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RESEARCH ARTICLE

GENETIC VARIABILITY STUDIES FOR YIELD COMPONENTSIN RICE (*ORYZA SATIVA* L.)

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Abstract: Forty eight genotypes were assessed for variability atRARS Karjat Dist. Raigad during *Kharif* 2020. The analysis of variance revealed highly significant differences due to treatments for all the fifteen characters under study. The estimates of PCV were slightly higher than their corresponding GCV for all the traits studiedbut the difference is very less indicating the presence of environmental influence to some degree in the phenotypic expression of the traits. All the characters except no of tillers per plant showed high broad sense heritability. High heritability estimates coupled with high genetic advance as per cent of mean were observed for number of filled spikelets per panicle, total number of spikelets per panicle, straw yield per plant, number of unfilled spikelets per panicle, plant height, test weight, grain yield per plant and harvest index indicating the preponderance of additive type of gene action for the expression of these characters and selection may beeffective for improving these characters.Thus, these characters may serve as an effective selection parameter during breeding programme.

Keywords: Rice, Variability, Heritability, Genetic advance, Yield components

INTRODUCTION

Rice (*Oryza sativa* L.) is a self pollinating, short day, monocotyledonous angiosperm having genus *Oryza* and family Poaceae (Gramineae). It is one of the three major food crops of the world and forms the staple diet of about half of the world's population. Asia is the leader in rice production accounting for about 90% of the world's production. Over 75% of the world supply is consumed by people in Asian countries and thus rice is of immense importance to food security of Asia. The demand for rice is expected to increase further in view of expected increase in the population.

The development of high yielding rice varieties for diverse ecologiesrely upon the nature and amount of variability present in the genetic stock. 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 and are used for devising suitable selection strategy for high yield in rice crop. Heritability is a good index of the transmission of character from parents to their offspring (Falconer, 1981). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations. In addition, high genetic advance coupled with high heritability offers the most effective condition for selection for a specific character.

In view of above, the present investigation was undertaken to estimate the extent of variation for yield and yield contributing traits in rice genotypes by studying the genetic parameters like, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, which will help in formulation of suitable selection indices for crop improvement and to explore high yield potential and quality traits in rice.

MATERIALS AND METHODS

The present experiment was conducted at Regional Agricultural Research Station, Karjat Dist. Raigad, Maharashtra state during *Kharif*, 2020. Forty-eight rice genotypes collected from Rice Specialist, RARS Karjat were laid out in randomized block design with three replications.

All genotypes along with check were sown on 19th June, 2020 separately in the nursery on raised beds. Recommended agronomic and plant protection measures were adopted to raise a healthy nursery. The seedlings were transplanted on 15th July, 2020 i.e. after 27 days of sowing. Seedlings were transplanted with a spacing of 20 cm between rows and 15 cm between plants in a row. The plot size was

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2.25 m×0.06 m for each genotype. Each genotype was planted in three rows and each row with fifteen plants. So, forty five seedlings of each genotype per replication were maintained.

Five competitive plants were selected randomly from each genotype per replication for recording observations on fifteen yield and yield attributing characters *viz;* days to 50 per cent flowering, plant height (cm), number of tillers per plant, panicle length (cm), number of filled spikelets per panicle, number of unfilled spikelets per panicle, total number of spikelets per panicle, spikelet fertility (%), test weight (g), straw yield per plant (g), harvest index (%), grain length (mm), grain breadth (mm), length/breadth ratio and grain yield per plant (g).

The data recorded on various traits were statistically analyzed using software WINDOSTAT version 9.2. Analysis of variance carried out by the method suggested by Panse and Sukhatme (1961). The variability parameters, phenotypic and genotypic coefficient of variation (PCV and GCV) were computed as per Burton and De Vane (1953). Heritability and genetic advance were categorized into low, medium and high as per Johnson *et al*. (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences due to treatments for all the characters under study (Table 1). It implies that all the genotypes had substantial variation for all the characters. Highly significant variation was obtained for total number of spikelets per panicle, number of filled spikelets per panicle, plant height, number of unfilled spikelets per panicle and days to 50 per cent flowering. These results are in accordance with Tiwari *et al*. (2011), Paswan *et al*. (2014) and Rashid *et al*. (2017) in rice.

Components of variation

The estimates of components of variation, coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean for various yield contributing characters are presented in Table 2. Graphical presentation of phenotypic and genotypic coefficient of variation is shown in fig. 1 and that of heritability and genetic advance as per cent of mean is shown in fig. 2.

The environment considerably influenced most of the polygenic characters of economic importance. Therefore, available total variation of the population was partitioned into phenotypic, genotypic and environmental variance. The perusal of coefficient of variability indicated that wide range of variation was present at both phenotypic and genotypic levels for all the characters under study. In general, phenotypic variances were found to be maximum than corresponding genotypic variances for different characters under study. The highest phenotypic and genotypic variance was observed for the characters total number of spikelets per panicle followed by number of filled spikelets per panicle, plant height andnumber of unfilled spikelets per panicle. These results are in agreement with Akinwale *et al*. (2011), Rashid *et al*. (2017) and Adhikar *et al*. (2018) in rice.

The amount of genetic variability present, decides the effectiveness of selection. The extent of variability as measured by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides information regarding the relative amount of variation for various traits (Pratap *et al*. 2018). Here, the estimates of PCV were slightly higher than their corresponding GCV for all the traits studied, but the difference is very less indicating the presence of environmental influence to some degree in the phenotypic expression of the traits. The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence Akinwale *et al*. (2011).

High phenotypic and genotypic coefficients of variation (>20%) was recorded for number of unfilled spikelets per panicle, number of filled spikelets per panicle, grain yield per plant, straw yield per plant and total number of spikelets per panicleindicating the greater scope of improvement through selection. Moderate for plant height, test weight and harvest index while, low for days to 50 per cent flowering, spikelet fertility, grain length, grain breadth and L/B ratio. These findings are in conformity with Idris *et al*. (2013), Gokulakrishnan *et al*. (2014), Paswan *et al*. (2014) and Rashid *et al*. (2017) in rice.

Heritability and genetic advance are important selection parameters. All the characters under study exhibited high heritability except number of tillers per plant which showed low heritability (22.40 per cent). This result indicates that these characters could be easily improved by selection. The broad sense heritability of these characters is in accordance with those of Akinwale *et al*. (2011), Kishore *et al*. (2015), Tiwari *et al*. (2019) and Lingaiah *et al*. (2020) in rice.

The results further revealed that high estimates of genetic advance observed for total number of spikelets per panicle, no of filled spikelets panicle^{-1}and plant height whereas number of unfilled spikelets panicle^{-1} and days to 50 per cent flowering estimated moderate genetic advance.Straw yield plant^{-1}, harvest index, spikelet fertility, test weight, panicle length, grain yield plant^{-1}, grain length, no of tillers plant^{-1}, length/breadth ratio and grain breadth recorded genetic advance with low magnitude. This indicates that, mode of genetic advance was low to high. Gokulakrishnan *et al*. (2014), Sameera *et al*. (2015) and Kishore *et al*. 2015 also found the similar results for genetic advance in rice.

Further, a perusal of the results on genetic advance as per cent of mean revealed high values (>20%) for no of filled spikelets panicle^{-1}, number of unfilled spikelets panicle^{-1}, total number of spikelets panicle^{-1}, straw yield plant^{-1}, grain yield plant^{-1}, test weight and harvest index indicated the traitsare governed by additive genes and selection will be rewarding for its improvement. Moderate genetic advance as per cent of mean was noticed for days to 50 per cent flowering, panicle length and plant height which, indicated that these characters are governed by non-additive gene action and selection may not be effective. Thus, the similar results supported by Sreedhar (2017) andSameera *et al*. (2015) in rice.

Heritability alone provides no information on the amount of genetic progress that would result from the selection. In the present study, high heritability estimates coupled with high genetic advance as per cent of mean were observed for no of filled spikelets panicle^{-1}, total number of spikelets panicle^{-1}, straw yield plant no of unfilled spikelets panicle^{-1}, plant height, test weight, grain yield plant^{-1} and harvest index indicating the preponderance of additive type of gene action for the expression of these characters and selection may be effective for improving these characters.Similar observations were reported by Idris *et al*. (2013), Gokulakrishnan *et al*. (2014) and Kishore *et al*. (2015) in rice.

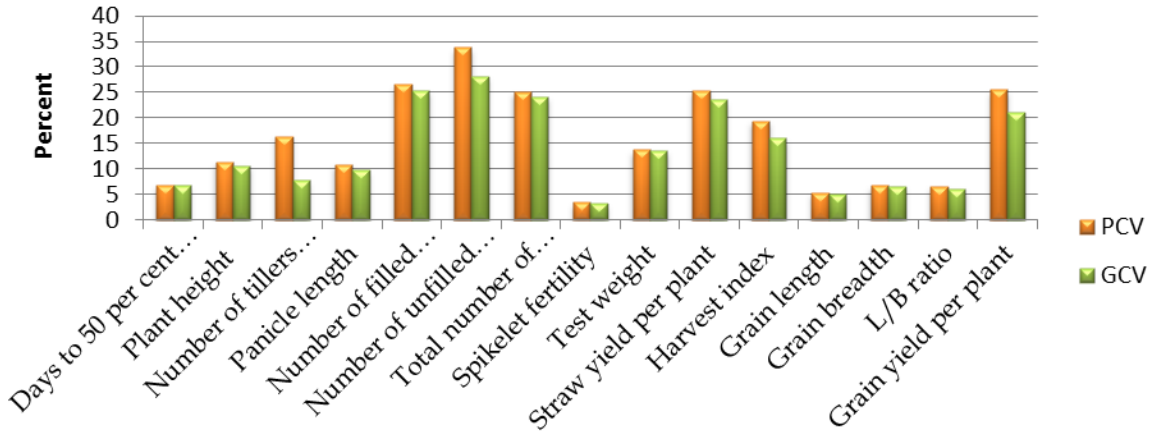

Fig. 1. PCV and GCV estimates for various traits in rice.

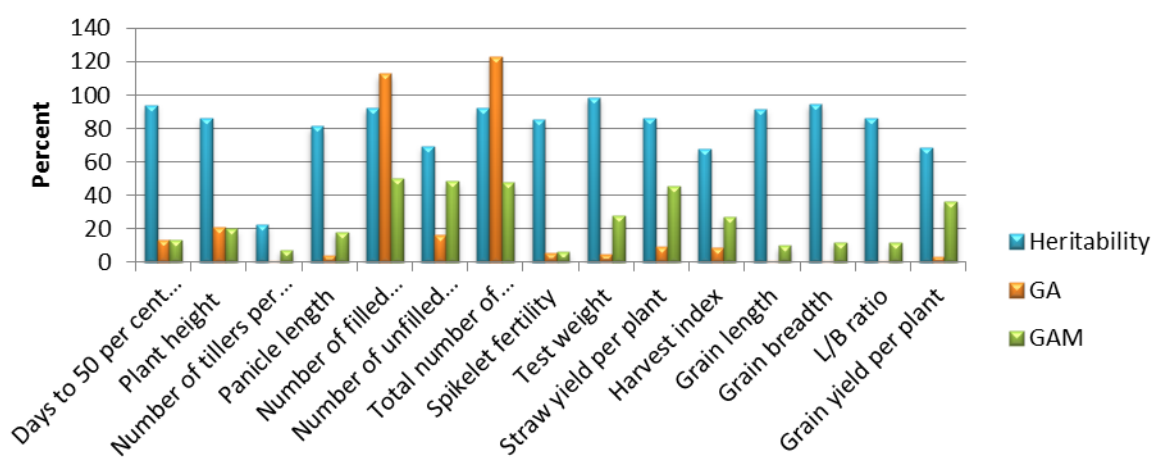

Fig. 2. Heritability, genetic advance and genetic advance as per cent of mean estimates for various traits in rice.

High heritability and moderate genetic advance as per cent of mean for days to 50 per cent flowering, panicle length, grain breadth and L/B ratio were also reported by Akinola et al., 2019 and Lingaiah *et al*. (2020) in rice. High heritability with low genetic advance as per cent of mean were observed for spikelet fertility and grain length which revealed the non- additive gene action in the expression of these characters in their inheritance, hence in this case selection may not be effective while low heritability and low genetic advance as per cent of mean for number of tillers per plant indicating that this

character is highly influenced by environmental effects and selection would be ineffective. These results are in conformity with the findings of Hasan *et al*. (2013), Idris *et al*. (2013) and Rashmi *et al*. (2017) in rice.

Table 1. Analysis of variance for yield attributing characters in rice.

Sr. No.	Characters	Mean sum of squares		
		Replication (df=2)	Treatment (df=47)	Error (df=94)
1	Days to 50 per cent flowering	0.27	143.14**	3.07
2	Plant height (cm)	54.98	374.06**	18.75
3	Number of tillers per plant	1.54	1.70**	0.91
4	Panicle length (cm)	3.43	16.31**	1.15
5	Number of filled spikelets per panicle	47.48	9988.16**	266.37
6	Number of unfilled spikelets per panicle	104.53	302.40**	38.44
7	Total number of spikelets per panicle	89.15	11883.98**	336.28
8	Spikelet fertility (%)	3.84	25.08**	1.36
9	Test weight (g)	0.10	15.13**	0.08
10	Straw yield per plant (g)	0.71	75.04**	3.73
11	Harvest index (%)	36.55	92.56**	12.49
12	Grain length (mm)	0.01	0.26**	0.008
13	Grain breadth (mm)	0.001	0.05**	0.001
14	Length/breadth ratio	0.004	0.10**	0.005
15	Grain yield per plant (g)	7.75	14.43**	1.92

*, ** - significant at 5% and 1%, respectively.

Table 2. Estimates of components of variation, coefficient of variation heritability, genetic advance and genetic advance as per cent of mean for yield attributing characters in rice.

Sr. No.	Characters	σ^2_p	σ^2_g	PCV (%)	GCV (%)	h^2b (%)	GA	GAM (%)
1	DTF	49.76	46.69	6.90	6.68	93.80	13.64	13.34
2	PH (cm)	137.19	118.44	11.37	10.57	86.30	20.83	20.22
3	NTPP	1.17	0.26	16.41	7.77	22.40	0.50	7.58
4	PL (cm)	6.20	5.06	10.81	9.76	81.50	4.18	18.15
5	NFSPP	3506.97	3240.60	26.50	25.47	92.40	112.73	50.44
6	NUSPP	126.42	87.99	33.80	28.19	69.60	16.12	48.45
7	TNSPP	4185.51	3849.23	25.20	24.16	92.00	122.57	47.73
8	SF (%)	9.27	7.91	3.51	3.24	85.30	5.35	6.16
9	TW (g)	5.10	5.02	13.76	13.64	98.40	4.58	27.87
10	SYPP (g)	27.50	23.77	25.36	23.57	86.40	9.34	45.14
11	HI (%)	39.18	26.69	19.37	15.99	68.10	8.78	27.19
12	GL (cm)	0.09	0.08	5.29	5.06	91.70	0.57	9.99
13	GB (cm)	0.02	0.02	6.73	6.55	94.80	0.26	13.14
14	L/B	0.04	0.03	6.53	6.07	86.40	0.33	11.63
15	GYPP (g)	6.09	4.17	25.53	21.13	68.50	3.48	36.03

CONCLUSION

It can be concluded that, significant differences were found among the genotypes for all the characters under study, indicated presence of sufficient genetic variability for different traits. The genotypes *viz*; CR 3783-3-2-1-1-1-4-1, KPS-6262, Pusa 1702-10-271, GNV 1904, AD 16168, RP 6334-111-5-2-1 and JGL 3245 showed their superiority for yield based on their mean performances. The characters *viz*; total number of spikelets per panicle, number of filled spikelets per panicle, plant height, number of unfilled spikelets panicle^{-1}, days to 50 per cent flowering, harvest index and straw yield plant^{-1} showed more contribution of genotypic variance to total variance. All the characters under study exhibited high magnitude of heritability except number of tillers plant^{-1}. Wide variability was observed for no of filled spikelets panicle^{-1}, number of unfilled spikelets panicle^{-1}, total no of spikelets panicle^{-1}, straw yield

plant^{-1} and grain yield plant^{-1}. These characters also had higher estiamtes of heritability coupled with high genetic advance as per cent of mean which can be utilize for further improvement through selection in rice.

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