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Breeding potential of the basmati rice germplasm under water stress condition

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Eight parents were selected on the basis of phenotypic and genotypic screening for the development of F_1. All the possible combinations were made between the parents excluding reciprocals in diallel mating design. Data were analyzed by using Hayman graphical approach and Griffing's approach to study the genetics of the parents and their F_1 hybrids. Based on the genetic component analysis, both additive and non-additive components appeared which is important in the inheritance of most of the traits. Both additive and dominance type of gene action were found important in inheritance for different traits under study. Most of the traits showed constant gene action in both environments, but the gene action of some traits was affected by the environment. Morphological traits like plant height, productive tillers per plant and 1000 seed weight showed over dominance type of gene action in both environments (control and drought environments), while seeds per panicle and seed length width ratio showed this type of gene action only in drought conditions. The seeds per panicle and length width ratio showed additive type of gene action with partial dominance only in normal irrigation conditions. From Griffing analysis, genotypes CB-17, CB-32 and Basmati-198 were found to be good general combiners for productive tillers per plant, primary branches per panicle and yield per plant, especially under water stress condition. Also, maximum specific combining ability was found in Basmati-198 × CB-17 for productive tillers per plant, Basmati-198 × CB-42 for primary branches per panicle and CB-32 × CB-14 for yield per plant.

Key words: *Oryza sativa* L., gene action, combining ability, stress, yield traits.

INTRODUCTION

Rice is one of the most important crops around the world. It is a staple food and ranks second among the world as well as in Pakistan. It is considered to be a main food grain crop in many regions of the world, especially in Asian countries. More than 3 billion people feed on rice crop, providing 50 to 80% of their daily calorie intake (Khush, 2005). It is widely cultivated in more than 100 countries, including Pakistan. The total paddy production area is about 162 million hectares and the annual production of rice is about 700.7 million metric tons globally; 3% more than previously reported in year 2009(Anonymous, 2010). Asian countries are the main rice producer, with its rice production accounting for about 92% of the world's total production (Ohtsubo et al., 2005). In Pakistan, rice is a major source of export earnings in recent years. It accounts for 4.4% of value added in agriculture and 0.9% in GDP. Pakistan grows high quality rice to meet both domestic demand and exports. Area sown for rice is estimated at 2365 000 hectares; 17.9% less than last year (2883 thousand hectares). The production of the crop is estimated at 4823 thousand tons, 29.9 percent less than last year 2009 (Anonymous, 2010-11).

The diallel analysis is used to get information about the genetic structure of populations and controlling genetic mechanism of various traits (Hayman, 1954; Griffing, 1956) under study. The analyses provide the information

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of various genetic parameters, general combining ability, specific combining ability, narrow sense heritability, broad sense heritability and heterosis of the parents and their crosses. The diallel theory was developed by (Hayman, 1954) based on Mather's (1949) components of variation, D (additive) and H (dominance). Some of the developments have been made in this method in detail by (Mather and Jinks, 1982). Griffing's approach divides the genotypic variance in to two components, general combining ability and specific combining ability. These estimates also determine the additive and dominance components of phenotypic variation (Griffing, 1956). The practical application of diallel method was carried out for the improvements of almost all the crop plants such as rice (Zhang et al., 1994; Verma and Srivastava, 2004; Rahimi et al., 2010; Muthuramu et al., 2010) and maize (Crosbie et al., 1978).

Researchers indicated that the relative importance of general combining ability (GCA) and specific combining ability (SCA) vary from different studies. Greater magnitude of variance due to GCA than SCA for any traits indicates a predominant role of additive gene action (Verma and Srivastava, 2004). On the other hand, in general most of the investigations showed that the amount of SCA and heterosis is greater than the general combining ability (Bagheri and Jelodar, 2010; Saleem et al., 2009). Sometimes both additive and non additive gene action are involved in the inheritance of characters (Mohanty and Khush, 1985; Farshadfar et al., 2008). Genetic variation for grain weight and some other yield contributing traits were reported due to predominately additive and complemented with additive × additive epistatic variation, indicating that selection for increased grain weight can be practiced in segregating generations (Gravois, 1992; Ahangar et al., 2008). Gene action are studied for different yield traits, total number of tillers, panicle length, number of grains per panicle, pollen fertility, spikelet fertility and grain weight per panicle. Durai et al. (2009) and Gravois and McNew, (1993) identified different parents on the basis significant general combining ability and their heterosis performance.

The objectives of this study were: (1) identify the physio-morphological traits responsible for the yield difference among the genotypes; and (2) select and screen out the water stress tolerant and susceptible genotypes in order to determine the gene action/ inheritance pattern among various traits suitable for further use in rice breeding program aimed at the development of new rice genotypes suitable for water stress prone areas.

MATERIALS AND METHODS

The experiment was conducted in experimental field of department of plant breeding and genetics during 2009. Eight basmati lines/varieties CB-14, CB-17, CB-32, CB-40, CB-42,Super-Bas, Bas-198 and Bas-2000 were used under normal and water stress conditions. The parents were grown in green house in pots with RCBD design in three replications. These parents were used for making the crosses in half diallel fashion to develop the F_1 seed for the future studies. Genotypes were grown in three replicated trials after one week interval of each trial to get the maximum crosses. The pollinated panicles were identified with tag indicating the names of female and male parents with date of pollination. The fertilized panicles were harvested after the maturation to collect the F_1 seed. The parents and the F_1 generation were tested under water stress condition to see genetic potential in replicated trial in 2010.

The experiments were carried out under green house in pots with controlled temperature and adequate moisture. The moderate water stress was imposed at about 50% of applied irrigation in a control plot (35% relative humidity) at both seedling stage and reproductive stage. The 35°C temperature was maintained for all experiments. The weather conditions were normal during the experiments and sandy clay loam type soil was used for all the experiments. Stress was given both at seedling and reproductive stage of the parents and their F_1 crosses. Data for plant height, tiller per plants, seeds per panicle, 1000 seed weight, seed length width ratio and yield per plant at maturity stage of each genotype/F_1 population. A replication comprised of 36 entries (28 F_1s+ parents). One seed of each cross and parent was planted in each pot. Five seeds of each parent and their respective crosses were planted separately in pots. Data was recorded of each parent plant and their respective cross on the basis of following observations:

(1) Plant height: The plant height was measured in centimeters from the base of the main tiller to the tip of the panicle.
(2) Tillers per plant: Tillers per plant of each plant was counted separately. The standard to decide productive tillers was 5 seeds per panicle.
(3) Seeds per panicle: Seeds per panicle of main tiller of each plant was counted separately.
(4) 1000 seed weight: The 1000 seed weight of each genotype was measured in grams.
(5) Yield per plant: The whole plant yield of each genotype was measured in grams.
(6) Length width ratio: The seed length width ratio of each genotype was calculated by using the following formula;

$$\text{Seed length width ratio} = \frac{\text{Seed length (mm)}}{\text{Seed width (mm)}}$$

Statistical analysis

The data recorded were subjected to the statistical analysis. Analysis of variance was carried out for all parameters, and then estimated genetic parameters and their proportional ratios were determined according to Hayman (1954) and Mather (1949). The general combining ability and specific combining ability were calculated according to the Griffing's (1956) procedure using model 1 and method 11, where block and variety effects are assumed fixed and only one set of the crosses were used with the parents.

RESULTS

Study of genetic parameter

All the genetic parameters are described in Table 1 for various morphological traits.

Table 1. Analysis of the genetic parameters of various morphological traits under normal condition and water stress conditions.

Genetic parameter	Plant height		Tillers/plant		Seeds/panicle		1000 seed weight		Yield/plant		Seed length width ratio	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
D	192.93*	164.40*	8.52*	4.45*	14.57*	0.13*	13.64*	20.12*	1187.64*	899.67*	0.10*	-0.024ns
H1	707.37*	599.73*	24.84*	17.79*	515.82*	0.98*	508.07*	499.05*	4111.09*	4231.19*	0.95*	0.57*
H2	591.63*	490.47*	16.91*	13.49*	438.51*	0.86*	432.71*	479.23*	3173.32*	3256.02*	0.80*	0.49*
F	211.07*	128.32*	10.67*	5.55*	-21.35*	0.11*	-22.03*	2.75*	1535.92*	1300.04*	0.17*	-0.016ns
h2	42.15*	3.68ns	2.19*	0.193*	1269.14*	0.036ns	1229.37*	2141.95*	63.07*	40.60ns	0.33*	0.012ns
E	4.46*	12.32*	0.116*	0.017*	0	0.036*	0	0	3.30*	17.14*	0.011*	0.053*
(H1/D)1/2	1.910	1.91	1.7	1.99	5.95	2.66	6.1	4.98	1.86	2.16	2.99	0
h2/H2	0.081	0.0086	0.148	0.016	3.3	0.048	3.24	5.1	0.022	0.014	0.46	0.029
H2/4H1	0.209	0.2	0.17	0.19	0.21	0.21	0.21	0.24	0.19	0.19	0.21	0.21
h2b	0.978	0.94	0.98	0.99	1	0.88	1	1	0.99	0.98	0.95	0.74
h2n	0.243	0.35	0.4	0.32	0.34	0.22	0.33	0.13	0.27	0.25	0.148	0.15

Value is significant when it exceeds 1.96 (t-tabulated value) after dividing it with its standard error. D = Additive variance; H_1, H_2 and h^2= Dominance variance; F= Product of additive and dominance alleles; E= Environmental variance; $(H_1/D)1/2$= Degree of dominance; h^2/H_2 = Number of effective factors; $H_2/4H_1$= Balance of positive and negative alleles; h^2b= Broad sense heritability; h^2n= Narrow sense heritability.

Plant height

In both cases (under normal and water stress conditions), the genetic component showed the positive and significant values of "D", indicating that genetic differences occur in the parents. Significant values of both H_1 and H_2 combined with the situation represent the unequal distribution of positive and negative effects of alleles at the additive loci in the parents. On the other hand, different proportional ratios give the information about the degree of dominance, such as the positive and negative effects of alleles within the parents, number of effective factors that control the trait and narrow sense heritability of the parents. A graphical representation of plant height showed that in both watering conditions, it was controlled by over-dominance type of gene action as regression line cuts the Wr-axis below the point of origin. Since the regression line followed the unit slope, epistasis was therefore absent for this trait. In both watering conditions variety super basmati contains maximum dominant genes followed by CB-40 since it was nearest to the point of origin (Figure 1).

Tillers per plant

The positive and significant values of different genetic components for productive tillers per plant under normal and water stress conditions. The entire genetic parameters showed positive signifi-cant variations under both irrigation conditions. Different proportional ratios were also formed from the variance components that give the information about the types of gene action among the parents and their cross combinations. Graphical repre-sentation of this trait showed that it was controlled by over dominance type of gene action as regression line intersects the Wr-axis below the point of origin in both environments. Also, since the regression line did not deviate from the unit slope, epistasis was absent for this trait. Distribution of genotypes in the graph showed that Super Basmati contains maximum dominant genes for this trait in normal conditions, but when drought was imposed, the trend of genes changed in the varieties and variety CB-42 became the maximum dominant genes containing variety (Figure 2).

Seed per panicle

The positive and significant values of different genetic components for seeds per panicle under normal and water stress conditions are shown in Table 2. All the genetic components showed positive and significant variation in both irrigation conditions except h^2 that showed positive non-significant variation under water stress condition. Different proportional ratios were also formed from
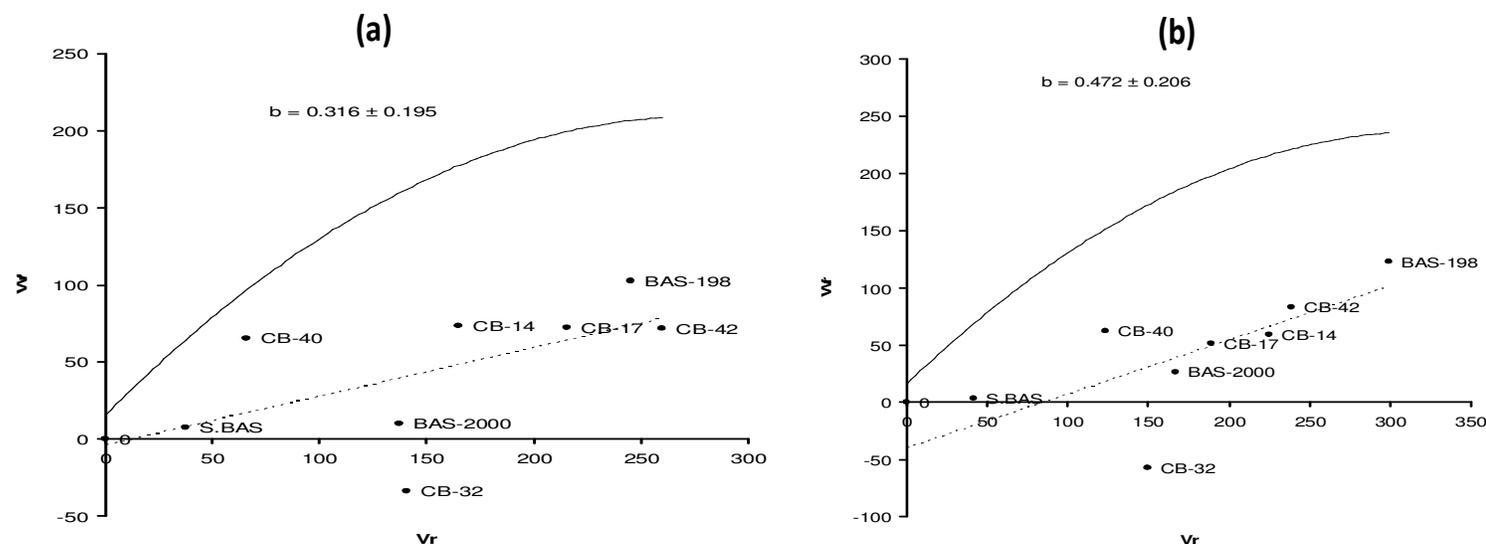
Figure 1. Vr-Wr graph for plant height under normal (a) and water stress (b) condition.
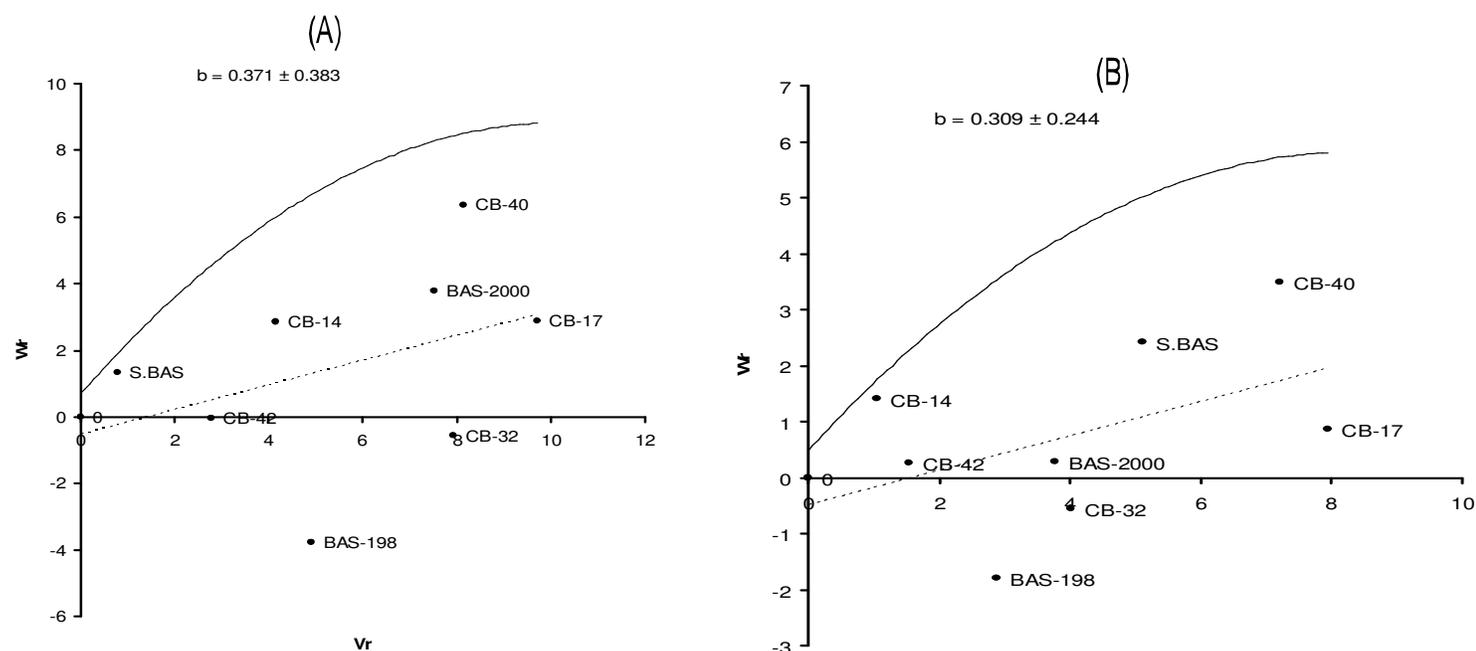

Figure 2. Vr-Wr graph for productive tillers per plant under normal (a) and water stress (b) conditions.

the variancecomponents that give the information about the types of gene action among the parents that were used in the cross combination. Seeds per panicle were controlled by additive type of gene action with partial dominance in normal irrigation conditions, but this mode of gene action changed to over dominance in water stress conditions as point of interception was below the axis. This may be due to the interaction of genes with the environment. Moreover, since the regression line followed the unit slope, epistasis was not present. Distribution of array points along the regression line showed

that Basmati-198 contains maximum dominant genes in normal conditions, but in water stress conditions CB-42 was the maximum dominant containing genotypes as it was closest to the point of origin (Figure 3).

1000-seed weight

The positive and significant values of different genetic components for 1000 seed weight under normal and water stress conditions are shown in Table 2. All the

Table 2. General and specific combining ability analysis under normal and water stress conditions.

Source of variation	Under normal water condition						
	D.F	PH (cm)	T/P	S/P	1000SW (g)	Y/P (g)	LWR
Rep.	2	1.25	0.12	6.33	0.36	0.529	0.091
GCA	7	243.60**	12.74**	1391.60**	25.84**	14.57**	0.151**
SCA	28	168.21**	5.15**	894.73**	10.59**	54.21**	0.233**
Error	70	0.844	0.14	1.30	0.11	0.157	0.012

Source of variation	Under water stress condition						
	D.F	PH (cm)	T/P	S/P	1000SW (g)	Y/P (g)	LWR
Rep.	2	0.308	0.149	1.13	0.258	0.0005	0.235
GCA	7	270.56**	6.76**	457.93**	25.16**	11.78**	0.099**
SCA	28	141.27**	3.85**	671.26**	12.07**	12.84**	0.116**
Error	70	0.064	0.018	0.771	0.038	0.091	0.037

PH= Plant height; T/P= Tillers per plant; S/P= Seeds per panicle; 1000SW= Seed weight; Y/P= Yield per plant; LWR= Length width ratio. Level of significance p<0.05= * and P<0.01= **
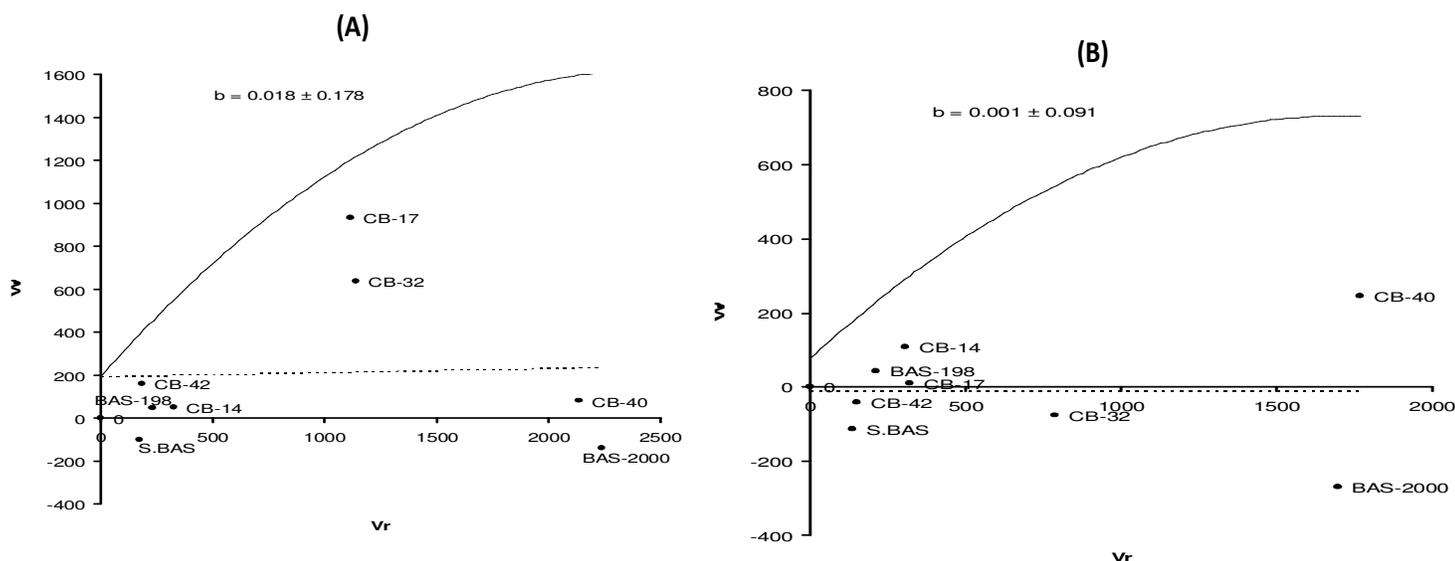
Figure 3. Vr-Wr graph for seeds per panicle under normal (a) and water stress (b) conditions.

genetic parameters showed positive and significant variation among the parents. In this case there were no environmental effects on genotypes in both irrigation conditions. Different proportional ratios were also formed from the variance components that give the information about the types of gene action among the parents that were used in various cross combination. Graphs in the figure below showed that this trait was controlled over dominance type of gene action as point of interception was below the point of origin in both environments. Unit slope of regression line indicates that epistasis was absent. Distribution of array points showed that CB-42 contains maximum dominant genes for this trait in both environmental conditions as it was nearest to the point of origin. However, recessive genes were present in

Basmati-2000 (Figure 4).

Seed length-width ratio

The positive and significant values of different genetic components for length width ratio under normal and water stress conditions are shown in Table 2. The entire genetic parameter showed positive significant variation among all the genotypes that used in the study under normal water condition. On the other hand, two genetic components (D and F) showed negative non-significant variation and one genetic component h^2 showed positive non-significant variation among the genotypes that used in this study. Different proportional ratios were also
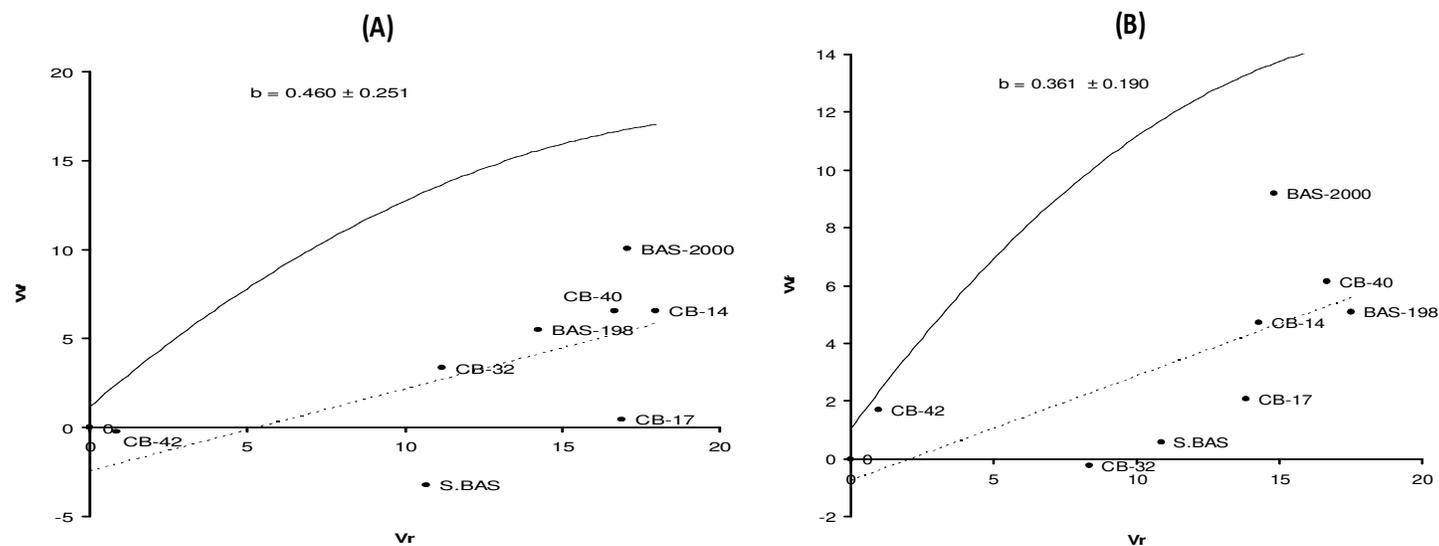
(A)

b = 0.460 ± 0.251

(B)

b = 0.361 ± 0.190

Figure 4. Vr-Wr graph for 1000 seed weight under normal (a) and water stress (b) conditions.

(A)

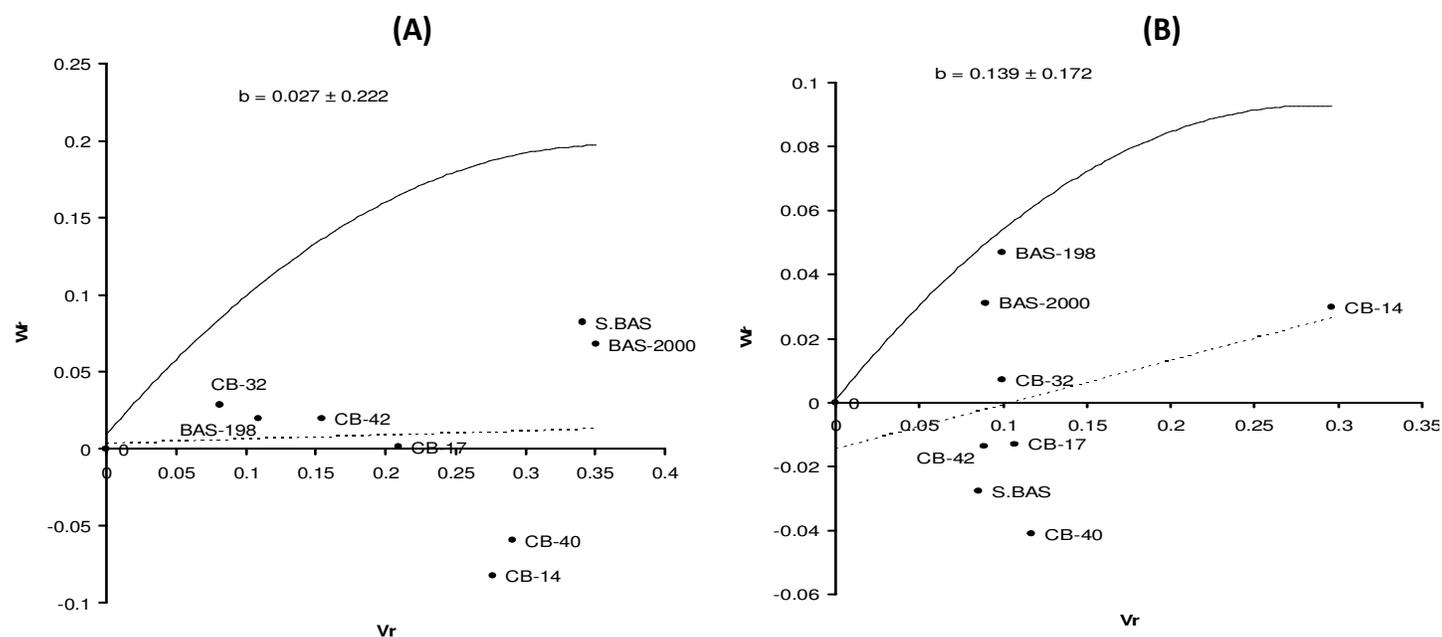b = 0.027 ± 0.222

(B)

b = 0.139 ± 0.172

Figure 5. Vr-Wr graph for yield per plant under normal (a) and water stress (b) conditions.

formed from the variance components that give the information about the types of gene action among the parents. Vr/Wr graph for length width ratio showed that this trait was controlled by additive type of gene action with partial dominance in normal irrigation conditions, but this mode of gene action changed to over dominance in water stress conditions as point of interception was below the axis. This may be due to the interaction of genes with the environment. And since the regression line followed the unit slope, epistasis was not present. The distribution of array points along the regression line showed that

Basmati-198 contains maximum dominant genes in normal conditions, but in water stress conditions CB-42 was the maximum dominant containing genotypes as it was closest to the point of origin (Figure 5).

Yield per plant

Table 2 shows the positive and significant values of different genetic components for yield per plant under normal and water stress conditions. The genetic
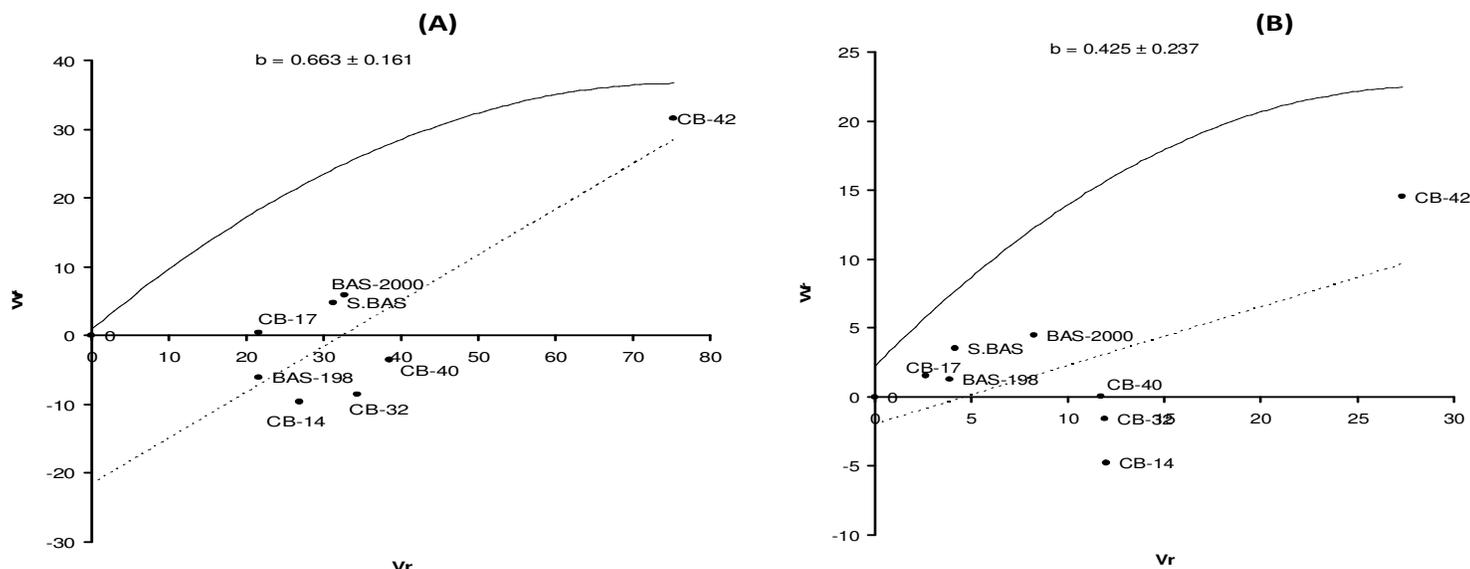
Figure 6. Vr-Wr graph for seed length width ratio under normal (a) and water stress (b) conditions.

components showed positive and significant variation among the parents in both cases. Different proportional ratios were also formed from the variance components that give the information about the types of gene action among the parents. High value narrow sense heritability under water stress condition showed that more additive types of genes were present in parents that used in the study. Graphical presentation of the data showed that this trait was controlled over dominance type of gene action as point of interception was below the point of origin in both environments (Figure 6). Unit slope of regression line indicates the absence of epistasis. The distribution of array points showed that CB-17 contains maximum dominant genes for this trait in both environmental conditions as it was nearest to the point of origin.

Combining ability estimates

The goal of a plant breeder in a self-pollinated crop like rice is to develop a true breeding (homozygous) population among various desirable characteristics contributing to the yield of rice crop with great genetic potential. The accomplishment of this objective would be based on the selection of suitable parents and nature of the gene action controlling the various traits in plants. The nature of gene action controlling the plant traits helps in developing the selection strategy in segregating populations.

According to Griffing (1956), the combining ability analysis partitions the genotypic variability into variances due to general combining ability (GCA) and specific combining ability (SCA), which represent the additive type of gene action and dominance type of gene action for the controlling of various traits of parents and their hybrids under normal and water stress conditions.

Combining ability analysis in this research work was carried out for different morphological traits following the method of Griffing (1956). The data were initially subjected to the analysis of variance that showed the significant variation among the eight parents and their 28 F_1 hybrids. Varietal differences were highly significant both at normal and water stress conditions in respect of all the six traits studied. The results of mean square values of all the traits were presented in the (Table 2).

General combining ability (GCA) effects

All drought tolerant parents viz., CB-17, CB-40, Basmati-198 and susceptible parents CB-14, CB-32, CB-42, Super basmati and Basmati Pak., showed themselves as good general combiners for some of the traits both under normal and water stress conditions. Some parents showed highly significant positive GCA effects for some traits, while others showed negative significant GCA effects for some traits (Table 3).

Specific combining ability (SCA) effects

The specific combining ability effects are summarized in Table 4. Some crosses showed highest positive significant effects under both normal and water stress condition for specific traits The crosses productive tillers per plant (Basmati-198 × CB-17), seeds per panicle (Basmati-2000 × CB-42, Basmati-198 × CB-14), seeds per panicle (Bas-198 × CB-14, Bas-2000 × CB-42, Super Bas × CB-40) 1000 seed weight (Basmati-2000 × CB-32, CB-42 × CB-32), yield per plant (CB-32 × CB-14) and seed length width ratio (Bas-2000 × CB-14) showed

Table 3. General combining ability effects of the parents.

Parent	Plant height		Productive tillers/ plant		Seeds/ panicle		1000 seed weight		Yield per plant		Seed Length- width ratio	
	Normal	Water stress	Normal	Water stress	Normal	Water stress	Normal	Water stress	Normal	Water stress	Normal	Water stress
CB-14	-8.22**	-59.00**	-11.91**	-27.00**	-25.21**	-12.04**	11.78**	32.00**	-5.27**	1.40	2.00**	-1.20
CB-17	-9.78**	-34.00**	-5.36**	-11.50**	63.33**	20.88**	14.00**	21.40**	18.18**	11.50**	-5.00**	0.60
CB-32	-18.56**	-53.57**	-5.73**	1.25**	2.73**	5.76***	-15.78**	-26.40**	4.73**	3.80**	0.67	-1.80**
CB-40	-4.00**	-13.00**	5.45**	18.00**	39.97**	37.96**	7.33**	4.00**	-5.82**	-3.30**	6.00**	0.80
CB-42	-14.11**	-52.71**	-9.00**	-21.00**	-18.79**	-7.36**	23.67**	40.00**	13.73**	16.60**	4.00**	3.40**
Super Basmati	10.78**	45.71**	13.45**	23.00**	-38.76**	-42.52**	-30.33**	-53.80**	-11.91**	-14.30**	-0.67	1.60*
Basmati-198	5.63**	5.57**	15.18**	26.25**	-28.39**	-25.88**	-10.22**	-17.80**	-7.09**	-13.10**	-4.67**	-1.20
Basmati-2000	38.26**	161.29**	-1.91**	-9.00**	5.12**	23.16**	-0.33	0.16	-6.55**	-2.50**	-2.67**	-2.00**
S.E (gi)	0.27	0.07	0.11	0.04	0.33	0.25	0.09	0.05	0.11	0.1	0.03	0.05

Level of significance p<0.05= * and P<0.01= **

promising results for yield and yield related traits. Thus, these hybrids could be used as such or further selection to develop high yielding rice genotypes suitable for cultivation under water stress condition. In addition, those crosses which showed highest positive significant SCA effects under normal and water stress conditions consi- dered to be more important specific combiners for the development of new high yielding varieties. Various morphological traits were studied to see the SCA effects of different cross combinations. Those cross combinations that had high SCA effects were considered to be good specific combiners and those having a negative significant SCA effects were considered to be the poorest specific combiners.

DISCUSSION

Genetic parameter analysis indicated the pre- sence of significant variation among all the genetic components for various morphological traits studied under normal and water stress conditions for all the traits as described separately in Table 1. Among all the traits, only the seed width in normal condition and length-width ratio under water stress condition showed additive non- significant variance that showed that less additive genes occur in the case. The positive and significant values of additive variance "D" and dominance variance "H_1, H_2 and h^2"showed that genetic differences occurred among genotypes used in the study. Significant values of both H_1 and H_2 showed the unequal distribution of positive and negative alleles within the parents. Lower values of D indicate the higher degree of domi- nance gene action than the additive gene action. In most of the traits, positive significant environ- mental effects occur on all the genotypes. The proportional value $(H_1/D)^{1/2}$ estimates the average degree of dominance over the loci (Mather, 1949). Hence in the present study, over dominance occur in most of the traits in both irrigation conditions. On the other hand, $H_2/4H_1$ ratio indicates the number of positive and negative alleles within the parents and also shows the dominance of the parents. It has maximum value of 0.25 (because it is squared quantity, the actual proportion being v = V = 0.5), when positive and negative alleles are equally distributed over the loci. If this ratio is greater than one, it indicates the excess of dominant alleles among the parents. The ratio h^2/H_2 indicates the number of effective factors within parents and controls the specific character and exhibit the dominance. In the present study, the overall results indicated that both additive and dominant types of gene action occur within the parents. Additive effects are important for the fixation of the trait and for early selection of the plants. On the other hand, dominance effects are not fixable due to segregation and late selection may be fruitful for the selection of genotypes for the next generation of the future breeding studies to develop new rice varieties. Additive and non- additive gene actions play a very important role in the determination of heritability in those traits which are controlled by additive gene effects (Dabholkar, 1992; Falconar, 1988). In the present study, different heritability was estimated for each trait. Different researchers also estimated the heritability for different traits (Kato, 1990) grain weight and number of grains per panicle.The nature and magnitude of gene action involved in phenotypic expression of plant traits is crucial for

Table 4. Specific combining ability effects of F$_1$ crosses.

Cross	Plant height		Productive tillers/ plant		Seeds/ panicle		1000 seed weight		Yield per plant		Seed width ratio	Length-
	Normal	Water stress	Normal	Water stress	Normal	Water stress	Normal	Water stress	Normal	Water stress	Normal	Water stress
CB-17 × CB-14	-4.30**	-12.78**	-5.32**	-1.42*	-23.06**	-15.99**	-10.47**	-23.53**	-10.20**	-3.30**	3.54**	0.29
CB- 32 × CB-14	-0.93	19.17**	-2.85**	3.08**	-28.05**	-32.72**	-4.83**	8.18**	16.06**	16.33**	2.53**	0.47
CB-40 × CB-14	-0.02	-0.01	-5.56**	-4.25**	27.32**	48.99**	7.80**	15.24**	-9.74**	-0.85	0.30	-2.82**
CB-42 × CB-14	-6.04**	57.61**	-0.24	1.92**	-9.62**	-10.27**	-1.80**	-6.71**	-8.40**	-7.12**	-0.91	3.00**
Super Bas× CB-14	28.48**	-25.35**	-4.91**	-21.00**	-17.48**	-5.24**	-12.47**	-21.18**	5.77**	7.88**	5.25**	-1.29*
Bas-198 × CB-14	-5.69**	50.70**	-9.50**	-19.75**	34.93**	39.19**	-10.17**	-18.82**	-1.80**	0.42	-1.01	-3.47**
Bas-2000 × CB-14	14.43**	-105.04**	-1.79**	0.60	7.01**	1.22	-3.37**	-11.41**	-15.06**	-13.85**	6.97**	2.00**
CB-32 × CB-17	-28.19**	77.13**	8.21**	-11.75**	-2.07**	14.76**	2.60**	3.47**	-14.37**	-5.61**	-0.71	2.06**
CB-40 × CB-17	18.08**	23.35**	1.26*	-5.00**	-11.66**	-17.08**	1.57**	5.82**	-21.14**	-14.24**	-4.44**	-1.12
CB-42× CB-17	6.80**	-36.17**	-6.47**	-16.17**	-25.85**	-26.59**	-2.03**	-3.18**	-24.80**	-17.33**	-0.10	0.24
Super Bas × CB-17	-7.43**	-14.78**	2.65**	-6.83**	-15.51**	-16.77**	-17.13**	-36.71**	-16.71**	-7.73**	-4.34**	3.24**
Bas-198 × CB-17	-5.00**	-17.74**	4.06**	22.33**	-16.57**	-0.19	8.83**	13.47**	-1.17	2.30**	-6.57**	-1.18
Bas-2000 × CB-17	14.90**	49.87**	5.15**	10.75**	-17.23**	-17.00**	-2.17**	-7.65**	-15.57**	-8.45**	3.54**	-1.41*
CB-40 × CB-32	-7.20**	-26.17**	1.50*	25.17**	-3.66**	-0.70	-12.47**	-22.59**	-13.80**	-5.82**	6.97**	0.59
CB-42 × CB-32	9.05**	32.83**	3.47**	8.83**	12.25**	11.70**	5.93**	13.82**	-4.40**	3.12**	1.62*	1.06
Super Bas × CB-32	-14.24**	-42.87**	4.24**	4.75**	17.91**	17.29**	10.13**	11.47**	7.94**	10.94**	-1.31*	-4.06**
Bas-198 × CB-32	-14.24**	-44.39**	12.50**	35.08**	-17.18**	-1.99**	-20.50**	-38.24**	-3.77**	-1.76**	2.73**	0.29
Bas-2000 × CB-32	-33.07**	-111.78**	5.24**	3.00**	-9.04**	-11.29**	15.43**	22.88**	-10.77**	-2.33**	-3.33**	1.65*
CB-42 × CB-40	8.93**	37.00**	-6.91**	-15.83**	-10.42**	-8.82**	14.80**	25.59**	-13.54**	-6.33**	-5.25**	1.06
Super Bas × CB-40	10.30**	37.78**	-4.32**	-3.83**	31.46**	35.30**	3.23**	9.12**	-7.74**	-0.88	-1.52**	-0.47
Bas-198 × CB-40	-4.83**	-7.52**	-4.18**	-0.83	21.42**	25.75**	-7.17**	1.47*	-9.89**	1.12	-4.04**	-0.88
Bas-2000 × CB-40	-6.53**	-23.57**	3.12**	-9.50**	-12.50**	-23.89**	7.17**	6.18**	-13.66**	-8.42**	-8.28**	-3.29**
Super Bas × CB-42	24.36**	89.04**	-2.29**	8.58**	-28.25**	-17.86**	13.17**	32.88**	-10.03**	-4.94**	-4.34**	2.24**
Bas-198 × CB-42	-11.45**	-49.04**	10.91**	33.75**	-11.17**	-15.18**	-7.83**	-17.65**	-10.94**	-8.91**	1.01	0.94
Bas-2000 × CB-42	-20.55**	-37.00**	2.74**	-0.17	101.03**	116.63**	-8.13**	-14.94**	-9.77**	-3.73**	-8.18**	0.06
Bas-198 × Super Bas	12.72**	35.04**	-1.12	2.33**	-2.65**	-10.52**	3.60**	9.71**	-9.94**	-6.70**	-2.53**	-1.94**
Bas-2000×Super Bas	-8.92**	-40.70**	-3.91**	-22.33**	2.71**	0.68	-6.80**	-9.65**	-6.29**	0.09	-3.84**	0.04
Bas-2000×Bas-198	8.10**	20.43**	10.00**	-8.42**	-21.51**	-24.82**	-9.50**	-14.35**	-12.77**	-4.88**	6.57**	0.08
S.E. (sii)	0.83	0.23	0.34	0.12	1.03	0.79	0.3	0.17	0.35	0.33	0.099	0.17

Level of significance p<0.05= * and P<0.01= **

successful development of crop cultivars. The right selection of parents for hybridization is very important for development of varieties as well. In breeding high yielding varieties of crop plant, the breeders often face the problem of selecting promising parents and crosses. Gene action studies provide such information so as to frame the breeding programme effectively. From the diallel analysis, Hayman (1954) behavior of gene action of different yield related traits was studied in normal and water stress conditions. Although most of the traits show constant gene action in both environments, gene action of some traits was, however, affected by the environment. Morphological traits like plant height, productive tillers per plant, days to maturity, 1000 seed weight and yield per plant showed over dominance type of gene action in both environments (normal and drought environments), while seeds per panicle and seed length width ratio showed this type of gene action only in water stress conditions. These results are supported by the findings of Akram et al. (2007), Nematzadeh (1987), Singh et al. (1970) and Kaushik (1984).

The analyses of variance (mean square values) from the combining ability analysis for all the morphological traits are presented in Table 2. It showed that the variances due to GCA effects were higher than that due to SCA effects, suggesting predominance of additive type of gene action. The combining ability analysis also helps in the identification of desirable parents (Venkatesan et al., 2007) and new superior cross combination for the improvement and development of new rice varieties. This will help plant breeders for the future breeding studies, and it may be useful for making improvements and manipulation of component traits. However, not all the variations were due to additive effects. Specific effects were also significant for all the traits. The finding of the present study showed that the additive gene effect generally plays a more important role than the dominance gene effects for the traits studied. These findings were confirmed by several earlier findings of Malini et al. (2006), Pradhan et al. (2006), Ramkrishan et al. (2006), Verma and Srivastava (2004) and Vanaja et al. (2003). Non-additive type of gene action was also important for the appropriate breeding studies. Some researcher have also reported similar results related to yield and yield related traits of non-additive type of gene action (Vyas and Kumar, 2008; Allahgholipour and Ali, 2006; Vanaja et al., 2003; Manuel and Palanisamy 1999; Yadav et al., 1999 and Kausik and Sharma, 1988)

The parents (Super basmati, Basmati-198 and Basmati-2000) showed positive significant GCA effects in plant height with respect to other parents under both conditions. On the other hand, CB-40, Super basmati and Basmati-198 showed a positive significant effect in productive tillers per plant. Genetic variability and diversity is based on the basmati rice germplasm and various phenotypic/genotypic traits that are used for the germplasm enhancement and development of new rice

varieties under normal and water stress condition (Ashfaq et al., 2012; Ashfaq and Khan, 2012). In rice, stress associated genes play a very important role for the protection of plants against abiotic stresses. On the other hand, fragrance gene in Basmati is also associated with a loss of function of a gene involved in abiotic stress tolerance and causing loss of performance (Fitzgerald et al., 2010). Akhtar et al. (2010) studied the genetic variation/association between eight basmati rice varieties under different water regimes, on the basis of various morphological and physiological traits for the screening of future breeding studies. Basmati fragrant rice cultivars possess the genetic potential in comparison with non-fragrant rice (Hussain et al., 1987; Lorieux et al., 1996; Bradbury et al., 2005) for accumulating 2-AP (volatile compounds having a characteristic of aroma).

The present study indicated that some specific cross combinations showed high positive significant effects, while others showed negative effects under both conditions. On the other hand, it was noted that some good general combiners may not produce good F_1 combinations instead of high GCA effects. Good combiner parents sometimes showed negative SCA effects in the hybrids. Similar results have been reported for grain yield (Khanorkar et al., 1984; Mohanty and Khush, 1985; Falconer and Mackay, 1996).

Conclusion

These study present sufficient exploitable genetic variability for various yield related traits among the rice genotypes. A good number of rice genotypes were screened and identified on the basis of various morphological traits that would be used in the development of F_1 hybrid seed. The genotypes CB-17, CB-42 and Basmati-198 were good general combiners for productive tillers per plant, 1000 seed weight and yield per plant especially under water stress condition, and also gave specific cross combinations for good yield and yield related traits. The crosses productive tillers per plant (Basmati-198 × CB-17), seeds per panicle (Basmati-2000 × CB-42, Basmati-198 × CB-14), 1000 seed weight (Basmati-2000 × CB-32, CB-42 × CB-32) and yield per plant (CB-32 × CB-14) showed promising results for yield and yield related traits. Thus, these hybrids could be used as such or further selection in order to develop high yielding rice genotypes suitable for cultivation under water stress condition. There is also a great genetic potential for the specific traits contributing to increase yield of the basmati rice crop and equally beneficial for the farmers' community to generate more income by using these rice materials.

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