	48.88
8	TS	223.71	134.40	357.60	3522.51	4064.18	26.53	28.50	86.70	113.82	50.88
9	SF	82.17	66.98	92.27	37.59	42.14	7.46	7.90	89.20	11.93	14.52
10	GY	19.56	9.49	33.22	21.68	33.88	23.81	29.76	64.00	7.68	39.24
11	TGW	21.00	13.01	29.30	17.99	18.20	20.20	20.32	98.90	8.69	41.37
12	GL	8.89	7.45	10.88	0.78	0.82	9.93	10.20	94.80	1.77	19.92
13	GW	2.75	2.18	3.49	0.10	0.11	11.41	11.84	92.90	0.62	22.66
14	GT	1.68	1.33	2.00	0.01	0.02	7.09	7.35	92.90	0.24	14.07
15	L/B	3.28	2.28	4.77	0.25	0.26	15.10	15.59	93.70	0.99	30.10

DFF : Days to 50% flowering; CG : Number of chaffy grains panicle⁻¹; TGW : Thousand grain weight (g); DM : Days to maturity; FG : Number of filled grains panicle⁻¹; GL : Grain length (mm); PH : Plant height (cm); TS : Number of spikelets panicle⁻¹; GW : Grain width (mm); PL : Panicle length (cm); SF : Spikelet fertility (%); GT : Grain thickness (mm); ET : Total number of effective tillers plant⁻¹; GY : Grain yield plant⁻¹ (g); L/B : Grain L/B ratio

A similar kind of results for high heritability coupled with high genetic advance was earlier reported by Devi *et al.* (2022), Bhargavi *et al.* (2021) and Lakshmi *et al.* (2021) for days to 50% flowering, grain yield plant⁻¹, thousand grain weight; Lakshmi *et al.* (2021), Singh *et al.* (2021) and Saha *et al.* (2019) for number of chaffy grains panicle⁻¹ and number of filled grains panicle⁻¹; Singh *et al.* (2022) and Saha *et al.* (2019) for number of spikelets panicle⁻¹; Singh *et al.* (2022), Lakshmi *et al.* (2021) and Dhavaleswar *et al.* (2019) for plant height; Gupta *et al.* (2022) and Bhargavi *et al.* (2021) for grain L/B ratio.

Grain length ($h^2_{bs} = 94.80\%$; GAM = 19.92%), grain thickness ($h^2_{bs} = 92.90\%$; GAM = 14.07%), spikelet fertility % ($h^2_{bs} = 89.20\%$; GAM = 14.52%) and panicle length ($h^2_{bs} = 68.80\%$; GAM = 15.66%) had high heritability but moderate genetic advance as per cent of mean. The high heritability is exhibited due to favourable environment effect rather than the genotype and selection for such characters may not be rewarding. These characters showing high heritability along with moderate genetic advance can be improved by intermating superior genotypes of segregating population developed from combination breeding.

These results were in accordance with Bhargavi *et al.* (2021) and Saha *et al.* (2019) for panicle length; Bhargavi *et al.* (2021) for grain length and Sudeepthi *et al.* (2022) for spikelet fertility.

Number of effective tillers plant⁻¹ showed moderate heritability and high genetic advance as per cent of mean ($h^2_{bs} = 55.00\%$; GAM = 27.41%). It shows the presence of additive gene action. Hence, selection may be effective for the improvement of this character.

From the foregoing discussion, it was evident that number of chaffy grains panicle⁻¹, number of filled grains panicle⁻¹, number of spikelets panicle⁻¹, grain yield plant⁻¹ and thousand grain weight exhibited sufficient variation among genotypes and hence direct selection may be effective for these characters. PCV is greater than GCV for all these characters which indicates less influence of environment on expression of traits.

High heritability coupled with high genetic advance as per cent of mean was recorded in number of days to 50% flowering, days to maturity, thousand grain weight, number of chaffy grains panicle⁻¹, grain L/B ratio, grain width, plant height, number of spikelets panicle⁻¹, number of filled grains panicle⁻¹ and grain yield plant⁻¹. It indicates the presence of additive gene action in inheritance of these characters and the influence of

environment is less on expression of these characters. Early and simple selection could be exercised due to fixable additive gene effects observed for yield and its components in the present study material.

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