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GENETIC VARIABILITY FOR MORPHOLOGICAL PARAMETERS IN F_2 SEGREGATING POPULATIONS OF RICE

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Abstract

This study was conducted to evaluate genetic variation among four parents and their 12 F_2 populations for various morphological attributes at The University of Agriculture, Peshawar during 2012 rice crop growing season. Significant variation among the genotypes was manifested for all the traits studied. F_2 population Kashmir-Basmati/Kangni-27 manifested minimum days to heading (100) while the F_2 population Dilrosh/Kashmir-Basmati took minimum days to maturity (135). F_2 population Kashmir-Basmati /Dilrosh had the longest panicles (29.5 cm) while F_2 population Dilrosh/ Kashmir-Basmati excelled for number of primary (12.4) and secondary (35.9) branches panicle^{-1}. Maximum broad sense heritability for panicle length (0.85), number of primary branches (0.87) and secondary branches (0.93) panicle^{-1} was observed for F_2 populations Kashmir-Basmati/Dilrosh, Dilrosh/Kangni-27 and Kashmir-Basmati/TN-1, respectively. F_2 population Kashmir-Basmati /Dilrosh showed the highest genetic advance for panicle length (22%). F_2 population Dilrosh/Kangni-27 manifested maximum genetic advance (34.7%) for primary branches panicle^{-1} while TN-1/ Kashmir-Basmati revealed the highest value (48.8%) of genetic advance for secondary branches panicle^{-1}. The above mentioned segregating populations on account of better performance for maturity and panicle traits could be advanced further to develop desirable recombinant inbred lines and rice cultivars.

Key words: Rice; F_2 populations; Genetic variation; Broad sense heritability; Genetic advance, Maturity traits, Panicle traits.

Introduction

Rice (*Oryza sativa* L.) is the world's most important food crop. It serves as the staple food for more than half of the globe's population (Khan *et al*., 2013). Worldwide, it is grown on an area of 166.1 million hectares with yield of 745.2 million tones (Anon., 2013). Rice is the second leading cereal crop of Pakistan after wheat with 2.3 million hectares area planted and 5.5 million tones production (Anon., 2014). In the Punjab and Sindh provinces, world's famous Basmati rice is grown while in the Khyber Pakhtunkhwa province northern regions cool tolerant rice cultivars and landraces are planted. Long grain IRRI type heat stress tolerant rice cultivars are planted in the southern areas of Khyber Pakhtunkhwa and the province of Balochistan (Salim *et al.*, 2003; Shah *et al*., 2011).

The existence of genetic variability for various desirable maturity and yield related traits in segregating generations is of utmost importance in crop breeding programs to develop desirable recombinant inbred lines and cultivars (Shinwari *et al*., 2013). Heritability (h^2) estimates for the desired traits takes into account the extent of transmission of the traits from the parents to progeny and serve as a analytical role in crop breeding programs (Khan & Naqvi, 2011). Heritability values are valuable resources for assessing the response of the desired traits to selection in segregating generations. Genetic advance is an estimate of the expected genetic progress of the selected genotypes for various traits over their parental populations and is influenced by the extent of amount of genetic variation, heritability and selection intensity (Allard, 1960). Relatively high heritability and genetic advance estimates for the desired traits helps in advancing the potential segregating generations to develop desirable recombinant inbred lines and commercial cultivars (Pervaiz *et al*., 2010). The present study was, therefore, carried out to figure out the genetic variability, heritability and genetic advance for the desired maturity and panicle traits in rice F_2 segregating populations and to identify the better performing F_2 populations for advancement in rice breeding programs.

Materials and Methods

Four parents and their 12 F_2 populations (developed in our own rice breeding program) were grown in a randomized complete block design using three replications in a field experiment at the Plant Breeding and Genetics Research Farm, The University of Agriculture Peshawar, during 2012 rice crop growing season. Parental and F_2 populations used the study have been presented in Table 1. Each rice genotype was planted in a two rows plot with row length was 1.5 m. Row to row and plant to plant distances of 30 and 15 cm were kept, respectively. It is worth mentioning that during the1st week of June, nursery was grown and seedlings of each genotype were transplanted into a highly puddled field in the first week of July. Data were recorded on flag leaf area, days to heading, culm length, days to maturity, panicle length, primary branches panicle^{-1} and secondary branches panicle^{-1} using ten randomly selected plants of each genotype in each replication.

Statistical analysis: Data were analyzed using analysis of variance (ANOVA) technique as proposed by Singh & Chaudhary (1985). For means separation and comparison, least significant difference test was used. Broad sense heritability was estimated for each F_2 population separately using the formula (Mahmud & Kramer, 1951):

$$h^2 = \frac{V_{F2} - \sqrt{V_{P1} \times V_{P2}}}{V_{F2}}$$

where, V_{F2} = Variance of F_2 population variance for a trait; V_{P1} and V_{P2} = Parental variances of a particular F_2 population. Expected genetic advance in each cross combination for the studied traits was estimated as GA = K x $\sqrt{\sigma^2_P}$ x h^2 (Panse & Sukhatme, 1965); where GA = Genetic advance, K = 1.76 (10% selection intensity), h^2 = Heritability coefficient and $\sqrt{\sigma^2_P}$ = Phenotypic standard deviation. Genetic advance was given as percent of mean using the formula:

GA % = GA/$\bar{x}$ x100 where $\bar{x}$ is mean of a particular F_2 population for a trait

Results

Days to 50% heading: Overall, highly significant ($p<0.01$) differences among the rice genotypes were manifested for days to heading. Significant ($p<0.05$) differences among the parents and also among the F_2 populations were observed for this trait. However, differences between parents vs F_2 populations were observed as non-significant ($p>0.05$) (Table 2). Among the parents, Kashmir-Basmati took the least number of days to heading (100). The value for this trait among the F_2 populations ranged from 100 to 105. F_2 population Kashmir-Basmati/Kangni-27 took the least number of days (100) while F_2 populations Dilrosh/ Kashmir-Basmati and TN-1/ Kashmir-Basmati showed maximum number of days (105) to heading (Table 3). Parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 showed variances of 1.7, 0.83, 1.8 and 0.83, respectively. Among the F_2 populations, the lowest variance (2.6) was observed for F_2 population TN-1/Dilrosh while the highest variance (6.1) was observed for F_2 population Kashmir-Basmati/TN-1. F_2 population Dilrosh/Kashmir-Basmati showed maximum broad sense heritability (0.78) whereas F_2 population TN-1/Dilrosh revealed minimum heritability (0.33). The highest genetic advance (3.2%) was observed for F_2 population Kashmir-Basmati/TN-1while the lowest genetic advance (0.9%) was observed for F_2 population TN-1/Dilrosh (Table 4).

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

Rice genotypes	
Parents	**F_2 Populations**
1. Dilrosh	1.Dilrosh/ Kashmir-Basmati
2. Kashmir-Basmati	2. Dilrosh/Kangni -27
3. TN-1	3. Kashmir-Basmati/TN-1
4. Kangni-27	4. Kangani -27/TN-1
	5. TN-1/Kashmir-Basmati
	6. Kangni-27/ Kashmir-Basmati
	7. Kashmir-Basmati / Kangni -27
	8. Kangni-27/Dilrosh
	9. TN-1/Dilrosh
	10. Dilrosh/TN-1
	11. Kashmir-Basmati /Dilrosh
	12. TN-1/Kangni-27

Flag leaf area: Mean squares displayed non-significant ($p>0.05$) differences among the rice genotypes for flag leaf area. Similarly, parents and parent vs F_2 populations revealed non-significant ($p>0.05$) differences for this trait. F_2 populations, however, manifested significant ($p<0.05$) differences for flag leaf area (Table 2). Kashmir-Basmati, among the parents, showed maximum flag leaf area (31.2 cm^2). Among the F_2 populations, F_2 population Kangni-27/Kashmir-Bas displayed the highest value (39.1cm^2) while F_2 population TN-1/Dilrosh had the lowest value (24.5 cm^2) for flag leaf area (Table 3). The parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 showed variances of 20.8, 19.6, 16.0 and 9.4, respectively. Among the F_2 populations, F_2 population Dilrosh/TN-1 had minimum variance (49.5) while F_2 population Dilrosh/Kashmir-Basmati manifested the highest variance (175.4) for this trait. F_2 population Dilrosh/KANGNI-27 displayed maximum broad sense heritability (0.85) while F_2 population Kashmir-Basmati/TN-1 had minimum (0.44) broad sense heritability for flag leaf area. Maximum genetic advance (57%) for the trait was observed for F_2 population of Kangni-27/TN-1 whereas minimum genetic advance (19.9%) was manifested for F_2 population Dilrosh/TN-1 (Table 4).

Culm length: Significant ($p<0.05$) differences among the rice genotypes were observed for culm length. F_2 populations revealed highly significant ($p<0.01$) differences whereas parents and parents vs F_2 populations had non-significant ($p>0.05$) differences for this trait (Table 2). Among the parents, Dilrosh showed the lowest value (90.0 cm) for culm length while Kangni-27 manifested the highest value (113.4 cm) for this trait. Among the F_2 populations, F_2 population Kashmir-Basmati/TN-1 displayed the minimum culm length (71.97 cm) while F_2 population Dilrosh/Kashmir-Basmati had maximum culm length (105.6 cm) (Table 3). Variances of 9.4, 11.9, 12.7 and 9.9 were observed for parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27, respectively. F_2 population Kashmir-Basmati/Dilrosh, among the F_2 populations, showed minimum variance (69.4) while F_2 populations TN-1/Kangni-27 manifested maximum variance (215.6). The highest broad sense heritability (0.96) was observed for F_2 population TN-1/Kangni-27 while the lowest (0.71) value was observed for F_2 population Dilrosh/Kangni-27. The highest value (29.3%) of genetic advance was revealed for F_2 population Dilrosh/TN-1 while the lowest value (11.6%) of genetic advance was observed for F_2 population Kashmir-Bas/TN-1 (Table 4).

Days to maturity: Rice genotypes displayed significant ($p<0.05$) differences for days to maturity. Significant ($p<0.05$) differences among the F_2 populations were observed for this trait while non-significant ($p>0.05$) differences were observed for parents and parent vs F_2 populations (Table 2). Among the F_2 populations, minimum days to maturity (134) were observed for F_2 population Dilrosh/Kashmir-Basmati while maximum days to maturity (140) were manifested for F_2 population Kashmir-Basmati/Dilrosh (Table 3). Parental genotypes Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 showed variances of 3.7, 3.9, 2.2 and 4.0, respectively. Among the F_2 populations, the lowest variance (9.7) was observed for F_2 populationTN-1/Kashmir-Basmati while the highest variance (22.1) was revealed for F_2 population TN-1/Dilrosh. F_2 population TN-1/Dilrosh displayed maximum broad sense heritability (0.83) while F_2 population Kashmir-Basmati/Kangni-27 revealed minimum heritability (0.53) for this trait. F_2 population TN-1/Dilrosh showed highest genetic advance (5.1 %) whereas F_2 populations Kashmir-Bas/Kangni-27 had minimum genetic advance (2.2 %) (Table 4).

Panicle length: Highly significant ($p<0.01$) differences among the rice genotypes were revealed for panicle length. F_2 populations manifested significant ($p<0.05$) differences while parental genotypes showed non-significant differences ($p>0.05$) for this trait. Highly significant ($p<0.01$) differences were observed among Parents vs F_2 populations for panicle length (Table 2). Among the parental genotypes, Dilrosh produced longest panicles (26.5 cm) while among the F_2 populations, Kashmir-Basmati/Dilrosh manifested the longest (29.5 cm) panicle. F_2 population TN-1/Dilrosh, however, displayed minimum panicle length (23.9 cm) among the studied F_2 populations (Table 3). Variances of 4.6, 2.2, 1.9 and 3.3 were observed for parental genotypes Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 showed, respectively. Among the F_2 populations, TN-1/Dilrosh had minimum variance (5.7) while Kashmir-Basmati/Dilrosh revealed maximum variance (19.2). The highest broad sense heritability (0.85) was manifested for F_2 population Kashmir-Basmati/Dilrosh whereas F_2 population TN-1/Kangni-27showed minimum (0.47) heritability. Maximum genetic advance (22%) was observed for F_2 population Kashmir-Basmati/Dilrosh whereas minimum genetic advance (8.6%) was revealed for F_2 population TN-1/Dilrosh (Table 4).

Table 2. Mean squares for various morphological traits of rice genotypes evaluated at the University of Agriculture, Peshawar during 2012.

Traits	Replications (df=2)	Genotypes (df=15)	Parents (P) (df=3)	F_2 populations (F_2) (df=11)	P vs F_2 (df=1)	Error
Days to heading	10.6	11.0**	14.5*	10.6*	5.1	3.84
Flag leaf area	14.2	65.4	0.60	88.3*	8.0	38.8
Culm length	62.7	301.5*	18.8	405.2*	9.0	138.0
Days to maturity	2.8	9.2*	3.5	11.4*	3.0	4.6
Panicle length	7.4	8.6*	3.3	8.5*	25.8**	3.3
Primary branches panicle^{-1}	0.65	1.8*	0.16	2.0**	4.0*	0.73
Secondary branches panicle^{-1}	27.7	49.3*	5.9	63.6*	21.6	24.3

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

Table 3. Means values for various morphological traits of rice genotypes evaluated at the University of Agriculture, Peshawar during 2012.

Genotypes	Days to heading	Flag leaf area (cm^2)	Culm length (cm)	Days to maturity	Panicle length (cm)	Primary branches panicle^{-1}	Secondary branches panicle^{-1}
				Parents			
Dilrosh	105	30.8	91.0	136	26.5	10.3	30.2
Kashmir-Basmati	100	31.2	94.8	137	24.1	10.0	27.4
TN-1	102	30.2	90.2	136	24.9	10.5	28.0
Kangni-27	104	30.9	95.0	137	24.6	10.3	29.9
Parental means	**103**	**30.8**	**92.8**	**136**	**25.4**	**10.3**	**28.9**
				F_2 Populations			
Dilrosh/ Kashmir-Basmati	105	37.0	97.5	134	28.0	12.4	35.9
Dilrosh/Kangni-27	101	33.7	97.4	138	26.8	9.8	25.3
Kashmir-Basmati /TN-1	104	26.0	71.2	135	27.5	11.9	34.8
Kangni-27/TN-1	101	25.1	74.1	138	25.3	10.9	34.7
TN-1/ Kashmir-Basmati	105	26.6	101.5	139	27.7	10.3	25.4
Kangni-27/ Kashmir-Basmati	104	39.1	100.9	134	24.0	10.0	25.1
Kashmir-Basmati / Kangni-27	100	37.2	85.9	137	27.2	11.1	33.7
Kangni-27/Dilrosh	103	33.7	97.1	138	27.9	9.7	26.6
TN-1/Dilrosh	100	24.5	76.8	134	23.9	10.9	24.6
Dilrosh/TN-1	102	34.6	94.7	138	25.6	11.6	35.0
Kashmir-Basmati /Dilrosh	101	27.0	100.4	140	29.5	11.3	31.3
TN-1/Kangni-27	100	36.0	103.5	137	26.9	11.0	32.6
F_2 Population means	102	31.7	91.7	137	26.7	10.9	30.4
Genotypes means	102	31.5	92	137	26.3	10.8	30
$LSD_{(0.05)}$ parents	2.1	8	12.5	2.5	3.6	1.4	8.7
$LSD_{(0.05)}$ F_2 populations	3.4	11.5	22.5	3.8	3.2	1.3	8.1
$LSD_{(0.05)}$ genotypes	3.3	10.4	19.5	3.6	3.02	1.43	1.6

Table 4. Variance (V), heritability (h^2) and genetic advance as percent of mean (GA) for various morphological traits of rice genotypes evaluated at the University of Agriculture, Peshawar during 2012.

Genotypes	Days to heading			Flag leaf area			Culm length			Days to maturity			Panicle length			Primary branches panicle^{-1}			Secondary branches panicle^{-1}		
	V	h^2	GA	V	h^2	GA	V	h^2	GA	V	h^2	GA	V	h^2	GA	V	h^2	GA	V	h^2	GA
										Parents											
Dilrosh	1.7			20.8			9.4			3.7			4.6			0.57			9.3		
Kashmir-Basmati	0.8			19.6			11.9			3.9			2.2			0.53			5.9		
TN-1	1.8			16.0			12.7			2.2			1.9			1.27			4.9		
Kangni-27	2.8			9.4			12.7			4.0			3.3			0.57			14.5		
										F_2 Populations											
Dilrosh/ Kashmir-Basmati	5.1	0.78	3.0	175.0	0.83	52.2	142.0	0.87	27.5	16.4	0.62	3.3	11.0	0.64	13.2	4.5	0.86	25.8	73.4	0.69	29.0
Dilrosh/Kangni-27	5.7	0.63	2.6	90.6	0.85	42.1	81.4	0.71	18.7	14.8	0.67	3.3	10.6	0.69	14.6	5.1	0.87	34.7	50.0	0.84	41.1
Kashmir-Basmati/TN-1	6.1	0.77	3.2	63.2	0.44	23.5	73.0	0.83	11.6	14.7	0.82	4.1	11.7	0.79	17.1	2.9	0.51	12.6	64.6	0.93	37.6
Kangni-27/TN-1	5.0	0.54	2.1	96.4	0.83	57.0	86.0	0.81	17.6	13.2	0.80	3.7	6.2	0.67	11.5	3.2	0.73	21.1	54.0	0.69	25.6
TN-1/Kashmir-Basmati	5.0	0.76	2.9	58.9	0.71	36.1	91.3	0.84	17.8	9.7	0.59	2.3	5.7	0.59	9.0	3.5	0.77	24.3	59.8	0.91	48.8
Kangni-27/Kashmir-Basmati	5.8	0.73	3.0	110.0	0.84	39.6	83.1	0.90	13.9	13.8	0.71	3.4	8.9	0.50	10.8	4.6	0.84	32.0	33.9	0.77	31.5
Kashmir-Basmati/Kangni-27	5.2	0.66	2.6	88.6	0.80	35.5	140.0	0.93	14.3	10.6	0.53	2.2	19.9	0.67	18.4	2.0	0.69	15.3	83.1	0.86	40.9
Kangni-27/Dilrosh	4.4	0.51	1.8	59.0	0.56	22.5	141.0	0.94	22.6	12.4	0.73	3.3	7.7	0.55	9.7	3.0	0.8	24.7	59.9	0.74	38.0
TN-1/Dilrosh	2.6	0.33	0.9	54.8	0.66	35.1	194.0	0.92	20.2	22.1	0.83	5.1	5.7	0.49	8.8	4.3	0.79	26.6	51.1	0.76	39.0
Dilrosh/TN-1	4.5	0.61	2.3	49.5	0.56	19.9	84.2	0.87	29.3	16.1	0.75	3.8	8.6	0.72	14.5	2.5	0.70	16.4	53.4	0.89	32.6
Kashmir-Basmati/Dilrosh	4.4	0.75	2.8	83.8	0.62	37.0	69.4	0.81	14.8	16.9	0.77	4.0	19.2	0.85	22.0	4.6	0.87	29.2	77.6	0.91	45.0
TN-1/Kangni-27	3.3	0.34	1.1	94.0	0.58	27.5	216	0.96	11.9	10.7	0.57	2.4	7.7	0.47	8.6	3.9	0.77	24.5	69.4	0.89	39.9

Primary branches panicle^{-1}: The rice genotypes displayed significant ($p<0.05$) differences for primary branches panicle^{-1}. Highly significant ($p<0.01$) differences were revealed among the F_2 populations while non-significant ($p>0.05$) differences among the parents were observed for this trait. Parents vs F_2 populations showed significant ($p<0.05$) differences for primary branches panicle^{-1} (Table 2). Among the F_2 populations, Dilrosh/Kashmir-Basmati showed the highest number (12.4) of primary branches panicle^{-1} (Table 3). Parental genotypes Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 showed variances of 0.57, 0.53, 1.3 and 0.57, respectively. The highest variance (5.1), among the F_2 populations, was observed for F_2 population Dilrosh/Kangni-27 while the lowest variance (2.0) was revealed for F_2 population Kashmir Basmati/Kangni-27. F_2 population Dilrosh/Kangni-27 had maximum broad sense heritability (0.87) whereas F_2 population Kashmir-Basmati/TN-1 showed the lowest broad sense heritability (0.51) for primary branches panicle^{-1}. Maximum genetic advance (34.7%) for this trait was observed for F_2 population Dilrosh/Kangni-27 while minimum genetic advance (12.6%) was manifested for F_2 population Kashmir-Basmati/TN-1 (Table 4).

Secondary branches panicle^{-1}: The rice genotypes displayed significant ($p<0.05$) differences for secondary branches panicle^{-1}. Significant ($p<0.05$) differences among the F_2 populations were observed while non-significant differences ($p>0.05$) were manifested for parents and parents vs F_2 populations (Table 4). Among the parental genotypes, Dilrosh showed the highest number of secondary branches panicle^{-1} (30.2) while among the F_2 populations, Dilrosh/Kashmir-Basmati displayed the highest number of secondary branches panicle^{-1} (35.9) (Table 3). Variances of 9.1, 5.9, 4.9 and 14.5 were observed for parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27, respectively. Among the F_2 populations, F_2 population Kangni-27/Kashmir-Basmati displayed maximum variance (83.1) while F_2 population of Kashmir-Basmati/Kangni-27 had minimum variance (33.9). F_2 population Kashmir-Basmati/TN-1showed the highest broad sense heritability (0.93) for secondary branches panicle^{-1} whereas F_2 populations Kangni-27/TN-1 and Dilrosh/Kashmir-Basmati displayed the lowest heritability (0.69) for this trait. Maximum genetic advance (48.8 %) was observed for F_2 population TN-1/Kashmir-Basmati while minimum genetic advance (25.6 %) was manifested for F_2 population Kangni-27/TN-1 (Table 4).

Discussion

Early heading is usually considered as one of the desirable attributes as it is usually positively associated with early maturity and at the same time grain filling duration is enhanced in the genotypes displaying early flowering. Enhanced grain filling duration in turn increases the grain weight (Sattar, 2010). The rice genotypes used in the study manifested highly significant ($p<0.01$) differences for days to heading which is compatible with the results of Khan *et al.* (2009). Khan *et al.* (2009) also observed significant differences for this trait in a study consisting of four rice parental genotypes and their respective three F_2 populations. However, non-significant genetic differences among the rice genotypes for flag leaf area as observed in the present study are different from the findings of Khan *et al.* (2009) which could be due to differences in the germplasm used in the both the studies. Some of the studied F_2 populations showed relatively high heritability estimates of >0.70 for days to heading and flag area. These results are also supported by the findings of Khan *et al*. (2009) who also observed high heritability values of >0.70 for these traits.

Significant genetic variation among the rice genotypes used in the study for culm length is in agreement with the findings of Padmaja *et al.* (2008); Rabbani *et al*. (2010) and Bharadwaj *et al.* (2007). Padjama *et al.* (2008) evaluated rice germplasm comprising 150 genotypes for various quantitative characteristics and observed significant differences among the studied genotypes for culm length along with other studied characteristics. Bharadwaj *et al.* (2007) assessed F_2 progenies of the three crosses along with respective parents for various traits. They also reported genetic variation for this trait in their studied germplasm. In the present study, we observed high heritability values of >0.80 for all the studied F_2 populations with the exception of Kangni-27/Dilrosh which also showed high heritability of 0.71. Nandeshwar *et al.* (2010) studied 25 F_2 populations derived from crosses of 25 parents. They observed high heritability value of 0.94 for culm length.

Significant genetic differences among the rice genotypes for days to maturity as observed in the present is compatible with results of Bharadwaj *et al.* (2008). They also observed sufficient genetic variation in their studied F_2 populations and their respective parents for days to maturity. Most of the studied F_2 populations displayed relatively high heritability estimates for days to maturity. Akhtar *et al.* (2011) studied four parental genotypes along with their three F_2 populations and reported high heritability estimate of 92.5for this trait.

Panicle length serves as an important selection for rice breeders to develop rice cultivars with high grain yield as longer panicles could support high number of spikelets and grains. We observed significant genetic variation for this trait among the F_2 segregating populations. Bharadwaj *et al.* (2007) also reported significant genetic differences among parental and their respective derived F_2 populations of rice for this panicle length. F_2 population Kashmir-Bas/Dilrosh displayed high heritability (0.85). These results are in line with the findings of Nandeshwar *et al.* (2010). They also reported high heritability value (0.80) for panicle length in a study comprising 25 parents and 25 F_2 populations of rice.

Significant genetic differences among the rice genotypes were displayed for primary branches and secondary branches panicle^{-1}. These results are in line with the findings of Karim *et al.* (2007) and Parikh *et al.* (2011). Karim *et al.* (2007) observed significant differences for primary branches panicle^{-1} in a study comprising 41 rice genotypes whereas Parikh *et al.* (2011) reported significant variation for secondary branches panicle^{-1}using 24 rice genotypes.

Overall, high values of variances were observed for F_2 populations when compared with variances of parental populations for all the studied traits. This shows the presence of sufficient genetic variability in the segregating populations for the development of the desirable genotypes.

Conclusions

High magnitude genetic variation was observed among the parents and F_2 populations for yield and yield related traits. Minimum days to heading were observed for F_2 population Kashmir-Bas/Kangni-27 while minimum days to maturity were exhibited by the F_2 population Dilrosh/Kashmir-Basmati. F_2 population Kashmir-Basmati/Dilrosh displayed maximum panicle length while the highest number of primary and secondary branches panicle^{-1} was observed for F_2 population Dilrosh/Kashmir-Basmati. Maximum broad sense heritability for panicle length, primary and secondary branches panicle^{-1} was observed for F_2 populations Kashmir-Bas/Dilrosh, Dilrosh/Kangni-27 and Kashmir-Basmati/TN-1, respectively. F_2 population Kashmir-Bas/Dilrosh showed the highest genetic advance for panicle length while F_2 population Dilrosh/Kangni-27 displayed maximum genetic advance for primary branches panicle^{-1}. For secondary branches panicle^{-1}, F_2 population TN-1/Kashmir-Basmati manifested the highest genetic advance. On account of superior performance for maturity and panicle related traits, the segregating F_2 populations of Kashmir-Basmati / Kangni-27, Dilrosh/Kashmir-Basmati, Kashmir-Basmati/Dilrosh, Dilrosh/Kangni-27, Kashmir-Basmati/TN-1 and TN-1/Kashmir-Basmati are recommended for further advancement to develop recombinant inbred lines and commercial rice cultivars.

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