

ASSESSMENT OF GENETIC PARAMETERS OF MAINTAINER LINES FOR HIGH OUT CROSS AND QUALITY THROUGH MORPHOLOGICAL TRAITS IN RICE (*Oryza sativa* L.)

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ABSTRACT

An investigation was carried out to study the genetic variability, heritability and genetic advance for 18 traits in 40 genotypes of rice during Kharif, 2018. Analysis of variance revealed that significant differences for all 18 characters studied. Magnitudes of phenotypic and genotypic coefficients of variation were high for number of grains per panicle (37.2 % and 34.1 %), followed by the gel consistency (28.2 % and 27.4 %) and 1000-grain weight (24.9 % and 24.4 %). High heritability coupled with high genetic advance as percent of mean was observed for number of effective tillers per plant, number of grains per panicle, 1000-grain weight, grain yield per plant, kernel length, kernel breadth, kernel L/B ratio, amylose content, gel consistency and kernel length after cooking indicated that these traits were controlled by additive type of gene action in the inheritance. These characters can be further improved by following a simple selection procedure. Whereas the remaining traits, days to 50% flowering, plant height, panicle length, angle of flower opening, stigma exertion, hulling percentage, head rice recovery and milling percentage were controlled by non-additive type of gene action, based on their moderate and low genetic advance as percent of mean respectively.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most predominant food crops in India in terms of area, production and consumer preference and it is the premier food crop in India occupying nearly 42.9 million hectares with an annual production of 111.01 million tonnes and productivity of 2585 Kg ha⁻¹ (Indiastat, 2017- 2018).

In Telangana annually rice is cultivated in an area of about 17.2 million hectares with producing 5.83 million tonnes annually with a productivity of 3387 kg ha⁻¹ (Indiastat, 2017-2018).To meet the demands of the growing population and to achieve food security in the country, the present production levels need to be increased by two million tonnes every year. It is estimated that 150 million tonnes of rice are required to feed the increasing population by 2030 in India. Hybrid rice can out yield the promising varieties and it is a key technology to meet the increasing global demand for rice. Several traits contribute to the hybrid seed production efficiency, among which the stigma exertion and angle of flower opening are important for Cytoplasmic Male Sterile lines, account for improved seed set (Sheeba *et al.*, 2006). It is mandatory to develop high yielding hybrids of good quality suiting the needs of the market.

The selection criteria may be yield or one or more of the yield component characters and quality aspects. However, breeding for high yield crops requires information on nature and

magnitude of variation in the available material, the relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters. Since grain yield in rice is quantitative and poly genetically controlled, effective yield improvement and simultaneous improvement of yield components are imperative, variability in genotypes for yield and its component traits forms the essential factor to be considered while making selection. A critical assessment of genetic variability present in the germplasm of crop and its estimation is a pre-requisite for successful exploitation and improvement of yield through breeding. Heritability is the measure of transmission of characters from generation to generation and the estimates of heritability will be of immense help to the breeder in selecting superior individuals for a desired trait for successful utilization in the breeding programme. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Johnson *et al.* (1955) suggested that heritability estimates along with genetic advance would be more useful in predicting genetic gain under selection than heritability estimates alone. Keeping in view the above perspectives, the present investigation is carried out with the objective of estimating the genetic variability for yield, yield contributing character, heritability and genetic advance which would help in selection and further improvement of

rice genotypes.

Keeping this in view the present investigation aimed to assess genetic parameters in maintainer lines across the 40 rice genotypes and for selection of suitable genotypes with high outcross potential and better quality for further utilization as parents in development of heterotic hybrids.

MATERIALS AND METHODS

Forty genotypes (Table.1) were utilized in this study and sown separately in the nursery on raised beds. Thirty days old seedlings of each genotype were transplanted in two rows each in a 4 m length plot by adopting a spacing of 20cm between rows and 15cm between plants in a Randomized Block Design replicated thrice during Kharif, 2018 at Rice Research Centre, Agriculture Research Institute, Rajendranagar, Hyderabad, Telangana State.

Five random plants in each plot were selected to record data on plant height (cm), number of effective tillers per plant, panicle length (cm), number of grains per panicle, grain yield per plant (g). Ten random plants of each genotype in each replication were selected to record data on angle of flowering opening and stigma exertion. Days to 50% flowering was recorded on whole plot basis whereas a random sample in each plot was used to record kernel length (mm), kernel breadth (mm), L/B ratio, 1000-grain weight (g), hulling percentage, milling percentage, head rice recovery, amylose content, gel consistency and kernel length after cooking.

The data recorded for all the characters whose mean values were subjected to analysis of variance to test the significance for each character as per methodology proposed by Panse and Sukhatme (1961). The genotypic and phenotypic variances as well as the genotypic (GCV) and phenotypic (PCV) coefficient of variation were calculated by the formulae given by Burton (1952). Heritability in broad sense [h² (b)] was calculated by the formulae given by Lush (1940), from the heritability estimates the genetic advance (GA) was calculated by the formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences for all 18 traits studied which was presented in Table 2.

The genotypic and phenotypic coefficients of variation for days to 50 % flowering were low *i.e.*, 6.8% and 7.0% respectively. The observed heritability estimate for this trait was high (93.9 %) while, genetic advance as per cent of mean (13.7%) was moderate. These results are in conformity with findings of Chandra Mohan *et al.* (2016) for low GCV and PCV, Pragnya *et al.* (2018) for high heritability, Sandeep *et al.* (2018), for moderate genetic advance as per cent of mean.

Number of effective tillers per plant had moderate genotypic and phenotypic coefficients of variation *i.e.*, 14.5% and 15.8% respectively. The observed heritability estimate was high (83.8%) with high genetic advance as per cent of mean (27.4%). The similar results were reported by Edukondalu *et al.* (2017) for moderate GCV and PCV, Kumar *et al.* (2018) for high heritability, Sandeep *et al.* (2018) for high genetic advance as per cent of mean for number of effective tillers per plant in

rice.

The genotypic and phenotypic coefficients of variation estimates observed for plant height (cm) were low *i.e.*, 9.6% and 9.9% respectively. The observed heritability estimates for this character was high (95.0%) with moderate genetic advance as per cent of mean (19.4%). The similar results were reported by Chandra Mohan *et al.* (2016) for low GCV and PCV, Pragnya *et al.* (2018) for high heritability, Yadav *et al.* (2010) for moderate genetic advance as per cent of mean for plant height.

The GCV and PCV were low (*i.e.*, 6.9% and 7.5% respectively) for panicle length (cm). The heritability observed for this trait was high (85.8%). This character recorded moderate genetic advance as per cent of mean (13.3%). The results agree with findings Chakraborty and Chakraborty (2010), for low GCV and PCV.

The high estimates of GCV (34.1%) and PCV (37.2%) were observed for number of grains per panicle. The heritability estimate for this trait was also high (84.0 %) with high genetic

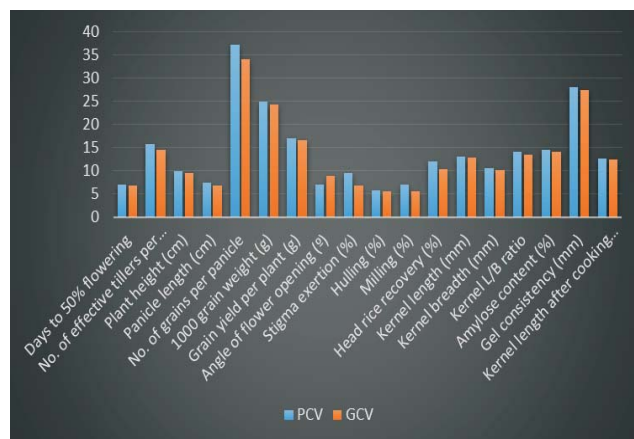
Table1: List of genotypes (maintainer lines) utilized for the research programme in rice.

S.No.	Genotype	Source
1	CMS 11B	IRRI, Philippines
2	CMS 14B	IRRI, Philippines
3	CMS 23B	IRRI, Philippines
4	CMS 46B	IRRI, Philippines
5	CMS 52B	IRRI, Philippines
6	CMS 59B	IRRI, Philippines
7	CMS 64B	IRRI, Philippines
8	JMS 11B	RARS, Jagtial
9	JMS 13B	RARS, Jagtial
10	JMS 14B	RARS, Jagtial
11	JMS 17B	RARS, Jagtial
12	JMS 18B	RARS, Jagtial
13	JMS 20B	RARS, Jagtial
14	JMS 21B	RARS, Jagtial
15	RNR 21280	RRC, ARI, Hyderabad
16	WGL 44	RARS, Warangal
17	TELLAHAMSA	RRC, ARI, Hyderabad
18	RP 5950-24-6-2-1-1-B	IIRR, Hyderabad
19	GNV 14-25	IIRR, Hyderabad
20	GNV 14-05	IIRR, Hyderabad
21	R 1919-537-1-160-1	IIRR, Hyderabad
22	RP 4993-183-9-2-1-1	IIRR, Hyderabad
23	SYE 160-7-19-7-23-16	IIRR, Hyderabad
24	MTU 1216	RARS, Maruteru
25	TP 30494	IRRI, Philippines
26	JGL 1798	RARS, Jagtial
27	HMT Sona	RRC, ARI, Hyderabad
28	IR 10 F 388	IIRR, Hyderabad
29	CT – 18615-1-S-1-2-4	IIRR, Hyderabad
30	TULASI	IIRR, Hyderabad
31	RNR 26119	RRC, ARI, Hyderabad
32	RNR 26032	RRC, ARI, Hyderabad
33	RNR 26061	RRC, ARI, Hyderabad
34	RNR 26075	RRC, ARI, Hyderabad
35	OR 2573-11	IIRR, Hyderabad
36	Sharbati	NRRI, Cuttack
37	IR – BLZ-F4	IIRR, Hyderabad
38	RNR 26992	RRC, ARI, Hyderabad
Checks		
39	RNR 15048	RRC, ARI, Hyderabad
40	MTU1010	ARS, Maruteru

Table 2: Analysis of variance for yield and quality traits in rice (*Oryza sativa* L.)

S.No	Characters	Replications (d.f. = 2)	Mean sum of squares	
			Treatments (d.f. = 39)	Error (d.f. = 78)
1	Days to 50% flowering	7.9	134.1**	2.84
2	No. of effective tillers per plant	3.42	19.09**	1.14
3	Plant height (cm)	2.78	282.0**	4.48
4	Panicle length (cm)	0.56	9.54**	0.49
5	No. of grains per panicle	62.8	17,044.8**	1011
6	1000 grain weight (g)	1.57	59.5**	0.79
7	Grain yield per plant (g)	6.11	70.8**	2.53
8	Angle of flower opening (°)	6.74	14.64**	2.43
9	Stigma exertion (%)	11.8	37.05**	8.2
10	Hulling (%)	3.5	55.6**	2.5
11	Milling (%)	20.6	48.2**	8.2
12	Head rice recovery (%)	11.15	113.18**	11.26
13	Kernel length (mm)	0.07	2.02**	0.028
14	Kernel breadth (mm)	0.0014	0.126**	0.002
15	Kernel L/B ratio	0.013	0.588**	0.016
16	Amylose content (%)	1.11	30.74**	0.62
17	Gel consistency (mm)	18.1	658.7**	12.75
18	Kernel length after cooking (mm)	0.01	3.77**	0.03

** Significant at 1 level of probability

**Figure 1: graphical representation of PCV and GCV**

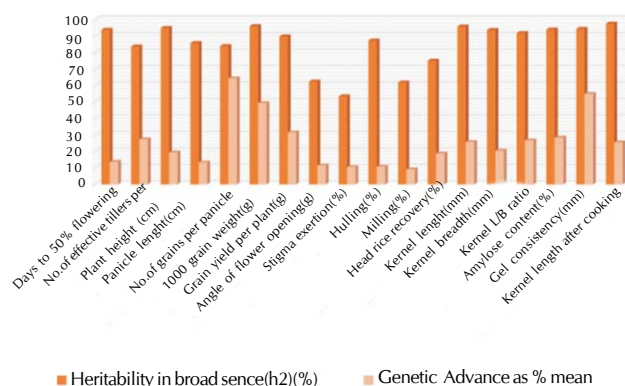
advance as per cent of mean (64.4%) and these results are comparable with findings of Singh and Verma (2018).

A high genotypic coefficient of variation (24.4%) and phenotypic coefficient of variation (24.9%) were observed for 1000-grain weight (g). A high heritability estimate (96.1%) coupled with high genetic advance as per cent of mean (49.4%). The results are in conformity with findings of Gampala *et al.* (2015) for high heritability.

Moderate genotypic (16.7%) and phenotypic (17.0%) coefficients of variation were recorded with high heritability estimate of (89.9 %) and high genetic advance as per cent of mean (31.6) for grain yield per plant (g). The similar results were reported by Dhurai *et al.* (2014).

Angle of flower opening (°) recorded low genotypic (8.9%) and phenotypic (7.0%) coefficients of variation. The heritability estimate for this trait was high (62.5%) with moderate genetic advance as per cent of mean (11.5%). similar results were reported Ali *et al.* (2013).

Stigma exertion (%) trait exhibited low genotypic (6.9%) and

**Figure 2: graphical representation of heritability and genetic advance as percent of mean**

phenotypic (9.5%) coefficients of variation, moderate heritability (53.5%) with moderate genetic advance as per cent of mean (10.5%). similar results were reported Hossain *et al.* (2016) for moderate genetic advance as per cent of mean.

A low genotypic (5.5%) and phenotypic (5.9%) coefficients of variation were observed for hulling percentage. The heritability estimate for this trait was very high (87.4%) with moderate genetic advance as per cent of mean (10.7%). The similar results were reported by Sahu *et al.* (2017).

Milling percentage recorded genotypic and phenotypic coefficients of variation is low *i.e.*, 5.6% and 5.9% respectively. The heritability estimate observed was high (61.9 %) with a low genetic advance as per cent of mean (9.1%). These results are in agreement with findings of Edukondalu *et al.* (2017)

Estimates of genotypic and phenotypic coefficients of variation were moderate *i.e.*, 10.4% and 12.1% respectively, high heritability estimates (75.1%) along with moderate genetic advance as per cent of mean (18.7%) for head rice recovery percentage. The similar results were reported by Rukmini Devi

Table 3: Magnitude of variability, heritability and genetic advance for yield and quality traits in rice (*Oryza sativa* L.)

S. No	Characters	Mean	Range		Pheno typic Variance	Geno typic Variance	PCV (%)	GCV (%)	Herit ability in broad sense (h ²) (%)	Genetic Advance as % mean
			Min	Max						
1	Days to 50% flowering	96	83	109	46.5	43.7	7	6.8	93.9	13.7
2	No. of effective tillers per plant	16.8	13.2	24.1	7.1	5.9	15.8	14.5	83.8	27.4
3	Plant height (cm)	99.5	85.3	121	97.3	92.5	9.9	9.6	95	19.4
4	Panicle length (cm)	24.8	21.4	29.7	3.5	3	7.5	6.9	85.8	13.3
5	No. of grains per panicle	214	119	365	63.5	53.4	37.2	34.1	84	64.4
6	1000 grain weight (g)	18.06	11.23	26.43	20.3	90.5	24.9	24.4	96.1	49.4
7	Grain yield per plant (g)	29.49	15.85	43.12	25.2	22.7	17	16.7	89.9	31.6
8	Angle of flower opening (°)	28.5	24.23	35.93	6.5	4	7	8.9	62.5	11.5
9	Stigma exertion (%)	44.4	37.83	53.63	17.8	9.5	9.5	6.9	53.5	10.5
10	Hulling (%)	75.4	61.7	86.33	20.2	17.6	5.9	5.5	87.4	10.7
11	Milling (%)	64.9	54.3	71.4	21.5	13.3	7.1	5.6	61.9	9.1
12	Head rice recovery (%)	55.5	41.4	65.26	45.2	13.9	12.1	10.4	75.1	18.7
13	Kernel length (mm)	6.33	5.21	8.15	68.9	66.1	13.1	12.8	95.9	25.8
14	Kernel breadth (mm)	1.98	1.61	2.4	0.04	0.04	10.5	10.2	93.7	20.4
15	Kernel L/B ratio	3.21	2.36	4.61	0.2	0.1	14.1	13.5	91.9	26.7
16	Amylose content (%)	22.2	16.1	27.6	10.6	10	14.6	14.2	94.1	28.4
17	Gel consistency (mm)	53.3	21	85.66	228	215.3	28.2	27.4	94.4	55
18	Kernel length after cooking (mm)	8.86	7.51	11.56	1.2	1.2	12.7	12.5	97.6	25.6

et al. (2014) and Rukmini Devi *et al.* (2016)

Kernel length (mm) exhibited moderate genotypic (12.8%) and phenotypic (13.1%) coefficients of variation. high heritability (95.9%) coupled with a high genetic advance as per cent of mean (25.8%). Similar results were observed by Edukondalu *et al.* (2017), Sahu *et al.* (2017) for moderate GCV and PCV and high heritability coupled with high genetic advance as per cent of mean.

Estimated genotypic (10.2%) and phenotypic (10.5%) coefficients of variation were moderate for kernel breadth (mm). The heritability estimate was high (93.7%) with high genetic advance as per cent of mean (20.4%) were also observed for this trait. Similar results were reported by Rukmini Devi *et al.* (2014).

A moderate genotypic (13.5%) and phenotypic (14.1%) coefficients of variation were observed for kernel length/breadth ratio. Estimates of heritability estimate was very high (91.9 %) with a high genetic advance as per cent of mean (26.7%) recorded for this trait. These results are in accordance with findings of Anant Kumar and Verma (2016) for moderate GCV and PCV, Gampala *et al.* (2015) for high heritability, and high genetic advance as per cent of mean.

Amylose Content (%) recorded moderate genotypic (14.2%) and phenotypic (14.6%) coefficients of variation. The heritability estimate was very high (94.1%) with a high genetic advance as per cent of mean (28.4%) for this trait. These results are in accordance with findings of Rathi *et al.* (2010) for moderate GCV and PCV and for high heritability coupled with high genetic advance as per cent of mean.

A high genotypic (27.4%) and phenotypic (28.2%) coefficients of variation and the heritability estimate was very high (94.4%) with a high genetic advance as per cent of mean (55.0 %) were exhibited by gel consistency (mm). These results are in accordance with findings of Dhanwani *et al.* (2013).

Kernel length after cooking (mm) recorded the low genotypic

(12.5%) and phenotypic (12.7%) coefficients of variation. The heritability estimate was very high (97.6%) with a high genetic advance as per cent of mean (25.6%). These results are in accordance with findings of Pathak *et al.* (2015) and Gampala *et al.* (2015).

CONCLUSION

Keeping in view of the facts, by considering all factors like *per se* performance, and quality the most promising genotypes may be utilized as parents in hybridization programme as they were expected to produce high heterotic crosses. The traits recorded high heritability coupled with high genetic advance as per cent of mean were number of effective tillers per plant, number of grains per panicle, 1000-grain weight, grain yield per plant, kernel length, kernel breadth, kernel L/B ratio, amylose content, gel consistency and kernel length after cooking indicated that these traits were controlled by additive type of gene action in the inheritance. These characters can be further improved by following simple selection procedure. High estimates of heritability coupled with moderate genetic advance as percent of mean were observed for days to 50% flowering, plant height, panicle length, angle of flower opening, head rice recovery percentage and hulling percentage. The high estimates of heritability coupled with low genetic advance as percent of mean for milling percentage indicated the presence of non-additive gene effects in addition to influence of environment to some extent.

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