



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(2): 1732-1735
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www.thepharmajournal.com

Received: 03-11-2021

Accepted: 09-12-2022

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Studies on genetic variability for yield and yield contributing traits in aromatic rice (*Oryza sativa* L.)

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Abstract

Fifteen genotypes of rice were evaluated in a field study to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. The analysis of variance revealed that there were significant differences among the entries for all the traits studied. A wide range of variation was recorded for days to 50% flowering, plant height (cm), number of tillers per plant, length of panicle (cm), total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), amylose content (%), kernel length (mm), kernel breadth (mm), L/B ratio (mm), kernel elongation (mm).

The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters studied which shows the influence of the environmental effect on the characters. High values for genotypic and phenotypic coefficient recorded for number of tillers per plant, total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, straw yield per plant (g), kernel length (mm) and L/B ratio (mm). High heritability along with high genetic advance as percent of mean were observed for plant height (cm), number of tillers per plant, total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, test weight (g), grain yield per plant (g), straw yield per plant and kernel length (mm) indicating that the characters were controlled by additive gene action. Therefore, the overall result indicates the presence of enough variability for development of improved rice varieties and the studied traits can be used for selection.

Keywords: Aromatic rice, genetic variability, heritability, genetic advance

Introduction

Rice (*Oryza sativa* L.) belonging to the family Poaceae is one of the oldest domesticated crop which provides food for more than half of the world's population. It contributes significantly in Indian economy and serves as a staple food for more than 70 per cent of the people dwelling in Asia. India is one of the world's largest producers of white rice, accounting for 20 per cent of all world rice production.

Aromatic rice (*Oryza sativa* L.) is known for its characteristic fragrance when cooked. This constitutes a small but special group of rice, which is considered the best in quality. Aromatic varieties fetch a higher price in the rice market than non-aromatic ones. Cultivation of aromatic rice has been gaining popularity in India over recent years because of its huge demand for both national and international trade (Dutta *et al.*, 2002; Gupta and Kumar, 2008) [2, 4]. The area under scented rice varieties is increasing day by day with the opening of the world market as well as domestic consumption (Singh *et al.* 2008) [12]. India is a natural repository for long and short-grained aromatic rice which are conserved by farmers over centuries. Among these, basmati rice cultivated in the foothills of the Himalayas is gifted with unique quality features; unique fragrance, taste and texture which develop under specific geographic demarcation making it best among the aromatic rice of the world (Singh *et al.* 1997) [13].

The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programme. Presence of high variability in the genotypes of this crop offers much scope for its improvement (Poehlman, 1987) [10]. Estimation of genetic parameters in the context of trait characterization is an essential component in developing high yielding varieties. Hence, an attempt was made to estimate the extent of variation for yield contributing traits in fifteen

aromatic rice genotypes by studying the genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, which may contribute to formulation of suitable selection indices for improvement in this crop.

Material and Methods

The field experiment was conducted on the field of Department of Agricultural Botany, College of Agriculture, Dr. B.S.K.K.V., Dapoli by taking three replications in Randomized Block Design during *Kharif*, 2019. Experimental material comprises of 15 different genotypes from different diverse sources of country. The materials was grown in randomize block design with three replications 20 cm spacing was kept between the rows while, 15 cm spacing was kept between the plants. The plot size was 4.50 m x 1 m maintained. All the agronomic practices were performed for better performance of the trial. The data was recorded in five random plants per entry in each replication *viz.*, days to 50% flowering, plant height (cm), number of tillers per plant, length of panicle (cm), total number of grains panicle⁻¹, number of filled spikelets panicle⁻¹, number of unfilled spikelets panicle⁻¹, spikelet fertility (%), test weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), amylose content (%), kernel length (mm), kernel breadth (mm), L/B ratio (mm), kernel elongation (mm).

The mean of all the plants for each trait under each replication was subjected to analysis (Panse and Sukhathme, 1967) [9]. The estimate of genotypic variance and phenotypic variance were worked out according to the method suggested by Johnson *et al.*, (1955) [5] using mean square values from the ANOVA table. Phenotypic and genotypic coefficient of variance was calculated based on the method advocated by Burton *et al.*, (1952) [1]. Heritability percentage in broad sense was estimated as per the method described by Lush (1940) [6] and traits were classified as having high, moderate and low heritability as per the method of Robinson *et al.*, (1949) [11]. Genetic advance was estimated according to the method suggested by Johnson *et al.*, (1955) [5], and expressed as percentage of mean. Traits were classified as having high, moderate or low genetic advance as per the method suggested by Johnson *et al.*, (1955) [5].

Results and Discussion

In the present investigation, the genetic variability of a metric trait can be studied through the use of various statistical parameters like mean, range, variance components and coefficients of variation. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitivity of crop to environment, heritability of the character and genetic advance. The analysis of variance showed a wide range of variation and significant differences for all the characters under study, indicating the presence of adequate variability for further improvement (Table 1).

The analysis of variance revealed that the differences among the genotypes were significant for all the characters under study. The genotypes were thus suitable for genetical studies, as their contribution to the genotypic sum of squares was significant for all the characters. The total variability in each

of these characters could be partitioned into three components *viz.*, phenotypic, genotypic and environmental. The phenotypic variance and genotypic variance was maximum for total number of grains per panicle followed by number of filled spikelets per panicle, plant height, number of unfilled spikelets per panicle and straw yield per plant indicating wide variability for these characters.

A wide range of variation was recorded for days to 50% flowering, plant height, number of tillers per plant, length of panicle, total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, straw yield per plant (g) and harvest index (%). The estimates of phenotypic coefficient of variation ranged from 2.894 for spikelets fertility (%) to 34.129 for L/B ratio (mm) and the corresponding values for genotypic coefficient of variation were 2.779 for spikelets fertility (%) to 32.359 for L/B ratio (mm), respectively.

Similarly, high genotypic and phenotypic coefficient of variation was also found number of tillers per plant, total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, straw yield per plant (g), kernel length (mm) and L/B ratio (mm). However, plant height (cm), grain yield per plant (g) and kernel breadth (mm) showed moderate phenotypic coefficient of variation and genotypic coefficient of variation.

In general, the differences between phenotypic coefficient of variation and genotypic coefficient of variations for most of traits were less indicating the ample scope for improvement through selection. Low values of phenotypic coefficient of variation and genotypic coefficient of variation were observed for days to 50% flowering, length of panicle (cm), spikelets fertility (%), test weight (%), harvest index (%), amylose content (%) and kernel elongation (mm) indicating narrow range of variability for these traits there by restricting the scope for selection.

Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1981). In the present study, the heritability estimates were high for all the characters as per Robinson's (1966) classification. Genetic advance as percentage of mean is impendent until the measurement and hence it is used for comparison among characters. The heritability values for different yield and yield attributing traits ranged from 81.6% to 99.8%.

Heritability estimates were high for all the characters studied. The values were especially high for plant height (cm), total number of grains per panicle and number of filled spikelets per panicle. High heritability indicates the amenability of the traits in the selection process. In present study, the values of genetic advance ranged from 0.322 to 86.91. Total number of grains per panicle recorded highest genetic advance (86.91). Similarly, the values of genetic advance as percent of mean ranged from 19.26 to 63.20.

Johnson *et al.*, (1955) [5] suggested that high heritability combined with high genetic advance is an indicative of additive gene action and selection based on these parameters would be more reliable. In the present investigation, high heritability estimates in conjunction with high genetic advance in percent of mean were observed for plant height (cm), number of tillers per plant, total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, test weight (g), grain yield per plant (g), straw yield per plant and kernel length (mm). Hence

these characters were controlled by additive gene action. Therefore, the selection based on phenotypic values will be instrumental for effective improvement in these characters. These findings are in agreement with Gokulakrishnan *et al.* (2014) [3] and Mirarab *et al.* (2011) [7].

Heritability estimates along with genetic advance are normally 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 (Johnson *et al.*, 1955) [5]. According to Panse (1957) [8], if the heritability is mainly owing to non

additive gene effect, the expected genetic advance would be low and if there is additive gene effect, a high genetic advance may be expected. Taking into consideration the amount of variability, heritability and genetic advance as per cent of mean in the present study it may be concluded that selection would be effective in plant height (cm), number of tillers per plant, total number of grains per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle, test weight (g), grain yield per plant (g), straw yield per plant and kernel length (mm) for developing high yielding varieties.

Table 1: Analysis of variance for yield and yield contributing characters in aromatic rice

Sr. No.	Characters	Mean sum of square		
		Replication	Treatment	Error
1	Days to 50% flowering	1.27	321.66**	2.62
2	Plant height (cm)	12.80	1673.82**	1.76
3	Number of tillers per plant	0.11	34.94**	1.15
4	Length of panicle (cm)	0.11	15.03**	0.50
5	Total number of grains panicle ⁻¹	4.06	5349.35**	2.58
6	Number of filled spikelets panicle ⁻¹	1.38	4289.64**	3.02
7	Number of unfilled spikelets panicle ⁻¹	3.29	142.36**	2.04
8	Spikelet fertility (%)	0.83	18.81**	0.51
9	Test weight (g)	0.13	21.84	0.23
10	Grain yield per plant (g)	0.40	37.10**	1.04
11	Straw yield per plant (g)	0.22	140.96**	2.24
12	Harvest index (%)	0.38	34.08**	1.06
13	Amylose content (%)	0.85	12.94**	0.55
14	Kernel length (mm)	0.14	5.57**	0.02
15	Kernel breadth (mm)	0.01	0.28**	0.02
16	L/B ratio (mm)	0.09	3.44**	0.12
17	Kernel elongation (mm)	0.07	0.11**	0.03
	D.F	2	14	28

Table 2: Components of variation for yield attributing characters aromatic rice

Sr. No	Characters	Phenotypic variance	Genotypic variance	Environmental variance
1	Days to 50% flowering	108.96	106.34	2.624
2	Plant height (cm)	570.65	568.28	2.370
3	Number of tillers per plant	12.41	11.26	1.145
4	Length of panicle (cm)	5.51	4.76	0.752
5	Total number of grains panicle ⁻¹	1786.30	1783.15	3.151
6	Number of filled spikelets panicle ⁻¹	1433.58	1429.39	4.192
7	Number of unfilled spikelets panicle ⁻¹	48.81	46.77	2.038
8	Spikelet fertility (%)	6.61	6.09	0.512
9	Test weight (g)	7.43	7.20	0.234
10	Grain yield per plant (g)	13.05	12.02	1.036
11	Straw yield per plant (g)	47.25	44.67	2.585
12	Harvest index (%)	12.07	11.00	1.064
13	Amylose content (%)	4.67	4.12	0.549
14	Kernel length (mm)	1.87	1.85	0.024
15	Kernel breadth (mm)	0.105	0.08	0.017
16	L/B ratio (mm)	1.23	1.10	0.124
17	Kernel elongation (mm)	0.03	0.03	0.007

Table 3: Genetic variability parameters for yield and yield attributing traits in aromatic rice

Sr. No	Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	Genetic Advance	Genetic Advance as % of mean
1	Days to 50% flowering	108.46	94-130	9.624	9.507	97.5	20.98	19.34
2	Plant height (cm)	125.75	96.80-167.17	18.996	18.957	99.5	49.00	38.96
3	Number of tillers per plant	13.42	10.27-23.60	26.238	24.998	90.7	6.58	49.06
4	Length of panicle (cm)	26.77	23.60-31.80	8.769	8.148	86.3	4.17	15.59
5	Total number of grains panicle ⁻¹	197.17	150.80-320.73	21.435	21.416	99.8	86.91	44.07
6	Number of filled spikelets panicle ⁻¹	175.23	130.53-284	21.607	21.576	99.7	77.76	44.38
7	Number of unfilled spikelets panicle ⁻¹	21.92	11.40-36.73	31.860	31.188	95.8	13.79	62.89
8	Spikelet fertility (%)	88.85	84.26-94.57	2.894	2.779	92.2	4.88	5.49

9	Test weight (g)	21.60	17.53-25.57	12.623	12.423	96.8	5.44	25.18
10	Grain yield per plant (g)	18.82	12.57-24.59	19.192	18.415	92.0	6.85	36.39
11	Straw yield per plant (g)	32.70	20.47-43.57	21.021	20.438	94.5	13.38	40.93
12	Harvest index (%)	36.62	30.19-41.01	9.486	9.058	91.1	6.52	17.81
13	Amylose content (%)	20.40	16.45-23.94	10.597	9.956	88.2	3.93	19.26
14	Kernel length (mm)	6.37	4.09-8.06	21.463	21.328	98.7	2.78	43.65
15	Kernel breadth (mm)	2.05	1.61-2.63	15.765	14.475	84.3	0.56	27.38
16	L/B ratio (mm)	3.25	1.69-4.69	34.129	32.359	89.9	2.05	63.20
17	Kernel elongation (mm)	1.47	1.08-1.70	12.993	11.743	81.6	0.322	21.864

Conclusion

The overall result showed the presence of wide range of variability in the genotypes studied. This indicated that there is ample scope for selection of promising genotypes for yield improvement. 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.

On the basis of per se performance, the genotypes Pawana, Chimansal, Indrayani and Super Basmati were found to be the best for yield and yield contributing traits. Therefore, these genotypes can be successfully utilized as parents in hybridization programme for evolving aromatic rice variety.

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