

Assessment of genetic parameters for various quantitative and qualitative traits in hybrid rice (*Oryza sativa* L.)

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ABSTRACT: The present investigation was carried out during kharif 2012 and kharif 2013 at research cum instructional farm IGKV, Raipur to evaluate the genetic parameters for thirty three quantitative and qualitative traits in thirty three rice genotypes. Analysis of variance revealed highly significant differences for almost all the traits under study. The characters, viz., pollen fertility percent, productive tillers per plant, harvest index, fertile spikelet per panicle, sterile spikelets per panicle, grain yield per plant, biological yield per plant, seed index, kernel L/B ratio and head rice recovery exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. Pollen fertility percent, fertile spikelet per panicle, sterile spikelet per panicle, total spikelet per panicle, spikelet fertility percent, productive tillers per, days to 50% flowering, flag leaf area, plant height, 100 seed weight, grain yield per plant, biological yield per plant, harvest index, head rice recovery, brown rice L/B ratio and kernal L/B ratio exhibited high heritability coupled with high genetic advance as percent of mean, suggesting that These characters are governed by additive gene action direct selection for the improvement of these characters may be rewarding.

Key words: Genetic advance, selection, heritability, GCV, PCV,

INTRODUCTION

The development of superior rice population involved the intelligent use of available genetic variability both indigenous as well as exotic to cater the need of various farming situations of rice. The grain yield with good quality is the primary trait targeted for improvement of rice productivity. Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology (Babu *et al.*, 2012). It is essential to find out the relative magnitude of additive and non additive genetic variances, heritability and genetic gain with regard to the characters of concern to the breeder (Paikhomba et al., 2014). The systematic breeding programme involves the steps like creating genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. The large spectrum genetic variability in segregating populations depends on the level of genetic diversity among genotypes offer better scope

for selection. Improvement in grain quality that does not lower yield is the need of hour at present context in order to benefit all rice growers and consumers (Dhanwani et al., 2013). Like grain yield, its quality is not easily amenable to selection due to its complex nature. Lack of clear cut perception regarding the component traits of good quality rice is one of the important reasons for tardy progress in breeding for quality rice varieties. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Ghosh and Sharma, 2012). Therefore, estimates of GCV, PCV, heritability and genetic advance will play an important role in exploiting future research projections of rice improvement. In the present investigation, an attempt has been made to elucidate information on nature and magnitude of genetic parameters for grain yield and quality components in certain parents and rice hybrids.

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MATERIALS AND METHODS

The present experiment was conducted at research farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh.) in kharif 2012 and kharif 2013. The materials comprised of thirty three rice genotypes (including three CMS lines, seven testers and twenty one hybrids). The experimental material was planted in a completely randomized block design (RCBD) with two replications in two blocks. Each block consisted of thirty three genotypes randomized within each block. Twenty one days old seedlings were transplanted at 20 cm apart between rows and 15 cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a good crop. Five representative plants for each genotype in each replication were randomly selected to record observations on the quantitative and quality characters under study. The mean of five observations were used for analysis. In order to obtain information on the three CMS-lines, their respective maintainer lines were grown, as A-line and B-line are isogenic line except for male sterility. The data recorded on thirty three characters were subjected to the following statistical analysis: Analysis of variance (ANOVA) was calculated by the suggested formula of Panse and Sukhatme (1967). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated by the formula given by Burton (1952). Heritability in broad sense (h²) was calculated by the formula suggested by Hanson *et al.* (1956). From the heritability estimates, the genetic advance (GA) was estimated by the formula given by Johnson et al. (1955).

RESULTS AND DISCUSSION

The analysis of variance indicated the highly significant differences among all the genotypes for almost all the traits studied (Table 1) indicating presence of high variability among the genotypes. Thus, there is an ample scope for selection of different quantitative and qualitative characters for rice improvement (Prasad *et al.*, 2013). A wide range of variation was observed in the rice genotypes for all the quantitative and qualitative characters (Table 2). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for almost all traits indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The magnitude of coefficient of variation was categorized as high (> 20%), moderate (10- 20%) and low (< 10%). The variation between genotypic and phenotypic coefficient of variation was less for all characters studied (Table 2). The slight difference between GCV and PCV was also reported by Prasad et al., (2013), Dhanwani et al., (2013) and Sao et al., (2013). The highest genotypic and phenotypic coefficient of variation were recorded for the characters, sterile spikelets per panicle (61.48% and 62.07%), pollen fertility percent (46.13% and 46.42%), productive tillers per plant (37.40% and 41.83%), harvest index (36.62% and 37.40%), fertile spikelet per panicle (33.91% and 34.72%), grain yield per plant (30.26% and 31.05%) and biological yield per plant (30.21% and 30.29%). The moderate genotypic and phenotypic coefficient of variation were recorded for the characters, 100 seed weight (17.62% and 18.68%) followed by head rice recovery (17.31% and 17.31%), plant height (16.01% cm and 16.16%), Brown rice L/ B ratio (12.73 % and 14.52%) and The low genotypic and phenotypic coefficient of variation was recorded for the characters, kernel breadth (8.49% and 10.65%), kernel length (8.27% and 8.62%), cooked rice length (8.11% and 8.22%), paddy length (8.05% and 8.39%), brown rice length (7.93% and 8.27%) and elongation ratio (7.91% and 8.11%). The high magnitude of genotypic coefficient of variation reveals the high genetic variability present in the material studied. Similar results for high GCV and PCV in rice were also reported by Dhanwani et al., (2013) and Sao et al., (2013) in grain yield per plant; Panwar (2005) in spikelet fertility percent and grain yield per plant; Prasad et al., (2013) and Jayashudha and Sharma (2010) in spikelet fertility percent; and Babu et al. (2012) in fertile spikelet per panicle and sterile spikelet per panicle.

The reliability of the phenotypic value depends on the estimates of heritability for a particular character. Therefore high heritability helps in the effective selection for a particular character. The magnitude of heritability was categorized as high (>70%), moderate (31-70%) and low (<30%). In the present investigation most of all the characters exhibited high broad sense heritability (Table 2). Heritability was recorded the highest for head rice recovery (100%), biological yield per plant (99.73%), pollen fertility percent (99.37%), plant height (99.07%), spikelet fertility percent (98.51%), harvest index

		ANO	WA for diffe.	rrent quantita	ative and qua	Table 1 ality charact	ers of hybric	l rice and th	ieir parental	lines		
Source of variation	df						Mean square.	s				
		Days to 50% Flowering	% Plant height (cm)	t Chlorophyll content	Flag leaf length (cm)	Flag leaf width (cm)	Flag leaf area (cm²)	Productive tillers	Panicle length (cm)	Pollen fertility (%)	Fertile spikelets/ panicle	Sterile spikelets/ panicle
		1	2	3	4	5	6	7	8	9	10	11
Replicates Treatments Error	1 32 32	0.06 54.42*** 3.97	0.39 640.74*** 5.89	0.04 16.21*** 4.33	4.39 14.98*** 2.66	0.01 0.11*** 0.00	25.53* 116.12*** 4.78	0.74 39.47*** 4.40	1.25 10.02*** 2.57	0.36 1596.27*** 10.00	348.22* 2487.06*** 58.68	134.45 4610.64*** 44.48
Source of variation	df						Mean Square	Sč				
		Total spikelets/ panicle 12	Spikelet fertility (%) 13	100 seed weight 14	Grain yield/ plant 15	Biological yield/ Plant 16	Harvest index 17	Paddy length (cm) 18	Paddy bredth (cm) 19	Paddy L/B ratio 20	Brown rice length (cm) 21	Brown rice bredth (cm) 22
Replicates Treatments Error	1 32 32	20.30 3475.13*** 118.06	0.05 561.68*** 8.51	0.15* 0.41*** 0.02	0.09 70.38*** 1.82	1.23 635.35*** 1.74	0.38 300.80*** 6.33	$\begin{array}{c} 0.02 \\ 1.24^{***} \\ 0.05 \end{array}$	$\begin{array}{c} 0.01 \\ 0.18^{***} \\ 0.02 \end{array}$	0.03 0.54*** 0.07	0.03 0.68*** 0.03	0.01 0.12*** 0.02
Source of variation	df						Mean square.	S				
		Brown rice L/B ratio 23	Kernel length (cm) 24	Kernel bredth (cm) 25	Kernel L/B ratio 26	Cooked rice length(cm) 27	Cooked rice bredth(cm) 28	Cooked rice L/B ratio 29	Hulling (%) 30	Milling (%) 31	Head rice recovery 32	Elongation ratio 33
Replicates Treatments Error	1 32 32	$\begin{array}{c} 0.03 \\ 0.41^{***} \\ 0.05 \end{array}$	0.00 0.62*** 0.03	0.01 0.08*** 0.02	0.01 0.37*** 0.05	0.00 1.09*** 0.02	$\begin{array}{c} 0.00 \\ 0.12^{***} \\ 0.01 \end{array}$	$\begin{array}{c} 0.00 \\ 0.11^{***} \\ 0.01 \end{array}$	0.00 5.49** 1.84	$\begin{array}{c} 0.02 \\ 19.46^{***} \\ 0.38 \end{array}$	0.00 216.12*** 0.01	0. 00 0.02*** 0.00
*= Significant P >0.()5				**= Significe	ant P > 0.01				***= Signific	cant P > 0.00	-

Vol. 33, No. 1, January-March 2015

(97.91%), milling percent (97.85%), fertile spikelets per panicle (97.66%), elongation ratio (97.53%), grain yield per plant (97.45%), total spikelet per panicle (96.67%), flag leaf area (95.97%), paddy length (95.95%), kernel length (95.93%), brown rice length (95.88%). High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder, therefore adopt simple selection method on the basis of the phenotype of the characters which ultimately improves the genetic background of these traits. Similar results were also quoted by Jayashudha and Sharma (2010), Babu *et al.* (2012), Ghosh and Sharma, (2012), Dhanwani *et al.*, (2013), Sao *et al.*, (2013) and Karuppaiyan *et al.*, (2013).

The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population. Genetic advance estimates are depicted in Table 2. The genetic advance as per cent of mean was categorized as high (>20%), moderate (10-20%) and low (<10%). The high estimate of genetic advance were exhibited as per cent of mean by the characters for sterile spikelet per panicle (125.42%), pollen fertility percent (94.44%), harvest index (73.87%), productive tillers per plant (68.88%), fertile spikelet per panice (68.22%), biological yield per plant (62.05%), grain yield per plant (60.74%), spikelet fertility percent (57.98%), head rice recovery (35.65%), 100 seed weight (34.22%), brown rice L/B ratio (22.98%), kernel L/B ratio (22.38%) whereas, it were moderate for paddy breadth (19.63%), Brown Rice Bredth (18.33%), elongation ratio (15.87%), panicle length (11.36%), days to 50% flowering (10.47%) and chlorophyll content (10.44%) and it were low for hulling percent (8.29%) and milling percent (2.42%) (Table 2).

Table 2
Genotypic and phenotypic coefficient of variance (GCV and PCV), Heritability (h ²) and genetic advance as
percentage of mean (GA as percent of mean) for different characters

S.No	Characters	Genotypic	Phenotypic	Heritability	Genetic	Genetic advance
		coefficient of	coefficient of	(%) Broad	advance	as% mean
		variation	variation	sense		(5%)
		GCV (%)	PCV (%)			
1.	Days to 50% Flowering	5.47	5.88	93.03	9.62	10.47
2.	Plant Height (cm)	16.01	16.16	99.07	36.37	32.69
3.	Chlorophyll Content	6.66	8.76	76.03	3.81	10.44
4.	Flag Leaf Length(cm)	7.16	8.57	83.55	4.27	12.34
5	Flag Leaf Width (cm)	16.66	17.15	97.14	0.46	33.32
6.	Flag Leaf Area (cm ²)	20.05	20.89	95.98	14.75	39.63
7.	Productive Tillers/ Plant	37.40	41.83	89.41	7.71	68.88
8.	Panicle Length (cm)	7.17	9.32	76.93	3.05	11.36
9.	Pollen Fertility (%)	46.13	46.42	99.38	57.65	94.44
10.	Fertile Spikelets/ Panicle	33.91	34.72	97.67	70.10	68.22
11.	Sterile Spikelets/ Panicle	61.48	62.07	99.05	97.48	125.42
12.	Total Spikelets/ Panicle	22.70	23.48	96.68	81.57	45.20
13.	Spikelet Fertility (%)	28.58	29.01	98.52	33.74	57.98
14.	100 Seed Weight	17.62	18.68	94.33	0.85	34.22
15.	Grain Yield/ Plant	30.26	31.05	97.46	11.75	60.74
16.	Biological Yield/ Plant	30.21	30.29	99.74	36.56	62.05
17.	Harvest Index	36.62	37.40	97.91	24.47	73.87
18.	Paddy Length	8.05	8.39	95.95	1.52	15.90
19.	Paddy Bredth	10.82	12.29	88.04	0.51	19.63
20.	Paddy L/B Ratio	12.99	14.74	88.13	0.88	23.56
21.	Brown Rice Length	7.93	8.27	95.89	1.12	15.67
22.	Brown Rice Bredth	10.25	11.80	86.86	0.40	18.33
23.	Brown Rice L/B Ratio	12.73	14.52	87.67	0.76	22.98
24.	Kernal Length	8.27	8.62	95.94	1.07	16.35
25.	Kernal Bredth	8.49	10.65	79.72	0.28	13.93
26.	Kernal L/B Ratio	12.42	14.19	87.53	0.72	22.38
27.	Cooked Rice Length	8.11	8.22	98.66	1.48	16.46
28.	Cooked Rice Bredth	7.55	8.00	94.38	0.45	14.67
29.	Cooked Rice L/B Ratio	7.80	8.46	92.20	0.43	14.81
30.	Hulling (%)	1.66	2.36	70.34	1.95	2.42
31.	Milling (%)	4.10	4.19	97.85	6.23	8.29
32.	Head Rice Recovery	17.31	17.31	100.00	21.41	35.65
33.	Elongation Ratio	7.91	8.11	97.53	0.20	15.87

The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population. The high heritability along with high genetic advance were registered as per cent of mean for pollen fertility percent, fertile spikelet per panicle, sterile spikelet per panicle, total spikelet per panicle, biological yield per plant, plant height, spikelet fertility percent, harvest index, head rice recovery, flag leaf are, grain yield per plant, days to 50% flowering, productive tillers per, 100 seed weight, brown rice L/B ratio and kernal L/B ratio. The characters that show high heritability coupled with high genetic advance are controlled by additive gene action (Panse, 1957) and can be improved through simple or progeny selection methods while the characters which showed high heritability coupled with moderate or low genetic advance can be improved by intermitting superior genotypes of segregating population developed from combination breeding (Samadhia, 2005). Similar findings were also supported by Jayashudha and Sharma (2010),

Subbaiha *et al.* (2011) Seyoum *et al.* (2012), Ghosh and Sharma, (2012), Babu *et al.* (2012), Dhanwani *et al.*, (2013), Sao *et al.*, (2013) and Karuppaiyan *et al.*, (2013).

In the present investigation, considerable variability was present in the experimental material under study. Therefore, it is concluded that the characters which showed high heritability coupled with high genetic advance as percent of mean indicated the broad sense of additive gene effects in its inheritance and such characters could be improved by direct selection. Here grain yield per plant, productive tillers per plant, plant height, spikelet fertility percentage, spikelet sterility per cent, filled grain per panicle, grain yield per plant, 100-seed weight, biological yield per plant, biological yield per plant, harvest index, head rice recovery, flag leaf area, rice L/B ratio and kernal L/B ratio showed high GCV, PCV, heritability and genetic advance (Figure 1). Thus one should select these characters for direct selection. However, characters showing high values of heritability coupled with moderate genetic advance suggested that selection for the improvement of these characters may be rewarding.



Figure 1: Relationship among GCV, PCV, Heritability and Genetic advance

REFERENCES

- Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G. and Nagesh, P. (2012), Genetic Variability Studies for Qualitative and Quantitative traits in popular Rice (Oryza sativa L.) hybrids of India. *International Journal of Scientific and Research Publications* 2: 2250-3153.
- Burton, G.W. and Devane, E.H. (1952), Estimating heritability in tall fescue (Festuca arundinaceae) from replicated clonal material. *Agronomy Journal* 45: 478-481.
- Dhanwani, R.K., Sarawagi, A.K., Solanki, A. and Tiwari, J.K. (2013), Genetic variability analysis for various yield attributing and quality traits in rice (O. sativa L.). The bioscan, 8(4): 1403-1407.
- Hanson, W.D., Robinson, H.F. and Comstock, R.E. (1956), Biometrical studies of yield in segregating population Korean Lespandeza. *Agronomy Journal* 48: 268-272.
- Jayashudha, S. and Sharma, D. (2010), Identification of maintainers and restorers for CMS lines of rice under shallow low lands. *Electronic Journal of Plant Breeding*, 1: 311-314.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955), Estimation of genetic and environmental variability in soybean. *Agronomy Journal* 47: 314-318.
- Karuppaiyan, R., Kapoor, C. and Gopi, R. (2013), Variability, heritability and genetic divergence in lowland rice genotypes under the mid-hills of Sikkim. *Oryza*, 50 (1) 81-84.

- Paikhomba, N., Kumar, A., Chaurasia, A.K. and Rai, P.K. (2014), Assessment of Genetic Parameters for Yield and Yield Components in Hybrid Rice and Parents. *Journal* of Rice Research, 2: 117.
- Panse, V.G. (1957), Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics*, 17: 318-328.
- Panse, V.G., Sukhatme, P.V. (1967), Statistical methods for agricultural workers (2nd Ed) ICAR publications, New Delhi, India.
- Panwar, L.L. (2005), Line x Tester analysis of combining ability in rice. *Indian Journal of Genetics* 65: 51-52.
- Samadhia, D. K. (2005), Genetic variability studies in Lasora (Cordia myxa Roxb.). *Indian J. Plant Genetic Resources*. 18(3): 236-240.
- Seyoum, M., Sentayehu, A. and Kassahum, B. (2012), Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice. *J. Plant Sciences*. 7(1): 1320.
- Shiva Prasad, G., Sujatha, M., Subba Rao, L.V. and Chaithanya U. 2013. Studies on variability, heritability and genetic advance for quantitative characters in Rice (Oryza sativa L.). Annals of Biological Research, 4 (6): 372-375.
- Ghosh S. C. and Sharma, Deepak. (2012), Genetic parameters of agro-morpho-physiological traits in rice (Oryza sativa L.). *Electronic Journal of Plant Breeding*, 3(1): 711-714.