RESEARCH PAPER

Heritability and genetic advance for yield and yield related attributes in F2 rice populations

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Abstract

This study was performed to assess genetic variation, heritability and genetic advance for yield and yield associated traits using sixteen rice genotypes. Four parents and their 12 F$_2$ populations were grown in a randomized completed block design using three replications at Peshawar-Pakistan during 2012 rice crop growing season. The analyses of variance showed significant differences among the genotypes for all the studied traits. F$_2$ populations Kashmir-Basmati/TN-1 and Kangni-27/TN-showed maximum 100-grain weight (2.9 g) while F$_2$ population Dilrosh/TN-1 produced the highest grain yield plant^{-1} (38.3 g). The highest heritability for 100-grain weight (0.82) was observed for F$_2$ population Kangni-27/TN-1 whereas F$_2$ population Dilrosh/Kashmir-Basmati displayed maximum heitability for grain yield (0.95). F$_2$ populations Dilrosh/Kashmir-Basmati and Kashmir-Basmati/Kangni-27 displayed the highest genetic advance values for 100-grain weight (50.5%) and grain yield (82%), respectively. On the basis of superior performance for yield traits, F$_2$ populations Dilrosh/TN-1, Kashmir-Basmati/TN-1, Kangni-27/TN-1, Dilrosh/Kashmir-Basmati and Kashmir-Basmati/Kangni-27 could be advanced further to develop desirable rice recombinant inbred lines and cultivars.

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Introduction

Rice is considered as the world's most important cereal crop and serves as the staple food of more than half of the world's population. Rice grows well in warm and humid conditions and is grown extensively in tropical and sub-tropical regions of the world. Rice is also an important food crop of Pakistan and is grown under different climatic and soil conditions. The presence of genetic variation in the segregating populations for yield and its associated traits is highly important for identification of desirable genotypes and selecting the desirable forms of crop plants in crop breeding programs (Rahman *et al.,* 2015). Genetic variation for the desired traits in the segregating generations is helpful in the commencement of effective crop improvement programs (Babu *et al.,* 2012).

Heritability separates the available variation for a particular trait into genetic and non-genetic components and takes into consideration the heritable component of variation. The heritability (h^2) estimates for yield and yield associated traits are necessary for determining their response to selection in segregating generations. It is an index of transmissibility of the characters from the parents to offspring and has a predictive role in crop breeding programs (Khan and Naqvi, 2011). The traits lesser influenced by the environment usually have a high heritability (Bhadru *et al.,* 2012) and vice versa. The high heritability for a particular trait facilitates direct selection, while indirect selection is an effective approach for improving traits with low heritability. Genetic advance is an important selection index for estimating genetic improvement of the selected genotypes for various traits over the parental populations. The genetic advance for various traits of interest depends on magnitude of genetic variation, heritability and selection intensity (Allard, 1960). High heritability coupled with high genetic advance is an indicator of additive gene action and favors the selection of desirable genotypes. Traits with low genetic advance reveal the presence of non-additive gene action in controlling their expression.

The present study was, therefore, focused on heritability and genetic advance among the F_2 segregating populations of rice for various yield and yield associated traits and to identify the desirable F_2 populations for onward use in rice breeding program.

Materials and methods

This research was conducted at the Plant Breeding and Genetics Research Farm, The University of Agriculture Peshawar, during 2012 rice crop growing season. Twelve F_2 populations and their four parents were planted in a randomized complete block design using three replications.

The list of genotypes used in the study is given in Table 1. Each rice genotype was planted in a two-row plot with row length of 1.5 m. Row-row and plant-plant distances of 30 and 15 cm were maintained, respectively. Nursery was planted in the 1st week of June while transplantation of seedlings into well-puddled field was done during the first week of July. Ten randomly selected plants were used to collect data on number of spikelets panicle^{-1}, 100-grain weight, biological yield, grain yield and harvest index.

Statistical analysis

Data were analyzed using analysis of variance (ANOVA) technique as outlined by Singh and Chaudhary (1985). Least Significant Difference (LSD) test was also used for means separation and comparison. Broad sense heritability was determined for each trait from parental and F_2 populations of each cross combination using the formula as suggested by Mahmud and Kramer (1951):

$h^2 = \frac{V_{F2} - \sqrt{V_{P1} \times V_{P2}}}{V_{F2}}$ where V_{F2} = Variance of F_2 population for a trait, V_{P1} and V_{P2} = Variances of parent 1 and parent 2 of each F_2 population. Expected genetic advance was also computed using the following formula proposed by Panse and Sukhatme (1965)**:** GA = K x $\sqrt{\sigma^2_P}$ x h^2 where GA = Genetic advance; K = 1.76 at 10 % selection intensity**;** h^2 = Heritability coefficient and $\sqrt{\sigma^2_P}$ = Phenotypic standard deviation. Genetic advance expressed as percent of the mean was computed as GA % = GA/$\bar{x}$ x100 where $\bar{x}$ is mean of a specific F_2 population.

Table 1. List of the studied genotypes.

	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. Kangni-27/TN-1	
	5. TN-1/Kashmir-Basmati	
	6. Kangni-27/Kashmir-Basmati	
	7. Kashmir-Basmati/K-27	
	8. Kangni-27/Dilrosh	
	9. TN-1/Dilrosh	
	10. Dilrosh/TN-1	
	11. Kashmir-Basmati/Dilrosh	
	12. TN-1/ Kangni-27	

Results

Spikelets panicle^{-1}

Mean squares showed significant (p<0.05) differences among the rice genotypes for spikelets panicle^{-1}. F$_2$ populations displayed significant (p<0.05) differences while parents and parent vs F$_2$ populations manifested non-significant (p>0.05) differences for this trait (Table 2). Among the parents, mean data for spikelets panicle^{-1} ranged from 106.3 to 130.5. Kangni-27 produced the lowest number of spikelets panicle^{-1} (106.3) while TN-1 gave the highest number of spikelets panicle^{-1} (130.5).

Spikelets panicle^{-1} among the F$_2$ populations varied from 103.2 to 145.5. F$_2$ population TN-1/Kashmir-Basmati showed minimum spikelets panicle^{-1} (103.2) while F$_2$ population Kashmir-Basmati/TN-1 revealed maximum spikelets panicle^{-1} (145.5) (Table 3).

Parental populations Dilrosh, Kashmir-Basmati, TN-1 and K-27 displayed variances of 37.7, 51.2, 46.3 and 63.5, respectively. Variances among the F$_2$ populations for spikelets panicle^{-1} ranged from 551 to 2030.5. F$_2$ populations Dilrosh/Kangni-27 showed maximum variance (2030.5) while F$_2$ population Kangni-27/Kashmir-Basmati revealed minimum variance (551).

Overall, all the studied F$_2$ populations showed high broad sense heritability values (>0.94) for this trait. F$_2$ population Kangni-27/Dilrosh showed the highest genetic advance (64.1%) while F$_2$ population Kangni-27/Kashmir-Basmati displayed the lowest genetic advance (37.6%) for spikelets panicle^{-1} (Table 4).

Hundred-grain weight

Highly significant (p<0.01) differences among the rice genotypes were observed for 100-grain weight. Parents, F$_2$ populations and parent vs F$_2$ populations also showed significant (p<0.05) differences for this trait (Table 2). Among the parents, mean data for 100-grain weight ranged from 1.9 to 2.6 g. Kashmir-Basmati showed the lowest (1.9 g) 100-grain weight while Kangni-27 displayed the highest value (2.6 g) for 100-grain weight. Hundred-grain weight among the F$_2$ populations ranged from 2.1 to 2.9 g. F$_2$ population TN-1/ Kashmir- Basmati revealed minimum (2.1 g) while F$_2$ population Kashmir-Basmati/TN-1 and Kangni-27/TN-1 showed maximum (2.9 g) 100-grain weight (Table 3).

Variances for parental population Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 were observed as 0.08, 0.25, 0.02 and 0.07, respectively. Among the F$_2$ populations, variances for this trait ranged from 0.08 to 0.39. F$_2$ populations Dilrosh/Kashmir-Basmati and Dilrosh/Kangni-27 displayed the highest variances (0.39) while F$_2$ population Kashmir-Basmati/TN-1 showed the lowest variance (0.08).

Heritability values among the F$_2$ populations for 100-grain weight varied from 0.47 to 0.82. Maximum broad sense heritability (0.82) was observed for F$_2$ population Kangni-27 /TN-1 whereas minimum heritability (0.47) was manifested for F$_2$ population Kashmir-Basmati/TN-1. Maximum genetic advance (50.5%) was observed for F$_2$ population Dilrosh/K-27 whereas minimum genetic advance (4%) was observed for F$_2$ population Kashmir-Basmati/TN-1 (Table 4).

Biological yield plant[-1]

Mean squares revealed highly significant (p<0.01) differences among the rice genotypes for biological yield plant[-1]. F_2 populations showed significant (p<0.05) differences while parents and parents vs F_2 populations displayed non-significant (p>0.05) differences for this trait (Table 2).

Among the parents, mean values for biological yield plant[-1] ranged from 87. 1 to 125.3 g. Kangni-27 displayed minimum (87.1 g) while Dilrosh produced maximum (125.3 g) biological yield plant[-1].

The value of this trait among the F_2 populations ranged from 72.4 to 124.5 g. F_2 population Kashmir-Basmati/Kangni-27 produced the lowest (72.4 g) while Dilrosh/Kashmir-Basmati had the highest (124.5 g) biological yield (Table 3).

Parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 showed variances of 50.9, 27.1, 34.7 and 38.0, respectively. Variances among the F_2 populations for biological yield ranged from 241.7 to 434.9. F_2 population Kangni-27/TN-1 displayed minimum (241.7) variance while F_2 population Kashmir-Basmati/ Kangni-27 revealed maximum variance (434.9) for this trait.

Heritability values among the F_2 populations varied from 0.51 to 0.93. Maximum broad sense heritability (0.93) for the trait was observed for F_2 population Kashmir-Basmati/ Kangni-27 whereas minimum (0.51) was observed for F_2 population Kashmir- Basmati/ Dilrosh. The highest genetic advance (47.1%) was observed for F_2 population Kashmir-Basmati/K-27 whereas minimum (13.4 g) was observed for F_2 population Kashmir-Basmati/Dilrosh (Table 4).

Grain yield plant[-1]

The analysis of variance showed highly significant (p<0.01) differences among the rice genotypes for grain yield plant[-1]. F_2 populations and parents vs F_2 populations displayed highly significant (p<0.01) differences while parental populations showed significant (p<0.05) differences for this trait (Table 2).

Among the parents, mean data regarding grain yield plant[-1] ranged from 15.8 to 27.4 g. Kashmir-Basmati produced minimum (15.8 g) while Dilrosh showed maximum (27.4 g) grain yield plant[-1].

Grain yield plant[-1] among the F_2 populations ranged from 17.7 to 38.3 g. F_2 population TN-1/Kashmir-Basmati and Kangni-27/Dilrosh had the lowest (17.7 g) grain yield plant[-1] while F_2 population Dilrosh/TN-1 gave the highest (38.3 g) grain yield plant[-1] followed by Kangni-27/TN-1 with grain yield plant[-1] of 37.3 g (Table 3). Variances for parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 were manifested as 11.8, 4.1, 10.9 and 12.4, respectively.

Among the F_2 populations, variances for grain yield plant[-1] varied between 45.3 and 137.4. F_2 population Dilrosh/K-27 showed the lowest variance while F_2 population K-27/TN-1 displayed the highest variance. Heritability values among the F_2 populations varied from 0.62 to 0.95. F_2 population Kashmir-Basmati/Dilrosh showed maximum (0.95) broad sense heritability while F_2 population Dilrosh/K-27 displayed minimum (0.62) broad sense heritability. F_2 population Kashmir-Basmati/K-27 showed maximum genetic advance (82 %) while F_2 population K-27/Kashmir-Basmati displayed minimum (10.5 g) genetic advance (Table 4).

Harvest index

Highly significant (p<0.01) differences among the rice genotypes were observed for harvest index. F_2 populations and parents vs F_2 populations showed highly significant (p<0.01) differences while parents revealed non-significant (p>0.05) differences for this trait (Table 2). Mean data of parental genotypes varied from 16.6 to 24.7%.

Kashmir-Basmati displayed the lowest harvest index (16.6%) while Kangni-27 displayed the highest value (24.7%) for harvest index. The value of this trait among the F_2 populations ranged from 18.8 to 41.8%. F_2 population TN-1/Kashmir-Basmati revealed minimum (18.8%) harvest index while F_2 population TN-1/Kangni-27 had maximum (41.8%) harvest index (Table 3).

Parental populations Dilrosh, Kashmir-Basmati, TN-1 and Kangni-27 displayed variances of 4.9, 6.8, 9.5 and 29.3, respectively. Among the F_2 populations, variances for this trait ranged from 67.2 to 231.5. F_2 population Dilrosh/Kashmir-Basmati showed minimum variance while F_2 population Kashmir-Basmati/Kangni-27 displayed maximum variance. Heritability values among the F_2 populations ranged from 0.77 to 0.97.

The highest broad sense heritability (0.97) was observed for F_2 population TN-1/Dilrosh whereas the lowest (0.77) was observed for F_2 population Dilrosh/Kangni-27. The highest genetic advance (138.9%) was observed for F_2 population Kangni-27/Kashmir-Basmati while the lowest genetic advance (13.2%) was revealed for F_2 population TN-1/Kangni-27 (Table 4).

Table 2. Mean squares for various yield and yield related traits of rice genotypes at Peshawar during 2012.

Traits	Replications (df=2)	Genotypes (df=15)	Parents (df=3)	F_2 Populations (df=11)	P vs F_2 (df=1)	Error
Spikelets panicle^{-1}	181.0	678.8*	486.8	731.2*	678.6	337.6
100-grain weight	0.68	0.23**	0.26*	0.20*	0.46*	0.08
Biological yield plant^{-1}	2178.2	736.2**	832.1*	729.2*	526.7	242.1
Grain yield plant^{-1}	8.3	198.7**	67.3*	204.3**	531.7**	97.0
Harvest index	343.2	183.6**	34.7	166.2**	822.3**	92.2

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

Table 3. Means for yield and yield related traits of rice genotypes at Peshawar during 2012.

Genotypes	Spikelets panicle^{-1}	100-grain weight (g)	Biological yield plant^{-1} (g)	Grain yield plant^{-1} (g)	Harvest index (%)
			Parents		
Dilrosh	126.8	2.2	125.3	27.4	21.9
Kashmir-Basmati	107.2	1.9	95.3	15.8	16.6
TN-1	130.5	2.3	107.9	21.7	20.1
Kangni-27	106.3	2.6	87.1	21.5	24.7
Parental Means	117.7	2.3	103.9	21.6	20.8
			F_2 Populations		
Dilrosh/Kashmir-Basmati	137.3	2.5	124.5	32.7	26.3
Dilrosh/Kangni-27	132.6	2.7	80.7	18.9	23.4
Kashmir-Basmati/TN-1	145.5	2.9	100.5	35.0	34.8
Kangni-27/TN-1	140.2	2.9	101.3	37.3	36.3
TN-1/Kashmir-Basmati	103.2	2.1	93.9	17.7	18.8
Kangni-27/Kashmir-Basmati	106.6	2.7	101.3	35.4	34.9
Kashmir-Basmati/ Kangni-27	129.3	2.4	72.4	19.5	26.9
Kangni-27/Dilrosh	105.8	2.4	85.1	17.7	20.9
TN-1/Dilrosh	108.6	2.3	122.2	33.4	27.3
Dilrosh/TN-1	139.5	2.6	98.0	38.3	39.1
Kashmir-Basmati/Dilrosh	131.5	2.2	91.6	30.9	33.7
TN-1/ Kangni-27	136.2	2.3	83.0	34.7	41.8
F_2 Population Means	126.4	2.5	96.2	29.3	30.4
Genotypes Means	124.2	2.4	98.1	27.4	28.0
LSD (0.05) Parents	30.4	1.0	5.0	10.8	9.3
LSD (0.05) F_2 populations	33.2	0.4	27.3	17.3	6.7
LSD (0.05) Genotypes	30.6	0.5	30.8	16.4	7.7

Table 4. Variance (V), heritability (h²) and genetic advance as percent of mean (GA) for yield and yield related traits at Peshawar during 2012.

Genotypes	Spikelets panicle^{-1}			100-grain weight			Biological yield plant^{-1}			Grain yield plant^{-1}			Harvest index		
	V	h²	GA	V	h²	GA	V	h²	GA	V	h²	GA	V	h²	GA
Parents															
Dilrosh	21.2			0.80			50.9			11.8			4.9		
Kashmir-Basmati	18.0			0.14			27.1			4.1			6.8		
TN-1	8.7			0.02			34.7			10.9			9.5		
Kangni-27	14.1			0.07			38.0			12.4			29.3		
F₂ populations															
Dilrosh/Kashmir-Basmati	1632	0.99	51.3	0.89	0.76	50.5	353.0	0.65	17.3	114.6	0.95	54.7	67.2	0.93	51.0
Dilrosh/Kangni-27	2030	0.94	56.2	0.59	0.73	36.6	292.9	0.84	31.4	45.3	0.62	38.9	105.1	0.77	59.4
Kashmir-Basmati /TN-1	1063	0.99	39.0	0.07	0.25	4.0	301.8	0.90	27.4	107.1	0.93	48.4	131.7	0.94	54.6
K-27/TN-1	1996	0.96	53.8	0.25	0.82	24.9	241.7	0.83	22.4	137.4	0.94	52.0	109.9	0.87	44.2
TN-1/Kashmir-Basmati	973	0.99	52.7	0.13	0.65	19.6	387.2	0.90	33.2	59.7	0.73	56.1	207.9	0.94	126.9
Kangni-27/ Kashmir-Basmati	551	0.97	37.6	0.13	0.45	10.6	316.0	0.73	22.5	49.0	0.88	30.6	1128.8	0.82	138.9
Kashmir-Basmati /Kangni-27	1114	0.98	44.5	0.28	0.74	28.7	434.9	0.93	47.1	99.7	0.91	82.0	231.5	0.94	93.6
Kangni-27/Dilrosh	1548	0.98	64.1	0.35	0.59	25.6	433.1	0.91	39.2	70.7	0.74	61.9	118.0	0.9	82.3
TN-1/Dilrosh	956	0.99	49.6	0.24	0.80	30.0	370.5	0.79	21.9	111.7	0.88	49.0	164.4	0.97	80.2
Dilrosh/TN-1	1142	0.99	42.2	0.1	0.50	10.7	343.2	0.82	27.3	113.3	0.88	43.0	97.6	0.95	42.2
Kashmir-Basmati /Dilrosh	1226	0.99	46.4	0.21	0.53	19.4	323.2	0.51	17.6	96.7	0.81	45.4	118.1	0.96	54.5
TN-1/Kangni-27	1198	0.99	44.3	0.19	0.81	27.0	321.2	0.91	34.6	94.0	0.67	32.9	145.2	0.81	41.1

Discussion

Significant differences observed among the parents and F₂ populations in the present study for spikelets panicle^{-1} and 100-grain weight is in line with the findings of Ali *et al.* (2000). They studied four parents and their respective 10 F₂ populations and reported significant differences among the studied genotypes for these traits.

We observed high heritability values of >0.90 for spikelets panicle^{-1} for the different F₂ populations while Ali *et al.* (2000) observed heritability value of 0.65 for this trait.

The reason for this could be attributed to the differences of the genetic material of the two studies. Some of the studied F₂ populations like Kangni-27/TN-1, TN-1/Dilrosh, TN-1/Kangni-27 showed high heritability values of >0.80 for 100-grain weight which is similar to the findings of Ali *et al.* (2000) who reported significant differences among the parental and F₂ populations with high heritability value of 0.85 for 100-grain weight. Significant differences among the genotypes were manifested for biological yield, which is compatible with the results of Shukla *et al.* (2005). Shukla *et al.* (2005) studied 42 rice genotypes and observed significant differences for biological yield.

They also reported high heritability value (0.96) for this trait which is compatible with the findings of this study as some of F₂ populations like Kashmir-Basmati/TN-1, TN-1/Kashmir-Basmati, Kashmir-Basmati/Kangni-27, Kangni-27/Dilrosh and TN-1/Kangni-27 displayed heritability values of >0.90 for biological yield.

The studied genotypes displayed significant variation for grain yield while most of the F₂ populations displayed high heritability values for grain yield. These findings are similar with the results of Nandeshwar *et al.* (2010).

They reported significant variation among 25 parents and their 25 F₂ populations with high heritability value (0.72) for grain yield. Significant differences among the genotypes for harvest index as observed in the present study are in line with the findings of Sravan *et al.* (2012).

Sravan *et al.* (2012) studied 36 rice genotypes and reported significant differences for harvest index. Most of the studied F₂ populations displayed high heritability for harvest index, which supports the findings of Subbaiah *et al.* (2011).

They also observed reported high heritability for harvest index in a study comprising 16 parents and their 48 hybrid populations.

Conclusions

The present study revealed sufficient genetic variation among the parents and F_2 populations for yield and yield associated traits. F_2 populations Kashmir-Basmati/TN-1 and Kangni-27/TN-1 had maximum 100-grain weight while F_2 populations Kashmir-Basmati/TN-1 and Dilrosh/TN-1 produced maximum number of spikelets panicle^{-1} and grain yield, respectively. The highest heritability for 100-grain weight was observed for F_2 population Kangni-27/TN-1 while F_2 population Dilrosh/Kashmir-Basmati showed maximum heritability for grain yield. F_2 populations Dilrosh/Kashmir-Basmati and Kashmir-Basmati/Kangni-27 manifested maximum genetic advance values for 100-grain weight and grain yield, respectively. F_2 populations Dilrosh/TN-1, Kashmir-Basmati/TN-1, Kangni-27/TN-1, Dilrosh/Kashmir-Basmati and Kashmir-Basmati/Kangni-27 are, therefore, recommended for further advancement to develop desirable recombinant inbred lines and commercial rice cultivars.

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