

## STUDY ON GENETIC PARAMETERS IN F<sub>2</sub> GENERATION INVOLVING AROMATIC RICE GENOTYPES (*O.SATIVA*)

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**ABSTRACT:** A field experiment was conducted during *kharif*, 2010 and rabi 2010-11 at Rice section, ARI, Rajendranagar, involving 7 parents, 7 F<sub>1</sub> hybrids and their corresponding F<sub>2</sub> populations to study the genetic parameters i.e. variability, heritability and genetic advance cross-wise in aromatic rice. A critical examination of genetic parameters in each cross in F<sub>2</sub> generation revealed the presence of wider range of variability for both yield and quality traits. The estimates of heritability and genetic advance varied depending on the cross and also the character. Estimates of heritability in broad sense and genetic advance were high for number of grains per panicle, grain yield per plant and kernel length whereas, the estimates were relatively low-moderate for the remaining characters. Keeping in view the gene action known from the genetic parameters, selection on important yield components *viz.*, number of grains per panicle and grain yield per plant and the quality trait, kernel length was suggested to bring out further improvement in aromatic rice. The crosses, RNR 2354 × Sye 632002 and YAMINI × BM 71 for number of grains per panicle, PUSA 1121 X MTU 1010 for grain yield per plant, PUSA 1121 × BM 71 and PUSA 1121 × MTU 1010 for kernel length were identified as better crosses for further advancement to develop pure lines with high yield and quality.

**Key words:** Aromatic rice, heritability, GCV, PCV and Genetic advance

### INTRODUCTION

Aromatic rice has got paramount importance in breeding programmes in the countries, which are self sufficient in their production. Preference is given for kernel length, size, shape, appearance and cooking quality characters especially kernel elongation ratio. As such the plant breeders should focus their attention towards the improvement of both Basmati types and aromatic short grain rices for quality and high yield potential. Yield is a complex character determined by a large number of component characters which are considered important in plant breeding. The F<sub>2</sub> population is the correct stage for selection in any hybridization programme. A knowledge on the nature and magnitude of genetic variability is essential before launching any breeding programme. Similarly estimates of heritability along with genetic advance are helpful to breeder in exercising the selection effectively. Therefore the present investigation was undertaken with the objective of estimating genetic variability, heritability and genetic advance in 7 F<sub>2</sub> populations of aromatic rice

### MATERIAL AND METHODS

The experimental material consisted of 7 parents, 7 F<sub>1</sub> hybrids and their corresponding F<sub>2</sub> populations. The genotypic and phenotypic coefficients of variation in F<sub>2</sub> were calculated according to the formula given by Emphig et al. (1970).

$$\text{GCV} = \frac{(\text{Vg})^{1/2}}{\bar{X}} \times 100$$

$$\text{Where, } \text{Vg} = \text{VF}_2 - \left[ \frac{\text{V}(\text{P}_1) + \text{V}(\text{P}_2) + \text{V}(\text{F}_1)}{3} \right]$$

$$\frac{\sum \text{X}^2 - (\sum \text{X})^2}{\text{N}}$$

$$\text{Where, } \text{VF}_2 = \frac{\quad}{\text{N}-1}$$

Variance was estimated based on single plant observations

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{(\text{Vp})^{1/2}}{\bar{X}}$$

Where, Vp = Phenotypic variance of F<sub>2</sub>

Heritability (h<sup>2</sup>) in the broad sense for all characters in F<sub>2</sub> was computed as per formula given by Allard (1960).

$$h^2(b) = \frac{\text{VF}_2 - \left[ \frac{\text{V P}_1 + \text{V P}_2 + \text{V F}_1}{3} \right]}{\text{V F}_2}$$

h<sup>2</sup>(b) = heritability in broad sense

VF<sub>2</sub> = variance among F<sub>2</sub> plants

VP<sub>1</sub>, VP<sub>2</sub>, VF<sub>1</sub> = variance among female, male and F<sub>1</sub> plants respectively

From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$\text{Where, GA} = \text{K} \cdot h^2(b) \cdot \sigma_p$$

GA = Expected genetic advance

K = Selection differential, the value of which is 1.76 at 10 per cent selection intensity

σ<sub>p</sub> = Phenotypic standard deviation of F<sub>2</sub>

h<sup>2</sup>(b) = Heritability in broad sense

$$\text{Genetic advance as per cent of mean} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,  $\bar{X}$  = mean of F<sub>2</sub> population

## RESULTS

The range and the genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent of mean were estimated for 7 crosses in F<sub>2</sub> generation and the results were furnished in Table 1.

Table 1. PCV, GCV, H and GA for yield and quality traits in F<sub>2</sub> generation

Crosses	Days to 50% flowering	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of grains per Panicle	1000-Grain Weight (g)	Grain yield per plant (g)	Kernel Length (mm)	Kernel Breadth (mm)	L/B Ratio
<b>YAMINI X BM 71</b>										
Range	88-111	109-172	6-17	22.3-30.1	43-248	14.1-27.8	5.42-58.8	6.12-7.79	1.45-1.99	3.13-5.18
PCV	6.23	10.57	32.66	14.6	46.41	15.65	51.6	6.31	19.76	12.77
GCV	4.63	8.59	25.75	10.15	46.25	11.32	50.5	4.9	17.96	10.84
Heritability (%)	55.3	66	62.2	48.3	99.2	52.4	95.7	60	84.3	71.3
GA	6.14	17.6	4.29	3.37	103.18	3.09	24.39	0.47	0.49	0.67
GAM	6.05	12.28	35.76	12.42	81.03	14.43	87.10	6.66	29.31	16.02
<b>PUSA 1121 X BM71</b>										
Range	90-114	94-160	4-23	22.6-30.8	42-303	14.5-29.3	5.08-71.78	6.3-8.1	1.20-2.16	2.97-6.26
PCV	4.92	11.57	31.27	15.14	44.79	17.97	52.3	9	17.24	21.07
GCV	3.65	9.56	23	10.38	44.47	13.3	51.74	8.11	16.66	19.62
Heritability (%)	54.9	68.2	54.2	47.0	98.5	54.6	97.6	80	85	88
GA	6.04	18.26	3.28	3.47	88.01	3.80	25.49	0.92	0.45	1.39
GAM	4.74	13.88	29.83	12.52	77.66	17.27	89.98	12.78	25.79	32.56
<b>YAMINI X MTU1010</b>										
Range	89-112	105-176	8-18	19.8-27.4	55-221	13.2-27.3	8.41-35.54	6.35-7.94	1.52-2.06	3.42-4.88
PCV	6.35	12.70	32.62	14.24	51.42	19.57	41.81	8.13	13.81	13.15
GCV	4.5	10.51	22.36	9.98	51.12	13.91	38.86	6.97	12.15	11.51
Heritability (%)	50.4	68.5	46.8	39.3	98.8	50.7	86.5	74.6	81.4	78.1
GA	5.39	20.84	2.77	2.56	74.2	3.70	12.51	0.73	0.36	0.69
GAM	5.64	15.31	26.87	11.04	89.41	17.46	63.65	10.68	19.78	17.89
<b>YAMINI X Sye632002</b>										
Range	89-114	108-188	5-18	21.5-30	39-215	13.1-20.7	4.94-44.01	5.72-7.72	1.33-1.97	3.5-4.86
PCV	6.38	13.45	33.09	14.95	34.25	22.98	58.82	10.76	21.51	11.4
GCV	4.88	11.47	25.64	9.95	34.06	16.15	56.64	9.84	18.98	9.46
Heritability	58.6	78.4	59.6	44.5	98.9	57.3	92.8	84.2	80.3	71.3
GA	6.71	26.21	4.27	3.11	69.55	3.80	16.33	1.03	0.48	0.59
GAM	6.58	18.56	34.71	11.71	59.61	23.18	96.07	15.95	30.41	14.3
<b>PUSA 1121X MTU1010</b>										
Range	88-115	102-174	6-17	19.2-30.2	35-168	16.4-28.6	8.07-48.79	6.2-7.8	1.54-2	3.22-6.27
PCV	7.12	13.33	34.36	16.44	29.95	18.24	51.95	8.05	17.58	17.95
GCV	5.59	11.48	24.87	11.13	29.56	12.90	50.57	6.66	15.93	16.7
Heritability	61.6	74.2	52.4	45.9	97.4	49.9	95.2	69.1	86.4	85.9
GA	7.62	22.12	3.27	3.44	59.56	3.37	20.30	0.70	0.49	1.09
GAM	7.72	17.41	31.69	13.28	51.35	14.42	87.04	9.79	26.73	27.14
<b>RNR2354 X Sye632002</b>										
Range	90-113	82-141	4-14	17.6-28.6	41-433	8.2-19	4.58-46.12	5.08-6.8	1.26-1.91	3.3-4.88
PCV	6.82	11.85	36.12	15.66	45.37	29.76	66.39	8.72	14.28	16.11
GCV	5.31	8.80	24.65	9.74	44.90	20.51	62.71	6.98	12.92	14.06
Heritability	60.5	55.1	46.4	38.9	99	46.8	89.2	69.2	80.8	77.7
GA	7.38	12.16	2.75	2.44	120.97	3.07	13.89	0.60	0.29	0.86
GAM	7.27	11.49	29.49	10.72	79.06	24.51	104.22	10.62	20.31	22.03
<b>RNR 2354 X MTU1081</b>										
Range	89-114	95-148	7-18	19-29.1	42-220	15-19.7	8.32-43.83	6.13-7.5	1.42-1.91	3.18-5.17
PCV	6.08	13.02	35.16	14.56	52.29	23.5	47.38	8.97	17.72	12.74
GCV	4.26	10.91	25.95	10.12	51.86	16.77	45.38	7.53	15.82	11.27
Heritability (%)	49.2	70.3	54.6	47.9	98.3	51	91.6	71.6	84.8	79.4
GA	5.24	18.89	3.26	3.05	81.12	3.69	16.04	0.70	0.42	0.73
GAM	5.25	16.11	33.78	12.36	90.46	21.09	76.38	11.30	26.44	17.81

PCV= phenotypic coefficient of variation, GCV=genotypic coefficient of variation, GA = genetic advance, GAM = genetic advance as percent of mean H= heritability in broad sense

The range was wider and the genotypic coefficients of variation higher for 3 characters i.e. number of productive tillers per plant, number of grains per panicle and grain yield per plant in all cross combinations. While, for other characters it was low to moderate except for 1000 grain weight in cross combination RNR2354 X Sye632002 which was high. The GCV ranged from 3.65 for Days to 50% flowering to 62.71 for grain yield per plant. The highest GCV observed for grain yield per plant in cross combination RNR2354 X Sye632002 (62.71). The phenotypic coefficient of variation ranged from 4.92 for days to 50 % flowering to 66.39 for grain yield per plant. The PCV higher for number of grains per panicle, number of grains per panicle and grain yield per plant in all cross combinations. In addition, for the two crosses i.e. YAMINI X Sye632002 and RNR2354 X Sye632002 it was also high for 1000 grain weight. PCV was low to moderate for remaining characters. The heritability values ranged from 38.90% for panicle length to 99.2% for number of grains per panicle. In general, heritability was moderate to high for all the characters. Highest heritability values observed for number of grains per panicle in cross combination YAMINI X BM71 (99.2%). The expected genetic advance as per cent of mean ranged from 4.74 for days to 50 % flowering in cross PUSA 1121 X BM71 to 104.22 for grain yield per plant in cross RNR2354 X Sye632002. Higher heritability values along with higher genetic advance observed for number of grains per panicle in all cross combinations. Estimates of heritability and genetic advance were also high for grain yield per plant and kernel length. Whereas, the estimates were relatively low-moderate for the remaining characters. The investigation revealed that presence of significant differences in the material for all yield and quality traits. Overall examination of the seven F<sub>2</sub> populations indicated existence of a spectrum of variability and varying estimates of heritability and genetic advance offering a better scope for exercising selection on different metric traits in superior crosses in desirable direction. Nayudu *et al.* (2007) also reported similar findings earlier. Johnson *et al.* (1955) also emphasized that heritability, GCV along with genetic advance are more helpful in predicting the results of selection. High heritability coupled with moderate to high genetic advance for grain yield per plant was in conformity with the finding of Patra *et al.* (2006). High heritability estimates for kernel length was in agreement with findings of Surender Raju *et al.* (2002).

## CONCLUSION

Based on the results, the crosses, RNR 2354 × Sye632002 and YAMINI × BM 71 for number of grains per panicle, PUSA 1121 X MTU 1010 for grain yield per plant, PUSA 1121 × BM 71 and PUSA 1121× MTU 1010 for kernel length were identified as better crosses for further advancement to develop pure lines with high yield and quality.

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