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Priya Gupta

Department of Genetics and
Plant breeding, Indira Gandhi
Krishi Vishwavidyalaya,
Raipur, Chhattisgarh, India

Mangla Parikh

Department of Genetics and
Plant breeding, Indira Gandhi
Krishi Vishwavidyalaya,
Raipur, Chhattisgarh, India

Krishna Tandekar

Department of Genetics and
Plant breeding, Indira Gandhi
Krishi Vishwavidyalaya,
Raipur, Chhattisgarh, India

Genetic variability assessment in accessions of rice (*Oryza sativa* L.)

Priya Gupta, Mangla Parikh and Krishna Tandekar

Abstract

Forty eight rice (*Oryza sativa* L.) genotypes including four checks has been planted in Randomized Block Design, within two replications, were evaluated during kharif 2018 for twenty five quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among forty eight genotypes were significant for all the characters except length of leaf blade and width of leaf blade. Among the all traits gel consistency exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by unfilled grain per panicle, gel consistency, grain yield per panicle and number of effective tiller. Broad sense heritability was highest for Gel consistency, which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as per cent of mean was recorded for Gel consistency with high value of heritability.

Keywords: Genetic variability, rice (*Oryza sativa* L.), genotypic coefficient of variation

Introduction

Rice (*Oryza sativa* L.) is the most important cereal crop of the world and about 90 per cent of the people of south East Asia consume rice as staple food. Rice production in India was 113 million tonne for 2018-19 (The Economic Times) and estimated production for India for the year of 2019-20 is 114.1 mt (United States Department of Agriculture). According to United States Department of Agriculture rice production in world was 499.07 mt for 2018-19 and its estimated production for 2019-20 is reduced by 1.5 mt because of late monsoon. Development of high yielding varieties requires the knowledge of existing genetic variability. The large spectrum of genetic variability in segregating population depends on the amount of the genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype for further breeding programme. Assessment of variability for yield and its component characters becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. It helps in determining the influence environment on the expression the genotypic and reliability of characters. With the above background information the present investigation was undertaken to study the genetic parameters among the 45 rice genotypes.

Materials and Methods

A field experiment was conducted with forty eight rice genotypes including four checks (Pusa basmati 1, Swarna, IGKV R 1244, Indira sugandhitdhan 1) during kharif 2019 at research cum instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh) in Randomized Block Design (RBD) with two replications. Twenty seven days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and hills, respectively. Five representative plants for each genotypes in each replications were randomly selected to record the observations for 25 quantitative traits viz., Length of leaf blade, width of leaf blade, days to 50% flowering, Plant height, panicle length, effective tiller per plant, filled grain per panicle, spikelet fertility, 100 seed weight, biological yield per plant, harvest index, grain yield per plant, hulling percentage, milling percentage, head rice recovery percentage, brown rice length, brown rice width, brown rice l/b ratio, kernel length, kernel width, kernel length after cooking, kernel

Corresponding Author:

Priya Gupta

Department of Genetics and
Plant breeding, Indira Gandhi
Krishi Vishwavidyalaya,
Raipur, Chhattisgarh, India

width after cooking, cooked rice elongation ratio, kernel elongation ratio and gel consistency. The mean data after computing for each character was subjected to standard method of analysis of variance, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance as per cent of mean were estimated by OPSTAT software.

Results and Discussion

A wide range of variation was observed among forty four rice (*Oryza sativa* L.) accessions and four checks (Pusa basmati 1, Swarna, IGKV R 1244, Indira sugandhitdhan 1) for twenty five quantitative characters. The perusal of data revealed that variance due to treatment was highly significant for all the characters except length of leaf blade and width of leaf blade (Table 1). This suggested that there were inherent genetic differences among the genotypes. Significant genetic variation in various component characters exhibited by the genotypes indicated these characters might be effective. Among all important yield contributing characters coefficient of variation indicated that estimates of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters (Table 2). Among the all traits grain yield per plant (23.94%, 39.20%) exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by filled grain per panicle (21.08%, 34.36%) and biological yield (20.05%, 27.04%). The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Effective tiller per panicle (39.53%, 19.55%) and harvest index (27.043%, 11.604%) showed moderate value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The characters *viz.*, effective tiller (19.55, 39.53), filled grain per panicle (21.08, 34.36), unfilled grain per panicle (55.66, 67.67), spikelet fertility (82.27, 114.65), kernel L/B ratio (21.17, 24.88), gel consistency (40.26, 40.3) have high genotypic and phenotypic coefficient of variation that showed the presence of considerable amount of variability for these characters for all genotypes. Similar findings were reported by Limbani *et al.* (2017) [6], Prasad *et al.* (2017) [8] and Rashmi *et al.* (2017) [9], Iqbal *et al.* (2018) [3]. The coefficient of variation doesn't offer the full scope of heritable variation. It can be found out with greater degree of accuracy when heritability is conjunction with genetic advance study. Heritability and genetic advance are important selection parameters. High heritability estimates along with high genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johanson *et al.*, 1955) [4].

Heritability: Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. Broad sense heritability was high for gel consistency (99.82%), brown rice length (99.287%), brown rice width (95.55%), brown rice L/B ratio (98.01%), kernel length (98.72%), kernel width (86.69%), kernel L/B ratio (72.39%), cooked rice length (98.705%), cooked rice width (92.34%), cooker rice L/B ratio (98.08%), head rice recovery percentage (98%), biological yield per plant (98.62%), grain yield per plant (95.81%), hulling percentage (98.02%), milling percentage (95.81%) days to 50% flowering, (98.62%), plant height (84.16%), panicle length (60.7%) and harvest index (98.02%) which suggested that these traits would respond to selection owing is their high genetic variability and transmissibility. Similar finding was earlier reported by Paikhomba *et al.* (2014) [7].

Heritability and Genetic Advance: High heritability coupled with genetic advance as percent of mean was observed for plant height (84.16%, 25.96%), head rice recovery percentage (98.00%, 38.40%), grain yield per plant (95.81%, 30.13%) and biological yield (98.62%, 30.19%), milling percentage (95.81%, 22.79%), brown rice length (99.28%, 25.31%), brown rice width (95.55%, 25.24%), brown rice L/B ratio (98.01%, 40.71%), kernel length (98.72%, 23.4%), kernel width (86.69%, 25.01%), kernel L/ B ratio (72.39%, 37.1%), cooked rice length (98.7%, 23.48%), cooked rice L/B ratio (98.08%, 35.38%) and gel consistency (99.82%, 79.72%) were the important quantitative parameters among yield contributing traits. Low heritability coupled with low genetic advance was observed for the characters like length of leaf blade (35.89%, 9.95%) and width of leaf blade (28.92%, 6.98%). High heritability with moderate genetic advance was showed by characters days to flowering (98.62%, 17.12%) panicle length (98.62%, 17.12%), harvest index (98.02%, 18.4%), hulling percentage (98.02%, 18.4%) and cooked rice width (92.24%, 16.56%) with low genetic advance panicle length (60.70%, 11.54%), effective tiller per plant (24.45%, 19.91%) and 100 seed weight (35.89%, 38.25%). The characters having 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 selection. Whereas, low heritability and low genetic advance shows non-additive gene action. However, characters showing high values of heritability coupled with moderate genetic advance suggest that selection for the improvement of these characters may be rewarding. It also indicates greater role of non-additive gene action in their inheritance suggesting heterosis breeding could be useful for improving these traits. Similar findings were also reported by Sharma and Bhuyan (2004) [10], Das *et al.* (2005) [11], Kumar *et al.* (2013) [5], Iqbal *et al.* (2018) [3].

Table 1: Analysis of variance for different quantitative and qualitative traits of 44 rice accessions.

S.No	Sources of Variation	MSS		
		Treatment	Replication	Error
	DF	47	1	47
1	Length of leaf blade (cm)	64.324	10.69	30.344
2	Width of leaf blade (cm)	0.025	0.009	0.014
3	Days to 50% flowering (days)	134.89**	4.167	0.933
4	Plant height (cm)	732.07**	77.54	75.10
5	Panicle length(cm)	10.912*	0.113	0.735
6	Effective tiller per plant	56.88**	3.604	1.819
7	Filled grain/panicle	3545.49**	25.01	0.991
8	Spikelet fertility%	220.87**	0.510	39.494
9	100 seed weight (g)	0.370**	0.006	4.553
10	Biological yield per plant (g)	830.461**	7.849**	0.005
11	Grain yield per plant (g)	257.56**	3.64	0.735
12	Harvest index%	222.41**	3.454	
13	Hulling%	98.426**	3.08	1
14	Milling%	129.12**	30.488**	2.769
15	Head rice recovery%	187.95**	8.461*	1
16	Brown rice length (mm)	1.178**	0.011	0.004
17	Brown rice width (mm)	0.169**	0.006	0.004
18	Brown l/b ratio	0.615**	0.001	0.006
19	Kernel length (mm)	0.833**	0.004	0.005
20	Kernel width (mm)	0.179**	0.023	0.013
21	Kernel elongation ratio	0.733*	0.177	0.117
22	Kernel length after cooking (mm)	1.973**	0.001	0.01
23	Kernel width after cooking (mm)	0.125**	0.001	0.005
24	Cooked rice elongation ratio	0.538**	0.002	0.005
25	GC	446.829**	1.042	0.403

Table 2: Variability parameters of different quantitative and qualitative traits in rice

S. No.	Characters	Mean	Range		GCV%	PCV%	h ² % (bs)	GA as percent of mean
			Min.	Max.				
1	Length of leaf blade	51.09	32.43	67.43	8.06	13.46	35.89	9.95
2	Width of leaf blade	1.18	0.87	1.63	6.30	11.73	28.92	6.98
3	Days to 50% flowering	97.75	107	152	8.37	8.43	98.62	17.12
4	Plant height	133.144	84.6	160.2	13.73	14.97	84.16	25.96
5	Panicle length	26.16	21.82	31.21	7.191	9.23	60.70	11.54
6	Effective tiller	11.02	7.2	25.5	19.55	39.53	24.45	19.91
7	Filled grain per panicle	124.546	71.9	217.7	21.08	34.36	28.92	26.64
8	Spikelet fertility	8.01	0.83	60.27	82.27	114.65	51.49	121.63
9	100 seed weight	2.26	1.01	3.24	18.89	19.21	35.89	38.25
10	Biological yield	67.80	38.4	110.85	20.05	27.43	98.62	30.19
11	Harvest index	37.10	20.47	56.68	11.60	27.04	98.02	10.25
12	Grain yield per plant	25.22	11.7	43.6	23.94	39.20	95.81	30.13
13	Hulling%	77.40	51.67	84.93	9.02	9.11	98.02	18.4
14	Milling%	70.35	47.14	81.22	11.30	11.54	95.81	22.79
15	Head rice recovery%	51.21	37.84	68.98	18.83	19.02	98.00	38.40
16	Brown rice length	6.21	4.6	8	12.33	12.37	99.28	25.31
17	Brown rice width	2.29	1.6	3	12.53	12.82	95.55	25.24
18	Brown rice l/b ratio	2.76	1.75	4.29	19.96	20.16	98.01	40.71
19	Kernel length	5.62	4.1	7.2	11.43	11.50	98.72	23.40
20	Kernel width	2.21	1.5	2.95	13.04	14.01	86.69	25.01
21	Kernel l/b ratio	2.62	1.64	4.95	21.17	24.88	72.39	37.10
22	Cooked rice length	8.62	6.9	11.75	11.47	11.54	98.7	23.48
23	Cooked rice width	2.92	2.25	3.45	8.36	8.70	92.34	16.56
24	Cooked rice l/b ratio	2.97	2.32	5.2	17.34	17.51	98.08	35.38
25	Gel consistency	37.55	26	95.5	40.26	40.30	99.82	79.72

Conclusion

The overall result showed the presence of adequate variability in the genotypes studied. This variation could be effectively manipulated using appropriate breeding techniques and program to develop improved varieties. High estimate of heritability and genetic advance were observed in most of the

traits, indicating the predominance of additive gene action and the possibility of direct selection through these traits.

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