

Studies on Genetic Variability of Grain Yield and Quality in F₂ and F₃ Generations of Aromatic Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out for yield and quality related traits in the F₂ and F₃ populations of twenty eight rice cross combinations developed from five aromatic (Pusa 1121, Improved Pusa Basmati, Basmati 370, Sumathi and RNR 2354) and three non-aromatic (BPT 5204, Akshyadhan and NLR 145) parents. In F₂ generation, among the yield characters, the highest values of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were recorded for the number of filled grains/panicle followed by grain yield per plant while the lowest values were recorded for days to 50% flowering. However, for the grain quality characters the highest PCV and GCV values were recorded for head rice recovery and lowest for kernel breadth. In F₃ population, higher magnitudes of PCV and GCV were recorded for the number of filled grains/panicle and panicle weight, indicating greater scope of obtaining high selection response for these traits. High heritability in narrow sense along with medium to high genetic advance was noticed for the traits like days to 50% flowering, 1000 grain weight and the kernel traits.

Keywords: Rice; F₂ generation; F₃ generation; PCV; GCV; heritability; genetic advance.

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1. INTRODUCTION

The existence of variability in the breeding material is the first and foremost point in selection for improvement. Environmental effects influence the total observable variations of quantitative traits. Therefore, partitioning of overall variance due to genetic and non-genetic causes becomes necessary for effective breeding programme. The genotypic coefficient of variation estimates the heritable variability, whereas phenotypic component measures the role of environment on the genotype. High phenotypic coefficient of variance and low genotypic coefficient of variance for a character indicates high influence of environment in its expression. The phenomenon of transmission of characters from parents to offspring is usually measured in terms of heritability. When it is estimated in narrow sense based on the additive variance, which is fixable in nature gives highly fruitful results through simple selection procedures. The F_2 generation is critical for success of breeding programme because there are remote chances of finding superior recombinants in advanced generations if there is lack of desirable segregants in F_2 populations. Therefore the estimates of heritability in narrow sense and genetic advance would help to estimate realizable improvement through formulation of a sound breeding programme.

2. MATERIALS AND METHODS

The experimental material representing five generations (P_1 , P_2 , F_1 , F_2 , and F_3) 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 (Table 1) was chosen and evaluated during post rainy season in the randomized block design, replicating thrice at Agricultural Research Station, Kampasagar, Nalgonda district, Telangana. Parents and respective hybrids (F_1 's) were planted in one row of 3.0 m length adopting a spacing of 20 cm between the rows and 15 cm between the plants, within each row. Each cross of F_2 and F_3 generations were planted in twelve rows with same row length and spacing. Observations were recorded on ten random competitive plants from parents and F_1 's, 50 in F_2 and F_3 for yield and yield attributing characters 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 headrice recovery (%). Variability, heritability and genetic advance were estimated in F_2 as well as in F_3 generation separately by utilizing crosswise mean values of RBD and considering each generation as whole population to have a comparison between two generations (F_2 and F_3).

3. RESULTS AND DISCUSSION

GCV, PCV, heritability in narrow sense and genetic advance as percentage of mean were estimated for yield and quality characters to study F_2 and F_3 generations as whole population (Table 2). The values were treated as high, moderate and low as per the categorization proposed by Siva Subramanian and Madhavamenon [1] for variability and Johnson et al. [2] for heritability as well as genetic advance as per cent of mean.

A wide range of variation was observed among 28 F_2 crosses for fourteen characters. The perusal of data revealed that variance due to treatment was highly significant for all the characters exhibited by the genotypes. Significant genetic variation in various component characters was observed among the crosses and phenotypic variance was higher than genotypic variance for all the characters thus indicating the influence of environment factor on these traits. Similar findings were earlier reported by Sarkar et al. [3], Manoj Kumar Prajapati et al. [4] and Mohana Sundaram et al. [5].

The characters studied in the present investigation in F_2 generation exhibited low, moderate and high PCV and GCV values. Among the yield characters, highest PCV and GCV values were recorded for no. of filled grains/panicle followed by grain yield per plant and the lowest PCV and GCV values were recorded for days to 50% flowering. Among the grain quality characters highest PCV and GCV values were recorded for head rice recovery and lowest PCV and GCV was recorded for kernel breadth. Therefore, selection on the basis of phenotypic expression alone cannot be effective for the improvement of these traits. Similar opinion was expressed by Rather et al. [6] and Krishna et al. [7]. Studies of variation indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the

traits studied except panicle length and kernel elongation ratio.

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. This indicated greater scope of obtaining high selection response for these traits. 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. [8] 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. [9] 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.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. Among the yield characters in F₂ generation, highest heritability was registered for days to 50% flowering, kernel length and kernel L/B ratio, whereas kernel breadth had lowest heritability.

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,

Table 1. Cross combination of F₂ and F₃ progenies of 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. Mean, range and genetic parameters for yield and quality characters of rice in F₂ and F₃ progenies

Parameter	Generation	Mean	Range	PCV (%)	GCV (%)	h ² (broad sense) %	GA (%)	GAM (%)
Days to 50 % flowering	F ₂	110	113 - 118	5.59	5.26	62	14.25	13.08
	F ₃	98	82-114	8.14	7.87	94	19.78	20.09
Plant height (cm)	F ₂	122	91 - 148	12.01	11.57	50	35.09	29.44
	F ₃	101	61-127	14.86	12.97	76	30.18	29.87
No. of productive tillers/ plant	F ₂	12.5	9.5 - 15.1	18.52	16.17	32	4.45	37.26
	F ₃	14.8	11.8-22.7	18.93	16.06	72	5.31	35.98
Panicle length (cm)	F ₂	25.8	18.6 - 29.6	13.49	8.75	22	3.82	14.97
	F ₃	24.1	18.7 - 27.2	9.36	8.51	83	4.92	20.42
Panicle weight (g)	F ₂	2.2	0.9 - 3.2	19.49	18.09	29	12.26	44.32
	F ₃	1.6	0.4 - 2.3	23.07	21.44	86	12.53	52.61
No. of filled grains/ panicle	F ₂	91.1	34.4 - 135.1	34.79	33.54	37	84	85.39
	F ₃	75	21-130	35.73	35.1	97	68.71	91.02
1000 grain weight (g)	F ₂	21.39	14.8 - 28.9	18.38	18.1	47	9.89	47.08
Grain yield/ plant (g)	F ₂	20.7	14.0 - 26.2	16.42	15.62	90	8.13	39.2
	F ₃	19.9	7.3 - 27.6	26.92	23.67	70	11.05	54.92
Kernel length (mm)	F ₂	18.5	10.8 - 26.7	22.01	19.32	77	8.29	44.76
	F ₃	5.87	5.01 - 6.67	9.73	9.11	78	1.34	22.55
Kernel breadth (mm)	F ₂	5.95	4.81 - 7.10	9.83	8.28	71	1.1	18.39
	F ₃	1.64	1.50 - 1.78	6.54	5.53	25	0.21	12.31
Kernel l/b ratio	F ₂	1.63	1.47 - 2.00	7.8	6.3	65	0.22	13.41
	F ₃	3.59	3.14 - 4.17	10	8.88	78	0.75	20.8
Kernel length after cooking (mm)	F ₂	3.68	2.8 - 4.6	11.54	9.96	75	0.83	22.68
	F ₃	9.48	8.58 - 11.87	12.09	11.17	42	2.66	27.25
Kernel elongation ratio	F ₂	9.51	7.75 - 13.00	13.39	11.78	77	2.6	27.34
	F ₃	1.62	1.30 - 2.06	10.4	8.82	33	0.33	19.75
Head rice recovery (%)	F ₂	1.6	1.46 - 1.85	7.23	4.75	43	0.13	8.23
	F ₃	45.38	26.7 - 57.7	20.47	19.25	26	23.48	47.78
	F ₃	48.93	35.6 - 62.6	14.27	11.62	66	12.22	24.96

*h*² = heritability, GA = Genetic advance, GAM = Genetic advance as per cent of mean

kernel length after cooking and head rice recovery the values were low in F_3 generation. High estimates of heritability with high genetic advance in percent of mean have also been reported earlier for grain yield per plant [10], no. of filled grains/panicle [11] and for number of grains per panicle [12]. 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 genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value [2]. Genetic advance was highest for number of filled grains per panicle followed by plant height and lowest for panicle length among yield characters in F_2 generation. In case of grain quality characters, head rice recovery recorded highest genetic advance and the lowest for kernel breadth. The genetic advance as per cent of mean was highest in case of no. of filled grains/panicle followed by grain yield per plant, while it was low in case of days to 50% flowering. Whereas, with respect to grain quality characters, head rice recovery registered the highest genetic advance as per cent mean and the lowest value was associated with kernel breadth.

Significant genetic variation in various component characters was observed among the crosses and phenotypic variance was higher than genotypic variance for all the characters thus indicating the influence of environment factor on these traits. In F_2 generation, among the yield characters, highest PCV and GCV values were recorded for no. of filled grains/panicle followed by grain yield per plant and the lowest for days to 50% flowering and in grain quality characters highest PCV and GCV values were recorded for head rice recovery and lowest for kernel breadth and selection on the basis of phenotypic expression alone cannot be effective for the improvement of these traits. High heritability in narrow sense along with medium to high genetic advance was noticed for the traits, days to 50% flowering, 1000 grain weight and most of the kernel traits and these characters can be improved by direct selection and inter-mating superior genotypes in segregating

population (F_2) developed from recombination breeding [13].

In F_3 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.

4. CONCLUSION

These results suggested that, among the yield components panicle weight and filled grains per panicle and quality traits kernel length and kernel L/B ratio, which exhibited medium to high heritability and high genetic advance as percentage of mean in addition to high correlation with yield have to be concentrated upon in future selection programmes. Thus, in the present case selection based on panicle weight and filled grains per panicle will be more effective. Maurya and Chaudhury et al. [14,15] also observed that selection based on spikelets, panicle weight and test weight is more effective.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Siva Subramanian S, Madhavamenon P. Combining ability in rice. Madras Agricultural Journal. 1973;60:419-421.
2. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(7):314-318.
3. Sarkar KK, Bhutia KS, Senapati BK, Roy SK, Panda S, Mondal AB. Genetic variability and relationship between grain yield and its component traits in Rice (*Oryza sativa*). Journal of Environment and Ecology. 2005;23:702-706.
4. Manoj Kumar Prajapati, Chandra Mohan Singh, Suresh Babu G, Roopa Lavanya G,

- Priyadarshini Jadhav. Genetic parameters for grain yield and its component characters in rice. *Electronic Journal of Plant Breeding*. 2011;2(2):235-238.
5. Mohana Sundaram K, Rajeswari S, Saraswathi R, Jayaprakash P. Genetic variability studies for yield and its Components and quality traits with high iron and zinc content in segregating population of rice (*Oryza sativa* L.). *International Journal of Chemical Studies*. 2019;7(3):800-805.
 6. Rather AG, Mir GN, Sheikh FA. Genetic parameters for some quantitative traits in rice. *Advances in Plant Sciences*. 1998;19(2):163-166.
 7. Krishna L, Surender Raju Ch, Sudheer Kuamr S, Narender Reddy S, Bhave MHV. Genetic variability studies for qualitative and quantitative traits in F₂ generation of aromatic rice (*Oryza sativa* L.). *The Journal of Research, PJTSAU*. 2014;42(3): 26-30.
 8. Singh Y, Pani DR, Pradhan SK, Bajpai A, Singh US. Divergence analysis for quality traits in some indigenous basmati rice genotypes. *Oryza*. 2008;45(4):263-267.
 9. Khedikar VP, Bharose AA, Sharma D, Khedikar YP, Killare AS. Path coefficient analysis of yield components of scented rice. *Journal of Soils and Crops*. 2004;14(1):198-201
 10. Sarangi DN, Pradhan B, Sial P, Mishra CHP. Genetic variability, correlation and path-coefficient analysis in early rice genotypes. *Environment and Ecology*. 2009;27:307-312.
 11. Devi SL, Raina FA, Pandey MK, Cole CR. Genetic parameters of variation for grain yield and its components in rice. *Crop Research*. 2006;32(1):69-71.
 12. Anjaneyulu M, Reddy DR, Reddy KHP. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Research on Crops*. 2010;11:415-416.
 13. Samadia DK. Genetic variability studies in Lasora (*Cordia myxa* Roxb.). *Indian Journal of Plant Genetic Resources*. 2005; 18(3):236-240.
 14. Maurya DM. Heritability and genetic advance in rice. *Oryza*. 1976;13:97-100.
 15. Chaudhury D, Rao MJBK, Prasad AB, Suriya Rao AV. Heritability and correlations in rice. *Oryza*. 1980;17:184-199.

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