

## Heterosis for Yield, Protein Content and Quality Traits in Rice (*Oryza sativa L.*)

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### ABSTRACT

Heterosis for 28 cross combinations, evolved from 8 parents mating in diallel fashion were studied in three locations representing 3 agro-climatic zones of Telangana state to estimate standard heterosis for yield, its attributes, protein content and quality traits. The cross combinations viz., Suraksha × Jalanidhi, Suraksha × MTU1010, Suraksha × Swarna, Jalanidhi × Phalguna, Jalanidhi × Mahamaya, Jalanidhi × MTU1010, Phalguna × RP BIO226, Phalguna × Swarna, Mahamaya × RP BIO226, MTU1010 × BPT5204, RP BIO 226 × BPT5204, RP BIO 226 × Swarna were identified as most promising cross combinations for yield and quality characters based on *per se* performance and heterosis. Regarding

protein content, none of the cross combination showed significant heterosis in desirable direction, however, the crosses Mahamaya × Swarna (11.59%), Phalguna × Swarna (11.49%), Suraksha × Mahamaya (11.27%), Jalanidhi × MTU1010 (11.21%), Suraksha × Jalanidhi (11.18%), Phalguna × RP BIO226 (11.09%) had high Protein content among all cross combinations with optimum yield.

**Keywords** Rice, Standard heterosis, Cross combinations, Yield, Protein content.

### INTRODUCTION

The slogan ‘Rice is life’ aptly describes the importance of rice in food and nutritional security. Rice occupies the enviable prime place among the food crops cultivated around the world. In Asia, it has a very long history of cultivation and is deeply rooted in the daily lives of people (Narayanan *et al.* 2000). Cereals based food habits had created the situation of under nutrition and it is one of the ever increasing issues in the developing world most vulnerable to the protein deficiency.

Milled rice is the staple food of tropical Asia and it contributes 40 to 80% of the calories and 40% of the protein (Shobharani *et al.* 2006). Compared to other protein sources, rice protein is deficient in lysine, the sulfur containing amino acid and tryptophan, but the lysine content of rice protein (3.5 to 4.0%) is highest among cereal proteins. A positive correlation of tryptophan with lysine content ( $r = 0.076$ ) and a

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**Table 1.** Analysis of variance (Mean squares) for yield and its components, quality traits and protein in three different locations. I – Jagtial , II –Warangal, III –Hydeabad. \* Significant at 0.05 level of probability, \*\* Significant at 0.01 level of probability.

Source of variation	df	Location	Days to 50% flowering	Number of tillers per hill	Panicle length (cm)	Seed yield per plant (g)	1000 seed weight (g)	Protein content	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio
Replications	2	I	3.120	1.287	0.188	1.628	0.655	0.319	0.002	0.002	0.014
		II	10.065 *	0.583	1.820	3.418	1.086	0.335	0.061	0.005 *	0.007
		III	7.343	2.028 *	7.375 **	21.296 **	0.560	0.093	0.003	0.004	0.008
Genotypes	35	I	142.917 **	6.659 **	20.052 **	64.503 **	28.059 **	4.566**	0.806 **	0.071 **	0.219**
		II	159.085 **	7.895 **	12.563 **	48.851 **	25.889 **	3.438**	1.077 **	0.095 **	0.248**
		III	126.580 **	8.160 **	12.522 **	64.934 **	31.795 **	3.513**	0.859 **	0.082 **	0.236**
Error	70	I	2.301	0.630	1.326	3.794	1.534	1.009	0.031	0.002	0.011
		II	2.655	0.660	1.153	4.261	1.081	0.695	0.036	0.002	0.012
		III	2.428	0.504	1.024	3.825	1.271	0.876	0.028	0.002	0.011

strong negative correlation with total protein content ( $r = -0.923$ ) was recorded by Banerjee *et al.* (2011).

Environment affects the protein content of cereals and in rice, the grain protein accumulation of a variety exhibited a range of about 6% on dry weight basis (IRRI 1963). The average protein content of milled rice is relatively low (about 7% at 14% moisture) whereas brown or dehulled rice contains about 8% protein. Increasing the protein content of rice would mean an increased supply of protein in rice based diets. Improving protein content will have a significant social and economical impact worldwide, especially in the developing countries.

Enriching rice with protein either through conventional or marker assisted introgression holds a great promise for sustainable food based solutions (Graham *et al.* 2001). The primary objective of the present investigation was to estimate the heterosis for protein and yield and their subsequent utilization in the genetic enhancement of rice. Heterosis is useful to decide the direction of future breeding program and to identify the cross combinations which are promising in conventional breeding program.

## MATERIALS AND METHODS

The present investigation was carried out with 8 parents and 28 cross combinations developed in diallel fashion as per Griffing's Method II. The resulting 30

cross combinations were evaluated at three different locations viz., at ICAR-IIRR, Hyderabad (Southern Telangana agro-climatic zone), Regional Agricultural Research Station, Warangal (Central Telangana agro-climatic zone), Regional Agricultural Research Station, Jagtial (Northern Telangana agro-climatic zone) representing different agro-climatic zones of Telangana in Randomized Block Design (RBD) with three replications by adopting spacing of  $20 \times 15$  cm. Recommended package of practices and necessary prophylactic measures were adopted to raise a healthy crop. At flowering and maturity stages, observations were recorded on nine characters viz., Days to 50% flowering, number of productive tillers per plant, panicle length (cm), Seed yield per plant (g), 1000 grain weight (g), Protein content (%), Kernel length (mm), Kernel breadth (mm) and Kernel L/B ratio from five randomly selected plants in each entry in each replication. All the field observations were recorded according to minimal descriptor developed by Mahajan *et al.* (2000). Nitrogen content of rice was determined by Micro-kjeldahl distillation method (Piper 1966). Protein content was calculated by multiplying nitrogen content of seed with factor (Sadasivam and Manickam 1996).

$$\text{Protein content (\%)} = \text{Nitrogen content (\%)} \times 6.25 \\ (\text{Factor})$$

The analysis of variance for each character was found as per the standard statistical procedure to

**Table 2.** Standard heterosis for yield and its components, quality traits, protein in rice (*Oryza sativa L.*) at different locations and in pooled. I – Jagital, II – Warangal, III – Hyderabad, P – Pooled. \* Significant at 5% level, \*\*Significant at 1% level.

	Days to 50 % flowering			Number productive tillers hill <sup>1</sup>			Panicle length (cm)					
	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled
Suraksha× Jalanidhi	2.92 *	5.99 **	2.20 *	3.61 **	35.71 **	-15.79 **	-14.71 **	-1.00	30.57 **	18.44 **	27.42 **	25.18 **
Suraksha× Phalguna	-8.45 **	-12.62 **	-8.52 **	-9.77 **	-32.14 **	-44.74 **	-14.71 **	-31.00 **	-1.79	-2.21	-2.69	-2.22
Suraksha× Mahamaya	-19.53 **	-17.35 **	-18.68 **	-18.55 **	0.00	-13.16 *	8.82	-2.00	-5.85	-4.42	-12.37 **	-7.29
Suraksha× MTU1010	-9.33 **	-13.25 **	-9.34 **	-10.55 **	-32.14 **	-13.16 *	-26.47 **	-23.00 **	16.59 **	7.37	1.61	8.70 *
Suraksha× RPBIO 226	1.17	2.84 *	1.65	1.86	3.57	-23.68 **	-2.94		13.33 **	-3.10	-10.93 *	0.00
Suraksha× BPT 5204	-9.33 **	-7.89 **	-9.07 **	-8.79 **	-10.71	-10.53	-23.53 **	-15.00 **	27.97 **	11.65 **	12.37 **	17.29 **
Suraksha× Swarna	-11.37 **	-20.19 **	-12.09 **	-14.36 **	-17.86 *	-21.05 **	-17.65 **	-19.00 **	18.37 **	7.67	14.52 **	13.29 **
Jalanidhi× Phalguna	2.33 *	-12.93 **	-12.36 **	-7.62 **	-10.71	2.63	23.53 **	6.00	31.71 **	22.42 **	14.70 **	23.18 **
Jalanidhi× Mahamaya	-4.96 **	-9.46 **	-5.22 **	-6.45 **	-7.14	-15.79 **	-14.71 **	-13.00 *	8.13	8.47 *	-18.17 **	0.32**
Jalanidhi× MTU1010	-0.29	-3.15 *	1.37	-0.59	32.14 **	10.53	20.59 **	20.00 **	34.63 **	25.07 **	10.75 *	23.93 **
Jalanidhi× RPBIO 226	1.75	-1.26	-0.82	-0.10	21.43 **	0.00	5.88	8.00	16.13 **	1.03	-0.72	5.52
Jalanidhi× BPT 5204	-3.79 **	-9.78 **	-4.12 **	-5.76 **	14.29	-5.26	11.76 *	6.00	35.45 **	15.78 **	8.42	20.10 **
Jalanidhi× Swarna	-4.08 **	-15.77 **	-1.65	-6.84 **	-7.14	-28.95 **	-11.76 *	-17.00 **	19.77 **	1.18	-11.11 *	3.65
Phalguna× Mahamaya	-3.21 **	-3.47 **	-1.37	-2.64 *	-14.29	0.00	-8.82	-7.00	26.02 **	17.26 **	-0.54	14.80 **
Phalguna× MTU1010	-10.79 **	-20.19 **	-8.24 **	-12.79 **	-21.43 **	-31.58 **	11.76 *	-14.00 *	21.98 **	13.57 **	-5.02	10.76 *
Phalguna× RPBIO 226	-7.87 **	-10.09 **	-5.77 **	-7.81 **	0.00	-26.32 **	8.82	-7.00	-5.20	-0.74	6.99	0.11
Phalguna× BPT 5204	-4.96 **	-8.52 **	-3.85 **	-5.66 **	0.00	-5.26	26.47 **	7.00	27.97 **	24.93 **	8.60	21.02 **
Phalguna× Swarna	-6.41 **	-5.99 **	-3.30 **	-5.18 **	-7.14	-15.79 **	-17.65 **	-14.00 *	12.85 **	3.24	-5.02	3.94
Mahamaya× MTU1010	-13.99 **	-16.40 **	-11.54 **	-13.87 **	-3.57	-21.05 **	-23.53 **	-17.00 **	26.83 **	21.39 **	9.86 *	19.72 **
Mahamaya× RPBIO 226	-0.58	-11.67 **	-5.77 **	-5.86 **	0.00	-23.68 **	-2.94	-10.00	4.23	6.64	0.90	4.11
Mahamaya× BPT 5204	3.79 **	-1.26	-6.59 **	-1.46	10.71	-2.63	5.88	4.00	6.18	0.74	-17.03 **	-2.81
Mahamaya× Swarna	-9.04 **	-7.89 **	-7.97 **	-8.30 **	-10.71	5.26	-5.88	-3.00	15.45 **	2.06	2.33	6.59
MTU1010× RPBIO 226	-4.96	-13.56**	-11.81**	-10.06 **	25.00**	2.63	-8.82	5.00	8.94	9.14*	0.36	6.43
MTU1010× BPT 5204	-1.75	-1.26	-3.02 **	-2.05	14.29	-5.26	20.59 **	9.00	1.95	21.98 **	28.49 **	17.29 **
MTU1010× Swarna	-14.58 **	-19.87 **	-17.03 **	-17.09 **	-17.86 *	-2.63	-8.82		16.75 **	13.27 **	-5.38	8.81 *
RPBIO 226												
×BPT 5204	2.04	-1.26	-3.02 **	-0.78	3.57	5.26	-11.76 *	-1.00	13.01 **	4.90	5.91	7.90

**Table 2.** Continued.

	Days to 50 % flowering			Number productive tillers hill <sup>1</sup>						Panicle length (cm)		
	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled
RPBIO												
226×												
Swarna	-2.04	-10.41 **	-9.07 **	-7.13 **	10.71	0.00	2.94	4.00	17.89 **	0.44	9.32 *	8.91*
BPT												
5204×												
Swarna	3.50 **	-5.99 **	-7.14 **	-3.22 **	21.43 **	13.16 *	20.59 **	18.00 **	28.94 **	11.50 **	14.19 **	18.11 **

**Table 2.** Continued.

**Table 2.** Continued.

	Grain yield per plant (g)			Pooled	Test weight (g)			Pooled	JGL	Protein content (%)		
	JGL	WGL	HYD		JGL	WGL	HYD			WGL	HYD	Pooled
BPT 5204	10.24	29.38 **	-9.85	10.18	26.05 **	75.17 **	48.05 **	48.74 **	-8.08	-10.07	6.29	-4.28
Mahamaya <sup>x</sup>	-2.36	23.85 **	20.03*	13.75	12.97 *	34.59 **	18.18 **	21.35 **	2.50	-2.52	6.29	1.98
MTU1010 <sup>x</sup>												
RPBIO 226	-32.44 **	-23.70**	-6.57	-21.10 **	4.83	9.53	9.09	7.78	-15.86*	-23.53**	-0.94	-13.81*
MTU1010 <sup>x</sup>												
BPT 5204	11.50	48.03 **	32.35**	30.58 **	26.72 **	23.50 **	34.14 **	28.42 **	-15.30*	-26.52**	-5.97	-16.18*
MTU1010 <sup>x</sup>												
Swarna RPBIO 226 <sup>x</sup> BPT 5204	18.43 *	40.44 **	-13.14	15.61 *	9.82	27.49 **	23.19 **	19.95 **	-12.25	-31.82**	4.09	-13.77*
RPBIO 226 <sup>x</sup>												
Swarna BPT 5204 <sup>x</sup>	-2.36	41.67 **	37.60**	25.46 **	8.64	17.74 **	16.70 **	14.28 *	-11.41	-22.86**	-13.43	-15.90*
Swarna	-22.20 **	25.12 **	16.09	6.18	-0.20	45.45 **	-9.09	10.34	-13.91	-26.02**	-6.29	-15.62*

**Table 2.** Continued.

**Table 2.** Continued.

	Kernel length (mm)			Kernel breadth (mm)			Kernel L/B ratio					
	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled
MTU1010	23.09 **	19.27 **	25.43 **	22.57 **	16.40 **	16.01 **	8.35 **	13.50 **	6.44 *	-10.03 **	16.12 **	3.91
Phalgunax												
RPBIO 226	17.45 **	19.20 **	22.61 **	19.72 **	30.20 **	27.87 **	19.73 **	25.83 **	-9.22 **	-6.54 *	2.55	-4.59
Phalgunax												
BPT 5204	32.18 **	33.73 **	29.29 **	31.76 **	23.00 **	24.11 **	17.08 **	21.33 **	8.00 **	9.02 **	10.18 **	9.04 **
Phalgunax												
Swarna	24.88 **	10.40 **	22.95 **	19.38 **	33.80 **	33.60 **	26.57 **	31.25 **	-6.33 *	-17.14 **	-2.55	-8.81 **
Mahamaya												
MTU1010	25.48 **	11.20 **	24.88 **	20.48 **	30.80 **	31.82 **	28.08 **	30.20 **	-0.44	-15.56 **	-2.42	-6.20 *
Mahamaya												
RPBIO 226	3.12	10.20 **	24.60 **	12.49 **	11.40 **	7.11 **	3.61	7.31 **	-7.44 **	2.93	20.36 **	4.86
Mahamaya												
BPT 5204	2.32	4.53	-4.27	0.92	19.80 **	25.10 **	10.63 **	18.40 **	-14.33 **	-16.12 **	-13.21 **	-14.59 **
Mahamaya												
Swarna	-2.19	-5.80	-1.72	-3.25	27.00 **	21.94 **	20.49 **	23.09 **	-22.78 **	-22.44 **	-18.55 **	-21.32 **
MTU												
1010x												
RPBIO 226	19.58 **	17.47 **	19.99 **	19.00 **	10.80 **	15.22 **	8.35 **	11.42 **	8.22 **	2.48	10.79 **	7.08 *
MTU1010x												
BPT 5204	2.46	-1.60	-0.62	0.09	20.00 **	17.59 **	15.18 **	17.55 **	-14.78 **	-16.23 **	-13.33 **	-14.82 **
MTU												
1010x												
Swarna	10.55 **	8.73 **	15.51 **	11.55 **	4.80 *	2.57	1.52	2.94	5.67	6.09	14.30 **	8.54 **
RPBIO												
226x BPT												
5204	3.92	4.47	4.07	4.15	8.00 **	10.67 **	4.55 *	7.70 **	-3.22	-5.64	-0.73	-3.25
RPBIO												
226x Swarna	7.23 *	6.20	13.44 **	8.91 **	16.40 **	20.16 **	12.33 **	16.24 **	-7.22 *	-11.27 **	1.33	-5.90 *
BPT 5204x												
Swarna	8.29 **	5.40	10.82 **	8.14 **	26.60 **	29.64 **	20.87 **	25.64 **	-14.56 **	-18.60 **	-8.00 *	-13.86 **

determine the effects of the genotypes evaluated. Standard errors were computed to compare mean performances of the hybrids with popular checks. Standard heterosis was estimated by the method of Liang *et al.* (1971).

Standard heterosis was expressed as per cent increase or decrease observed in  $F_1$  over standard check as per the following formula

$$\text{Standard heterosis (\%)} = \frac{\bar{F}_1 - \text{Mean of superior check}}{\text{Mean of superior check}} \times 100$$

Standard heterosis against the best checks BPT 5204 for grain yield and Mahamaya for protein content.

## RESULTS AND DISCUSSION

The analysis of variance (ANOVA) of 36 genotypes (8 parents and 28 cross combinations) for protein content, yield, yield components and quality traits at 3 locations viz., Jagtial, Warangal and Hyderabad revealed the existence of significant differences among the genotypes studied for 9 characters (Table 1).

For days to 50% flowering, from the pooled analysis, all except seven hybrids recorded significant standard heterosis over standard check in desired direction (Table 2). Early maturing genotypes are desirable as they produce more yields per day and fit well in multiple cropping systems. Negative standard heterosis was observed by Tiwari *et al.* (2011).

Out of 28 cross combinations evaluated, fifteen

**Table 3.** Most promising cross combinations for protein content based on *per se* performance coupled with optimum grain yield per plant.

Cross combinations	Protein (%)	Grain yield (g)
Mahamaya×Swarna	11.59	20.67
Phalguna×Swarna	11.49	32.10
Suraksha×Mahamaya	11.27	22.50
Jalanidhi×MTU1010	11.21	22.10
Suraksha × Jalanidhi	11.18	34.10
Phalguna × RP BIO 226	11.09	25.60

hybrids exhibited significant positive standard heterosis over standard check BPT5204. Hybrids generally possess' very long panicle with more number of spikelets, which facilitates partitioning of assimilates into reproductive parts more efficiently. This is one of the important reasons for higher yields in hybrids. This trait directly contributes towards grain yield. Sharma *et al.* (2013), Singh *et al.* (2013) and Ravi *et al.* (2017) also observed highest significant heterosis for panicle length. Number of grains per panicle is the major yield attributing character; hence significant positive standard heterosis is desirable. Out of 28 cross combinations, two hybrids viz., Jalanidhi × MTU1010 and BPT 5204 × Swarna recorded significant positive standard heterosis over standard check. This trait directly contributes towards grain yields. Similar findings were also reported by Sharma *et al.* (2013) and Singh *et al.* (2013).

Test weight is considered as an important yield contributing character in rice, as higher yields are mostly associated with varieties having longer grains with good filling. Twenty five hybrids showed significantly greater standard heterosis over standard check BPT 5204 (Table 2). Sharma *et al.* (2013), Singh *et al.* (2013) and Ravi *et al.* (2017) also reported highly significant positive heterosis for test weight.

Heterosis for grain yield/plant in positive direction is desirable as higher grain yield is the main objective for almost all the breeding programs. In pooled analysis, seventeen hybrids registered significant positive standard heterosis (Table 2). The hybrid, Phalguna × Swarna exhibited the highest heterosis (62.07) followed by Suraksha × Jalanidhi (44.86%), Suraksha × MTU1010 (44.22%), RP-BIO226 × BPT5204 (38.52%), Phalguna × RP-

BIO226 (36.17%) and Jalanidhi × Phalguna (35.8%). Singh *et al.* (2013) and Shindae and Patel (2014) observed the similar results.

For some of the quality traits, negative heterotic value is considered to be desirable, while in others positive heterotic estimates are usually preferable. Kernel length before cooking is one of the important grain quality parameters and its higher value is perceived to be desirable. Higher as well as lower values of kernel length before cooking over standard check for different cross combinations were observed in the present study. In pooled analysis, for kernel length, twenty two hybrids showed significantly greater standard heterosis over standard check BPT5204 (Table 2). Earlier workers Krishna Veni *et al.* (2005) and Pratap *et al.* (2013) were also reported the similar results.

Lower value of kernel breadth before cooking ensures grain fineness. Thus, negative value of heterosis for kernel breadth before cooking would be desirable. None of the hybrids recorded significant negative standard heterosis. Kumar babu *et al.* (2010) reported varying levels of heterosis due to good interaction with environment like in the present case. Kernel length/breadth ratio before cooking is one of the important physical traits determining the quality of rice grain. A higher value of kernel length/breadth ratio before cooking is conceived as desirable. Four hybrids viz., Phalguna × Mahamaya, Phalguna × BPT 5204, MTU1010 × RPBI 226 and MTU1010 × Swarna showed significant standard heterosis for this trait over standard check (Table 2). These results are in agreement with earlier reports of Krishna Veni *et al.* (2005).

In pooled analysis, none of the hybrids exhibited significant positive standard heterosis over standard check Mahamaya for protein content (Table 2). However, the cross combinations viz., Mahamaya × Swarna, Phalguna × Swarna, Suraksha× Mahamaya, Jalanidhi × MTU1010, Suraksha × Jalanidhi and Phalguna × RPBI 226 were recorded high Protein content coupled with optimum yield among all cross combinations (Table 3).

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