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Studies on Variability, Heritability and Genetic Advance in Rice (*Oryza Sativa* L.) Hybrids

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ABSTRACT

The present investigation was carried out with 20 genotypes of Rice (*Oryza sativa* L.) which consists of 15 hybrids and 5 checks to elicit information on the nature and extent of variability, heritability and genetic advance for yield, yield contributing traits and quality traits. The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the presence of sufficient genetic variability among them. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association with the characters at genotypic level. The genetic parameters revealed that moderate to high variability and high heritability coupled with high genetic advance as per cent of mean were observed for grain yield per plant (g), number of total grains per panicle and water uptake suggesting the predominance of additive type of gene action in controlling these traits with less influence by the environment and improvement of these characters is possible through direct phenotypic simple selection. The remaining characters under study *viz*., days to 50% flowering, plant height (cm), panicle length (cm), head rice recovery percentage, L/B ratio, days to maturity, hulling percentage and kernel elongation ratio has high heritability coupled with moderate to low genetic advance as percent of mean indicating the operation of both additive and non-additive gene effects in the inheritance of these traits. Hence improvement of these characters is possible through mass selection, progeny selection or any other suitable modified selection procedure for exploitation of the mixed effects of both non-additive and additive gene actions.

Keywords : *Genetic advance, Heritability, Quality parameters, Variability, Yield, Yield contributing traits.*

Rice (*Oryza sativa* L.) is one of the most important cereal crops in the tropics as well as parts of temperate regions in the world. It is a grass belongs to family of Poaceae. It is a food crop of world-wide importance and forms the foundation of the diet of over 3 billion people, constituting over half of the world's population. In world, rice occupies an area of 161.54 million hectares, with production of 487.46 million tonnes of milled rice and productivity of 4.5 t/ha. (United States Department of Agriculture, 2016-17). India is next to China in production of rice. India has 43.7 million hectares of area, 110.00 million tonnes of milled rice production and productivity of 3.78 t/ha (United States Department of Agriculture, 2016-17). Andhra Pradesh has 2.16 million hectares of area, 7.49 million tonnes of production with productivity of 3.79 t/ha milled rice. (Directorate of Economics and Statistics, 2015-16).

For the estimated population of 1.63 billion people by the year 2050 with a per capita rice consumption of 225 to 275 g/day, country would require 133 to 162 Mt of rice (Directorate of Rice Research, 2013). At present the rice productivity has reached to a plateau and there is a need to develop the varieties with higher yield potential by breaking the existing yield plateau through utilizing more divergent lines in the breeding programmes.

Rice offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various qualitative and quantitative charectetrs (Kotaiah, 1983). The conservation of a large amount of genetic variability in rice gene pool provides plant breeder with raw material that can be recommended to produce new improved varieties for yield and quality traits.

The estimation of genotypic variation alone may not provide necessary information on heritable variation. Hence, information on heritability along with genetic advance will be of immense help to the breeder in selecting superior individuals for a desired trait and successfully utilizing them in breeding programme.

MATERIALS AND METHODS

The present investigation was carried out during *kharif,* 2017 at Agricultural College Farm, Bapatla. The experimental material consisted of twenty genotypes (15 Hybrids + 5 Checks) of Rice (*Oryza sativa* L.) obtained from Indian Institute of Rice Research (IIRR), Rajendranagar, Hyderabad, Telangana, which were sown in nursery beds and transplanted into the main field in Randomized Block Design in three replications with a spacing of 15 x 15 cm.

Table 1. Analysis of variance for yield and yield components among 20 genotypes of rice (*Oryza sativa* L.)

S. No	Source	Replications	Treatments	Error
	Degree of freedom	2	19	38
	MEAN SUM OF SQUARES			
1	Days to 50% flowering	2.5167	90.5649**	1.3939
2	Days to maturity	0.4500	82.2280**	1.6781
3	Plant height (cm)	2.6047	411.9068**	7.8124
4	Productive tillers per plant	1.2167	18.8236**	2.3395
5	Panicle length (cm)	0.1499	7.0572**	0.6626
6	Grains/ Panicle	206.8167	9886.7675**	292.6412
7	Grain Yield/ Plant	0.4167	317.0131**	10.1711
8	Hulling %	4.5167	28.3122**	3.9728
9	Milling %	10.5167	27.0973**	5.2711
10	Head Rice Recovery	9.2167	110.2315**	8.2868
11	Volume Expansion Ratio	0.0072	0.0419**	0.0123
12	Water Uptake	117.91	13463.4648**	157.8289
13	L/B Ratio	0.0048	0.1850**	0.0120
14	Kernel Elongation Ratio	0.0026	0.0227**	0.0022
15	Amylose Content	3.4042	4.0552**	1.2982

*significant at 5% level, **significant at 1% level

Table 2. Mean, variability, heritability and genetic advance as per cent of mean for yield, yield components and grain quality parameters in rice (*Oryza sativa* L.).

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5% level)
			Maximum	Minimum	PCV %	GCV %		
1	Days to 50% Flowering	97.43	105.00	84.00	5.73	5.60	96.40	11.27
2	Days to Maturity	126.50	134.00	114.00	4.22	4.10	94.50	8.19
3	Plant Height (cm)	128.74	146.20	96.66	9.27	9.01	95.10	18.05
4	Productive Tillers/ Plant	18.18	22.00	12.66	15.39	12.89	70.80	22.24
5	Panicle Length (cm)	23.60	26.25	21.03	7.08	6.18	76.20	11.13
6	Grains/ Panicle	326.58	428.00	220.00	18.09	17.32	92.10	34.14
7	Hulling %	83.63	90.33	80.33	4.16	3.41	67.50	5.75
8	Milling %	72.88	81.33	69.66	4.86	3.70	58.30	5.81
9	Head Rice Recovery	60.26	73.66	51.33	10.79	9.67	80.70	17.87
10	Volume Expansion Ratio	3.65	4.00	3.50	4.08	2.72	45.30	3.75
11	Water Uptake	158.66	275.00	85.00	42.71	41.97	97.70	84.97
12	L/B Ratio	2.87	3.24	2.32	9.18	8.36	83.90	15.66
13	Kernel Elongation Ratio	1.77	1.90	1.66	5.38	4.67	75.90	8.37
14	Amylose Content	23.18	24.66	20.23	6.42	4.13	41.30	5.48
15	Yield per plant (g)	46.41	63.66	28.66	22.85	21.79	91.40	42.81

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

Single plant observations were recorded on five plants selected at random per genotype per replication for characters *viz*., plant height (cm), number of productive tillers per plant, panicle length (cm), number of total grains per panicle, grain yield per plant (g) and their means were used for statistical analysis. However, observations on days to 50% flowering, days to maturity were recorded on plot basis and all grain quality parameters *viz.,* hulling percentage, milling percentage, head rice recovery percentage, L/B ratio, water uptake, kernel elongation ratio, volume expansion ratio and amylose content were done as per DRR laboratory manual on rice grain quality procedures. The mean values over three replications were used for statistical analysis and analysis was done as per Panse and Sukhatme (1967), Burton and Devane (1953) and Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability in the studied material (Table 1). The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association with the characters at genotypic level (Table 2). Low PCV and GCV is observed for characters like days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), hulling percentage, milling percentage, volume expansion ratio, L/B ratio, kernel elongation ratio and amylose content. Moderate PCV and GCV is observed for characters like number of productive tillers per plant and number of total grains per panicle. High PCV and GCV is observed for grain yield per plant and water uptake. The trait, head rice recovery percentage recorded moderate PCV and GCV. These results were in conformity with the findings of Nandan *et al.* (2010), Subbaiah *et al.* (2011), Babu *et al.* (2012), Krishnaveni *et al.* (2013), Rao *et al.* (2014), Ekka *et al.* (2015), Tejaswini *et al.* (2016), Prasad *et al.* (2017) and Mamata *et al.* (2018).

The genetic parameters revealed that moderate to high variability and high heritability coupled with high genetic advance as per cent of mean were observed for grain yield per plant (g), number of total grains per panicle and water uptake suggesting the predominance of additive type of gene action in controlling these traits with less influence by the environment. These results indicated the operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through direct phenotypic simple selection. Hence, good response to selection can be attained in early generations in improving these traits. The remaining characters under study *viz*., days to 50% flowering, plant height (cm), panicle length (cm), head rice recovery percentage, L/B ratio, days to maturity, hulling percentage and kernel elongation ratio with high heritability coupled with moderate to low genetic advance as percent of mean indicating the operation of both additive and non-additive gene effects in the inheritance of these traits. Hence, for improvement of these characters, mass selection, progeny selection or any other suitable modified selection procedure for exploitation of the mixed effects of both non-additive and additive gene actions. Similar results were reported by Tiwari *et al.* (2011), Bhadru *et al.* (2012), Krishnaveni *et al.* (2013), Sarwar *et al.* (2015), Sameera *et al.* (2016), Lakshmi *et al.* (2017) and Mamata *et al.* (2018).

CONCLUSION

High heritability coupled with high genetic advance as per cent of mean was observed for number of productive tillers per plant, number of total grains per panicle, grain yield per plant and water uptake, which indicated the predominance of additive gene action in the inheritance of these traits and simple selection can be practiced for the improvement these traits.

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