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Study of Variability, Heritability and Genetic Advance for Grain Yield and Yield Characters in Hybrid Rice (*Oryza sativa* L.)

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ABSTRACT

The experiment was conducted with an objective to estimate the variability, heritability and genetic advance of 77 rice genotypes for ten yield traits. Analysis of variance revealed significant differences for all the traits under study. The characters *viz.,* filled grains per panicle, total number of grains per panicle and grain yield per plant exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). High heritability coupled with high genetic advance was observed for productive tillers plant^{-1}, filled grains per panicle, total number of grains per panicle and grain yield per plant indicating the preponderance of additive gene action and further improvement of these characters can be possible through simple selection procedures.

Key words: Variability. Heritability, Genetic advance, Rice

Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world and it is the major food crop for nearly one half of the world population. Globally, rice is cultivated now on 159 million hectares with annual production of around 685 million tonnes and average productivity of 4.4 tonnes/ha. India has the largest area of 43.86 million hectares under rice cultivation and ranks second with an average production of 104.32 million tonnes with a productivity of 2404 kg ha^{-1} (Ministry of Agriculture, Directorate of Economics and Statistics, 2014-15) and about 65 per cent of the population has rice as a major constituent in the diet. It is estimated that the demand for rice will be 121.2 million tonnes by the year 2030 and 137.3 million tonnes by the year 2050. (CRRI -VISION 2050). To meet the food demand of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 million tonnes every year, which is possible through other innovative breeding approaches. Among the innovative breeding options available for enhancing the rice production in short term, hybrid rice is one of the technology which is practically feasible and readily adoptable one. In the present investigation, an attempt has been made to elucidate information on nature and magnitude of genetic parameters for grain yield in the parents and rice hybrids.

MATERIAL AND METHODS

The present investigation was carried out at Agricultural Research Station, Nellore during *rabi* 2015-16 with the objective of estimate genetic variability among the parents and rice hybrids. The experimental materials for the present study consisted of 77 genotypes (three female lines, 18 males, 54 hybrids produced by L x T mating design and two checks) (Table 1). The experimental material was planted in four rows with a row length of 4.5 m and two replications in a Randomized Block Design (RBD). Twenty five days old seedlings were transplanted with a spacing of 20 cm between rows and 15 cm between plants under recommended dose of fertilizers i.e., 120N: 40 P_2O5:40 K_2O per hectare along with necessary plant protection measures to raise a good crop. Observations were recorded for ten characters on ten randomly selected plants of each replication and the mean data was subjected to statistical analysis. The characters studied were., days to 50 % flowering, , plant height, productive tillers plant^{-1}, panicle length, filled grains panicle^{-1}, total grains panicle-^{1}, spikelet fertility per cent and grain yield plant^{-1}. The genotypic and phenotypic coefficients of variance (Burton and Devane, E.W. 1953), heritability and genetic advance as percentage of mean (Johnson *et al.* 1955) were estimated.

RESULTS AND DISCUSSION

The potentiality of a cross is measured not only by mean performance but also on the extent of variability. Knowledge on nature and magnitude of genotypic and phenotypic variability present in any crop species plays an important role in formulating successful breeding programmes (Allard, 1960). The analysis of variance revealed highly significant differences among the genotypes for all the ten yield attributing characters indicating the existence of significant amount of variability among the characters studied (Table 2).

In general, phenotypic coefficient of variation (PCV) values were higher than genotypic coefficient of variation (GCV) values. A wide range of phenotypic

Table 1. List of rice genotypes studied during *rabi*-2015

Parent	Designation	Source	Origin
CMS lines	IR-58025A	WA	IRRI, The Philippines
	IR-68888A	WA	IRRI, The Philippines
	IR-68897A	WA	IRRI, The Philippines
R lines		Parentage	
1	NLR 145	CICA-4 / IR-6425-32-2-3-1/ Tetep	ARS, Nellore
2	NLR 34449	IR 72 / BPT 5204	ARS, Nellore
3	NLR 40024	WGL 14280-1/ NLR 30491	ARS, Nellore
4	NLR 3041	BPT 5204 / NLR 145	ARS, Nellore
5	NLR 3010	WGL 3962/IET 9994	ARS, Nellore
6	NLR 3083	MTU 1001 / RNR 19994	ARS, Nellore
7	ADT 37	BG 280-12/ PTB 33	TNAU, Coimbatore
8	JGL 11118	IET 8585 / JGL 1798	ARS, Jagital
9	MTU 1010	MTU 2077 / IR 64	Andhra Pradesh
10	MTU1001	MTU 5249 / MTU 7014	RARS, Maruteru
11	RNR 2458	Chandan / BPT 5204	ARI, Rajendranagar
12	PS 4	Pusa 1121/Pusa 614-1-2/Pusa614-2-4-3	IARI, New Delhi
13	PS 5	Pusa 2511/Pusa 3A/ Pusa 1238-81-6	IARI, New Delhi
14	BPT 5204	GEB 24 / T (N) 1 // Mahsuri	RRU, Bapatla
15	Sumati	Chandan / Pakistan Basmati	ARI, Rajendranagar
16	WGL 32100	Divya x BPT 5204	RARS, Warangal
17	WGL 283	Chaitanya / TellaHamsa	RARS, Warangal
18	WGL 3962	Phalguna / IR 36	RARS, Warangal
Checks	DRRH-2	68897A/ DR 714-1-2R	DRR, Hyderabad
	KRH-2	IR 58025A x KMR 3R	Karnataka

coefficient of variation (PCV) was observed for yield contributing traits ranging (Table 2) from 4.34 per cent (Days to Maturity) to 34.13 per cent (grain yield plant^{-1}). Genotypic coefficient of variation (GCV) had the range of 4.18 per cent (Days to Maturity) to 31.74 per cent (grain yield plant^{-1}) among the characters. High phenotypic and genotypic coefficient of variation was recorded for grain yield per plant (34.13 and 31.74), filled grains per panicle (25.38 and 24.30) and total grains per panicle (23.87 and 22.14) indicated that these characters could be used as selection criteria for yield improvement, which is in accordance with results of Satyarajkumar *et al.* (2015), Vijay Kumar *et al.* (2015) and Shajedur Hossain *et al.* (2015). Phenotypic and genotypic coefficient of variation was moderate for productive tillers per plant (14.70 and 12.41) and test weight (14.20 and 13.94). These results were in agreement with the results obtained by Allam *et al.* (2015) and Keya *et al.* (2015).

High heritability along with high genetic advance as percent of mean was registered for test weight (96.37, 28.20), filled grains per panicle (91.68, 47.92), grain yield per plant (86.48, 60.79), total grains per panicle (86.01, 42.30) and productive tillers per plant (71.30, 21.58) suggesting preponderance of additive gene action in the expression of these characters. This type of characters could be improved by mass selection and other breeding methods based on progeny testing. Similar results were also reported by Lingaiah *et al.* (2014), Allam *et al.* (2015) and Sameera *et al.* (2015) for these characters. However, high heritability associated with moderate genetic advance as percent of mean was observed for days to 50% flowering (96.64, 11.11), panicle length (79.72, 16.52) and plant height (70.62, 15.07) suggesting greater role of non-additive gene action in their inheritance. Therefore heterosis breeding could be used to improve these traits. Similar findings of high heritability associated with moderate genetic advance were also reported by Keya *et al.* (2015) and Sameera *et al.* (2015). Whereas, high heritability (92.98) and low genetic advance as percent of mean (8.31) recorded for days to maturity indicated the inheritance was due to non-additive gene effects (Sameera *et al.* 2015 and Vijay Kumar *et al.* 2015).

Table No 2. Analysis of variance for yield and yield and yield contributing characters in rice (*Oryza sativa* L.) during *rabi*-2015

Source of Variations	df	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Productive Tillers Plant^{-1}	Panicle Length (cm)	Filled Grains Panicle^{-1}	Total Grains Panicle^{-1}	Spikelet Fertility (%)	Test Weight (g)	Grain Yield Plant^{-1} (g)
		Mean squares									
Replicate	1	0.000	0.006	0.407	0.015	0.16	14.645	30.318	3.534	0.005	1.14
Treatments	76	53.084**	56.938**	98.005**	3.589**	7.660**	3307.256**	4135.716**	64.785**	13.633**	124.873**
Error	76	0.908	2.072	16.873	0.601	0.864	143.635	310.972	16.465	0.252	9.054

Table 3. Genetic parameters for yield and yield and yield contributing characters in rice (*Oryza sativa* L.) during *rabi*-2015

S.No.	Characters	General Mean	Range		Coefficient of variation		Heritability (Broad Sense)	Genetic Advance	Genetic Advance as % of Mean
			Min.	Max.	GCV (%)	PCV (%)			
1	Days to 50% Flowering	93.13	79.00	106.00	5.48	5.58	96.64	10.34	11.11
2	Days to Maturity	125.20	113.00	137.50	4.18	4.34	92.98	10.40	8.31
3	Plant Height (cm)	73.16	59.50	94.30	8.71	10.36	70.62	11.03	15.07
4	Productive Tillers Plant^{-1}	9.85	6.78	13.30	12.41	14.70	71.30	2.13	21.58
5	Panicle Length (cm)	20.53	15.90	25.50	8.98	10.06	79.72	3.39	16.52
6	Filled Grains Panicle^{-1}	163.70	52.80	231.40	24.30	25.38	91.68	78.45	47.92
7	Total Grains Panicle^{-1}	197.53	71.80	288.20	22.14	23.87	86.01	83.55	42.30
8	Spikelet Fertility (%)	82.71	64.93	93.43	5.94	7.71	59.47	7.81	9.44
9	Test Weight (g)	18.55	13.82	28.51	13.94	14.20	96.37	5.23	28.20
10	Grain Yield Plant^{-1} (g)	23.98	6.99	41.45	31.74	34.13	86.48	14.58	60.79

CONCLUSION

From the present study it can be concluded that the genotypes possessed adequate variability for the yield and yield attributing characters and may provide good source of material for further breeding programmes. High PCV GCV and high heritability coupled with high genetic advance was observed for the characters viz., filled grains per panicle, total grains per panicle and grain yield per plant. While test weight and productive tillers per plant also recorded high heritability along with high genetic advance. This indicated the presence of high genetic variability for the traits which may facilitate selection and these characters attributable to additive gene effects which are fixable revealing that improvement in these characters would be possible through direct selection. Other characters showed high heritability along with moderate or low genetic advance indicating the operation of both additive and non additive gene action which can be improved by intermating superior genotypes of segregating population developed from combination breeding.

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