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Evaluation of early mature elite rice (*Oryza sativa* L.) hybrids for yield and quality traits

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Abstract

Field Experiment was conducted to evaluate 33 rice Hybrids for yield and quality traits in Department of Genetics and Plant Breeding, SHUATS, Allahabad during Kharif 2016 in Randomized Block Design with 3 replications of 33 Rice Hybrids received from AICRIP from Indian Institute of Rice Research (IIRR) Hyderabad. The data were recorded for 15 quantitative characters to assess Genetic variability. Analysis of variance showed highly significant for all the 15 characters except flag leaf width. The highest grain yield per plant was observed in hybrid IHRT-E-34 7t/ha. Highest of GCV and PCV were observed for number of spikelets per panicle followed by grain yield per plant and unfilled grains percentage. High Estimate of Heritability was observed for plant height and days to 50% flowering. High Genetic advance as % of mean was recorded for number of spikelets per panicle, grain yield per plant, unfilled grains and tillers per hill. High heritability coupled with high genetic advance as percent of mean was observed for spikelets per panicle followed by plant height and tillers per hill. With regards to hulling percentage and high Gel consistency recorded in IHRT-E-9 follows by IHRT-E-12.

Keywords: Hybrid rice, genetic variability, heritability & genetic advance, gel consistency

Introduction

Rice (*Oryza sativa* L.) is the staple food for 65% of the world population and forms the cheapest source of energy and protein. Globally rice is cultivated now 154 million tonnes and average productivity of 3.9 tonnes per hectare. In India rice play key role it contributes also 46% of Indian cereal production and also staple food for two third of the population. India stands first in area and second in production. India has 44.13 million hectare and production 104.8 tones and productivity of 2416 kg/ha (Agristatics at glance 2015)^[1].

The country witnessed an impressive growth in rice production due to adoption of semi dwarf varieties coupled with intensive input based management practices. In order to keep pace with growing population the estimated rice requirement by 2025 is about 130million tones. There is an extreme need to enhance the rice productivity in India which will be achieved by developing hybrids and high yield varieties. Hybrid rice technology is likely to play key role in increasing the rice production nearly 15-20% over the best pure lines varieties. Presently in India hybrid rice is cultivated about 5 million hectares, more than 80% of the total hybrid rice area is in the state of Uttar Pradesh, Jharkhand, Bihar, Punjab, Haryana, Gujarat, Odisha, Chhattisgarh. The rice hybrids have recorded yield in the range of 5 to 8 tones/ hectare and average yield of hybrid rice is around 5 tones/ hectare, (Directorate of Rice Research Annual Report (2014-15)^[1, 7].

Rice is the only cereal crop cooked and consumed mainly as whole grains, and quality considerations are much more important than for any other food crop (Hossein, 2009)^[8]. Grain quality currently represents a major problem in high yielding rice production in India and many other rice producing areas of the world. Much of this problem stems from the poor cooking and eating quality of many widely grown varieties, especially the indica varieties. The term rice quality encompasses milling quality, market quality, and nutritional quality, cooking and eating quality of the grains. Physical quality properties such as size, shape, uniformity and general appearance, the cooking and eating characteristics, gelatinization temperature, grain elongation, gel consistency. Development of high yielding varieties with superior milling and cooking qualities is now one of the most important objectives in all rice improvement programmes. Thus breeding materials is evaluated for four components grain quality via: grain size, shape, appearance, cooking and eating characteristics. (Rani *et al.*, 2007)^[13].

Materials and Methods

The material for the present investigation consists of 33 (including 2 checks) rice hybrids under AICRIP received from Indian Institute Rice Research (IIRR) Hyderabad. These were grown in Randomized block design design with three replications during kharif 2016 at field experiment farm of Department of Genetics and Plant Breeding, SHUATS, Allahabad Twenty five days old seedlings raised in nursery were transplanted at 20 cm x 15 cm. Five representative plants for each hybrid in each replication were randomly selected to record observations on plant height (cm), flag leaf length (cm), flag leaf width (cm), total tillers per plant, productive tillers per plant, panicle length, spikelets per panicle, biological yield, harvest index, test weight, filled and unfilled grains percentage, and grain yield per plant (g). Days to 50% flowering and days to maturity were computed on plot basis. Therefore quality parameters like hulling %, kernel length and kernel breadth before cooking, and kernel length, kernel breadth after cooking, L/B ratio, elongation ratio, gel consistency and alkali spreading value were evaluated for best performing hybrids in terms of yield. The genotypic and phenotypic co-efficient of variations were computed through Burton's method Heritability and genetic advance were worked out as per the method of (Jhonson *et al.* 1995) [9].

Results and Discussion

The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied except flag leaf width (table1) similar finding for Padmaja D *et al.* (2008) [11]. According to the mean performance wide range of variation was found in most of the

characters revealed that highest range of mean variation was noticed for number of spikelets per panicle (332.87), plant height (135.00) and days to maturity (126.00). Whereas the range was found to be lowest in flag leaf width (0.91) and unfilled grains (3.09). The hybrid IHRT-7 showed higher yield coupled with cooking qualities (table 3) high gel consistency, intermediate alkali spreading value, and L/B ratio.

Phenotypic variance was higher than the genotypic variances for all the characters thus indicated the influences of environmental factor on these traits. Grains per panicle and plant height exhibited high genotypic and phenotypic variances, followed by plant height, biological yield and grain yield per plant. Similar results were obtained earlier by Deb Choudhary and Das1998 [6]. Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV (table 2) Among the all traits number of spikelets per panicle (29.54 and 31.41) exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by grain yield per plant (27.27 and 29.62), unfilled grains (27.13 and 29.31). The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression showed moderate value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

Table 1: Analysis of variance for 15 characters in 33 Rice Hybrids during *Kharif-2016*

S. No.	Characters	Mean squares		
		Replication (d.f=2)	Treatments (d.f =32)	Error (d.f=64)
1	Days to 50% flowering	2.76	147.52**	1.55
2	Plant height	6.76	499.00**	2.73
3	Flag leaf length	9.66	120.00**	16.85
4	Flag leaf width	0.01	0.097	0.002
5	Panicle length	0.16	18.27**	0.420
6	Tillers / plant	0.136	20.00**	0.602
7	Panicles / plant	0.82	20.00**	1.13
8	Spikelets / panicle	184.29	10376.91**	502.92
9	Days to maturity	0.31	153.97**	0.56
10	Biological yield	4.33	453.36**	36.68
11	Harvest index	0.75	98.85**	4.19
12	Test weight	0.10	17.34**	0.22
13	Filled grain	0.94	11.83**	1.59
14	Unfilled grain	0.199	8.80**	0.46
15	Grain yield / plant	1.28	175.84**	9.94

** Significant at 1% level of significance

Similar findings of high GCV and PCV for number of spikelets per panicle and grain yield per plant were observed earlier by Anjaneyulu *et al.* 2010.

The coefficient of variation doesn't offer the full scope of heritable variation. It can be find out with greater degree of accuracy when heritability is conjunction with genetic advance study. Heritability is a good index of transmission of characters from parents to its progeny. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population. The estimates of heritability (%) in broad sense for 15 characters studied which range from 98.37 to 68.17%. Maximum heritability observed for the plant height (98.37%) followed by traits likewise days to 50% flowering (96.11%), days to maturity (95.44%), test

weight (95.20%), tillers per hill (93.98%), panicle length (93.40%), leaf width (92.13%) harvest index (87.65%), flag, grain yield (84.74%), biological yield (79.10%). Deepa S *et al.* 2006 observed that high heritability were obtained for the traits plant height, days to 50 per cent flowering, productive tillers/plant, panicle length, grains/panicle, 100 seed weight and single plant yield.

A character exhibited high heritability may not necessarily give high genetic advance have been shown that high heritability accompanied by high genetic advance to arrive reliable conclusion. The breeder should cautions in making selection based on heritability as it includes additive gene effects, so such variability. Thus genetic advance is through not independent represent the expected genetic advance under

selection. The Genetic advance varied from 0.35 to 110.74. Maximum genetic advance was recorded for spikelets per panicle (112.74) followed by plant height (26.28) biological yield (21.59), days to 50% flowering (14.14), days to maturity (14.65), grain yield (14.09), harvest index (11.52), flag leaf length (9.89). Bidhan *et al.* 2001^[3]. High genetic advance was observed for number. High genetic advance was observed for number of spikelets per panicle and plant height. In the present study, high heritability along with high genetic advance was noticed for the traits, number of spikelets per panicle and

plant height. Observed similar results earlier for number spikelets per panicle. Other characters like flag leaf width and UN filled grains, showed high heritability along with moderate or low genetic advance. The estimates of genetic advance as a percent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over original population.

Table 2: Genetic parameters for 15 quantitative characters in Rice Hybrids during *Kharif*-2016

S. No.	Characters	Mean	Range	σ^2g	σ^2p	Coefficient of variation		$h^2(\%)$	GA	GA as % of mean
						GCV	PCV			
1	Days to 50% Flowering	87.75	75.00-97.00	48.66	50.21	7.96	8.08	96.11	14.14	16.14
2	Plant Height	111.84	82.67-135.00	165.49	168.23	11.50	11.59	98.37	26.14	23.50
3	Flag Leaf Length	35.80	22.00-47.00	34.38	51.23	16.37	19.56	67.10	26.28	27.63
4	Flag Leaf Width	1.26	0.91-1.68	0.03	0.03	14.03	14.62	92.13	9.89	27.75
5	Panicle Length	27.10	22.11-32.17	5.95	6.37	8.99	9.31	93.40	4.85	17.91
6	Tillers/ Plant	13.38	8.97-22	9.40	10.03	22.90	23.62	93.40	6.12	45.74
7	Panicles/ Plant	10.92	6.63-17.20	6.28	7.42	22.96	24.95	84.74	4.75	43.52
8	Spikelets/ Panicle	196.10	93.67-32.87	3291.32	3794.25	29.54	31.41	86.74	110.74	56.12
9	Days to Maturity	114.60	98.33-126	53.63	56.19	6.27	6.30	98.11	14.65	12.84
10	Biological Yield/ Plant	62.26	33.03-86.43	138.89	175.57	18.82	21.27	79.10	21.59	34.67
11	Harvest Index	43.19	27.75-49.25	31.55	35.74	13.10	13.94	88.27	10.87	25.36
12	Test Weight	23.56	18.33-29.23	5.71	5.93	10.14	10.33	96.34	4.83	20.51
13	Filled grains (%)	94.15	91.06-97.33	3.41	5.00	1.96	2.37	68.17	3.14	3.33
14	Un Filled grains (%)	6.14	3.09-8.86	2.78	3.24	27.13	29.31	85.16	3.17	51.72
15	Grain Yield/ Plant	27.25	13.43-41.77	55.24	65.18	27.27	29.62	84.74	14.09	51.84

σ^2g = Genotypic variance. σ^2p = Phenotypic variance. h^2 = Heritability (broad sense), GCV = Genotypic coefficient of variation. PCV = Phenotypic coefficient of variation.

Table 3: Mean performances of best 10 Rice Hybrids for 9 quality parameters during *Kharif* 2016

S. No.	Characters Genotypes	Hulling %	Kernel Length (mm)	Kernel Width (mm)	L/B ratio	Kernel length after cooking (mm)	Kernel width after cooking (mm)	Elongation ratio	Gel consistency (mm)	Alkali spreading value	
											1
2	IHRT-E-9	78.00	6.72	2.39	2.81	8.02	2.90	1.20	37	High	
3	IHRT-E-12	69.33	7.28	1.89	3.85	8.46	2.44	1.09	68	Intermediate	
4	IHRT-E-13	70.00	7.25	2.23	3.25	8.25	2.67	1.12	52	High	
5	IHRT-E-17	66.00	6.53	2.53	2.58	8.10	3.17	1.24	36	High	
6	IHRT-E-23	70.67	6.81	2.11	3.23	8.19	2.60	1.20	85	Low	
7	IHRT-E-24	66.67	6.07	2.31	2.62	7.78	2.86	1.28	33	Intermediate	
8	IHRT-E-28	67.67	7.54	2.11	3.57	8.72	2.62	1.15	61	Low intermediate	
9	IHRT-E-30	65.67	6.01	1.84	3.16	7.84	2.34	1.30	55	Low	
10	IHRT-E-34	73.33	6.69	1.87	3.69	8.10	2.46	1.08	38	Intermediate	
	Mean	69.70	6.69	2.16	3.20	8.14	2.67	1.18	55.47		
	Range	Lowest	65.67	6.01	1.84	2.58	7.78	2.34	1.09	33	
		Highest	78.00	7.54	2.53	3.85	8.72	3.17	1.30	85	

Maximum genetic advance as percent of mean for spikelets per panicle (56.12), unfilled grain (51.72), grain yield (51.72), tillers per hill (45.74), panicles per hill (43.52), biological yield (34.67). The moderate genetic advance as a percent of mean was recorded for harvest index (25.36) followed by flag leaf width (27.75) and filled grains percentage (3.33) recorded low as low percentage. Thus it is interpreted that the characters viz., number of spikelets per panicle and plant height were controlled by additive gene action, which could be improved through simple selection methods. The characters showing high heritability with low genetic advance indicated the presence of non-additive gene action. Hence selection could be postponed for these characters or these characters could be improved by intermitting of superior genotypes of segregation population from recombination

breeding.

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