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# Genetic Analysis in F<sub>4</sub> Generation of Three Crosses in Rice (Oryza sativa L.)

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ABSTRACT: In rice (Oryza sativa L.), a study was conducted at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal during rabi, 2017-18 to assess the genetic potentialities of F4 populations of three crosses viz., ADT 46 × IET 2226, CO 50 × AD 06207 and AD 07302 × AD 09399. Mean, variability, heritability, genetic advance, correlation, path analysis and parent-progeny regression analysis were studied for eight traits viz., days to flowering, plant height, panicles per plant, panicle length, panicle weight, grains per panicle, grain weight and grain yield. Among the three crosses, ADT 46 × IET 2226 and CO 50 × AD 06207 were found to be suitable crosses to provide good source populations for exercising an effective selection for progenies with high yielding ability, as these crosses registered high mean and greater genetic variability for grain yield and many of its component traits. Cross AD 07302 × AD 09399 was suitable for making selection of high vielding progenies combined with fine grain quality based on mean performance and variability. All the characters studied recorded high heritability in F4 populations of all the three crosses. However, combination of high heritability and high genetic advance was observed for grain yield, grains per panicle and grain weight, revealing the predominance of additive gene effects for these traits.

**Keywords:**  $F_4$  population, Phenotypic variance, Genotypic variances, Heritability and Genetic advance.

## **INTRODUCTION**

Rice (Oryza sativa L.) is life and prince among cereals. This unique grain helps to sustain two thirds of world population. More than 90% of the world's rice output comes from Western and Eastern Asia, out of which China and India account for more than 33%. India has about 433.88 lakh hectare of area under rice with an annual production of 104.32 million tonnes recorded during 2016-17. It is estimated that India needs to produce 120 million tonnes of rice by 2030 to feed its projected one and half billion plus population by then as the rice is the staple food for more than 65 per cent of the people of India. Hence, to increase production, productivity of rice varieties has to be further enhanced (Adhya, 2011; Sudeepthi et al., 2017). Further, presently fine rice grain has also assumed importance based on consumer preference and market value. Thus, breeders want to develop rice varieties with high yield potential and fine grain. Recombination breeding involving hybridization and selection in the segregating populations is a time-tested breeding tool to produce such varieties. Exercise of effective selection in the segregating generations after crossing appropriate parents is crucial to achieve the progress. For this, the magnitude of variability available in the segregating generations, extent of this variability transferred to the next generation, breeding value of selected plants and association between yield and yield component traits have to be analysed and understood. Genetic parameters Naimuddin & Govindarasu

such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the segregating generations. The heritability  $(h^2)$  for yield and yield associated traits is also necessary for determining the response to selection in segregating populations. It is an index of transmissibility of the character from a generation to the next segregating generation and has a predictive role in breeding program (Shah et al., 2017).

### MATERIALS AND METHODS

Experimental site. The experiment was carried out under Agriculture Research Farm, Department of Plant Breeding and Genetics, Pandit Jawaharlal Nehru College of Agriculture and Research institute, Karaikal Puducherry.

Experimental material and details. Thirty F<sub>3</sub> plants selected for grain yield from the three crosses mentioned below were forwarded as F<sub>4</sub> families in the present study. Thus, a total of 90 F<sub>4</sub> families comprising 30  $F_4$  families in each of the three crosses constituted the material for present study. Cross 1(ADT 46  $\times$  IET 2226), Cross 2 (CO 50 × AD 06207) and Cross 3 (AD 07302 × AD 09399).

Observations recorded. Observations on yield and yield attributing characters were recorded, leaving border plants in each replication. Taken out five random plants from each entry of genotype of

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replications and tagged for data recording. Data was recorded on whole plot basis for Days to flowering, plant height (cm), panicles per plant (cm), panicle length (cm), panicle weight (g), grains per panicle (no), grain weight (g), grain yield from individual tagged plant.

#### RESULTS AND DISCUSSION

According to Goulden (1952), the potentiality of any cross is measured not only by mean performance but also on the basis of extent of variability generated. Therefore, the next criterion for evaluating crosses is to study the amount of variability available in the segregating populations. The genotypic coefficient of variation would be a useful estimate for assessing the variability in the populations, since this estimate reflects the heritable portion of the total phenotypic variability as the non-heritable environmental variability is eliminated. Therefore, the GCV estimates representing the genetic variability worked out for the traits under study were used to evaluate the efficiency of the three crosses for the exercising selection.

High magnitude of genetic variability of more than 20 per cent was recorded in the F4 populations of crosses 1 and 2 and an exploitable amount of moderate genetic variability was found in cross 3 for grain yield. Moderate genetic variability was also available for panicle weight, grains per panicle and grain weight in all the three crosses. Moderate to high genetic variability for these traits was also earlier observed in segregating populations of rice crosses by Bastia et al. (2008); Nandeshwar et al. (2010); Kumar et al. (2014); Bhuvaneswari et al. (2015); Pankaj et al. (2016). These findings of earlier studies and that of present investigation reveal that the F<sub>4</sub> populations of all the three crosses under study would be ideal for excising selection for yield and above mentioned important yield component traits viz., panicle weight, grains per panicle and grain weight as enough genetic variability was present in these populations for making effective selection. As the parents of crosses are of same duration group and have semi dwarf habit, days to flowering exhibited low genetic variability in F<sub>4</sub> population of all the crosses and plant height exhibited moderate variability in cross 1 and low variability in cross 2 and 3. Sabesan et al. (2009); Hossain et al. (2015) also recorded in their earlier studies low genetic variability for days to flowering. Low and moderate variability for plant height were earlier observed by Padmaja et al. (2008); Sabesan et al. (2009); Nandeshwar et al. (2010); Prajapati et al. (2011); Aditya and Bharatiya (2013).

In general, panicles per plant exhibited moderate genetic variability in crosses 1 and 2 and low variability in cross 3. Panicle length expressed low variability in all the three crosses. Such a low to moderate magnitude of variability for panicles per plant was reported in segregating generations by Savitha and Ushakumari (2015); Sala and Shanthi (2016); Pratap et al. (2012). Aditya and Bharatiya (2013); Sala and Shanthi (2016) recorded low variability for panicle length. Desirable mean coupled with enough genetic variability is highly

useful for an effective selection (Finkner et al., 1973). When this is considered as an index for selection,  $F_4$ population of cross 1 followed with cross 2 are found suitable for selection of high yielding progenies, since the high genetic variability was realized along with high mean performance for grain yield in these crosses. However, though considerable variability was exhibited for grain weight in these crosses, the mean grain weight of both the crosses is on higher side which is not desirable. Hence, selection of high yielding progenies along with fine grain type may not be possible in the  $F_4$ populations of crosses 1 and 2.

While, in cross 3 exploitable amount of genetic variability was existing for grain yield as well as for grain weight. The mean grain yield in this cross is also higher than its high yielding female parent and the check variety. Similarly, the mean grain weight of this cross is in desirable direction of lower value. Hence, this cross is suitable for selection of high yielding progenies with fine grain.

Heritability and genetic advance. High GCV alone would not indicate the true selection value and hence, heritability estimates should also be considered for an effective selection according to Burton (1952). High heritability represents the strong reflection of genotype on phenotype. Consequently, the superiority of selected plants is transferred to the next generation. High heritability along with high genetic advance is an indirect estimation of predominant role of fixable additive gene action on the respective characters. Hence, the study of heritability coupled with genetic advance would be more useful in estimating the efficiency of phenotypic selection than selection based only on heritability.

In the present study, heritability was of high magnitude of more than 60 per cent for all the traits studied in  $F_4$ populations of all the three crosses. However, high heritability combined with high genetic advances as per cent of mean (more than 20 per cent) was observed only for three traits viz., grain yield, grains per panicle and grain weight in all the three crosses. This indicates, these characters are predominantly controlled by additive gene action and improvement of these traits could be achieved through simple phenotypic selection in all three crosses. Such a combination of high heritability and high genetic advance was reported earlier for yield (Nandeshwar et al., 2010; Prajapati et al., 2011; Hossain et al., 2015; Rai et al., 2016) for plant height (Padmaja et al., 2008; Sabesan et al., 2009; Pratap et al., 2012); for panicles per plant (Sabesan et al., 2009; Pratap et al., 2012; Sala and Shanthi 2016); and for grain weight (Sabesan et al., 2009).

Whereas, the traits viz., plant height and panicle length showed high heritability along with moderate to high only in cross 1 for plant height and genetic advance in  $F_4$  populations of all the three crosses. The other traits viz., panicles per plant and panicle weight produced high heritability with high genetic advance in crosses 1 and 2, while in cross 3 these traits had high heritability with moderate genetic advance. Arumugasamy and Thiyagarajan (2006); Zahid et al. (2006); Nandeshwar et al. (2010); Kumar et al. (2014); Bhuvaneswari et al. (2015) also obtained similar results for these traits.

These findings suggested that selection for these traits would produce moderate to high gain in the subsequent generation. reveal the superiority of  $F_4$  population of cross 1 and 2 for an effective selection of plants with high yield potential and cross 3 for high yield with fine grain type.

Finally, the consideration of mean, genetic variability, heritability and genetic advance together as the criterion

Parameters	Range	Mean	PV	GV	PCV (%)	GCV (%)	Heritability (%)	GA	GA as % of mean
Days to flowering	C1	101.53- 130.0	115.19	92.09	84.69	8.33	7.98	91.97	18.18
	C2	100.67- 132.67	112.43	107.06	103.51	9.2	9.04	96.68	20.61
	C3	102.20- 130.33	111.45	81.75	79.21	8.11	7.98	96.89	18.05
Plant height (cm)	C1	102.73- 173.33	132.62	464.81	448.73	16.25	15.97	96.54	42.88
	C2	103.14- 149.33	126.15	102.21	80.41	8.01	7.1	78.67	16.38
	C3	102.20- 130.33	111.45	81.75	79.21	7.84	7.25	85.71	18.05
Panicle length (cm)	C1	22.28-28.60	24.39	0.24	0.21	7.11	6.29	78.35	0.88
	C2	22.52-31.35	24.55	5.3	4.26	9.38	8.41	80.49	3.81
	C3	20.47-28.68	23.49	3.74	2.93	8.23	7.29	78.39	3.12
Grains per panicle (no)	C1	135.55- 288.33	198.63	1371.63	1348.1	18.64	18.48	98.28	74.98
	C2	107.00- 212.33	140.87	696.29	671.23	18.73	18.39	96.47	52.4
	C3	111.00- 206.33	138.68	730.84	707.34	19.49	19.17	96.78	53.9
Panicles per plant	C1	13.07-36.67	24.88	30.67	20.32	22.26	18.11	66.26	7.56
	C2	21.33-33.00	26.17	13.51	10.38	14.05	12.31	76.86	5.82
	C3	20.00-30.00	24.98	6.85	4.77	10.47	8.72	69.63	3.76
Panicle weight (g)	C1	2.32-3.80	3.02	0.24	0.21	16.4	15.45	88.78	0.88
	C2	2.65-3.98	3.5	0.17	0.15	11.82	11.05	87.48	0.75
	C3	2.51-4.71	3.68	0.17	0.14	11.31	10.22	81.6	0.7
Grain weight (g)	C1	2.31-3.86	2.9	0.35	0.29	19.1	17.52	84.81	1.01
	C2	2.02-3.77	2.39	0.24	0.21	16.59	15.34	85.57	0.88
	C3	1.31-2.44	1.47	0.04	0.03	14.33	12.61	77.36	0.31
Grain yield (g)	C1	13.17-32.52	23.43	29.46	28.66	23.16	22.84	97.28	10.88
	C2	12.81-26.47	18.89	37.03	33.88	30.96	29.61	91.48	11.47
	C3	15.27-26.08	18.69	6.76	5.68	13.91	12.75	84.02	4.5

Table 1: Table of parameters PCV, GCV, Heritability and Genetic Advance in F<sub>4</sub> generation of three crosses.

#### CONCLUSIONS

High magnitude of genetic variability was recorded in the  $F_4$  populations of crosses 1 and 2 and an exploitable amount of moderate genetic variability was found in cross 3 for grain yield. Moderate genetic variability was also available for panicle weight, grains per panicle and grain weight in all the three crosses, suggesting the higher efficiency of selection for improving these component traits as well as grain yield. Panicle length, days to flowering and plant height only in cross 1 and cross 3 expressed low variability in all the three crosses, inferring that selection may not be fruitful in improving these traits in the populations under study.

High heritability combined with high genetic advances as per cent of mean was observed only for three traits *viz.*, grain yield, grains per panicle and grain weight in all the three crosses, suggesting that these characters are predominantly controlled by additive gene action and improvement of these traits could be achieved through simple phenotypic selection in the  $F_4$  populations of all three crosses. Plant height and panicle length showed high heritability along with moderate to high only in cross 1 for plant height and genetic advance in  $F_4$ populations of the three crosses, while panicles per plant and panicle weight produced high heritability with high genetic advance in crosses 1 and 2, while in cross 3 these traits had high heritability with moderate genetic advance. These results suggest that selection for these traits would produce moderate to high genetic gain in the subsequent generation.

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