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SHORT COMMUNICATION

Genetic Variation for Morphological, Grain Yield and Grain Quality Traits in Rice Landraces of Chhattisgarh

Richa Sao, Ritu R. Saxena, Namita Singh and Parmeshwar K. Sahu*
Department of Genetics and Plant Breeding, College of Agriculture,
Indira Gandhi Krishi Vishwavidyalaya, Raipur-492012 (Chhattisgarh)
*Corresponding author's email: parmeshwarsahu1210@gmail.com

ABSTRACT

An attempt was made to study the genetic parameters for yield, yield attributing and quality characters in forty seven rice genotypes. Analysis of variance for 27 yield and quality traits revealed significant differences for all the traits under study. Coefficient of variation ranges from 5.83% for hulling percentage to 66.97% for alkali spreading value. The high value of phenotypic coefficient of variation coupled with genotypic coefficient of variation was recorded in number of filled grains per panicle followed by number of unfilled grains per panicle, total spikelet per panicle, grain weight per plant, panicle weight, and harvest index so on. The phenotypic variance was higher than the corresponding genotypic variance for the characters, indicating influence of environment on expression of these characters. High heritability with high genetic advance as percent mean was observed for all yield attributing traits like grain weight per plant, harvest index %, number of filled grains per panicle, panicle weight etc except for panicle length.These characters are governed by additive gene action and one should go for direct selection for improving these traits.

Keywords: *Rice, germplasm, genetic variability, grain yield*

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INTRODUCTION

Rice is the most important cereal crop of the world meeting the dietary requirement of the people living in tropics and sub-tropics. More than half of the world's population depends on rice for a substantial amount of calories [15]. The rising demand, saturation of cultivable field and low gross domestic production of rice are likely to cause a supply shortage of a crop in the near future [14]. Therefore being the most important staple food of the population, improving its productivity by exploiting the genetic variability has become a crucial importance. For effective genetic improvement, knowing the nature and magnitude of various characters of rice is very essential. A critical analysis of genetic variability is a prerequisite for initiating any crop improvement also for adopting appropriate selection technique [13]. Environmental effects also influence the total observable variation of quantitative traits. Therefore, partitioning of total variance due to genetic and non genetic cause becomes necessary for effective breeding program. The genotypic coefficient of variance estimates the heritable variability, whereas phenotypic component measures the role of environment in its expression [7]. The phenomenon of transmission of characters from parents to offspring is usually measured in terms of heritability whereas genetic advance is a measure of genetic gain under selection. Therefore the estimates of heritability and genetic advance would help to formulate a sound breeding programme [10]. Keeping in view the above facts, the present investigation was undertaken to know genetic variability and heritability of rice genotypes for different yield and quality traits.

MATERIAL AND METHODS

The present research work was conducted at Research cum Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, during the *Kharif* season of 2016. Forty-seven genotypes including land races and released varieties of rice were included for the study (Table 1). Twenty-one days old seedlings were subsequently transplanted in the field with row to row & plant to plant distance of 20 cm X 20 cm in Randomized Block Design (RBD) with two replications. Standard agronomical practices were adopted for all the treatments. Five random plants from each of the treatment of each replication were taken for recording data.

Statistical analysis for ANOVA and variability parameters was done by software WINDOSTAT v9.3. ANOVA and test of significance was calculated as per the method of Fisher [4]. The genotypic and phenotypic coefficient of variance was calculated by the formula given by Burton [2]. Heritability in broad sense was calculated by the formula given by Hanson *et al.* [5]. From the heritability estimates, the genetic advance was calculated by the formula given by Johnson *et al.* [6].

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA) based on Randomized Complete Block Design

The result of analysis of variance of 27 yield and quality traits in 47 rice germplasm accessions is given in the table 2. The results of the analysis of variance indicated that all the genotypes were highly significant for all the yield attributing and quality characters. This clearly indicates that variability does exist in all the genotypes for all the traits and there is good chance to improve these traits through proper breeding methods. Presence of high variability might be due to presence of diverse germplasm lines where natural recombination taken place continuously. The presence of high variability for grain yield, yield attributing traits and grain quality traits were also reported by Subba Rao *et al.* [13], Sajid *et al*. [11] and Sahu *et al*. [10].

Variability parameters and mean performance for the traits

Genetic variability parameters and mean performance of 27 yield and quality traits of 47 rice germplasm accessions are given in table 3. Grain yield ranges from 6.32 to 26.02 with an average of 13.27±5.57 and CV 41.97%. Hundred seed weight ranges from 0.71 to 2.94 with an average 2.11±0.53 and CV 24.9%. Harvest index ranges from 19.62 to 51.25 with an average 31.66±8.74 and CV 27.62%. Hulling% ranges from 61.47 to 76.11 with an average 69.08±4.03 and CV 5.83%. Milling% ranges from 34.25 to 70.80 with an average 57.6±6.75 and CV 11.71%. HRR% ranges from 22.10 to 63.43 with an average 45.75±9.31 and CV 20.35%.

Genotypic and phenotypic coefficient of variation (GCV and PCV)

The magnitude of coefficient of variation was categorized as high (> 20%), moderate (10- 20%) and low (< 10%). Coefficients of variation indicated that the phenotypic coefficient of variation (PCV) were slightly higher than corresponding genotypic coefficient of variation (GCV) which showed the negligible influence of extraneous factors and therefore, selection for such traits on the basis of phenotype only could also be rewarding [1, 10]. The high value of PCV coupled with high GCV was recorded for number of filled grains/panicle, followed by total spikelet/panicle, number of unfilled grains per panicle, grain weight/plant, panicle weight, harvest index, milled grain length, hundred seed weight, number of panicles per plant, decorticated grain length, gel consistency, decorticated grain width, milled grain width, shoot dry weight/plant, HRR%. Results showed traits having high GCV and PCV could be improved through direct selection. Traits like leaf: length of blade, leaf: width of blade, plant height, stem: length (excluding panicle), spikelet fertility, paddy length, paddy width, milling (%), amylose content (%) showed intermediate GCV and PCV which indicated that selection for these traits in advance generation would be rewarding. Two traits *viz.,* panicle length and hulling (%) showed low GCV and PCV which indicated the presence narrow genetic base and improvement in these traits could be done by hybridization or induced mutagenesis followed by pedigree selection in advanced generations [9]. These results were in accordance with the findings of Babu *et al.* [1], Karuppaiyan *et al.* [7], Lingaiah *et al.* [8] and Sahu *et al.* [10].

Heritability (bs):

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. Heritability was classified as high (above 60%), medium (30%-60%) and low (below 30%). High estimate of heritability was found for all characters except for panicle length which showed intermediate heritability. The highest heritability was estimated for decorticated grain length followed by 100-grain weight, total spikelet per panicle and number of filled grains per panicle. 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. This finding is in agreement with Choudhary *et al*. [3], Babu *et al.* [1], Sarawgi *et al*., [12], Tuhina Khatun *et al.* [14] and Sahu *et al.* [10].

Genetic advance:

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 as percent of mean was categorized as high (>20%), moderate (10-20%) and low (<10%). Most of the traits under investigation possessing high values of genetic advance indicate that the characters are governed by additive genes and selection will be rewarding for improvement of such trait. Only some traits *viz.,* width of leaf blade, panicle length, spikelet fertility, hulling% showed moderate genetic advance.

Heritability estimates along with genetic advance is more useful than heritability alone in predicting the effectiveness of selection [6]. High heritability coupled with high genetic advance was observed for leaf: length of blade, plant height, stem length, panicle weight, panicle: number/ plant, hundred grain weight, number of filled grains/panicle, number of unfilled grains/panicle, total spikelet/panicle, grain weight/plant, shoot dry weight/plant, harvest index, paddy length, decorticated grain length, decorticated grain width, length of milled grain, width of milled grain, milling%, HRR, amylose content and gel consistency. Characters which showed high genetic advance coupled with high heritability are governed by additive gene action and would be considered for direct selection. High heritability with moderate or low genetic advance as percentage of mean was observed for width of leaf blade, spikelet fertility, width of paddy, hulling % which indicated that these traits are also governed by additive gene action and can be improved by selection methods with proper care [9]. These findings are in agreement with findings of Veni and Rani [15], Babu *et al.* [1], Tuhina Khatun *et al.* [14], Sahu *et al.* [10].

Table 1: List of 47 rice genotypes (33 landraces and 14 released varieties) included in the study.

S. N.	CGR No.	Name	S. N.	CGR No.	Name
1	CGR NO- 17976	Dhaur	24	CGR NO- 569	Basmati
2	CGR NO- 17978	JS-5	25	CGR NO- 741	Dhamna panda
3	CGR NO-18029	Badal phool	26	CGR NO- 1599	No :21 (A)
4	CGR NO-1	Amakoyali	27	CGR NO- 1845	Badi barik
5	CGR NO- 14	Rambhoj	28	CGR NO- 2181	Basmati
6	CGR NO- 72	Churhala dhan	29	CGR NO- 1718	Kondi ajan
7	CGR NO- 218	Lal batra	30	CGR NO- 2176	Basmati (I)
8	CGR NO- 242	Lallo-14	31	CGR NO- 2210	Beo (I)
9	CGR NO- 255	Machhri kata	32	CGR NO- 2328	Bodi
10	CGR NO- 300	Parra dhan	33	CGR NO- 1712	Bhata ajan
11	CGR NO- 320	Pinna basengi	34		Swarna sub 1
12	CGR NO- 369	Sakra	35		Jaya
13	CGR NO- 389	Satka	36		IGKVR 1244
14	CGR NO- 447	Shyam jir	37		Karma mahsuri
15	CGR NO- 529	Banko –II	38		Badshabhog Selection 1
16	CGR NO- 659	Changadi	39		Dubraj Selection 1
17	CGR NO- 746	Dhaura	40		Tarunbhog Selection 1
18	CGR NO- 930	Kadam phool	41		Mahamaya
19	CGR NO- 953	Kakdo	42		Safri 17
20	CGR NO- 993	Kanji	43		IGKVR 2
21	CGR NO- 1211	Machhari ankhi	44		Indira Aerobic Dhan 1
22	CGR NO- 1267	Nalla wadlu	45		Swarna sub 1
23	CGR NO- 1319	Parra	46		IGKVR 1
			47		MTU1010

Table 2: Analysis of variance (ANOVA) for 27 yield and quality traits in rice genotypes

SV	DF	Mean Sum of Squares									
		1	2	3	4	5	6	7	8	9	10
Replications	1	23.585*	0.01	739.42*	282.65*	107.75*	4.53	1.53	0.00	29.88	53.63**
Treatments	46	102.24**	0.064**	721.72**	717.31**	12.45**	83.42**	16.52**	0.55**	5907.92**	588.09**
Error	46	2.21	0.01	34.28	24.56	4.79	1.70	3.25	0.00	21.41	8.85

SV	DF	Mean Sum of Squares									
		11	12	13	14	15	16	17	18	19	20
Replications	1	163.57**	43.53**	0.14	1.41	5.82	74.00**	0.02	0.03	0.01	0.23
Treatments	46	9922.71**	109.68**	61.99**	137.41**	152.87**	1.93**	0.19**	2.78**	102.24**	0.064**
Error	46	34.03	9.11	1.12	5.05	4.89	65.27	0.01	0.01	2.21	0.01

SV	DF	Mean Sum of Squares						
		21	22	23	24	25	26	27
Replications	1	0.01	13.41	13.18*	38.15*	7.19	0.01	4.04
Treatments	46	721.72**	717.31**	12.45**	83.42**	16.52**	0.55**	19.66**
Error	46	0.03	24.56	4.79	1.70	3.25	0.25	21.41

** Significant at 1% level of significance; * Significant at 5% level of significance

1= Leaf: Length of blade ; 2 = Leaf: Width of blade ; 3= Plant height ;4= Stem: Length(excluding panicle ; 5= Panicle length ; 6= Panicle weight (g) ; 7= Number of panicles per plant ; 8= 100 seed weight (g) ; 9= Number of filled grains/panicle ;10= Number of unfilled grains/panicle ;11= Total spikelets/ panicle; 12= Spikelet Fertlity % ; 13= Grain weight/plant (g) ; 14= Shoot dry weight/plant (g) ; 15=Harvest Index (%) ; 16= Paddy length ; 17= Paddy width ; 18= Decorticated grain length (mm) ; 19=Decorticated grain width(mm) ; 20= Milled grain length ; 21 ; Milled grain width ; 22= Hulling% ; 23= Milling% ; 24=HRR% ; 25= Gel consistency ; 26=Alkali spreading value ; 27= Content of amylose %

Table 3: Mean and Variability parameters for 27 yield and quality traits of 47 rice germplasm accessions

Traits	Mean (X)	Range		SD	CV%	GCV (%)	PCV (%)	h^2 (bs) (%)	GA as % mean
		Min.	Max.						
Leaf: Length of blade (cm)	40.38	28.18	60.49	7.15	17.70	17.51	17.89	95.77	35.30
leaf: width of blade (cm)	1.62	1.23	2.15	0.18	11.10	10.33	11.82	76.43	18.61
Plant height (cm)	132.05	91.26	176.04	19.00	14.39	14.04	14.72	90.93	27.58
Stem: Length(excluding panicle)	107.99	67.50	147.50	18.94	17.54	17.23	17.84	93.38	34.31
Panicle length (cm)	24.06	18.64	29.39	2.49	10.37	8.14	9.42	44.47	11.18
Panicle weight (g)	15.58	7.60	31.00	6.46	41.46	41.04	41.88	96.00	82.83
Number of panicles per plant	10.72	6.00	19.00	2.87	26.80	24.02	29.32	67.12	40.54
100 seed weight (g)	2.11	0.71	2.94	0.53	24.90	24.87	24.94	99.44	51.09
Number of filled grains/panicle	85.41	7.00	232.50	54.35	63.63	63.52	63.75	99.28	50.0
Number of unfilled grains/panicle	26.63	8.00	67.00	17.15	63.34	62.86	63.81	97.04	45.8
Total spikelets/ panicle	112.49	17.50	304.00	70.44	62.62	62.51	62.72	99.32	40.8
Spikelet Fertility (%)	74.42	39.87	87.60	7.41	9.95	10.23	10.96	84.66	18.06
Grain weight/plant (g)	13.27	6.32	26.02	5.57	41.97	41.58	42.34	96.46	84.13
Shoot dry weight/plant (g)	40.76	26.00	62.00	8.29	20.33	20.06	20.70	92.91	39.63
Harvest Index (%)	31.66	19.62	51.25	8.74	27.62	27.17	28.06	93.80	54.21
Paddy length (mm)	9.29	5.40	47.80	5.82	62.67	11.43	11.79	91.91	25.45
Paddy width (mm)	2.97	2.30	3.50	0.31	10.27	10.34	10.89	88.06	19.21
Decorticated grain length(mm)	5.50	2.85	7.13	1.18	21.44	21.41	21.47	99.45	43.99
Decorticated grain width(mm)	1.97	1.10	2.55	0.41	20.66	20.58	20.76	98.25	42.01
Milled grain length (mm)	4.10	1.68	5.63	1.04	25.47	25.22	25.71	96.19	50.95
Milled grain width (mm)	1.94	1.08	2.53	0.41	20.90	20.8	21	98.08	42.43
Hulling (%)	69.08	61.47	76.11	4.03	5.83	5.54	6.11	82.06	10.33
Milling (%)	57.60	34.25	70.80	6.75	11.71	11.53	11.89	93.89	23.00
HRR (%)	45.75	22.10	63.43	9.31	20.35	20.41	21.24	83.52	36.55
Gel consistency	69.34	33.00	97.00	15.75	22.72	22.34	23.08	93.69	44.55
Alkali spreading value	2.71	1.00	7.00	1.82	66.97	23.4	23.6	88.1	15.41
Amylose content (%)	21.77	15.91	29.37	3.10	14.22	13.82	14.6	89.70	26.97

CONCLUSION

Increasing the rice production per unit of land is essential to feed the global population. Therefore study about genetic variations in rice germplasm keeps a prime importance. This study gives idea to the plant breeders about the variations available in rice germplasm lines for grain yield attributing traits and grain quality traits which would be useful for improvement of studied traits.

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