



Assessment of Genetic Parameters for Yield and Quality Components Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

An experiment was conducted to determine the genetic variability, heritability, genetic advance for yield and quality related traits of 30 rice genotypes in direct seeded rice condition during 2016 kharif season. Significant genotypic differences were observed for most of the traits. Generally PCV was higher than GCV for all the characters. High GCV and PCV estimates over the environments observed for number of tillers per plant, biological yield, grain yield, harvest index, kernel length breadth ratio before cooking, kernel length after cooking, kernel breadth after cooking, kernel length breadth ratio after cooking. Heritability estimates were high for all the characters except biological yield. Plant height, number of tillers/plant, kernel length before cooking, length breadth ratio before cooking, kernel length after cooking, kernel breadth after cooking, length breadth ratio after cooking and elongation ratio exhibited high heritability with high genetic advance as percent of mean over the environments indicating that these characters are more reliable for effective selection. Medium range of heritability with high genetic advance as percent of mean was found for grain yield, harvest index and thousand grains weight.

Key words: Rice Genotypes, Yield, Quality, Genetic variability, Heritability.

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's leading cereal crop as more than half of the world's population is dependent on rice as their staple food. In India rice is cultivated on 44.10mha, with a production 165.30 mt and productivity 3.78t/ha¹. In Haryana, rice is mainly grown as transplanted crop over an area of 1.42 million hectare with the production and productivity levels of 4.88 mt and 3.25t/ha, respectively. The presence of genetic variability for yield and quality related traits is of utmost

importance for identification and development of desirable genotypes as improvement in any trait and it depends upon the genetic variability present in the breeding materials. The genotypic coefficient of variation estimates the heritable variability, whereas phenotypic component measures the role of environment on the genotype. High phenotypic coefficient of variation (PCV) and low genotypic coefficient of variation (GCV) for a trait indicated high influence of environment in its expression.

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Similarly, heritability is the measure of transmission of traits from parents to progeny and the estimates of heritability will be of immense help to the breeder in selecting superior genotypes with a desired trait and successfully utilizing them in breeding programme.

MATERIAL AND METHODS

A field experiment with 30 rice genotypes was conducted under direct seeded condition at RRS, Kaul, Haryana during winter (*kharif*) season 2016. The description of genotypes is given in Table 1. All the genotypes were grown in a randomized block design (RBD) with three replications in a single row of 5 meter in length, keeping row to row distance of 20 cm. Observations for all the traits were recorded on five randomly selected plants for each genotype in each replication. Observations were recorded on the characteristics like days to 50% flowering (DH), days to maturity (DM), plant height

(PH), number of tillers per plant (NTTP), panicle length (PL), number of grains per panicle (NGPP), thousand grains weight (TGW), biological yield per plant (BY), grain yield per plant (GY), harvest index (HI), hulling % (H%), milling % (M%), head rice recovery % (HRR %), kernel length before cooking (KLBC), kernel breadth before cooking (KBBC), length breadth ratio before cooking (LBBC), kernel length after cooking (KLAC), kernel breadth after cooking (KBAC) and elongation ratio (ER). Analysis of the observations recorded on different characters was carried out as per the standard procedure. The data for all the parameters was subjected to analysis of variance following Panse and Sukhatme¹² to evaluate the significant differences among the genotypes. Phenotypic and genotypic coefficients of variation were calculated using Burton⁵ method and heritability estimates were computed according to the method described by Johanson *et al.*⁷.

Table 1: List of genotypes (scented and non- scented)

Sr. No.	Genotypes(non scented)	Sr. No.	Genotypes(scented)
1	HKR 12-1	16	PAU 6297-1
2	HKR 12-2	17	UPR 3886-9-1-1
3	HKR 126	18	Haryana Basmati 2
4	HKR 11-87	19	Haryana Basmati 1
5	HKR 07-147	20	PUSA 1637-12-8-20-5
6	HKR 11-79	21	PUSA 1656-10-705
7	IR 91648-B-89-B-1402	22	PUSA 1718-14-2-150
8	IR 99784-255-29-1-2	23	HKR 12-408
9	IR 91648-B-59-B-1-1	24	HKR 12-411
10	IR 93835-90-3-2-1	25	HKR 13-409
11	IR 93928-195-2-1-1	26	HKR 13-418
12	IR 91648-B-2-38-B-1-2	27	Pusa Basmati 1
13	HKR 128	28	Pusa Basmati 1121
14	HKR 47	29	Taraori Basmati
15	HKR 48	30	CSR 30

RESULTS AND DISCUSSION

Analysis of variance

The mean sum of squares for all the studied traits viz. days to 50% flowering, days to maturity, plant height, number of tillers per plant, panicle length, number of grains per

panicle, thousand grain weight, biological yield per plant, grain yield per plant, harvest index, hulling %, milling %, head rice recovery %, kernel length before cooking, kernel breadth before cooking, length breadth ratio before cooking, kernel length after

cooking, kernel breadth after cooking, length breadth ratio after cooking, elongation ratio over the environments has been showed in table 2 and showed significant differences among the genotypes. These results clearly indicate that the material had sufficient amount of variability present in the material and give

to valid estimate for further studies for different traits. It reveals that selection of superior cultivars in developing and release of new varieties for different ecologies. Similar findings were also reported by by Keten *et al.*⁸, Kumar *et al.*¹⁰ and Edukondalu *et al.*².

Table 2: Analysis of variance for grain yield and quality components in scented and non-scented rice genotypes

Source of variation	df	Mean Sum of Square									
		DH	DM	PH	NTPP	PL	NGPP	TGW	BY	GY	HI%
Replication	2	0.03	0.03	9.64	1.44	1.35	11.21	1.30	10.66	14.22	62.92
Treatments	29	260.44**	260.44**	630.92**	7.19**	13.05**	272.47**	8.22**	161.39**	32.37**	70.97**
Error	58	1.44	1.44	5.69	0.66	0.72	18.54	1.02	29.69	4.78	12.24
Source of variation	df	H%	M%	HRR%	KLBC	KBBC	LBBC	KLAC	KBAC	LBAC	ER
Replication	2	0.26	0.05	0.34	0.04	0.004	0.06	0.32	0.02	0.11	0.01
Treatments	29	8.74**	6.02**	12.08**	1.46	0.070	0.97	19.26**	0.80	7.32**	0.14
Error	58	0.40	0.61	0.52	0.01	0.004	0.02	0.11	0.01	0.05	0.003

Phenotypic and genotypic coefficient of variation

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficients of variation (GCV), heritability in broad sense (h^2) and expected genetic advance as per cent of mean (GAM) are presented in Table 3 and Figure 1. The phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV); indicated that the apparent variation is not only due to genotypes but also due to influence of environment. The estimates of genotypic variances showed a considerable range of variation for most of the characters. Selection and interpretation based on such findings may be sometimes misleading. Similar results found by the Keten *et al.*⁸, Savitha *et al.*¹⁵ and Edukondalu *et al.*².

High values of PCV and GCV were observed for number of tillers per plant, biological yield, grain yield, harvest index, Length breadth ratio before cooking, kernel length after cooking, kernel breadth after cooking and length breadth ratio after cooking. These results are in accordance with the findings in rice by Subbaiah *et al.*¹⁷, Keten *et al.*⁸, Rao *et al.*¹³ and Edukondalu *et al.*². Days to 50% flowering, plant height, number of grains per plant, kernel length before cooking and elongation ratio exhibited medium PCV and GCV values whereas, low PCV and GCV values were found for the days to maturity, panicle length, thousand grain weight, hulling %, milling %, head rice recovery % and kernel breadth before cooking. These results supported by the findings of Mustafa *et al.*¹¹, Kumar *et al.*⁹ and Shankar *et al.*¹⁶.

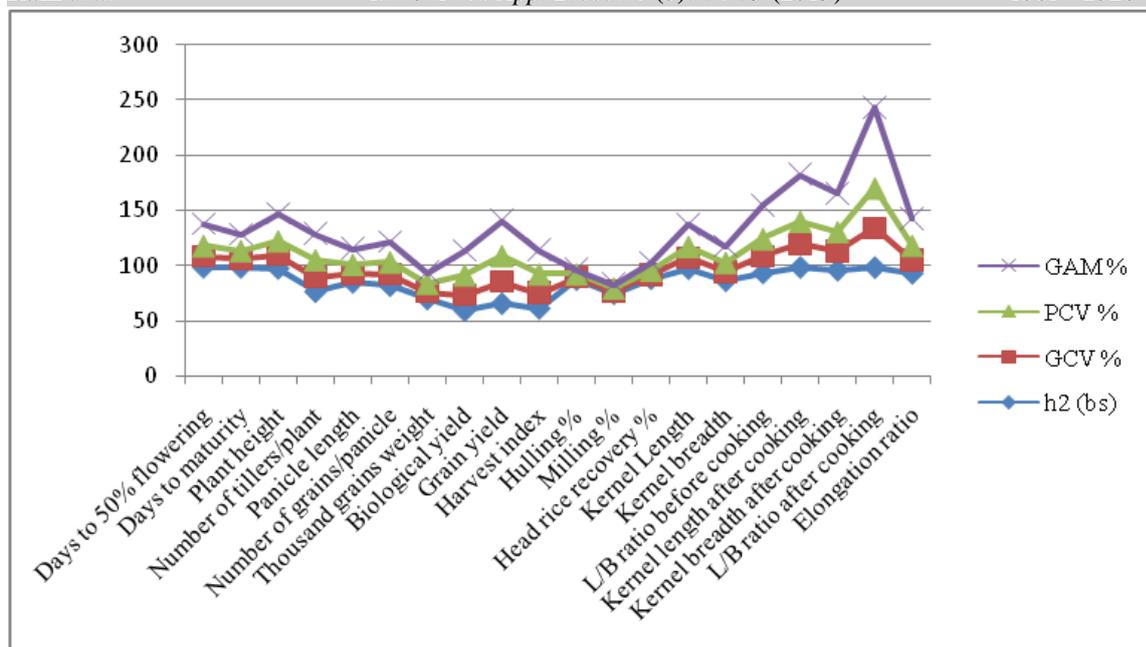


Fig. 1: Genetic parameters for yield and quality traits in rice

Heritability and genetic advance

High heritability and high genetic advance as percent of mean over the environments was observed in case of plant height, number of tillers per plant, kernel length, length breadth ratio before cooking, kernel length after cooking, kernel breadth after cooking, length

breadth ratio after cooking and elongation ratio. It indicated the presence of additive gene effect hence these traits can be improved by simple selection. Similar findings were observed by Bisne *et al.*⁴, Bekele *et al.*³ and Chowdhury *et al.*⁶ in rice.

Table 3: Genetic components of variance, heritability and genetic advance of different traits

Characters	Genetic components of variance			
	h^2_{bs} (%)	GCV (%)	PCV (%)	GAM (%)
Days to 50% flowering	98.364	9.757	9.838	19.934
Days to maturity	98.364	7.419	7.481	15.159
Plant height	97.342	12.341	12.508	25.083
Number of tillers/plant	76.674	13.154	15.022	23.727
Panicle length	85.011	7.595	8.237	14.425
Number of grains/panicle	82.028	9.965	11.003	18.592
Thousand grains weight	70.079	6.12	7.311	10.555
Biological yield	59.659	13.748	17.799	21.875
Grain yield	65.827	19.178	23.638	32.054
Harvest index	61.522	13.412	17.099	21.671
Hulling %	87.455	2.174	2.325	4.189
Milling %	74.785	1.999	2.312	3.561
Head rice recovery %	88.078	3.571	3.805	6.905
Kernel Length	97.223	9.879	10.019	20.066
Kernel breadth	86.346	7.782	8.374	14.895
L/B ratio before cooking	93.282	15.222	15.761	30.286
Kernel length after cooking	98.33	20.787	20.963	42.463
Kernel breadth after cooking	95.824	17.216	17.587	34.717
L/B ratio after cooking	98.167	35.952	36.287	73.38
Elongation ratio	92.964	12.308	12.765	24.445

High heritability and moderate genetic advance as percent of mean over the environments was observed for days to 50% flowering, days to maturity, panicle length, number of grains/panicle and kernel breadth before cooking indicated the presence of both additive and non additive type of gene action. Similar findings were also reported in rice by Savitha *et al.*¹⁵ Sangare *et al.*¹⁴. High heritability and low genetic advance as percent of mean over the environments was observed for hulling %, milling % and head rice recovery % indicated the role of both additive and non-additive variance. Hence, selections based on progeny values may be more effective.

CONCLUSION

In the present investigation, Analysis of variance indicated highly significant differences among the genotypes for all the traits except kernel length before cooking, kernel breadth before cooking, L/B ratio before cooking, kernel breadth after cooking and elongation ratio under study. A perusal of genetic variability parameters revealed that PCV and GCV were high for number of tillers/plant, biological yield, grain yield, harvest index, L/B ratio before cooking, kernel length after cooking, kernel breadth after cooking and L/B ratio after cooking. High heritability coupled with high genetic advance as percent of mean was observed for plant height, number of tillers/plant, kernel length before cooking, length breadth ratio before cooking, kernel length after cooking, kernel breadth after cooking, length breadth ratio after cooking and elongation ratio, which indicated that these traits were controlled by additive type of gene action. Moderate heritability with high genetic advance as percent of mean was found for grain yield, harvest index and thousand grains weight, indicated the presence of non additive gene effects, in addition to influence of environment to some extent. Thus evaluation of material for genetic variability parameters among various yield and quality traits would be more useful to the plant breeders and parents identified on

the basis of these parameters for any breeding programme would be more promising.

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