



RESEARCH PAPER

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Genetic variability and heterosis among rice genotypes for yield and yield associated traits

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Key words: Rice, Genotypes, Genetic variability, Heterosis, Heritability

<http://dx.doi.org/10.12692/ijb/9.2.137-146>

Article published on August 31, 2016

Abstract

The present research was performed to assess genetic variability and heterosis among 30 rice genotypes for yield and yield associated traits. Sixteen F₁ hybrids and their 14 parents were planted in a randomized complete block design using two replications at The University of Agriculture Peshawar, during 2011 rice crop growing season. Highly significant differences among the parents and F₁ hybrids were observed for all the traits studied. The parental genotypes Bas-370, Pakhal and IR-8 displayed maximum values for panicle length (32.5 cm), primary branches panicle⁻¹ (15.1) and secondary branches panicle⁻¹ (47.0), respectively. Among the F₁ cross combinations, IR-8/Sugdesi manifested higher mean values for primary branches panicle⁻¹ (15.0) and secondary branches panicle⁻¹ (55.0) whereas Bas-6129/Bas-370 showed maximum value for panicle length (34.0cm). Moderate and low phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for most of the traits. High broad sense heritability values were observed for all the studied traits except primary branches panicle⁻¹. Bas-2008/Kashmir-Bas showed the highest positive values of mid and better parent heterosis for primary branches panicle⁻¹ (33.3 and 19.0%) while Bas-2008/Kashmir-Bas and Dokri-Bas/Bas-6129 for secondary branches panicle⁻¹ (44.2% and 30.6%), respectively. On the basis of superior performance for yield and yield associated traits, the parental genotypes IR-8 and Pakhal whereas the F₁ hybrids IR-8/Sugdesi and Bas-2008/Kashmir-Bas are recommended for onward use in rice hybridization programs.

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Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crops worldwide. More than half of the world's population, particularly in the developing countries depends on rice for calories and protein. Worldwide it is planted on 163 million hectares with production of 728.7 million tones (FAOSTAT, 2012). In Pakistan, it is planted on an area of 2.4 million hectares with production of 7.2 million tons. It accounts for 6.4 percent of value added in agriculture and 1.4 percent in GDP (MINFAL, 2009-10).

Heterosis has been exploited extensively and is one of the major achievements of crop breeding programs (Birchler *et al.*, 2003). Jones (1926) first noticed heterosis in rice and observed that some F₁ hybrids as compared to their parents showed excellence for culm number and yield. Heterosis for a trait could be both positive and negative while the desired value of heterosis is dependent on the nature of the particular trait. The positive heterosis in general is used for yield whereas heterosis in negative is desired for earliness (Nuruzzaman *et al.*, 2002). The exploitation of heterosis can enhance yield from 30 to 400% and can also enrich the domesticated crops with most important traits of qualitative and quantitative nature (Srivastava, 2000).

Improvement of yield and its component traits is the main focus of most crop breeding programs and their genetic improvement largely depends upon the presence of genetic variability; its nature and magnitude (Fisher, 1981). Information on the nature and magnitude of genetic variability for quantitatively inherited traits like yield and its components is very essential and is the first step towards the commencement of any judicious crop breeding programs (Babu *et al.*, 2012; Singh and Narayanam, 2006). The extent of variability in a population is measured by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) providing valuable information about the variability for different traits (Roychowdhury and Tah, 2011).

PCV values when higher than the respective GCV values for a particular trait depicts that major portion of total phenotypic variance is constituted by the environmental variance and differences of low magnitude are the indices of additive gene action (Sunday *et al.*, 2007, Karim *et al.*, 2007). In plant breeding, low heritability of quantitative traits such as yield is a major limiting factor in increasing the productivity of crops. Heritability indicates the extent of transmissibility of a trait from parents to off springs. Traits which are lesser influenced by the environment usually have a high heritability and indicates the scope of genetic improvement through selection (Bhadru *et al.*, 2012; Bisne *et al.*, 2009).

Therefore, the present study was undertaken to assess genetic variability, estimate heritability and study heterosis for yield and yield associated traits among F₁ hybrids of rice and their parents.

Materials and methods

In the present research 16 F₁ rice hybrids along with their 14 parents were studied at the Plant Breeding and Genetics Research Farm, The University of Agriculture Peshawar, during 2011 rice crop growing season. Randomized complete block design with two replications was used. Each rice genotype was planted in a two-row plot with row length of 3 m. Row - row and plant - plant distances of 30 and 15 cm were maintained, respectively. First, nursery was raised in the last week of May and then transplantation of seedlings into well puddled field was done during the last week of June. Data were recorded on 8 quantitative traits using ten randomly selected plants from each entry. Traits used in the study were flag leaf area, culm length, peduncle length, panicle length, days to 50% flowering, days to maturity, primary branches panicle⁻¹ and secondary branches panicle⁻¹, respectively.

Statistical Analysis

Data were subjected to analysis of variance (ANOVA) technique as outlined by Steel and Torrie (1980). Least Significant Difference (LSD) test was also used for means separation.

Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability and broad sense heritability were computed as per the method suggested by Singh and Chaudhary (1985).

$$V_g = [MSG - MSE / r]$$

$$V_p = V_g + V_e$$

$$V_e = MSE$$

Where,

MSG and MSE are mean squares of genotypes and error whereas r is number of replications, respectively.

$$PCV = [\sqrt{V_p} / X] \times 100$$

$$GCV = [\sqrt{V_g} / X] \times 100$$

Where,

V_p ; phenotypic variance, V_g ; genotypic variance and X ; grand mean. Values of PCV and GCV were classified by Burton (1952) as follows:

Low = Less than 10, Moderate = Less than 20 and High = More than 20. Heritability in broad sense (h^2B) was calculated as the ratio of the genotypic variance (V_g) to the total (phenotypic) variance (V_p) in percents. Heritability values were classified as low (less than 0.30); moderate (0.30 – 0.60) or high (greater than 0.60) (Johnson *et al.*, 1955).

Mid parent and better parent heterosis for each trait were determined by using the following formula (Sharma and Singh, 1978).

$$\text{Mid parent heterosis (\%)} = (F_1 - MP) / MP \times 100$$

$$\text{Better parent heterosis (\%)} = (F_1 - BP) / BP \times 100$$

Where

F_1 = Mean of hybrid

MP = Average mean of parents = (Parent 1 + Parent 2)/2

BP = Mean of better parent in the cross

For significance of the F_1 hybrid means t-test was used (Wynne *et al.*, 1970).

t value for mid parent heterosis

$$t = F_1 - MP / \sqrt{(3/8 \text{ EMS})}$$

t value for better parent heterosis

$$t = F_1 - BP / \sqrt{(1/2 \text{ EMS})}$$

Where,

F_1 = Mean value of F_1 hybrid in the cross

MP = Mean mid parent value ($P_1 + P_2/2$) of the respective cross

BP = Mean better parent value (P_1 or P_2) of the respective cross

EMS = Error mean square

Table 1. List of the genotypes used in the study.

Rice genotypes			
Parents		Hybrids	
1.	NIAB-IR-9	1.	NIAB-IR-9 × IR-8
2.	Dokri-Bas	2.	Dokri-Bas × DR-92
3.	Bas-2008	3.	Dokri-Bas × DR-83
4.	DR-92	4.	Dokri-Bas × Sugdesi
5.	Bas-6129	5.	Dokri-Bas × Pakhal
6.	IR-8	6.	Dokri-Bas × Bas-6129
7.	DR-83	7.	Bas-2008 × Kashmir-Bas
8.	Sugdesi	8.	Bas-2008 × TN-1
9.	Pakhal	9.	Bas-2008 × Dilrosh
10.	Kashmir-Bas	10.	DR-92 × Dokri-Bas
11.	TN-1	11.	DR-92 × DR-83
12.	Dilrosh	12.	Bas-6129 × Bas-370
13.	Bas-370	13.	Bas-6129 × Dokri-Bas
14.	Shahdab-31	14.	IR-8 × NIAB-IR-9
15.	IR-8 × Sugdesi	15.	IR-8 × Shahdab-31

Results and discussion

Genetic variability

Highly significant differences ($p \leq 0.01$) among the parents and F_1 hybrids were observed for all the studied traits viz., flag leaf area, culm length, peduncle length, panicle length, days to 50%

flowering, days to maturity, primary branches panicle⁻¹ and secondary branches panicle⁻¹ (Table 2). These results are compatible with the findings of Rahimi *et al.* (2010), Bagheri and Jelodar (2010), Soni and Sharma (2011), Subbaiah *et al.* (2011) and Ghosh and Sharma (2012).

Table 2. Mean square values for morphological traits of 30 rice genotypes.

Traits	Mean squares		
	Replications	Genotypes	Error
Flag leaf area	848.2	191.7**	37.1
Culm length	1.07	1277.4**	34.0
Peduncle length	0.16	73.0**	5.27
Panicle length	0.73	14.8**	3.45
Days to flowering	4.27	224.3**	1.3
Days to maturity	5.4	269.4**	1.47
Primary branches panicle ⁻¹	0.02	3.09**	0.88
Secondary branches panicle ⁻¹	68.3	111.5**	21.8
Degrees of freedom	1	29	29

** , * : Significant at 1 and 5% levels of probability, respectively.

Flag leaf area

Mean values of parents ranged from 30.3 to 60.7 cm². Minimum value was observed for the parent NIAB-IR-9 while maximum for Sugdesi. Among rice hybrids the values ranged between 35.8 (Dokri-Bas/DR-83) and 63.5 (Bas-2008/TN-1) cm² (Table 4). High PCV (23.0%), moderate GCV (18.9%) and high heritability (67.6%) was observed for this trait (Table 3).

Rahman *et al.* (2012) also reported similar results of high PCV, GCV and heritability for flag leaf area. Mid and better parent heterosis values varied from -24.2 to 49.0% and -33.3 to 18.4%. The hybrid IR-8/NIAB-IR-9 exhibited maximum mid parent heterosis (49.0%) whereas IR-8/NIAB-IR-9 and Bas-2008/TN-1 showed significant better parent (29.9% and 25.2%) heterosis (Table 5).

Saleem *et al.* (2008) also reported significant mid (60.13%) and better parent (42.99%) heterosis for flag leaf area.

Culm length

Mean values of parents varied from 67.0 (DR-83) to 134.7 (Bas-370) cm. F_1 hybrids showed a range of 71.7 and 151.5 cm. Minimum value was observed for the hybrid Dokri-Bas/DR-83 while maximum for Bas-2008/Kashmir-Bas (Table 4). High PCV, GCV and heritability with values of 24.7, 24.0% and 94.8% were observed (Table 3).

The findings of Nuruzzaman *et al.* (2002) and Yadav *et al.* (2010) are in line. Heterosis over mid parent ranged between -14.4 and 37.0%, whereas better parent heterosis values varied from -2.14 to 73.4%. The hybrid Dokri-Bas/Pakhal manifested significant negative mid parent heterosis (-14.4%) (Table 5).

Alam *et al.* (2004) also observed significant negative mid and better parent heterosis of values -77.03 and -86.82%, respectively for this trait.

Table 3. Phenotypic (Vp), genotypic (Vg) and environmental variances (Ve), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and broad sense heritability (h²bs) for different traits of 30 rice genotypes.

Traits	Vp	Vg	Ve	PCV	GCV	h ² bs
Flag leaf Area	114.3	77.2	37.1	23.0	18.9	67.6
Culm length	655.9	621.9	34.0	24.7	24.0	94.8
Peduncle length	39.1	33.9	5.23	16.1	15.0	86.6
Panicle length	9.13	5.67	3.46	10.8	8.53	62.1
Days to flowering	112.8	111.5	1.30	10.0	9.98	98.9
Days to maturity	135.4	134.0	1.47	8.32	8.28	98.9
Primary branches panicle ⁻¹	2.01	1.09	0.92	11.3	8.31	54.3
Secondary branches panicle ⁻¹	66.0	44.6	21.4	19.8	16.3	67.6

Table 4. Mean values for flag leaf area, culm length, peduncle length, panicle length and days to flowering of 30 rice genotypes.

Rice genotypes	Flag leaf area (cm ²)	Culm length (cm)	Peduncle length (cm)	Panicle length (cm)	Days to flowering	Days to maturity	Primary branches panicle ⁻¹	Secondary branches panicle ⁻¹
NIAB-IR-9/IR-8	46.6	83.3	35.9	27.3	116.5	151.5	13.5	39.8
Dokri-Bas/DR-92	36.4	82.3	38	26.7	98	131	11.5	39
Dokri-Bas/DR-83	35.8	71.7	32.2	22.9	99	132	12.7	50.6
Dokri-Bas/Sugdesi	55.1	117.5	44.4	28.8	96.5	129.5	12.2	45
Dokri-Bas/Pakhal	36.4	82.5	40.8	30.2	91.5	124.5	11.3	42.6
Dokri-Bas/ Bas-6129	57	105.4	31.16	27.7	132	168	11.4	52.5
Bas-2008/Kashmir-Bas	57.6	151.5	43.4	28.8	100	133.5	13.8	45.2
Bas-2008/TN-1	63.5	130.7	40.5	26.2	100.5	134	13.1	40.9
Bas-2008/Dilrosh	53.4	139.6	46	30.2	96	129	13.2	45.5
DR-92/Dokri-Bas	39.9	85.8	40.8	27.7	96	129	12	48.1
DR-92/DR-83	36.3	85.5	39	28.4	96	129	11.7	47.6
Bas-6129/Bas-370	42.8	132.3	50.6	34	112.5	147.5	12.4	42.5
Bas-6129/Dokri-Bas	51.8	130.5	46.1	31.9	106	140	12	47.1
IR-8/NIAB-IR-9	60.8	89.1	36.4	27.8	118	153	14.3	49.1
IR-8/ Sugdesi	55.7	132.8	40.4	33.5	122.5	158.5	14.6	54.8
IR-8/Shadab-31	48.9	88.6	37.9	28.9	115	150	13.2	42.8
NIAB-IR-9	30.3	87.1	33.9	25.4	111.5	146.5	12.7	34.5
Dokri-Bas	41.4	75.2	32.6	24.8	104.5	138.5	12.3	40.2
Bas-2008	54.2	133.2	44.8	25.9	97.5	130.5	11.6	42.3
DR-92	38.8	87.5	33.1	26.7	103.5	137.5	11.9	37.2
Bas-6129	55.5	134	45.2	28.7	108	142	12.6	39.1
IR-8	51.4	85.1	32.3	26.9	111.5	146.5	13.4	47.2
DR-83	36.8	67	32.4	22.7	106	140	12	35.3
Sugdesi	60.7	108.8	28.9	28.5	128	164	11.2	36.6
Pakhal	54.5	117.6	43.6	27.7	95	128	15.1	32.1
Kashmir-Bas	34.5	130.3	48.2	28.5	93.5	126.5	9.1	20.4
TN-1	47.2	79.8	32.4	24.4	97.5	130.5	13.4	32.6
Dilrosh	38.1	87	37.8	27.8	97.5	130.5	14.5	32.2
Bas-370	38.3	134.7	46.3	32.5	115.5	150.5	12.5	32.9
Shahdab-31	33.1	78.3	30.8	26.2	108.5	142.5	11.4	33.6
LSD _(0.05)	12.5	11.9	4.69	3.8	2.33	2.48	1.92	2.55

Table 5. Mid parent and better parent heterosis for flag leaf area, culm length, peduncle length and panicle length among F₁ hybrids of rice.

F ₁ hybrid combinations	Flag leaf area		Culm length		Peduncle length		Panicle length	
	Mid parent heterosis (%)	Better parent heterosis (%)	Mid parent heterosis (%)	Better parent heterosis (%)	Mid parent heterosis (%)	Better parent heterosis (%)	Mid parent heterosis (%)	Better parent heterosis (%)
NIAB-IR-9/IR-8	14.2	-9.28	-3.28	-2.14	8.62	6.02	4.43	1.49
Dokri-Bas/DR-92	-9.19	-12.1	1.16	9.4	15.7**	14.9**	3.51	-0.15
Dokri-Bas/DR-83	-8.62	-13.7	0.83	7.05	-0.89	-1.2	-3.6	-7.74
Dokri-Bas/Sugdesi	7.85	-9.23	27.7**	56.2**	44.6**	36.4**	8.2	1.23
Dokri-Bas/Pakhal	-24.2**	-33.3**	-14.4**	9.69	7.17	-6.4	15.2**	9.29
Dokri-Bas/Bas-6129	17.7*	2.81	0.73	40.1**	-19.9**	-31.1**	3.51	-3.52
Bas-2008/Kashmir-Bas	29.9**	6.29	15.0**	16.3**	-6.74*	-10.0**	5.88	0.95
Bas-2008/TN-1	25.2**	17.2*	22.7**	63.7**	4.89	-9.67*	4.06	1.12
Bas-2008/Dilrosh	15.7	-1.47	26.8**	60.5**	11.5**	2.79	12.4**	8.65
DR-92/Dokri-Bas	-0.4	-3.61	5.48	14.1*	24.4**	23.5**	7.55	3.74
DR-92/DR-83	-3.95	-6.36	10.7*	27.7**	19.3**	18.0**	15.1**	6.48
Bas-6129/Bas-370	-8.79	-22.9**	-1.57	-1.31	10.6**	9.41*	11.1**	4.69
Bas-6129/Dokri-Bas	6.87	-6.66	24.7**	73.4**	18.4**	1.86	19.3**	11.2*
IR-8/NIAB-IR-9	49.0**	18.4*	3.42	4.64	9.95*	7.32	6.38	3.38
IR-8/Sugdesi	-0.62	-8.24	37.0**	56.1**	32.2**	25.3**	21.0**	17.7**
IR-8/Shadab-31	15.8	-4.86	8.46	13.2*	20.2**	17.5**	8.56	7.13

** , * : Significant at 1% and 5% levels of probability, respectively.

Peduncle length

Parental genotypes and F₁ rice hybrids displayed a range of 28.9 (Sugdesi) to 48.2 (Kashmir-Bas) cm and 31.2 (Dokri-Bas/Bas-6129) and 50.6 (Bas-6129/Bas-370) cm (50.6 cm) (Table 4). The studied genotypes displayed moderate PCV (16.10%) and GCV (14.98%) whereas high heritability of value 86.6% (Table 3). Mean values of mid and better parent heterosis ranged between -19.9 to 44.6% and -31.1 to 36.4%. Ten F₁ hybrids exhibited significant positive mid parent heterosis with maximum value of 44.6% (Dokri-Bas/Sugdesi). The F₁ hybrids Dokri-Bas/ Sugdesi (36.4%), IR-8/Sugdesi (25.3%) and DR-92/Dokri-Bas (23.5%) depicted significant positive better parent heterosis for peduncle length (Table 5). These results are in line with the findings of Shahid *et al.* (2012).

Panicle length

Among the parents and F₁ hybrids, panicle length ranged from 22.7 (DR-83) to 32.5 (Bas-370) cm and 22.9 (Dokri-Bas/DR-83) and 34.0 (Bas-6129/Bas-370) cm (Table 4). The studied genotypes showed moderate PCV (10.8%), low GCV (8.53%) and high (62.1%) heritability (Table 3). Bhadru *et al.* (2012) also showed similar results of moderate PCV, low GCV and high heritability.

Mid and better parent heterosis values among hybrids varied from -3.60 to 21.0% and -7.74 to 17.7%. Six F₁ hybrids manifested significant positive mid parent heterosis in which IR-8/Sugdesi, Bas-6129/Dokri-Bas and Dokri-Bas/Pak-hal showed values of 21.0, 19.3 and 15.2%. Only two F₁ hybrids, IR-8/Sugdesi (17.7%) and Bas-6129/Dokri-Bas (11.2%) manifested significant positive better parent heterosis (Table 5). The findings of Bagheri and Jelodar (2010) and El-Rewainy *et al.* (2011) further strengthen our results.

Days to flowering

Among the parents, the values varied between 93.5 (Kashmir-Bas) and 128 (Sugdesi) days whereas among the rice hybrids mean data ranged between 91.5 and 132 days. The hybrid Dokri-Bas/Pakhal took minimum while Dokri-Bas/Bas-6129 maximum days to flowering (Table 4). Moderate PCV (10.0%), low GCV (9.98%) and high heritability (98.9%) was observed for this trait (Table 3). Sravan *et al.* (2012) also reported moderate PCV and GCV whereas high heritability. Among the hybrids, seven F₁ cross combinations depicted significant negative mid parent heterosis with highest negative values of -17.0% (Dokri-Bas/Sugdesi) and -8.27% (Dokri-Bas/Pakhal).

Significant negative better parent heterosis was observed for six cross combinations with maximum values of -7.66% (Dokri-Bas/Sugdesi), -7.25% (DR-92/Dokri-Bas) and -7.25% (DR-92/DR-83) for this trait (Table 6). Bagheri and Jelodar (2010) and Shahid *et al.* (2012) also reported significant negative mid and better parent heterosis for days to flowering.

Days to maturity

The mean values of parents ranged between 126.5 (Kashmir-Bas) and 164 (Sugdesi) days. The F₁ rice hybrids showed a range of mean values between 124.5 (Dokri-Bas/Pakhal) and 168 (Dokri-Bas/Bas-6129) days (Table 4).

The study showed low PCV (8.32%), GCV (8.28%) and high (98.9%) heritability (Table 3). Fukrei *et al.* (2011) and Ovung *et al.* (2012) supported our results. Mid parent heterosis values ranged between -14.4 and 19.8% whereas better parent heterosis values varied from -6.5 and 21.3%. Significant negative mid and better parent heterosis was observed for six cross combinations in which maximum values were observed for F₁ hybrids Dokri-Bas/Sugdesi (-14.4 and -6.50%), DR-92/DR-83 (-7.03 and -6.52%) and DR-92/Dokri-Bas (-6.18% and -6.18%) (Table 6). Similar results were also reported by Nuruzzaman *et al.* (2002) and Islam *et al.* (2010).

Table 6. Mid parent and better parent heterosis for days to flowering, days to maturity, primary branches panicle⁻¹ and secondary branches panicle⁻¹ among F₁ hybrids of rice.

F ₁ hybrid combinations	Days to flowering		Days to maturity		Primary branches panicle ⁻¹		Secondary branches panicle ⁻¹	
	Mid parent heterosis (%)	Better parent heterosis (%)	Mid parent heterosis (%)	Better parent heterosis (%)	Mid parent heterosis (%)	Better parent heterosis (%)	Mid parent heterosis (%)	Better parent heterosis (%)
NIAB-IR-9/IR-8	4.48**	4.48**	3.41**	3.41**	3.45	0.75	-2.57	-15.7**
Dokri-Bas/DR-92	-5.77**	-5.31**	-5.07**	-4.73**	-4.96	-6.5	0.78	-2.99
Dokri-Bas/DR-83	-5.94**	-5.26**	-5.21**	-4.69**	4.53	3.25	34.0**	25.9**
Dokri-Bas/Sugdesi	-17.0**	-7.66**	-14.4**	-6.50**	3.83	-0.81	17.2*	11.94
Dokri-Bas/Pakhal	-8.27**	-3.68**	-6.57**	-2.73**	-17.5**	-25.2**	17.8**	5.97
Dokri-Bas/Bas-6129	24.2**	26.3**	19.8**	21.3**	-8.43	-9.52	32.4**	30.6**
Bas-2008/Kashmir-Bas	4.71**	6.95**	3.89**	5.53**	33.3**	19.0**	44.2**	6.86
Bas-2008/TN-1	3.08**	3.08**	2.68**	2.68**	4.8	-2.24	9.2	-3.31
Bas-2008/Dilrosh	-1.54*	-1.54	-1.15	-1.15	1.15	-8.97	22.2**	7.57
DR-92/Dokri-Bas	-7.69**	-7.25**	-6.52**	-6.18**	-0.83	-2.44	24.3**	19.7*
DR-92/DR-83	-8.35**	-7.25**	-7.03**	-6.18**	-2.09	-2.5	31.3**	28.0**
Bas-6129/Bas-370	0.67	4.17**	0.85	3.87**	-1.2	-1.59	18.1*	8.7
Bas-6129/Dokri-Bas	-0.24	1.44	-0.18	1.08	-3.61	-4.76	18.8*	17.2*
IR-8/NIAB-IR-9	5.83**	5.83**	4.44**	4.44**	9.58*	6.72	20.2**	4.03
IR-8/Sugdesi	2.3**	9.87**	2.09**	8.19**	18.7**	8.96	30.8**	16.1*
IR-8/Shadab-31	4.55**	5.99**	3.81**	5.26**	6.45	-1.49	5.94	-9.32

** , * : Significant at 1% and 5% levels of probability, respectively.

Primary branches panicle⁻¹

Mean values among the parents and F₁ hybrids varied from 9.1 (Kashmir-Bas) to 15.1 (Pakhal) and 11.3 (Dokri-Bas/Pakhal) to 14.6 (IR-8/Sugdesi) (Table 4). Moderate PCV (11.3%), heritability (54.3%) and low GCV (8.31%) were observed for primary branches panicle⁻¹ (Table 3). Sanghera *et al.* (2013) also reported moderate PCV, low GCV and moderate heritability for this trait. Three F₁ hybrids Bas-2008/Kashmir-Bas (33.3%), IR-8/Sugdesi (18.7%) and IR-8/NIAB-IR-9 (9.58%) displayed significant

positive mid parent heterosis. F₁ cross combination Bas-2008/Kashmir-Bas manifested significant positive better parent heterosis (19.0%) (Table 6). Islam *et al.* (2010) also reported significant positive mid (60.0%) and better parent heterosis (50.0%) for primary branches panicle⁻¹.

Secondary branches panicle⁻¹

Among the parental genotypes, the values ranged from 20.4 to 47.2. Minimum value was recorded for Kashmir-Bas while IR-8 showed maximum value.

Among the hybrids, the trait values varied from 39.0 (Dokri-Bas/DR-92) to 54.8 (IR-8/Sugdesi) (Table 4). The studied genotypes showed moderate PCV (19.8%) and GCV (16.3%) while high (67.6%) heritability (Table 3). Chakravorty *et al.* (2012) supported the present findings by observing high heritability for this trait. Heterosis over mid parent varied between -2.57 and 44.2% and better parent heterosis ranged from -15.7 and 30.6%. Twelve F₁ hybrids displayed significant positive mid parent heterosis with highest values observed for Bas-2008/Kashmir-Bas (44.2%), Dokri-Bas/DR-83 (34.0%) and Dokri-Bas/Bas-6129 (32.4%). Six F₁ crosses displayed significant positive better parent heterosis. Maximum value (30.6%) was observed for Dokri-Bas/Bas-6129 followed by DR-92/DR-83 (28.0%) and Dokri-Bas/DR-83 (25.9%) (Table 6). Islam *et al.* (2010) also observed similar results of significant positive mid and better parent heterosis.

Conclusions

Significant differences among the parents and F₁ hybrids were observed for all the studied traits. The parental genotypes Bas-370, Pakhal and IR-8 displayed maximum values for panicle length, primary branches panicle⁻¹ and secondary branches panicle⁻¹, respectively. Among the F₁ cross combinations, IR-8/Sugdesi manifested the highest values for primary branches panicle⁻¹ and secondary branches panicle⁻¹ whereas Bas-6129/Bas-370 showed maximum value for panicle length. Moderate PCV and GCV values were observed for secondary branches panicle⁻¹ whereas moderate PCV and low GCV values were recorded for primary branched panicle⁻¹ and panicle length. High broad sense heritability values were observed for all of the studied traits except primary branches panicle⁻¹. Bas-2008/Kashmir-Bas showed highest positive values of mid and better parent heterosis for primary branches panicle⁻¹ and mid parent heterosis for secondary branches panicle⁻¹ while Dokri-Bas/Bas-6129 observed maximum positive value of better parent heterosis for secondary branches panicle⁻¹.

The parental genotypes IR-8 and Pakhal whereas the F₁ hybrids IR-8/Sugdesi and Bas-2008/Kashmir-Bas performed excellent for most of the yield and yield associated traits and could be used onward in rice yield improvement programs.

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