Heritability, genetic advance, genotypic and phenotypic correlation studies for yield and yield related traits in F₂ segregating populations of rice (Oryza sativa)

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Abstract:

   To estimate heritability, genetic advance and correlation for yield traits in rice genotypes, 7 parents and their 16 F₂ populations were planted in a randomized complete block design with three replications at The University of Agriculture, Peshawar during 2012. Significant ($p \leq 0.05$) differences among the genotypes were observed for days to 50 % heading, culm length, days to maturity, panicle length, primary and secondary branches panicle^{-1} and grain yield plant^{-1}. Among the F₂ populations Dokri-Bas/Bas-6129 produced early heading (94 days) and matured earlier (123.6 days). IR-8/NIAB-IR-9 displayed maximum primary branches panicle^{-1} (12.13) while Bas-6129/Dokri-Bas showed maximum secondary branches panicle^{-1}(43.6). The highest grain yield (59.5 g) was recorded for Dokri-Bas/Pakhal. High heritability estimation was observed for all the studied traits associated with high selection response. IR-8/Shahdab-31 showed maximum heritability (0.92) and maximum selection response (6.91 cm) for panicle length. For primary branches panicle^{-1}, maximum

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heritability (0.89) was displayed by Bas-6129/Dokri-Bas while maximum selection response (2.67) was observed for Bas-2008/TN-1. For secondary branches, Bas-2008/TN-1 had maximum heritability (0.97) and maximum selection response (19.82). The highest heritability (0.95) and selection response (25.60 g) was manifested for Dokri-Bas/DR-92 for grain yield plant^{-1}. Positively significant phenotypic correlation of days to heading was observed with days to maturity, panicle length, and primary and secondary branches panicle^{-1}. As a result of high heritability and high genetic advance for yield related traits, the populations IR-8/Shahdab-31, Bas-6129/Dokri-Bas, Bas-6129/Bas-370, Bas-2008/TN-1, IR-8/NIAB-IR-9, Dokri-Bas/DR-92 and Dokri-Bas/Pakhal could be utilized as progenitors in succeeding generations of rice breeding programs.

Key words: Heritability, genetic advance, genotypic and phenotypic correlation studies, yield, F₂ segregating populations of rice (Oryza sativa)

Introduction

Rice (*Oryza sativa*) is one of the most important cereal crops of the world. It belongs to the family *Graminae* and genus *Oryza*. The cultivated species are *Oryzasativa* and *O. glaberrima*.*O. Sativa (2n = 24 AA)* is grown worldwide, while *O. glaberrima (2n = 24 BB)* is planted on a limited scale in West Africa. About half of the world's population depends on rice as their staple food. The major rice producing countries are China, India, Indonesia, Bangladesh, Vietnam, Thailand, Myanmar and Philippines with annual productions of 205.2, 150, 68.6, 51.3, 43.4, 36, 30.0 and 18.0 million tons respectively (FAOSTAT, 2012). Pakistan is a rice producing and exporting country. In Pakistan rice is grown in total area of 2.57 million hectares with annual production of 6.16 million tons (FBS, 2011). It is grown in different climatic conditions. Rice Basmati is cultivated in Punjab. The cold-tolerant rice cultivars are grown

at high altitude mountainous valleys of Swat, while in southern Khyber Pakhtunkhwa, Sindh and Baluchistan long grain heat resistant IRRI type genotypes are cultivated (PARC, 2005-06). Mostly breeders are interested in developing rice cultivars with improved yield and quality.

In the early stages of breeding programs, direct selection for grain yield is not practiced due to its complex quantitative nature and low heritability. Knowledge of the heritability is fundamental for selection to quantify the transfer of a trait in future generations (Sabesan et al., 2009). The heritability and genetic advance is the essential framework for the selection, their collective estimation is beneficial for the prediction of gain during the selection (Habibullah et al., 2015). High heritability along with a strong genetic gain is a useful tool for selection in segregating generations (Larik et al., 2000). Frankel (1935) and Adams (1967) suggested that the components of performance are strongly influenced by the environment and the negative correlations between them are common. Therefore, the selection for one of the components may fail in increased performance due to the negative associations between performance components. Genotypic and phenotypic associations between yield and yield contributing traits are of immense importance to plant breeders to develop probable and better performance rice cultivars (Agarwal et al, 1978, Amin, 1979 Ragarathiram et al. 1992). The objectives of this research study were to evaluate the F$_2$ segregating populations of rice for yield and yield associated traits, to study phenotypic and genotypic correlations, BS heritability and genetic advance estimation and find out superior F$_2$ populations for onward use in rice breeding programs for different traits of interest.

Materials and Methods

Experimental site

The research study was conducted at the The University of Agriculture, Peshawar-Pakistan in Plant Breeding and Genetics Research Farm, during 2012 rice crop growing season.

Breeding materials

Thirty rice genotypes composing 16 F_2 populations and 14 parental cultivars were cultivated in randomized complete block design with 3 replications. The studied genotypes in this research study are listed below.

List of the rice genotypes studied in research study

	Parents		F₂ Populations
1.	IR-8	1.	NIAB-IR-9/IR-8
2.	DR-92	2.	IR-8/NIAB-IR-9
3.	Dilrosh	3.	IR-8/Shahdab-31
4.	TN-1	4.	IR-8/Sugdesi
5.	Basmati-370 (Bas-370)	5.	Bas-6129/Bas-370
6.	Sugdesi	6.	Bas-6129/Dokri-Bas
7.	Kashmir Basmati-100 (K-Bas-100)	7.	Bas-2008/K-Bas-100
8.	Pakhal	8.	Bas-2008/TN-1
9.	NIAB-IR-9	9.	Bas-2008/Dilrosh
10.	DR-83	10.	Dokri-Bas/DR-92
11.	Basmati-6129 (Bas-6129)	11.	Dokri-Bas/Pakhal
12.	Basmati-2008 (Bas-2008)	12.	Dokri-Bas/Bas-6129
13.	Shahdab-31	13.	Dokri-Bas/DR-83
14.	Dokri-Basmati (Dokri-Bas)	14.	Dokri-Bas/Sugdesi
		15.	DR-92/DR-83
		16.	DR-92/Dokri-Bas

Field experimentation and procedure

Thirty rice genotypes composing 16 F_2 populations and 14 parental cultivars were grown in randomized complete block design with three replications. Each rice genotype was planted in a plot containing two rows of 2 meters length keeping row space 30 cm while the planting space was 15 cm. In the end of

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May 2012 the nursery was prepared and was transplanted to
field in July 2012 start. Data were taken on days to 50%
heading, culm length (cm), days to maturity, panicle length
(cm), primary branches panicle^{-1}, secondary branches panicle^{-1}
and grain yield plant^{-1} (g). Days to heading were counted from
the nursery date to the day when 50% tillers of each selected
plant exposed panicles. Culm length is the length of stem in
centimeters (cm) from base of culm at ground level to the base
of panicle. Panicle length was measured in cm from panicle
base to its tip. Different panicle traits like primary branches
panicle^{-1} and secondary branches panicle^{-1} were also studied for
the selected genotypes. Days to maturity were calculated from
nursery date to the day when above 80% of the grains on
panicles of each selected plant was ripened, while grain yield
plant^{-1} was determined after threshing the plants.

Statistical analysis

Data were compiled and analyzed using analysis of variance
(ANOVA) technique appropriate for randomized complete block
design. Broad sense heritability of a specific trait was
calculated from the variances of parents and F$_2$ populations of
each cross combination following the formula of Mahmud and
Kramer (1951):

$$h^2_{BS} = \frac{VF_2 - \sqrt{VP_1 \times VP_2}}{VF_2}$$

Where
V_{F2} = Variance of F$_2$ population for a specific trait.
V_{P1} and V_{P2} = Variances of Parent 1 and Parent 2 of a specific
F$_2$ population

Genetic advance was calculated using the following formula of
Panse and Sukhatme (1965):

$$GA = K \times \sqrt{o^2_P} \times h^2$$

Where

K = 1.47 for 20 % selection intensity

h^2 = heritability coefficient

$\sqrt{\sigma^2_P}$ = Phenotypic Standard Deviation

GA = genetic advance

Genotypic (r$_G$) and "phenotypic (r$_P$) correlations among various traits were worked out from genotypic, phenotypic and environmental co-variances following Singh and Chaudhary (1985) as under:

$$Genotypic \ Co-var iance \ (\delta^2_{g1g2}) = \frac{GMCP - EMCP}{r}$$

$$Evironmental \ Co-var iance \ (\delta^2_{e1e2}) = EMCP$$

$$Phenotypic \ Co-var iance \ (\delta^2_{p1p2}) = \delta^2_{g1g2} + \delta^2_{e1e2}$$

$$Genetic \ correlation \ (r_G) = \frac{COV_{G(x_1 x_2)}}{\sqrt{\delta^2_{G(x_1)}.\delta^2_{G(x_2)}}}$$

$$Phenotypic \ correlation \ (r_P) = \frac{COV_{P(x_1 x_2)}}{\sqrt{\delta^2_{P(x_1)}.\delta^2_{P(x_2)}}}$$

Where,

GMCP = Genotypic mean cross product

EMCP = Environmental mean cross product

COV$_{G(x1x2)}$ = Genetic covariance among traits x$_1$ and x$_2$

δ^2_{g} (x1) = Genotypic variance of trait x$_1$

δ^2_{g} (x2) = Genotypic variance of trait x$_2$

COV$_{P(x1x2)}$ = Phenotypic covariance among traits x$_1$ and x$_2$

δ^2_{p} (x1)= Phenotypic variance of trait x$_1$

δ^2_{p} (x2)= Phenotypic variance of trait x$_2$

Results and Discussion

Days to 50% heading

Analysis of variance exhibited highly significant differences (p < 0.01) among the rice genotypes for days to 50% heading. Parents, F_2 populations and parents vs F_2 populations revealed highly significant differences (p $\leq$ 0.01) for this trait (Table 1). Among the parents, mean data showed a range from 95 to 142.5 days. Bas-2008 took minimum days (95) to heading while maximum days (142.5) were recorded for Sugdesi. Among the F_2 populations, mean data showed a range from 94 to 119.8 days. Dokri-Bas/Bas-6129 showed minimum days to 50% heading (94) while maximum days (119.8) were recorded for IR-8/Sugdesi (Table 2). Among the parental populations, variances ranged from 1.1 to 16.6. Shahdab-31 showed minimum variance whereas maximum variance was observed for Sugdesi (Table 3). Among the F_2 populations, variances ranged from 4.0 to 153.6. Dokri-Bas/Bas-6129 showed minimum variance whereas maximum variance was observed for IR-8/Sugdesi (Table 3). Among the F_2 populations minimum and maximum limits of heritability were 0.49 and 0.96. Dokri-Bas/Bas-6129 revealed minimum broad sense heritability (0.49) while maximum heritability (0.96) was displayed by Bas-6129/Bas-370 and Bas-6129/Dokri-Bas (Table 3). F_2 populations of Dokri-Bas/Bas-6129 manifested minimum selection response (1.45 days) whereas maximum selection response (17.06 days) was observed for IR-8/Sugdesi (Table 3). Positively significant phenotypic correlation of days to heading was observed with days to maturity, panicle length, primary and secondary branches panicle[-1], while it was significantly and negatively correlated with culm length. Genotypic correlation of days to heading with days to maturity, panicle length, primary and secondary branches panicle[-1], was observed positively significant while negatively significant with culm length (Table 5). Significant

differences for days to heading were observed by the Seyoum et al. (2012). Kole et al. (2008) also studied 18 rice genotypes and reported high heritability value (0.94) for days to heading, which are in line with our current results. Qamar et al. (2005) reported significantly positive correlation of days to heading with days to maturity at both levels which support our results.

Table 1: Mean squares and co-efficient of variations (CV) for days to heading (DH), culm length (CL), days to maturity (DM), panicle length (PL), primary branches panicle^{-1} (PBP), secondary branches panicle^{-1} (SBP) and grain yield plant^{-1} of rice genotypes.

Source	Replications	Genotypes	Parents	F₂ Populations	P vs F₂	Error	CV (%)
Df	2	29	13	15	1	58	
DH	14.7 NS	346.3 **	548.4 **	185.2 **	135.1 **	13.4	3.48
CL	454.9 **	1055.5 **	909.1 **	1221.5 **	469.3 **	42	8.42
DM	84.9 *	331.7 **	511.7 **	189.3 **	126.7 **	17.3	3.07
PL	1.5 NS	31.5 **	47.9 **	17.8 **	24.30 **	1.5	4.71
PBH	0.76 NS	3.4 **	5.2 **	2.04 **	0.07 NS	0.46	6.55
SBH	1.9 NS	142.1 **	207.1 **	84.6 **	160.7 **	9.6	9.87
GY	26.5 NS	492.8 **	736.5 **	225.9 *	1329.2 **	99.7	19.94

*, ** = Significant at 0.05and 0.01 levels of probability, NS = Non significant

Culm length

Statistical analysis revealed highly significant differences (p ≤ 0.01) among the rice genotypes for culm length. Parents, F₂ populations and parents vs F₂ revealed highly significant differences (p ≤ 0.01) for this trait (Table 1). Among the parents, mean data varied between 56.1 and 100.1 cm for this trait. IR-8 manifested minimum culm length (56.1 cm) while maximum culm length (100.1 cm) was observed for Shahdab-31. Among the F₂ populations, mean data ranged from 55.5 to 115.6 cm. NIAB-IR-9/IR-8 showed minimum culm length (55.5 cm) while maximum culm length (115.6 cm) was displayed by Bas-2008/Dilrosh (Table 2).

Among the parental populations, variances ranged from 7.5 to 41.7. Dokri-Bas showed minimum variance whereas maximum variance was observed for Sugdesi (Table 3). Among the F₂ populations, DR-92/Dokri-Bas showed minimum variance (26.1) whereas maximum variance (447.7) was

observed for Bas-2008/TN-1 (Table 3). Among the F_2 populations minimum and maximum limits of heritability were 0.36 and 0.96. IR-8/NIAB-IR-9 revealed minimum broad sense heritability (0.36) while maximum heritability (0.96) was displayed by Bas-2008/TN-1 and Dokri-Bas/DR-92 (Table 3). F_2 population IR-8/NIAB-IR-9 manifested minimum selection response (2.72 cm) whereas maximum selection response (29.79 cm) was noted for Bas-2008/TN-1 (Table 3). Culm length showed positively significant phenotypic correlation with panicle length and secondary branches panicle[-1] while significantly negatively correlated with days to heading, days to maturity and primary branches panicle[-1]. Culm length manifested significant positive genotypic correlation with panicle length and secondary branches panicle[-1] while significantly negative correlation with days to heading, days to maturity and to the number of primary branches panicle[-1] (Table 5). Significant differences have been reported for culm length by Bharadwaj et al. (2007). Kole et al. (2008) studied18 rice genotypes and reported high heritability value (0.85) for culm length which are in the conformity of our current results.

Days to maturity

The genotypes exhibited highly significant differences ($p \leq 0.01$) for days to maturity. Parents, F_2 populations and parents vs F_2 revealed highly significant differences ($p \leq 0.01$) for this trait (Table 1). Among the parents, range varied between 127.7 to 171.7 days. TN-1 manifested minimum days to maturity (127.7) while maximum days (171.7) were observed for Sugdesi. Among the F_2 populations, the value for this trait varied between 123.6 to 150.1 days. Dokri-Bas/Bas-6129 was observed for minimum days (123.6) to maturity while maximum days (150.1) had taken by IR-8/Sugdesi (Table 2). Among the parental populations, variances ranged from 2.5 to 12.4. Dilrosh showed minimum variance whereas maximum variance was observed

for Pakhal (Table 3). Among the F_2 populations, Dokri-Bas/Pakhal showed minimum variance (6.5) whereas maximum variance (159.5) was observed for IR-8/Sugdesi (Table 3). Among the F_2 populations, minimum and maximum limits of heritability were 0.37 and 0.96. Dokri-Bas/Bas-6129 revealed minimum broad sense heritability (0.37) while maximum heritability (0.96) was displayed by Bas-6129/Bas-370 (Table 3). F_2 populations of Dokri-Bas/Bas-6129 manifested minimum selection response (1.39 days) whereas maximum selection response (17.65 days) was noted for IR-8/Sugdesi (Table 3). Days to maturity showed significantly positive phenotypic correlation with days to heading, panicle length and primary branches panicle[-1], while it was significantly negatively correlated with culm length. Genotypic correlation of days to maturity was observed positively significant with days to heading, panicle length, and primary branches panicle[-1] while it was significant and negatively correlated with culm length (Table 5). Significant differences for days to maturity were observed by the Seyoum et al. (2012). Seyoum et al. (2012) assessed 14 rice genotypes and estimated high heritability values (0.85) for days to maturity which supports our current findings. Qamar et al. (2005) reported significantly positive correlation for days to maturity at both levels which support our results.

Panicle length

Highly significant differences ($p \leq 0.01$) were observed among the rice genotypes for panicle length. Parents, F_2 populations and parents vs F_2 revealed highly significant differences ($p \leq 0.01$) for this trait (Table 1). Among the parents, mean data limits for panicle length were 19.8 and 34.9 cm and were manifested by Bas-2008 (19.8 cm) and Sugdesi (34.9 cm). Among the F_2 populations mean data ranged from 20.8 to 30.7 cm and were manifested byDokri-Bas/DR-83 (20.8 cm) and Bas-

6129/Bas-370 (30.7 cm) respectively (Table 2). Among the parental populations, variances ranged from 1.2 to 3.8. IR-8 showed minimum variance whereas maximum variance was observed for Sugdesi and Pakhal (Table 4). Among the F₂ populations, variances ranged from 3.5 to 26.1. Dokri-Bas/DR-83 showed minimum variance whereas maximum variance was observed for IR-8/Shahdab-31 (Table 4). For panicle length, heritability values ranged from 0.40 to 0.92 among the F₂ populations. Dokri-Bas/DR-83 revealed minimum broad sense heritability (0.40) while maximum heritability (0.92) was displayed by IR-8/Shahdab-31 (Table 4). F₂ populations of Dokri-Bas/DR-83 manifested minimum selection response (1.10 cm) whereas maximum selection response (6.91 cm) was noted for IR-8/Shahdab-31 (Table 4). Phenotypic and genotypic correlations of panicle length were observed positively significant with days to heading, culm length, days to maturity, primary branches panicle[-1] and secondary branches panicle[-1] (Table 5). Our significant results for panicle length are parallel to that of Nandeshwar et al. (2010) who also reported highly significant differences during their studies for panicle length. Seyoum et al. (2012) assessed 14 rice genotypes and estimated high heritability values (0.79) for panicle length which support our current findings.

Primary branches panicle[-1]

Mean squares displayed highly significant differences (p < 0.01) among the rice genotypes for number of primary branches panicle[-1]. Parents and F₂ populations revealed highly significant differences (p < 0.01) while the parents vs F2 differences were observed non significant (p > 0.05) for this trait (Table 1). Among parental cultivars, mean data range varied from 7.7 to 12.3 primary branches. Bas-2008 exhibited minimum number of primary branches (7.7) while maximum number of primary branches (12.3) was observed for IR-8.

Among the F_2 populations, mean data varied from 9.1 to 12.13 branches panicle^{-1}. Dokri-Bas/DR-92 exhibited minimum number of primary branches (9.1) while maximum number of primary branches (12.13) was divulged for IR-8/NIAB-IR-9 (Table 2). Among the parental populations, variances ranged from 0.3 to 2.0. Bas-6129 showed minimum variance whereas maximum variance was observed for Shahdab-31 (Table 4). Among the F_2 populations, variances ranged from 1.2 to 4.6. Bas-6129/Bas-370 showed minimum variance whereas maximum variance was observed for Bas-2008/TN-1 (Table 4). For primary branches, heritability values ranged from 0.44 to 0.89 concerning the F_2 populations. DR-92/DR-83 revealed minimum broad sense heritability (0.44) while maximum heritability (0.89) was displayed by Bas-6129/Dokri-Bas (Table 4). F_2 populations of DR-92/DR-83 manifested minimum selection response (0.86) whereas maximum selection response (2.67) was observed for Bas-2008/TN-1 (Table 4). Phenotypic and genotypic correlations of primary branches panicle^{-1} were observed positively significant with days to heading, days to maturity, panicle length and secondary branches panicle^{-1} while significantly negative for culm length (Table 5). Significant differences have been reported by Karim et al. (2007) and Parikh et al. (2011) for primary branches panicle^{-1}. Moderate to high heritability was observed for primary branches panicle^{-1} by Karim et al. (2007) which are in conformity with our reported results.

Secondary branches panicle^{-1}

The genotypes revealed highly significant differences ($p < 0.01$) for number of secondary branches panicle^{-1}. Parents, F_2 populations and parents vs F_2 revealed highly significant differences ($p < 0.01$) for this trait (Table 1). Among the parents, range limits of mean data were 21.2 and 47.9. NIAB-IR-9 manifested minimum number of secondary branches

panicle^{-1} (21.2) while maximum (47.9) were observed for Bas-6129. Among the F$_2$ populations, mean data ranged from 24.1 to 43.6 branches panicle^{-1}. Dokri-Bas/Pakhal showed the lowest number of secondary branches panicle^{-1} (24.1) while the highest number (43.6) was displayed by Bas-6129/Dokri-Bas (Table 2). Among the parental populations, variances ranged from 3.8 to 30.8. NIAB-IR-9 showed minimum variance whereas maximum variance was observed for DR-83 (Table 4). Among the F$_2$ populations, variances ranged from 31.9 to 194.8. NIAB-IR-9/IR-8 showed minimum variance whereas maximum variance was observed for Bas-2008/TN-1 (Table 4). For secondary branches panicle^{-1}, heritability values ranged from 0.59 to 0.97 relating to the F$_2$ populations. DR-92/DR-83 revealed minimum broad sense heritability (0.59) while maximum heritability (0.97) was displayed by Bas-2008/TN-1 (Table 4). F$_2$ populations of DR-92/DR-83 manifested minimum selection response (6.60) whereas maximum selection response (19.82) was noted for -Bas-2008/TN-1 (Table 4). Phenotypic and genotypic correlation of secondary branches panicle^{-1} was observed positively significant with days to heading, culm length, panicle length and primary branches panicle^{-1} while it was significantly negatively correlated with grain yield plant-1 (Table 5). Significant differences have been reported by Karim et al. (2007) and Parikh et al. (2011) for secondary branches panicle^{-1}. Moderate to high heritability was reported for secondary branches panicle^{-1} by Karim et al. (2007) which are in conformity with our reported results.

Grain yield plant^{-1}
The genotypes displayed highly significant differences (p < 0.01) for grain yield plant^{-1}. Parents and parents vs F$_2$ revealed highly significant differences (p < 0.01) while F$_2$ populations exhibited significantly differences (p $\leq$ 0.05) (Table 1). Among the parents, mean data for grain yield ranged from 34.1 to 81.4

g. Bas-370 manifested minimum grain yield (34.1g) while maximum grain yield (81.4g) was observed for Pakhal. Among the F$_2$ populations, mean data ranged from 34.7g to 59.5g. Bas-6129/Bas-370 showed minimum grain yield (34.7g) while maximum grain yield (59.5g) was displayed by Dokri-Bas/Pakhal (Table 2). Among the parental populations, variances ranged from 5.2 to 37.2. K-Bas-100 showed minimum variance whereas maximum variance was observed for Dilrosh (Table 4). Among the F$_2$ populations, variances ranged from 93.8 to 336.6. Bas-6129/Bas-370 showed minimum variance whereas maximum variance was observed for Dokri-Bas/DR-92 (Table 4). For grain yield, heritability values ranged from 0.75 to 0.95 regarding the F$_2$ populations. Bas-2008/Dilrosh revealed minimum broad sense heritability (0.75) while maximum heritability (0.95) was displayed by Dokri-Bas/DR-92 (Table 4). F$_2$ populations of Bas-2008/Dilrosh and Bas-2008/TN-1 manifested minimum selection response (12.95g) whereas maximum selection response (25.60g) was noted for Dokri-Bas/DR-92 (Table 4). The phenotypic and genotypic associations of grain yield plant^{-1} were observed significantly negative with secondary branches panicle^{-1} (Table 5). Significant genetic differences for grains yield were revealed which are analogous to the observations of Shukla et al. (2005). They have been observed wide range of variation in 39 rice genotypes. Kole et al. (2008) observed high heritability (0.76) for grain yield in F$_2$ populations which support our findings. Significant associations were observed for grain yield with days to maturity by (Chang and Tagumpay, 2005).

Conclusions and Recommendations

Parental cultivars and F$_2$ populations used in this research study manifested sufficient genetic variation for yield and yield related traits. Among the F$_2$ populations early heading and

early maturity was showed by Bas-6129/Dokri-Bas. Maximum numbers of primary and secondary branches panicle-1 were manifested by IR-8/NIAB-IR-9 and Bas-6129/Dokri-Bas respectively. Dokri-Bas/Pakhal was observed the highest yielding. Maximum heritability along with maximum genetic advance was manifested by Dokri-Bas/DR-92 for grain yield plant^{-1}. On the basis of high heritability and high genetic advance for yield related traits, the populations Bas-6129/Dokri-Bas, IR-8/NIAB-IR-9, Dokri-Bas/DR-92 and Dokri-Bas/Pakhal could be utilized and recommended for onward use in future rice breeding programs.

Table 2: Mean values for days to heading (DH), culm length (CL), days to maturity (DM) panicle length (PL) primary branches panicle^{-1} (PBP), secondary branches panicle^{-1} (SBP) and grain yield (GYP) plant^{-1}.

Genotypes	DH	CL	DM	PL	PBP	SBP	GYP
Parents							
IR-8	111.3	56.1	140.3	27.5	12.3	44.9	41.4
DR-92	105.7	58.1	136.3	26.5	10.1	28.7	59
Dilrosh	98.1	73.4	128	25.1	10.7	29.6	42.2
TN-1	97.7	58	127.7	20.8	10.4	22	64.3
Bas-370	98.3	74.8	128.3	24.6	9.6	24.4	34.1
Sugdesi	142.5	56.8	171.7	34.9	11.5	37.9	39.1
K-Bas-100	95.3	95.1	135.3	26.6	8.7	21.7	69.5
Pakhal	99	97.2	129.3	27.5	11	29.8	81.4
NIAB-IR-9	127.7	59.2	156.9	22.2	10.1	21.2	69.1
DR-83	107.7	72.4	137.7	29.8	8.8	27.4	67.1
Bas-6129	103	92.4	133	28.9	12.1	47.9	60.8
Bas-2008	95	91.6	136	19.8	7.7	23.7	36.3
Shahdab-31	111.4	100.1	141.2	30.6	11	31.1	59.4
Dokri-Bas	100.1	57.3	133	26.1	10	28.8	34.9
F₂ Populations							
NIAB-IR-9/IR-8	115.1	55.5	145.4	24.5	11.7	35.3	54.6
IR-8/NIAB-IR-9	114.8	58.1	145	25.3	12.1	33.4	57.1
IR-8/Shahdab-31	110.7	58.2	141	23.2	11.3	30.3	43.9
IR-8/Sugdesi	119.8	78	150.1	28.2	10.6	34	37.6
Bas-6129/ Bas-370	109.2	111.9	139.5	30.7	10.6	40.2	34.7
Bas-6129/ Dokri-Bas	104.7	91.5	134.9	28.7	10.9	43.6	38.8
Bas-2008/K-Bas-100	106.8	95.1	137	26.4	10.3	34	35.2
Bas-2008/TN-1	104.1	96.1	134.4	25.5	9.9	31.9	44.9
Bas-2008/ Dilrosh	97.3	115.6	127.5	26.6	10	34.3	38.5
Dokri-Bas/DR-92	97.9	96.1	128.2	25.5	9.1	30.6	46.7

Dokri-Bas/Pakhal	100.9	60.5	131.1	22.6	9.4	24.1	59.5
Dokri-Bas/ Bas-6129	94	76.4	123.6	24.1	9.8	28.3	44.3
Dokri-Bas/ DR-83	97.7	57.7	128	20.8	10.2	24.9	41.2
Dokri-Bas/ Sugdesi	95.3	85.4	125.2	25.7	9.8	36	53.5
DR-92/ DR-83	97.6	64.6	127.9	23.4	9.7	25.6	54.3
DR-92/ Dokri-Bas	101	64.3	131.3	25.8	10.3	35.8	59.1
Genotypes Means	105.3	76.9	136.1	25.9	10.3	31.3	50
LSD(0.05)	5.98	10.59	6.8	2	1.1	5.06	16.32
Parental Means	106.6	74.4	138.1	26.4	10.2	29.9	54.16
LSD(0.05) (Parents)	6.14	10.88	6.98	2.05	1.13	5.2	16.7
F₂ Population Means	104.1	79.1	134.3	25.4	10.3	32.6	46.4
LSD(0.05) (F₂ populations)	6.1	10.81	6.94	2.04	1.13	5.16	16.65

Table 3: Variance, broad sense heritability (h²) and genetic advance (GA) values for days to heading (DH), culm length (CL) and days to maturity (DM) of rice genotypes.

Genotypes	DH			CL			DM		
Parents	Var			Var			Var		
IR-8	5.8			14.2			5.4		
DR-92	2.5			8.4			4.6		
Dilrosh	5.3			20.9			2.5		
TN-1	2.5			16.3			10.0		
Bas-370	2.8			33.9			4.2		
Sugdesi	16.6			41.7			11.5		
K-Bas-100	3.8			38.5			3.8		
Pakhal	11.8			30.3			12.4		
NIAB-IR-9	16.1			20.5			5.0		
DR-83	4.3			14.0			9.2		
Bas-6129	2.0			22.3			3.5		
Bas-2008	2.5			22.1			3.6		
Shahdab-31	1.1			15.9			2.6		
Dokri-Bas	2.1			7.5			4.7		
F₂ Populations	Var	h²	GA	Var	h²	GA	Var	h²	GA
NIAB-IR-9/IR-8	62.7	0.85	9.84	41.5	0.59	5.58	70.2	0.93	11.4
IR-8/NIAB-IR-9	34.6	0.72	6.23	26.6	0.36	2.72	47.1	0.89	9.0
IR-8/Shahdab-31	48.9	0.95	9.76	33.4	0.55	4.68	58.9	0.94	10.6
IR-8/Sugdesi	153.6	0.94	17.06	305.7	0.92	23.66	159.5	0.95	17.65
Bas-6129/Bas-370	63.9	0.96	11.31	159.3	0.83	15.35	84.9	0.96	12.9
Bas-6129/Dokri-Bas	49.6	0.96	9.92	205.4	0.94	19.73	60.5	0.93	10.7
Bas-2008/K-Bas-100	48.4	0.94	9.57	109.2	0.73	11.27	49.9	0.93	9.6
Bas-2008/TN-1	39.7	0.94	8.68	447.7	0.96	29.79	49.9	0.88	9.1
Bas-2008/Dilrosh	15.0	0.76	4.32	90.8	0.76	10.69	22.1	0.86	6.0
Dokri-Bas/DR-92	17.7	0.87	5.39	193.6	0.96	19.61	24.4	0.81	5.9
Dokri-Bas/Pakhal	34.5	0.86	7.39	40.1	0.62	5.79	41.0	0.81	7.7
Dokri-Bas/Bas-6129	4.0	0.49	1.45	49.3	0.74	7.61	6.5	0.37	1.39
Dokri-Bas/DR-83	19.0	0.84	5.39	37.7	0.73	6.56	28.4	0.77	6.0
Dokri-Bas/Sugdesi	15.1	0.61	3.48	219.1	0.92	20.00	20.7	0.64	4.3
DR-92/DR-83	38.0	0.91	8.27	47.6	0.77	7.83	44.7	0.85	8.4
DR-92/Dokri-Bas	43.0	0.95	9.12	26.1	0.70	5.22	59.5	0.92	10.5

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Table 4: Variance, broad sense heritability (h²) and genetic advance (GA) values for panicle length (PL), primary branches panicle⁻¹ (PBP), secondary branches panicle⁻¹ (SBP) and Grain yield plant⁻¹ (GYP) of rice genotypes.

Genotypes	PL			PBP			SBP			GYP		
Parents	Var			Var			Var			Var		
IR-8	1.2			1.4			10.5			25.0		
DR-92	1.8			0.9			19.0			19.0		
Dilrosh	3.5			1.8			20.6			37.2		
TN-1	1.7			1.1			8.8			16.2		
Bas-370	1.8			0.4			11.3			5.7		
Sugdesi	3.8			0.5			9.0			24.8		
K-Bas-100	1.8			1.3			27.9			5.2		
Pakhal	3.8			0.6			16.5			14.4		
NIAB-IR-9	1.7			0.9			3.8			27.9		
DR-83	2.0			1.1			30.8			20.8		
Bas-6129	2.5			0.3			10.8			7.8		
Bas-2008	1.6			0.4			5.0			32.0		
Shahdab-31	3.5			2.0			11.6			35.8		
Dokri-Bas	2.3			0.7			16.3			15.2		
F₂ Populations	Var	h²	GA	Var	h²	GA	Var	h²	GA	Var	h²	GA
NIAB-IR-9/IR-8	4.2	0.66	2.0	2.5	0.55	1.28	31.9	0.80	6.7	159.5	0.83	15.5
IR-8/NIAB-IR-9	4.6	0.68	2.1	2.3	0.49	1.09	61.0	0.90	10.3	286.8	0.91	22.6
IR-8/Shahdab-31	26.1	0.92	6.9	3.2	0.48	1.25	89.8	0.88	12.2	138.8	0.78	13.6
IR-8/Sugdesi	7.8	0.72	3.0	3.0	0.73	1.85	105.3	0.91	13.7	179.8	0.86	17.0
Bas-6129/Bas-370	12.2	0.83	4.2	1.2	0.71	1.16	96.8	0.89	12.8	93.8	0.93	13.2
Bas-6129/Dokri-Bas	5.8	0.59	2.1	4.1	0.89	2.64	79.3	0.83	10.9	144.1	0.92	16.3
Bas-2008/K-Bas-100	3.8	0.55	1.6	3.9	0.81	2.36	86.3	0.86	11.8	158.2	0.92	17.0
Bas-2008/TN-1	14.4	0.89	4.9	4.6	0.85	2.67	194.8	0.97	19.8	118.8	0.81	13.0
Bas-2008/Dilrosh	16.3	0.86	5.1	3.0	0.70	1.80	71.2	0.86	10.6	138.2	0.75	13.0
Dokri-Bas/DR-92	8.2	0.75	3.2	2.0	0.62	1.29	62.0	0.72	8.3	336.6	0.95	25.6
Dokri-Bas/Pakhal	5.0	0.41	1.3	2.5	0.74	1.72	50.7	0.68	7.1	243.1	0.94	21.5
Dokri-Bas/Bas-6129	5.6	0.58	2.0	1.8	0.75	1.49	55.3	0.76	8.3	171.9	0.94	18.0
Dokri-Bas/DR-83	3.5	0.40	1.1	2.0	0.58	1.21	75.3	0.70	8.9	157.9	0.89	16.4
Dokri-Bas/Sugdesi	9.2	0.68	3.1	3.7	0.85	2.40	99.7	0.88	12.9	154.2	0.87	16.0
DR-92/DR-83	10.2	0.81	3.8	1.7	0.44	0.86	58.6	0.59	6.6	193.4	0.90	18.3
DR-92/Dokri-Bas	10.7	0.81	3.9	1.8	0.59	1.18	105.6	0.83	12.6	297.1	0.94	23.9

Table 5: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among the traits of rice genotypes.

	DH	CL	DM	PL	PBP	SBP	GYP
DH	--	-0.29**	0.98**	0.45**	0.42**	0.25*	-0.06
CL	0.33**	--	-0.31**	0.29**	-0.21*	0.21*	-0.11
DM	0.97**	-0.28**	--	0.47**	0.41**	0.19	-0.08
PL	0.51**	0.30**	0.47**	--	0.40**	0.61**	-0.03
PBP	0.54**	-0.27**	0.40**	0.37**	--	0.63**	0.01
SBP	0.27**	0.23*	0.19	0.62**	0.67**	--	-0.21*
GYP	-0.01	-0.11	-0.01	-0.06	0.00	-0.31**	--

Acknowledgement

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