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Genetic variability, heritability and genetic advance of grain yield and quality in aromatic rice

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Abstract

F₃ generations of 28 crosses were evaluated for the genetic parameters in rice. The estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the quantitative and qualitative traits studied. In F₃ population, higher magnitudes of PCV and GCV recorded for no. of filled grains/panicle and panicle weight and indicated greater scope of obtaining high selection response for these traits. The high estimates of heritability in broad sense with moderate genetic advance were recorded for the yield components viz., panicle length, filled grains per panicle and 1000 grain weight and kernel traits viz., kernel length and L/B ratio, which suggested that additive genetic effects played greater role as such, the chances of obtaining desirable segregants with good yield potential and quality are very bright through direct selection.

Keywords: Rice, F₃ generation, PCV, GCV, heritability and genetic advance

Introduction

Aromatic rice (*Oryza sativa* L.) with an aroma and flavour similar to popcorn, constitutes a small group of rice that is regarded as best in quality (Singh *et al.*, 2000) ^[1]. Although, aromatic rices popular in world market are long-grain types forming the bulk of export, majority of the Indian indigenous aromatic rices are small and medium-grain types, mostly cultivated for local consumption. Few of the small and medium-grained aromatic rices possess excellent aroma and other quality traits viz., kernel elongation after cooking, taste etc. which could be excellent sources for improving quality in high yielding varieties.

To achieve genetic improvement in yield traits, it is imperative to generate information on variability, its heritable proportion and also interrelationships existing in the breeding material handled. The knowledge of mode of inheritance, variability and association studies is essential to have effective selection programme for identification of superior genotypes. The F₂ or F₃ derived lines are far from being homozygous and early generation selection relies on the assumption that the performance of a line at an early generation of selfing is predicative of its performance at homozygosity (Chahota *et al.* 2007) ^[3]. Empirical studies in different self pollinated crops have indicated that early generation selection is sometimes effective and sometime ineffective (Bernardo, 2003) ^[2]. The present study, reports the extent of genetic variability and interrelationships for yield and yield contributing traits in rice from F₃ generation of twenty eight crosses. The information reported will help in predicting of the effectiveness of selection in early generation selection to isolate high yield potential pure lines of aromatic rice.

Material and methods

In the present study, F₃ generation material obtained from eight rice genotypes viz., BPT 5204, Akshyadhan, NLR 145, PUSA 1121, RNR 2354, Sumathi, Improved Pusa Basmati and Basmati 370 which were crossed in a diallel fashion (8 x 8) without reciprocals (Tab. 1) was chosen and evaluated at Agricultural Research Station, Kampasagar, Nalgonda district in a Randomized Block Design with 3 replications. Recommended package of practices were followed as specified for transplanted rice. Each entry was grown in 12 rows of 3 m length adopting a spacing of 20 x 15 cm with single seedlings per hill.

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Observations were recorded on yield components and physical grain characteristics viz., days to 50% flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), panicle weight (g), number of filled grains per panicle, 1000 grain weight (g), grain yield per plant (g), kernel length (mm), kernel breadth (mm), kernel L/B ratio, kernel length after cooking (mm), kernel elongation ratio and head rice recovery (%) and the means were subjected to statistical analysis. Finally, the parameters genotypic and phenotypic coefficients of variation (Siva Subramanian and Madhavamenon, 1973) [12], heritability in narrow sense, genetic advance and genetic advance as percentage of mean were estimated using Window Stat statistical package.

Results and discussion

A wide range of variation was observed among 28 F₃ cross population for 14 characters which were evaluated (Table 2). The data revealed that variance due to treatments was highly significant for all the characters studied. The estimates of genetic parameters including co-efficient of variation, heritability and genetic advance deserve attention in deciding the selection criteria for improvement in the concerned characters.

In the present study, the phenotypic and genotypic coefficients of variation computed to assess the nature and magnitude of existing variability in the F₃ population, revealed presence of higher magnitudes of PCV and GCV with respect to no. of filled grains/panicle and panicle weight (Table 3). This indicated greater scope of obtaining high selection response for these traits. These results are in conformity with the findings of earlier workers viz., Pandey *et al.* (2009) [8], Yadav *et al.* (2010) [15], Maddeppa Mallimar *et al.* (2015) [7] and Venkatesan *et al.* (2020).

The moderate estimates of Coefficient of Variation at genotypic level were observed for plant height, no. of productive tillers/plant, 1000 grain weight, grain yield, kernel length after cooking and head rice recovery, as such these traits are likely to permit limited direct selection. Singh *et al.* (2011) found moderate PCV and GCV estimates for grain yield per plant and no. of productive tillers/plant.

Low estimates of PCV and GCV were observed for days to 50% flowering, plant height panicle length, kernel length, kernel breadth and kernel elongation ratio. Khedikar *et al.* (2004) [5] and Krishna *et al.* (2014) [6] also reported low estimates of genotypic and phenotypic coefficients with respect to days to 50% flowering and plant height. The occurrence of low estimates of genotypic and phenotypic coefficients of variation indicated that further selection directly based on these parameters would not be much rewarding.

Among the characters studied, high estimates of heritability in broad sense with high genetic advance in percentage of mean were observed in general for most of the characters including

grain dimensions whereas, in case of others, kernel length after cooking and head rice recovery the values were low. High estimates of heritability with high genetic advance in percent of mean have also been reported earlier for grain yield per plant (Sarangi *et al.* 2009) [9], no. of filled grains/panicle (Suman *et al.* 2005, Devi *et al.* 2006) [13, 4] and for number of grains per panicle (Anjaneyulu *et al.* 2010) [11]. The traits viz., plant height, no. of productive tillers/plant, panicle weight, 1000 grain weight and grain yield per plant also showed moderate to low heritability and genetic advance which suggested that inter mating of segregating genotypes to accumulate plus genes may provide very high response to selection for further improvement.

The high estimates of heritability with moderate genetic advance were recorded for the yield components viz., panicle length, filled grains per panicle and 1000 grain weight and kernel traits viz., kernel length and L/B ratio, which suggested that additive genetic effects played greater role as such, the chances of obtaining desirable segregants with good yield potential and quality are very bright through direct selection. However, for kernel elongation ratio and head rice recovery direct selection may not be much useful due low heritability coupled with low to medium genetic advance as percent mean.

Table 1: Cross combination of F₃ progenies of hill rice used as experimental material

S. No	Cross Combinations
1	BPT 5204 x Akshyadhan
2	BPT 5204 x NLR 145
3	BPT 5204 x Pusa 1121
4	BPT 5204 x RNR 2354
5	BPT 5204 x Sumathi
6	BPT 5204 x Improved Pusa Basmati
7	BPT 5204 x Basmati 370
8	Akshyadhan x NLR 145
9	Akshyadhan x Pusa 1121
10	Akshyadhan x RNR 2354
11	Akshyadhan x Sumathi
12	Akshyadhan x Improved Pusa Basmati
13	Akshyadhan x Basmati 370
14	NLR 145 x Pusa 1121
15	NLR 145 x RNR 2354
16	NLR 145 x Sumathi
17	NLR 145 x Improved Pusa Basmati
18	NLR 145 x Basmati 370
19	Pusa 1121 x RNR 2354
20	Pusa 1121 x Sumathi
21	Pusa 1121 x Improved Pusa Basmati
22	Pusa 1121 x Basmati 370
23	RNR 2354 x Sumathi
24	RNR 2354 x Improved Pusa Basmati
25	RNR 2354 x Basmati 370
26	Sumathi x Improved Pusa Basmati
27	Sumathi x Basmati 370
28	Improved Pusa Basmati x Basmati 370

Table 2: Analysis of variance (mean squares) for grain yield and kernel quality characteristics in rice

Source of variation	Replications (d.f = 2)	Treatments (d.f = 65)	Error (d.f = 130)	Total (d.f = 197)
Days to 50 % flowering	3.48	230.17 **	3.4	78.22
Plant height (cm)	12.21	492.78 **	12.11	170.71
No. of productive tillers/ plant	0.55	13.79 **	0.85	5.12
Panicle length (cm)	3.12	25.37 **	4.65	11.47
Panicle weight (g)	3.86	134.23 **	3.99	46.96
No. of filled grains/ panicle	195.72	8187.87 **	212.27	2843.65
1000 grain weight (g)	2.32 **	40.34 **	0.4	13.6

Grain yield/ plant (g)	3.4	125.62 **	5.85	45.35
Kernel length (mm)	0.001	1.25 **	0.03	0.43
Kernel breadth (mm)	0.001	0.02 **	0.002	0.01
Kernel l/b ratio	0.001	0.42 **	0.02	0.15
Kernel length after cooking (mm)	1.44 **	5.75 **	0.17	2.02
Kernel elongation ratio	0.04 **	0.14 **	0.01	0.05
Head rice recovery (%)	2.64	204.48 **	8.79	73.3

*Significant at 5 % level, ** Significant at 1 % level

Table 3: Genetic parameters for yield and of quality characters of rice in F₃ progenies

Parameter	PCV (%)	GCV (%)	h ² (broad sense) (%)	GA (%)	GAM (%)
Days to 50 % flowering	8.14	7.87	94	19.78	20.09
Plant height (cm)	14.86	12.97	76	30.18	29.87
No. of productive tillers/ plant	18.93	16.06	72	5.31	35.98
Panicle length (cm)	9.36	8.51	83	4.92	20.42
Panicle weight (g)	23.07	21.44	86	12.53	52.61
No. of filled grains/ panicle	35.73	35.1	97	68.71	91.02
1000 grain weight (g)	16.42	15.62	90	8.13	39.2
Grain yield/ plant (g)	22.01	19.32	77	8.29	44.76
Kernel length (mm)	9.83	8.28	71	1.1	18.39
Kernel breadth (mm)	7.8	6.3	65	0.22	13.41
Kernel l/b ratio	11.54	9.96	75	0.83	22.68
Kernel length after cooking (mm)	13.39	11.78	77	2.6	27.34
Kernel elongation ratio	7.23	4.75	43	0.13	8.23
Head rice recovery (%)	14.27	11.62	66	12.22	24.96

h² = heritability, GA = Genetic advance, GAM = Genetic advance as per cent of mean.

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