

## Estimation of combining ability and gene action for yield characteristics in rice under water-stress conditions

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### ABSTRACT

Rice maternal lines along for better combining abilities run an effective instrument for increasing rice manufacture. In this study, twenty-four combinations of four female and six male lines began by applying a line  $\times$  tester mating design. Two different water regimes: regular irrigation and water stress were used to test crosses and their maternal lines. In general, water deficit had a significant impact on yield component characteristics and was regulated by non-additive gene action. As it should have been, the non-additive effects played a big role in the grain yield (GY). The parental line Giza 178 and Sk104 were registered as the best combiners for GY under both conditions. The crosses combinations G.178  $\times$  N22, SK107  $\times$  IRAT112 and SK104  $\times$  AZUCENA showed considerably favorable SCA effects on grain yield. In general, the results of this study revealed that the GCA and SCA are important for the understanding of the genetic components and gene actions of rice yield attributes. As a result, we confirmed the importance of taking these findings into account when selecting superior parents for developing superior hybrid under the water-stress conditions in rice.

**Keywords:** genetic components, heritability, water deficit, rice.

### INTRODUCTION

Rice is the best worldwide crop that feeds the majority of the world's population. It will continue to play an important role in global food and livelihood security systems in Egypt. Researchers predicted that the global population would rise steadily from 7.7 billion today to 9 billion in 2035 (Leonilo *et al.*, 2020). As a result, an increase in overall rice consumption from 763 million tons to 852 million tons will be required (Khush, 2013).

The demand for continual strategies to boost rice production remains an enormous task, given fixed water supplies and many biotic and abiotic challenges. During the summer season, rice is about 22% of Egypt's total growing area and consumes about 20% of the country's total water resources. Because Egypt's water resources are restricted, in addition to the country's growing population, the overall water requirements for the rice crop are a severe challenge due to the river Nile's limited irrigation water supply. Some rice-growing areas, particularly those near the terminal irrigation canals in the northern part of the Nile Delta, face irrigation water shortages at various stages of growth, which is considered one of Egypt's most important restrictions on rice production (Abd Allah *et al.*, 2009). As a result, one of the main objectives of rice breeding for increasing rice production in Egypt is the development of water stress tolerance genotypes with high

yield potential. Even though rice is sensitive to drought, the crop provides a huge opportunity to breed for drought tolerance, due to its inherent capacity and availability of huge genetic variability for wider adaptations in varied ecosystems. Despite the realization of the importance of water use efficiency in crop improvement, the available genetic variability for drought tolerance has not been progressively exploited in drought improvement breeding endeavors (Venuprasad *et al.*, 2008). Breeding for drought tolerance requires knowledge of gene action and combining ability of yield traits under stress and non-stress environments (Ashfaq *et al.*, 2012). It is vital to identify possible rice parents and their hybrids that associate well for both high yielding and water stress tolerance in order to build an adequate program for the synthesis of genotypes with advantages of water stress tolerance and high yielding ability. The selection of an efficient breeding program is dependent on a thorough understanding of the type gene action involved in character expression. General combining ability (GCA) is a useful tool for determining which parents to choose based on the performance of their progenies (Sprague and Tatum, 1942). It represents additive gene action. A measure of hybrid performance called specific combining ability (SCA) evaluates the hybrids and counteract similar non-additive gene action that occurs with dominance, over-dominance, and epistatic effects in the presence of a dominant gene

(Latha *et al.*, 2013 and Su *et al.*, 2017). The most common method for producing hybrids is line  $\times$  tester mating design test analysis, which is a reliable biometric method for computing GCA and SCA, as well as conditional information about the nature of gene actions (Kempthorne, 1957). In hybrid combinations, genetic variation among parental lines plays a significant influence. In rice breeding, many morphological methodologies have been used to analyze the genetic variation of parental lines (Leonilo *et al.*, 2020). To assess the nature of gene action, combining ability for yield traits under stress and normal conditions, and to identify the best combining parents, and hybrid combinations for developing high yielding drought tolerant rice genotypes, ten parental genotypes with differential reactions to water stress were crossed in a line  $\times$  tester analysis fashion in the current study.

## MATERIALS AND METHODS

In season 2019, the four female parents (lines) and six male parents (testers) were crossed according to line  $\times$  tester mating design to obtain 24 F<sub>1</sub> crosses (Table 2). Parental lines and their crosses combinations were measured at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during one rice growing season in 2020. The mechanical properties of soil were clay (64.3%), sand (7.6%), and silt (28.1%) with a pH varying from 7.8 to 8.5.

In two experiments, F<sub>1</sub> crosses were produced with male and female parents. One of the experiments was done under normal (N) conditions of constant flooding. The second experiment was moved to water stress establishing (S) where it was quickly irrigated every 10 days without leaving any standing water. This arrangement is called "water stress." The stress status was assessed two weeks following the maturity date. All of the trials were designed using a randomized complete block design (RCBD) with three replicates. After thirty-day old seedlings were transplanted one per hill, with a gap of 20-centimeter between plants and rows. The Egyptian Rice Breeding Program recommended that all cultural concepts be followed. At maturity, phenotypic data for nine yield component traits were estimated by randomly selecting ten plants of each replication in each genotype. These yield traits contained days to heading (day; DH), plant height (cm, PH), panicle length (cm, PL), No. of panicles / plant (PP), No. of tillers / plant (TP), spikelet sterility (%; SS), 100-grain weight

(g; GW), grain yield plant (GY) and Harvest index (HI) according to (IRRI, 2013).

## Data analysis

Parental lines and the resulting F<sub>1</sub> crosses were aggregated based on nine agronomic traits using the UPGMA hierarchical clustering method (Esteves, 2018). Variance analysis: Phenotypic traits are analyzed with CV% using MSTAT software. Through package planning and performance analysis, the correlation between trait values was estimated and plotted using Pearson's correlation coefficients (Wei *et al.*, 2018 and Peterson *et al.*, 2018). Both general (GCA) and specific (SCA) combining ability analysis were achieved by using the line  $\times$  tester method according to (Kempthorne, 1957). The 5 % and 1 % L.S.D tests were used to achieve a significant test for the effects of GCA and SCA. Heritability was calculated in its broad sense ( $h^2 b$ ) and narrow sense ( $h^2 n$ ) for the traits studied according to (Griffiths *et al.*, 2000). Additive ( $\sigma^2 A$ ) and dominant ( $\sigma^2 D$ ) genetic variances, as well as additive and non-additive genetic methods were calculated, as explained (Verma and Srivastava, 2004).

## RESULTS

### Genotypes performance and variation

Ten parental lines and their F<sub>1</sub> crosses were analyzed based on their morphological data. The dendrogram analysis revealed two main clusters, each with sub-clusters of different types of diversity (Fig. 1). The dendrogram separated all genotypes (parent and their F<sub>1</sub> crosses) into two clusters. First cluster included only one genotype Giza 177. Two sub-clusters were constructed from the second cluster. Among the two sub-clusters, the first sub-cluster comprised SK104 $\times$  IRR1163, G.177  $\times$  IRR1163 and IRR1163. The second sub-cluster formed a separate sub-cluster with two groups. Among the second sub-cluster groups, first group included SK104 $\times$  IRGC1165, SK104 $\times$  N22, G.178  $\times$  IRR1163, SK104, IRR1-148, SK104 $\times$  AZUCENA, G.178  $\times$  AZUCENA, G.178  $\times$  N22 and G.178  $\times$  IRR1148. Second group was further divided into three sub-groups; first sub-group included two crosses namely; SK107  $\times$  IRR1148 and G.177  $\times$  IRGC1165. The second sub-group contained the following genotypes; G.177  $\times$  N22, SK107  $\times$  IRR1163, SK107  $\times$  IRAT112, SK104 $\times$  IRAT112, G.177  $\times$  IRAT112, G.177  $\times$  IRR1148, SK107  $\times$  AZUCENA, SK107  $\times$  N22, AZUCENA, IRR1148, N22, IRGC1165 and IRAT112. Third sub-group included G.178  $\times$  IRGC1165, G.178  $\times$

IRAT112, SK107 × IRGC1165, SK104, G.177 × AZUCENA, SK107 and G.178, (Figure 1). This revealed that depending on their origin, more comparable genotypes were grouped together in the same cluster (performance).

The average performance of males (testers), females (lines), and cross combinations under two irrigation environments are shown in (Table 1 and Figure 2). Water stress conditions had a significant impact on all attributes in this study when compared to normal irrigation conditions. PH, TP, PP, SS, GY, and HI were the attributes most influenced by water stress. Under normal conditions, the parental lines and their cross combinations performed better in all attributes than under water stress conditions (Table 1 and Figure 2).

In addition, the hybrids were reported to have higher levels of DH, PH, TP, PP, SS, PL, GY and GW comprised the parental lines evaluated. All 34 genotypes showed a significant decrease under water stress compared to normal irrigation conditions. Moreover, the cross combinations G.177 × IRGC 1165 followed by G.178 × IRI 163 and SK104 × IRR148 showed the highest number of panicle/plant under normal condition, meanwhile, the combinations Sk104 × N 22, G.178 × IRI 163 and SK104 × IRGC 1165 showed superiority under water stress conditions. The cross combination Sk104 × N 22 followed by Sk107 × IRR1 148 exhibited superiority in the 100-grain weight under normal condition and the cross combination Sk104 × N 22 followed by Sk107 × IRR1 148 exhibited dominance in 100-grain weight up the other tested genotypes under water stress. For grain yield trait, the crosses combinations G.178 × IRR148, Sk104 × IRR1-148 and SK104 × AZUCENA gave the highest values under normal irrigation. The cross G.178 × IRR148 followed by the cross G.178 × N 22 confirmed the highest grain yield under water-stress conditions (Table 1).

Figure 2 shows the correlation analysis for the nine characteristics of all materials under both normal irrigation and water-stress conditions. Under normal growth conditions, 14 correlation coefficients were found to be significantly associated with the characteristics (Figure 2, upper triangle). Among these, four had highly positive correlations. Two of the highly positive correlations were between the GY and TP and PP, and the other two were between the SS and TP.

There were varying degrees of correlations between all other traits in the same text (Fig. 2,

upper triangle). A total of 11 significant correlation coefficients ( $p < 0.05$ ) were established in terms of water stress conditions, ten of which were positive and one of which was negative (Fig. 2 bottom triangle). There were four absolute correlations among the positive correlations: GY with TP and PP, PP with TP, and PH with DH. There was also one negative association, which was between HI and SS (Fig. 2 bottom triangle).

#### Analysis of variance

Under both conditions, the ANOVA revealed significant differences between the 34 genotypes tested for nine variables (Table 2). Furthermore, no significant differences were found between replications for any of the attributes, demonstrating that all crosses have inherent variability. The mean squares of irrigation regimes were highly significant for all examined characteristics, indicating that the performance of genotypes tested differed under the two irrigation regimes. These findings corroborate those published by Perween *et al.* (2020) in rice.

Under the two irrigation conditions and their combined data, mean squares due to genotypes, parents, and combinations were highly significant for all analyzed variables, suggesting the considerable variation among the genetic materials used in this study. Highly significant mean squares due to interaction of genotypes, parents and crosses with irrigation treatments were obtained for most of the traits studied, reflecting the fact that these genotypes were inconsistent in their response to irrigation treatments. These findings agree with those reported in rice by Sabar and Arif (2014).

Under growing conditions, mean squares ascribed to parent *vs* cross were considerably higher for all attributes and their combined data (Table 2). Similarly, the differences generated by the line × tester (SCA) were significant for all traits under the growing conditions (Table 2). This result reflected interactions between females (lines) and males (testers) and resulted in significantly varied specialized combining ability effects, which might be explained by the parental lines' wide genetic variability.

#### Estimating of the genetic parameters and gene action

The dominant variance ( $\sigma^2 D$ ) attributable to the relative relevance of specific combining ability (SCA) for all examined traits was higher than the additional variance ( $\sigma^2 A$ ) attributed

to the relative importance of GCA in both normal and aqueous stresses, according to the findings (Table 3).

Regarding the estimate of heritability, in the broad sense ( $h^2_b$  %), the results showed that heritability was high values for most of the traits studied under the two irrigation environments. Under the two irrigation environments, the values of narrow-sense ( $h^2_n$  %) heritability ranged from low to high for most traits (Table 3).

#### Estimation of general combining ability:

Estimated significant differences in the effects of GCA for nine parental lines for nine agronomical traits under the two irrigation environments (Table 4). GCA estimates for the lines (local parents) revealed that G.177 (line) was the best pool due to the extremely negative GCA effect value of DH in both the two irrigation environments, respectively, this line (G.177) was a good standardized for SS under normal irrigation conditions as well. G.178 gave the best effect value of GCA for PH, PP, TP and GY under the two irrigation environments (Table 4). SK104 was the best aggregate for PP, PL, TP, GY and HI under the two irrigation environments. Under water stress, this parent was a good combiner for SS and GW. SK107 revealed the highest effect value of GCA in terms of DH, SS and GW under the two irrigation environments. This parent was a good PH combiner under normal conditions. In addition, it was the most effective combiner for HI under water stress. Similarly, with respect to the testers, IRR148 was found to be the best combiner of DH, PP, TP, GW, GY and HI under the two irrigation environments. It was well combiner in terms of PL in the case of water stress. (Table 4). IRAT112 was the best combiner for DH, PH and SS under both normal and water stress conditions. Under water stress conditions, it performed well in terms of HI. Under the two irrigation regimes, IRGC1165 was an excellent combiner for PH, PP, TP, SS, and GW, and it was found to be the best combiner of DH under water stress (Table 4).

N22 was found to be a good combiner of HI under the two irrigation environments. It was well combiner in terms of GW under water stress. Under normal conditions, IRR163 was a good combiner for HI, and under water stress conditions, it was a good combiner for SS (Table 4). AZUCENA was found to be the best general combiner for SS and GY under the two irrigation environments and was a good

combiner in terms of PH and HI under normal conditions (Table 4).

#### Estimating of specific combining ability:

SCA estimates for 24 cross combinations of traits studied under the two irrigation environments are presented in (Table 5). The findings revealed that six (under normal) and eight (under stress) of the 24 cross combinations had significantly detrimental SCA effects on DH. SCA had a negative effect on PH in 8 (below normal) and 7 (under stress). Under the two irrigation conditions, there were eight (under normal) and seven (under stress) significant positive SCA effects for PP (Table 5). Under two irrigation environments, five and four crosses exhibited superior SCA effects in terms of PL, respectively. Five and three crosses excepted the highest effect of SCA on TP under the two irrigation environments, respectively.

Ten (under normal) and 11 (under stress) recorded the highest SCA effects on GY. Similarly, 11 (under normal) and 10 (under stress) showed significantly negative SCA effects for HI (Table 5). Seven combinations, G.177 × IRGC1165, G.177 × IRR163, G.178 × N22, SK 104 × IRGC1165, SK 104 × AZUCENA, SK 107 × IRR148 and SK 107 × IRAT112 possess significantly positive SCA effects for GY under each of the two irrigation environments (Table 5). Seven groups, G.177 × IRGC1165, G.177 × IRR163, G.178 × N22, SK 104 × IRGC1165, SK 104 × AZUCENA, SK 107 × IRR148 and SK 107 × IRAT112 possess significantly positive SCA effects for GY under each of the two irrigation environments (Table 5).

#### Correlation and distribution of combining ability of yield traits

The correlation of the combining ability to all characteristics, such as GCA and SCA, contributed to the various traits in different ways. The correlation between GCAs or SCAs differs from the correlation between characteristics. The relationship between GCAs and SCAs for yield attributes under normal conditions is demonstrated in Figure 1. (Fig. 3A). The correlation between GCAs for two traits could be the same or different from the correlation between SCAs. We recorded that GCA PP was highly significant and positively correlated with GCA TP, which was comparable to SCA for these two traits. This indicates an additive positive effect between these two traits.

The data showed that GCA GY was positive and significantly correlated with GCA TP and GCA PP but SCA GY was not significantly correlated with SCA TP and PP. So, dissection of the phenotype into GCA and SCA helped explain the genetic relationships between traits related to yield. Correlations between GCAs and SCAs for yield attributes are demonstrated in the instance of stress conditions (Fig. 3B). The data indicated that GCA PP was significantly positively correlated with GCA TP.

PP SCA was highly significant and only positively correlated with TP SCA and a negative correlation was established between SCA GW, SCA DH and SCA PH (Fig. 3B). These data cleared a positive additive effect between PP and TP traits. There were non-additive negative effects between GW, DH, and PH. On the other hand, there was a negative correlation between GCA PH, GCA GY, GCA GW, GCA SS, GCA TP and GCA PP. However, SCA HI was negatively correlated with SCA PP, SCA TP, SCA SS and SCA GW. This suggests that those attributes have both positive and negative non-additive and additive effects. As a result of this association analysis, it was discovered that GCA and SCA are essential for understanding the genetic linkages between yield traits.

## DISCUSSION

### Variation analysis

The present study evaluated the yield traits properties of ten parental lines (4 lines and 6 testers), along with 24 F<sub>1</sub> crosses under each of the two irrigation environments. The assessment of genetic variation between parental genotypes is absolutely essential for the effective use of heterosis breeding. In our study, cluster analysis mentioned a significant difference in diversity between parental genotypes (Fig. 1), there may be a high potential for obtaining the best new combinations by crossing of the genotypes with the highest genetic distance (El-Refaei *et al.*, 2016). The study found that water stress conditions had a significant effect on all attributes when compared to normal conditions (Table 1).

The genotypes that displayed the lowest reduction under water deficit conditions were more tolerant to drought than others. Previous research has revealed similar findings (Manickavelu *et al.*, 2006 and Herwibawa *et al.*, 2019). According to the results for yield trait which showed high reduction in its value

under drought stress comparing with normal condition, this denotes that the yield has been reduced by terminal stress, which happens towards the end of the growth stage and can start before flowering. Furthermore, yield characteristics may be reduced as a result of vegetative stage drought (Ouk *et al.*, 2007), but this loss could be less than end stress due to recovery growing mostly in the latter growing season (Kamoshita *et al.*, 2008). In general, crosses performed better for traits related to yield than parental lines, reflecting the apparent hybrid vigor (Table 1). Except for DH and PH under both conditions and SS under water stress conditions, the data demonstrated a positive association between yield attributes. GY was found to have a positive relationship with TP, PL, PP, SS, and HI (Fig. 2). These findings were consistent with prior findings in which grain yield exhibited a significant correlation with yield-related attributes under normal conditions (Leonilo *et al.*, 2020).

### Genetic components of variance

All traits are under the genetic control of non-additive genetic effects, according to the assessment of genetic parameters. In each of the two irrigation conditions, non-additive gene action regulates all attributes (Table 3). Other research in the same text has revealed additive and non-additive gene action, showing their relevance in rice development (Huang *et al.*, 2015). The non-additive gene action controlled the traits that are in agreement with (Singh and Chaudhary 1979, Padmavathi *et al.* 2012, Hasan *et al.*, 2015 and Anis *et al.*, 2016).

Results of the present studies indicated that the values of broad sense heritability ( $h^2_b$ ) were higher than the values of narrow sense heritability ( $h^2_n$ ) for all traits studied under each of the two irrigation environments (Table 3). The total genetic variance for most variables was non-additive, according to these findings. Hybridization of target genotypes based on phenotypic performance may be helpful for yield component traits. Non-additive genes have been shown to have an effect on GY and other yield component variables in previous research (Anis *et al.*, 2016, El-Mowafi *et al.*, 2018 and Ganapati *et al.*, 2020).

### Combining ability and gene action

The ability to combine genotypes was investigated in order to discover genotypes with superior genetic potential for developing cross combinations with the desired trait and to track the action of genes involved in the trait's manifestation (Sprague and Tatum

1942). In terms of genetic view point, GCA assess the action of the additive and additive  $\times$  additive gene action, while the SCA measures the action of the non-additive gene. In the present study, in the case of the parents; Giza 178 and Sk104 were the best for GY and good combiners for most crop component traits under each of the two irrigation environments. However, in the case of (testers) male parents, IRR148 was the best combiner of GY and a good combiner of most traits under each of the two irrigation environments. This finding was superior to earlier research in which no parent had the best or worse effects of GCA on all yield component attributes (Latha *et al.*, 2013 and Yuga *et al.*, 2018).

The parental genotypes were discovered to be good general combiners, since they were able to participate genes that had positive effects on major quantitative characteristics. With regard to GCA effects of parents, it could be suggested that these parents may be preferred for hybridization and selection programs to extract desirable plants from segregating populations to improve the majority of the studied traits. Rahaman (2016) also concluded that parents with maximum GCA effects were found better responsive to produce high yielding hybrids.

The cross combinations SCA effects were all statistically positive for at least one yield attribute, according to the SCA estimation. Among these, crosses G.178  $\times$  N22, SK107  $\times$  IRAT112, and SK104  $\times$  AZUCENA exhibited significant and positive SCA effects on GY under each of the two irrigation environments (Table 5). These results indicated that these genotypes could be used for further exploitation. Furthermore, these findings revealed that no single combination exhibited positive SCA values for all of the traits investigated at the same time. This finding is consistent with earlier research findings (Huang *et al.*, 2015 and Yuga *et al.*, 2018). Furthermore, some of the cross combinations with high-significance SCA for many traits had both parents with good GCA or at least one parent reflecting the impacts of good GCA, according to the findings.

At the same time, other crosses exhibited higher significantly SCA in desirable traits than one parent reflects poor GCA effects. This could be because a good combiner parent has suitable additive effects while a bad combiner parent has epistatic effects (Tyagi *et al.*, 2018 and Singh *et al.*, 2019).

In terms of SCA, good  $\times$  good general combiners did not necessarily produce the best crosses. Even though both parents were GCA negative for that trait in each of the two irrigation conditions, crosses combinations SK 107  $\times$  IRAT112 and G.177  $\times$  IRR163 had the highest SCA for GY (Table 5). In contrast, the SK 104  $\times$  IRR148 cross showed negative effects of SCA even though both parents possessed good GCA for GY under each of the two irrigation environments. These results are achievable because of the complex combinations and interactions of the parents' genes positive and negative alleles. Previous study has revealed similar results (Sanghera and Hussain 2012 and Latha *et al.*, 2013).

### Correlation

Breeders use criteria such as the GCA: SCA variance ratio comparison in order to classify traits that have relatively more fixable additive variance, which will greatly aid in the exercise of selection in subsequent generations based on one or more traits. The relationships between GCAs or SCAs can vary from those between traits per se. This is due to the assessed traits additive and non-additive genetic effects. In our research, we revealed that the correlation between GCAs for two parameters could be the same or different from the relationship between SCAs, and that this inconsistent association between GCA and SCA indicates a complicated genetic interaction of quantitative traits (Su *et al.*, 2017 and Chen *et al.*, 2019). GCA and SCA are important for determining genetic relationships between yield variables, according to correlation analysis. As a result, we recommend that breeders consider both GCA and SCA when selecting elite genotypes for new combinations, particularly under water stress.

### CONCLUSIONS

A line  $\times$  tester analysis of yield component attributes under each of the two irrigation regimes was used to calculate the combining ability and gene action of four female genotypes (lines) and six male genotypes (testers). All characteristics are influenced by water shortage and governed by the actions of non-additive genes, according to the data analysis. Male and female parents who have the potential to arrive superior hybrids under each of the two irrigation environments were identified. Under these conditions, only the best hybrids with the greatest GY values were determined. The contrary connections between GCA and SCA in our study revealed the

relevance of both GCA and SCA for detecting genetic linkages between yield variables, thus we suggest using both in developing breeding programs to produce superior hybrids.

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**Table 1.** Performance of rice genotypes for five economic yield characteristics under normal irrigation (N), water-stress conditions (S) and their combined data.

Genotypes	No. of Panicles / Plant			100-grain weight (g)			Spikelet sterility %			Grain yield plant (g)			Harvest index (%)		
	N	S	Comb	N	S	Comb	N	S	Comb	N	S	Comb	N	S	Comb
Giza 177(L <sub>1</sub> )	16.97	9.33	13.15	2.95	2.08	2.52	7.73	25.60	16.67	36.07	17.77	26.92	39.73	20.03	29.88
Giza 178 (L <sub>2</sub> )	18.40	14.00	16.20	2.42	1.97	2.20	10.00	19.73	14.87	41.33	32.67	37.00	37.63	27.57	32.60
Sakha 104 (L <sub>3</sub> )	20.63	17.63	19.13	2.76	2.51	2.64	3.40	6.23	4.82	39.67	33.33	36.50	40.07	32.03	36.05
Sakha 107 (L <sub>4</sub> )	16.87	13.77	15.32	2.73	2.47	2.60	8.00	12.90	10.45	37.17	31.33	34.25	34.30	27.77	31.03
IRRI-148 (T <sub>1</sub> )	18.10	16.07	17.08	3.31	3.10	3.21	7.57	11.63	9.60	38.00	32.00	35.00	33.60	30.27	31.93
IRAT-112 (T <sub>2</sub> )	15.97	13.43	14.70	2.96	2.73	2.85	7.97	12.77	10.37	28.90	25.77	27.33	29.63	25.67	27.65
IRGC (T <sub>3</sub> )	14.10	12.07	13.08	3.08	2.87	2.98	6.20	8.40	7.30	30.00	26.67	28.33	30.67	26.23	28.45
N.22 (T <sub>4</sub> )	15.93	12.63	14.28	2.77	2.33	2.55	5.87	9.63	7.75	27.50	24.07	25.78	28.77	24.20	26.48
IRRI-163 (T <sub>5</sub> )	15.63	13.97	14.80	2.46	2.29	2.38	8.90	11.97	10.43	28.33	23.73	26.03	30.40	26.80	28.60
AZUCENA (T <sub>6</sub> )	17.43	14.20	15.82	2.63	2.37	2.50	8.17	12.53	10.35	37.57	32.17	34.87	31.63	27.33	29.48
G.177 X IRRI148	22.43	13.00	17.72	3.00	2.35	2.68	12.20	27.47	19.83	43.00	20.67	31.83	37.03	24.43	30.73
G.177 X IRAT112	21.33	15.17	18.25	2.81	2.32	2.57	10.63	15.10	12.87	30.75	18.80	24.78	31.73	23.80	27.77
G.177 X IRGC1165	30.73	20.17	25.45	3.11	2.60	2.86	10.03	13.90	11.97	37.67	24.67	31.17	31.40	20.07	25.73
G.177 X N22	16.60	13.00	14.80	2.60	2.17	2.39	15.57	29.50	22.53	32.80	21.80	27.30	43.80	24.77	34.28
G.177 X IRRI163	18.33	13.63	15.98	2.70	2.00	2.35	14.53	21.20	17.87	37.83	22.93	30.38	41.63	22.27	31.95
G.177 X AZUCENA	21.13	16.00	18.57	2.80	2.60	2.70	12.10	18.47	15.28	43.80	22.43	33.12	39.20	21.53	30.37
G.178 X IRRI148	27.53	21.50	24.52	3.07	2.82	2.95	18.13	28.07	23.10	54.00	49.33	51.67	35.30	24.87	30.08
G.178 X IRAT112	25.27	19.00	22.13	3.10	2.73	2.92	8.57	35.93	22.25	40.67	29.33	35.00	29.60	23.23	26.42
G.178 X IRGC1165	23.23	19.63	21.43	3.00	2.71	2.86	15.13	20.33	17.73	36.33	29.67	33.00	31.17	21.57	26.37
G.178 X N22	23.33	18.63	20.98	2.73	2.55	2.64	16.50	20.43	18.47	48.67	42.33	45.50	41.27	32.07	36.67
G.178 X IRRI163	30.37	23.93	27.15	2.12	1.79	1.96	20.40	25.03	22.72	40.67	32.67	36.67	37.60	23.07	30.33
G.178 X AZUCENA	27.13	20.87	24.00	2.97	2.54	2.76	11.03	17.13	14.08	49.33	37.67	43.50	40.27	23.17	31.72
SK104 X IRRI148	29.07	23.13	26.10	3.07	2.80	2.94	18.53	24.53	21.53	51.00	38.67	44.83	47.17	32.10	39.63
SK104 X IRAT112	17.53	15.73	16.63	2.63	2.59	2.61	10.07	11.33	10.70	37.60	28.07	32.83	40.37	30.33	35.35
SK104 X IRGC1165	28.10	23.43	25.77	2.70	2.31	2.51	9.63	12.20	10.92	42.00	37.67	39.83	40.23	29.03	34.63
SK104 X N22	27.73	25.23	26.48	3.27	3.07	3.17	15.90	19.23	17.57	34.33	27.67	31.00	33.13	25.17	29.15
SK104 X IRRI163	19.33	16.10	17.72	2.65	2.45	2.55	12.07	13.83	12.95	37.73	31.47	34.60	43.00	31.03	37.02
SK104 X AZUCENA	25.70	21.50	23.60	2.91	2.68	2.80	17.50	26.07	21.78	50.67	37.67	44.17	40.73	25.27	33.00
SK107 X IRRI148	22.60	19.67	21.13	3.21	2.98	3.10	5.03	8.53	6.78	47.33	40.67	44.00	40.03	27.23	33.63
SK107 X IRAT112	16.83	15.17	16.00	3.07	2.76	2.92	10.43	13.87	12.15	36.17	28.97	32.57	35.77	29.00	32.38
SK107 X IRGC1165	23.27	21.73	22.50	3.18	2.87	3.03	16.60	19.57	18.08	39.33	29.33	34.33	41.73	29.63	35.68
SK107 X N22	16.93	14.03	15.48	2.75	2.67	2.71	13.73	15.63	14.68	28.73	21.17	24.95	39.20	26.67	32.93
SK107 X IRRI163	18.03	15.03	16.53	2.97	2.87	2.92	11.13	13.17	12.15	30.70	28.97	29.83	31.47	27.93	29.70
SK107 X AZUCENA	16.40	15.43	15.92	2.59	2.49	2.54	10.77	13.27	12.02	30.33	27.20	28.77	37.83	29.77	33.80
Mean	21.15	17.00	19.07	2.85	2.54	2.70	11.47	17.51	14.49	38.41	29.69	34.05	36.68	26.35	31.51
drought Levels (T)															
L.SD 0.05	-	-	0.27	-	-	0.02	-	-	0.07	-	-	0.08	-	-	0.13
L.SD 0.01			0.36			0.02			0.09			0.11			0.17
Genotypes (G)															
L.SD 0.05	1.79	1.43	1.14	0.11	0.10	0.08	0.28	0.52	0.28	0.52	0.43	0.34	0.75	0.76	0.52
L.SD 0.01	2.38	1.90	1.50	0.15	0.14	0.11	0.38	0.69	0.37	0.69	0.57	0.45	0.99	1.02	0.69
Interaction (T×G)															
L.SD 0.05	-	-	1.61	-	-	0.11	-	-	0.40	-	-	0.48	-	-	0.74
L.SD 0.01			2.21			0.15			0.52			0.64			0.98

**Table 2:** Analysis of the line × tester mating design variances for nine yield traits under the two irrigation environments.

S.O.V	d.f		Days to heading (DH)			Plant height (PH)			No of panicles / Plant (PP)		
	S	Comb	N	S	Comb.	N	S	Comb.	N	S	Comb.
Replications / I	2	4	10.98	0.77	5.87	8.36	0.25	4.30	1.00	1.59	1.29
Irrigation (I)	-	1	-	-	4408.20**	-	-	14103.40**	-	-	879.18**
Genotypes (G)	33	33	269.90**	241.15**	434.58**	622.37**	447.79**	962.71**	70.67**	47.70**	110.78**
Parents (P)	9	9	221.19**	532.39**	686.77**	612.09**	749.97**	1245.07**	9.69**	14.81**	20.07**
Crosses (C)	23	23	298.50**	136.91**	352.02**	620.11**	336.48**	850.70**	65.88**	42.71**	100.11**
P vs C	1	1	50.57**	17.43**	63.69**	766.74**	288.34**	997.73**	729.74**	458.65**	1172.73**
Lines	3	3	581.52**	289.38**	800.69**	650.17**	592.41**	1074.01**	178.55**	142.50**	286.37**
Testers	5	5	345.07**	236.65**	486.35**	1301.02**	654.36**	1805.32**	72.51**	37.04**	104.22**
Lines × Testers	15	15	226.37**	73.17**	217.51**	387.13**	179.34**	487.82**	41.13**	24.64**	61.48**
G × I	-	33	-	-	76.47**	-	-	107.45**	-	-	7.59**
P × I	-	9	-	-	66.81**	-	-	116.99**	-	-	4.43**
C × I	-	23	-	-	83.39**	-	-	105.90**	-	-	8.48**
Lines × I	-	3	-	-	70.22**	-	-	168.57**	-	-	34.68**
Testers × I	-	5	-	-	95.37**	-	-	150.06**	-	-	5.33**
Lines × Testers × I	-	15	-	-	82.03**	-	-	78.64**	-	-	4.29**
P vs C × I	-	1	-	-	4.31**	-	-	57.35**	-	-	15.67**
Error	66	132	5.52	2.02	3.77	3.55	5.89	4.72	1.20	0.77	0.99
S.O.V	d.f		Panicle length (cm)			No. of tillers / plant			Spikelet sterility %		
	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
Replications / I	2	4	1.64	0.35	0.99	5.31	2.48	3.90	0.08	0.05	0.06
Irrigation (I)	-	1	-	-	405.43**	-	-	1039.60**	-	-	1857.06**
Genotypes (G)	33	33	22.42**	19.75**	37.47**	93.06**	61.53**	146.62**	53.18**	147.33**	156.44**
Parents (P)	9	9	15.04**	27.15**	35.91**	22.35**	17.77**	30.95**	10.07**	95.13**	71.65**
Crosses (C)	23	23	23.18**	15.65**	34.58**	90.23**	62.42**	145.97**	41.43**	138.94**	130.33**
P vs C	1	1	71.58**	47.59**	117.95**	794.49**	435.04**	1202.67**	711.49**	810.09**	1519.98**
Lines	3	3	79.33**	35.07**	105.60**	258.39**	177.84**	412.50**	46.86**	358.16**	305.02**
Testers	5	5	11.92**	17.40**	25.66**	95.97**	58.73**	150.00**	42.65**	50.24**	60.03**
Lines × Testers	15	15	15.70**	11.18**	23.35**	54.69**	40.56**	91.32**	39.93**	124.66**	118.82**
G × I	-	33	-	-	4.71*	-	-	7.97**	-	-	44.07**
P × I	-	9	-	-	6.28*	-	-	9.17*	-	-	33.55**
C × I	-	23	-	-	4.24*	-	-	6.68	-	-	50.03**
Lines × I	-	3	-	-	8.80	-	-	23.74**	-	-	100.01**
Testers × I	-	5	-	-	3.65	-	-	4.70	-	-	32.85**
Lines × Testers × I	-	15	-	-	3.53	-	-	3.92	-	-	45.77**
P vs C × I	-	1	-	-	1.22	-	-	26.86*	-	-	1.60**
Error	66	132	2.36	2.87	2.61	3.15	5.37	4.26	0.03	0.10	0.06

\* and \*\* denote significant differences at the 0.05 and 0.01 levels. N: Normal irrigation conditions. S: Water-stress conditions.

Table 2: Continued.

S.O.V	d.f		100-gain weight (g)			Grain yield plant (g)			Harvest index (%)		
	S	Comb.	N	S	Comb.	N	S	Comb.	N	S	Comb.
Replications / I	2	4	0.008	0.008	0.008	0.11	0.08	0.09	0.52	0.51	0.51
Irrigation (I)		1	-	-	4.983**	-	-	3883.28**	-	-	5441.53**
Genotypes (G)	33	33	0.208**	0.298**	0.457**	151.47**	153.86**	267.14**	70.82**	35.57**	70.62**
Parents (P)	9	9	0.228**	0.364**	0.526**	81.07**	79.94**	130.98**	52.66**	31.79**	46.82**
Crosses (C)	23	23	0.205**	0.276**	0.437**	156.66**	183.91**	302.09**	63.97**	38.23**	76.78**
P vs C	1	1	0.097**	0.210**	0.297**	665.78**	127.98**	688.77**	391.76**	8.23**	143.22**
Lines	3	3	0.064**	0.620**	0.510**	334.72**	748.63**	922.67**	75.70**	152.66**	184.02**
Testers	5	5	0.327**	0.287**	0.592**	314.87**	173.42**	465.91**	58.78**	11.72**	39.60**
Lines × Testers	15	15	0.193**	0.203**	0.371**	68.30**	74.46**	123.37**	63.36**	24.18**	67.72**
G × I	-	33	-	-	0.049**	-	-	38.19**	-	-	35.77**
P × I	-	9	-	-	0.066**	-	-	30.04**	-	-	37.63**
C × I	-	23	-	-	0.044**	-	-	38.48**	-	-	25.43**
Lines × I	-	3	-	-	0.175**	-	-	160.69**	-	-	44.33**
Testers × I	-	5	-	-	0.022**	-	-	22.38**	-	-	30.90**
Lines × Testers × I	-	15	-	-	0.025**	-	-	19.40**	-	-	19.82**
P vs C × I	-	1	-	-	0.011	-	-	104.98**	-	-	256.77**
Error	66	132	0.005	0.004	0.005	0.10	0.07	0.09	0.22	0.09	0.21

\* and \*\* denote significant differences at the 0.05 and 0.01 levels. N: Normal irrigation conditions. S: Water-stress conditions.

Table 3: Estimates of genetic parameters for 9 yield traits under the two irrigation environments.

S. O. V	Days to heading (days)		Plant height (cm)		No. of tillers / Plant		No. of panicles / plant		Panicle length (cm)	
	N	S	N	S	N	S	N	S	N	S
Parameter										
Additive variance ( $\sigma^2 A$ )	1.82	1.61	5.88	3.96	0.90	0.55	0.62	0.46	0.19	0.11
Dominant variance ( $\sigma^2 D$ )	73.61	23.72	127.86	57.81	17.18	11.73	13.31	7.96	4.45	2.77
Environmental variance ( $\sigma^2 E$ )	5.53	2.03	3.54	5.89	3.15	5.37	1.21	0.77	2.35	2.87
Genotypic variance ( $\sigma^2 G$ )	75.43	25.32	133.74	61.78	18.08	12.28	13.93	8.41	4.64	2.88
Phenotypic variance ( $\sigma^2 Ph$ )	80.96	27.35	137.28	67.67	21.23	17.65	15.14	9.18	6.99	5.75
Broad sense heritability ( $h^2 b$ ) %	93.18	92.61	97.41	91.30	85.15	69.59	92.06	91.62	66.28	50.16
Narrow sense heritability ( $h^2 n$ ) %	4.40	11.10	8.21	11.07	8.10	6.06	7.92	9.46	5.25	3.84
Relative importance of GCA% *	2.41	6.36	4.40	6.41	4.98	4.48	4.45	5.46	4.10	3.82
Relative importance of SCA% **	97.56	93.64	95.60	93.59	95.02	95.52	95.55	94.54	95.90	96.18
S. O. V	Spikelet sterility %		100-grain weight (g)		Grain yield / plant		Harvest index (%)			
	N	S	N	S	N	S	N	S		
Parameter										
Additive variance ( $\sigma^2 A$ )	0.04	0.36	0.0003	0.0018	2.23	2.76	0.02	0.35		
Dominant variance ( $\sigma^2 D$ )	13.30	41.52	0.0624	0.0662	22.73	24.80	21.05	7.99		
Environmental variance ( $\sigma^2 E$ )	0.03	0.10	0.0055	0.0043	0.10	0.07	0.21	0.22		
Genotypic variance ( $\sigma^2 G$ )	13.34	41.88	0.0627	0.0680	24.96	27.56	21.07	8.34		
Phenotypic variance ( $\sigma^2 Ph$ )	13.37	41.98	0.0682	0.0723	25.06	27.63	21.28	8.56		
Broad sense heritability ( $h^2 b$ ) %	99.78	99.77	92.0561	94.0337	99.59	99.75	99.00	97.48		
Narrow sense heritability ( $h^2 n$ ) %	0.56	1.70	0.9213	4.9495	16.33	18.17	0.15	7.95		
Relative importance of GCA% *	0.30	0.86	0.4785	2.6471	8.93	10.02	0.10	4.20		
Relative importance of SCA% **	99.70	99.14	99.5215	97.3529	91.07	89.98	99.90	95.80		

N: Normal irrigation conditions. S: Water-stress conditions; \* and \*\* denote significant at 0.05 and 0.01 levels.

**Table 4:** Estimates of the general combining ability (GCA) effects of parental genotypes for nine traits under the two irrigation environments.

Genotypes	Days to heading (days) (DH)		Plant height (cm) (PH)		No. panicles / plant (PP)		Panicle length (cm) (PL)		No. of tillers / plant (TP)	
	N	S	N	S	N	S	N	S	N	S
Lines										
G.177	-6.64 **	-4.21 **	5.71**	3.06**	-1.11**	-3.20**	-2.16**	-1.14**	-1.67**	-2.78**
G.178	3.83 **	-0.04	-6.77**	-8.59**	3.27**	2.23**	0.95*	-0.21	4.26**	2.62**
SK104	5.54 **	5.40 **	4.36**	2.37**	1.70**	2.49**	2.47**	2.02**	1.77**	2.83**
SK107	-2.73 **	-1.15 **	-3.30**	3.17**	-3.86**	-1.52**	-1.25**	-0.66	-4.36**	-2.66**
L.S.D 0.05	1.09	0.66	0.87	1.12	0.51	0.41	0.71	0.78	0.82	1.07
0.01	1.42	0.86	1.14	1.47	0.66	0.53	0.93	1.03	1.08	1.40
Tester										
IRRI148	-5.24**	-6.01**	-0.93	3.33**	2.53 **	0.96**	0.79	1.88**	2.69**	2.40**
IRAT112	-7.46 **	-1.01 *	-1.71**	-3.51**	-2.63 **	-2.10**	-1.98**	-1.51**	-3.54**	-2.70**
IRGC1165	2.96 **	-2.43 **	-12.41**	-11.42**	3.46 **	2.88**	0.16	-0.30	4.02**	2.95**
N22	1.17	3.15**	5.56**	1.72*	-1.72 **	-0.64*	0.28	-0.82	-1.72**	-0.70
IRRI163	6.92 **	6.74**	17.16**	10.73**	-1.36**	-1.19**	0.26	-0.05	-0.91	-0.52
AZUCENA	1.65*	-0.43	-7.68**	-0.86	-0.28	0.09	0.48	0.81	-0.54	-1.42*
L.S.D 0.05	1.33	0.80	1.07	1.37	0.62	0.50	0.87	0.96	1.00	1.31
0.01	1.74	1.05	1.40	1.80	0.81	0.65	1.14	1.26	1.32	1.72
Genotypes	Spikelet sterility % (SS)		100-grain weight (g) (GW)		Grain yield / plant (GY)		Harvest index (%) (HI)			
	N	S	N	S	N	S	N	S		
Lines										
G.177	-0.67**	1.61**	-0.038*	-0.233**	-2.42**	-8.53**	-0.48**	-3.36**		
G.178	1.78**	5.16**	-0.044*	-0.048**	4.88**	6.43**	-2.08**	-1.51**		
SK104	0.77**	-1.46**	-0.004	0.079**	2.16**	3.13**	2.83**	2.66**		
SK107	-1.89**	-5.32**	0.086**	0.202**	-4.63**	-1.03**	-0.27**	2.21**		
L.S.D 0.05	0.08	0.14	0.034	0.030	0.15	0.12	0.21	0.21		
0.01	0.10	0.19	0.045	0.040	0.19	0.16	0.28	0.28		
Tester										
IRRI148	0.30**	2.83**	0.211**	0.167**	8.77**	6.93**	1.94**	0.99**		
IRAT112	-3.25**	-0.27**	0.028	0.030	-3.76**	-4.12**	-3.58**	0.43**		
IRGC1165	-0.33**	-2.83**	0.123**	0.050**	-1.23**	-0.08	-1.81**	-1.09**		
N22	2.25**	1.88**	-0.037	0.042*	-3.93**	-2.17**	1.41**	1.00**		
IRRI163	1.36**	-1.02**	-0.267**	-0.294**	-3.33**	-1.40**	0.48**	-0.09		
AZUCENA	-0.33**	-0.59**	-0.058**	0.006	3.47**	0.83**	1.56**	-1.23**		
L.S.D 0.05	0.10	0.17	0.042	0.037	0.18	0.15	0.26	0.26		
0.01	0.13	0.23	0.055	0.049	0.24	0.19	0.34	0.34		

\* and \*\*—denote significant differences at the 0.05 and 0.01 levels respectively.

**Table 5:** Estimates of specific combining ability (SCA) effects of rice cross combinations for nine yield traits under each the two irrigation environments.

Hybrids	Days to heading (days) (DH)		Plant height (cm) (PH)		No. of panicles / plant (PP)		Panicle length (cm) (PL)		No. of tillers / Plant (TP)	
	N	S	N	S	N	S	N	S	N	S
G.177 x IRR1148	-2.67*	3.46**	0.53	2.51	-1.86**	-3.12**	-1.73	--2.48*	-1.68	-2.56
G.177 x IRAT112	5.52**	2.79**	7.02**	3.69**	2.20**	2.10**	2.38**	2.21*	2.42*	1.93
G.177 x IRGC1165	-17.63**	-8.13**	5.22**	4.79**	5.51**	2.13**	0.30	-0.17	4.92**	3.29**
G.177 x N22	1.56	4.29**	1.62	2.59	-3.44**	-1.52**	0.11	-0.02	-2.83**	-2.56
G.177x IRR1163	3.48*	0.71	5.32**	-0.86	-2.07**	-0.34	0.20	1.52	-3.21**	-1.95
G.177x AZUCENA	9.74**	-3.13**	-19.71**	-12.73**	-0.35	0.75	-1.26	-1.05	0.38	1.85
G.178 x IRR1148	5.83**	3.62**	9.69**	6.66**	-1.15	-0.06	1.13	2.89**	-1.64	0.44
G.178 x IRAT112	1.75	3.96**	-18.51**	-12.17**	1.75**	0.50	0.54	-0.89	1.82	1.27
G.178 x IRGC1165	-8.84**	-0.96	-4.17**	-7.46**	-6.37**	-3.84**	-2.77**	-1.90	-6.98**	-5.54**
G.178 x N22	-1.91	-5.21**	8.96**	2.84*	-1.09	-1.32**	2.74**	0.25	-0.60**	-2.16
G.178x IRR1163	5.67**	0.54	-4.31**	5.26**	5.58**	4.53**	-1.04	-1.11	7.76**	5.23**
G.178x AZUCENA	-2.50	-1.96*	8.34**	4.88**	1.27*	0.19	-0.60	0.75	-0.35	0.76
Sk104 x IRR1148	-2.22	-3.82**	-20.35**	-9.57**	1.95**	1.32**	1.77*	0.26	1.58	1.27
Sk104x IRAT112	-5.20*	-5.15**	6.76**	4.08**	-4.41**	-3.03**	-2.25*	-0.45	-4.90**	-3.38*
Sk104x IRGC1165	11.48**	9.60**	1.46	3.02	0.06	-0.30	1.71	2.74**	0.41	0.78
Sk104x N22	-2.29	-3.32**	-1.67	-8.52**	4.88**	5.02**	-0.85	-0.01	5.32**	6.63**
Sk104x IRR1163	-0.71	0.10	4.69**	-0.37	-3.89**	-3.57**	-3.03**	-3.11**	-5.15**	-5.28**
Sk104x AZUCENA	-1.07	2.60**	9.10**	11.36**	1.40*	0.56	2.65**	0.56	2.74**	-0.02
Sk107 x IRR1148	-0.95	-3.26**	10.12**	0.40	1.05	1.86**	-1.17	-0.66	1.74	0.85
Sk107x IRAT112	-2.07	-1.60	4.73**	4.41**	0.45	0.42	-0.66	-0.87	0.67	0.18
Sk107x IRGC1165	14.98**	-0.51	-2.51*	-0.35	0.80	2.01**	0.76	-0.68	1.64	1.47
Sk107x N22	2.64	4.24**	-8.91**	3.08*	-0.35	-2.17**	-2.00	-0.23	-1.88	-1.91
Sk107x IRR1163	-8.44**	-1.35	-5.71**	-4.03**	0.38	-0.62	3.86**	2.70**	0.61	2.00
Sk107x AZUCENA	-6.17**	2.49**	2.27*	-3.51*	-2.33**	-1.50**	-0.80	-0.26	-2.77**	-2.60
L.S.D 0.05	2.66	1.61	2.13	2.75	1.24	0.99	1.74	1.92	2.01	2.62
0.01	3.49	2.11	2.80	3.60	1.63	1.30	2.28	2.51	2.63	3.44

\* and \*\*—denote significant differences at the 0.05 and 0.01 levels of probability.

Table 5. Continued.

Hybrids	Spikelet sterility % (SS)		100-grain weight (g) (GW)		Grain yield / plant (GY)		Harvest index (%) (HI)	
	N	S	N	S	N	S	N	S
G.177 x IRR148	-0.61**	3.70**	-0.05	-0.16**	-3.41**	-8.14**	-2.37**	0.63*
G.177 x IRAT112	1.37**	-5.57**	-0.05	-0.05	-3.13**	1.03**	-2.16**	0.56*
G.177 x IRGC1165	-2.15**	-4.21**	0.15**	0.21**	1.25**	2.86**	-4.26**	-1.65**
G.177 x N22	0.81**	6.69**	-0.20**	-0.21**	-0.91**	2.08**	4.93**	0.96**
G.177x IRR163	0.67**	1.28**	0.13**	-0.04	3.52**	2.45**	3.69**	-0.45
G.177x AZUCENA	-0.08	-1.88**	0.02	0.26**	2.69**	-0.28	0.17	-0.04
G.178 x IRR148	2.87**	0.75**	0.03	0.13**	0.28	5.58**	-2.51**	-0.79**
G.178 x IRAT112	-3.14**	11.71**	0.24**	0.18**	-0.51**	-3.38**	-2.69**	-1.85**
G.178 x IRGC1165	0.50**	-1.33**	0.05	0.14**	-7.38**	-7.09**	-2.89**	-2.00**
G.178 x N22	-0.71**	-5.93**	-0.06	-0.02	7.65**	7.67**	3.99**	6.41**
G.178x IRR163	4.08**	1.56**	-0.45**	-0.44**	-0.95**	-2.77**	1.25**	-1.50**
G.178x AZUCENA	-3.60**	-6.76**	0.19**	0.01	0.92**	0.00	2.84**	-0.26
Sk104 x IRR148	4.28**	3.84**	-0.02	-0.02	0.01	-1.79**	4.46**	2.29**
Sk104x IRAT112	-0.63**	-6.27**	-0.27**	-0.08*	-0.85**	-1.35**	3.17**	1.09**
Sk104x IRGC1165	-3.99**	-2.84**	-0.29**	-0.39**	1.00**	4.21**	1.27**	1.30**
Sk104x N22	-0.30**	-0.51**	0.43**	0.37**	-3.96**	-3.70**	-9.04**	-4.66**
Sk104x IRR163	-3.24**	-3.02**	0.05	0.09*	-1.16**	-0.67**	1.75**	2.30**
Sk104x AZUCENA	3.88**	8.79**	0.10*	0.03	4.97**	3.30**	-1.60**	-2.32**
Sk107 x IRR148	-6.55**	-8.30**	0.04	0.04	3.13**	4.36**	0.42	-2.13**
Sk107x IRAT112	2.40**	0.13	0.08*	-0.04	4.50**	3.70**	1.67**	0.20
Sk107x IRGC1165	5.64**	8.39**	0.10*	0.05	5.13**	0.02	5.87**	2.35**
Sk107x N22	0.20*	-0.25	-0.17**	-0.15**	-2.77**	-6.05**	0.12	-2.71**
Sk107x IRR163	-1.51**	0.18	0.27**	0.39**	-1.41**	0.98**	-6.69**	-0.35
Sk107x AZUCENA	-0.19*	-0.15	-0.31**	-0.29**	-8.57**	-3.02**	-1.40**	2.63**
L.S.D 0.05	0.19	0.35	0.08	0.07	0.36	0.30	0.52	0.53
0.01	0.25	0.46	0.11	0.10	0.47	0.39	0.68	0.69

\* and \*\*—denote significant differences at the 0.05 and 0.01 levels of probability.

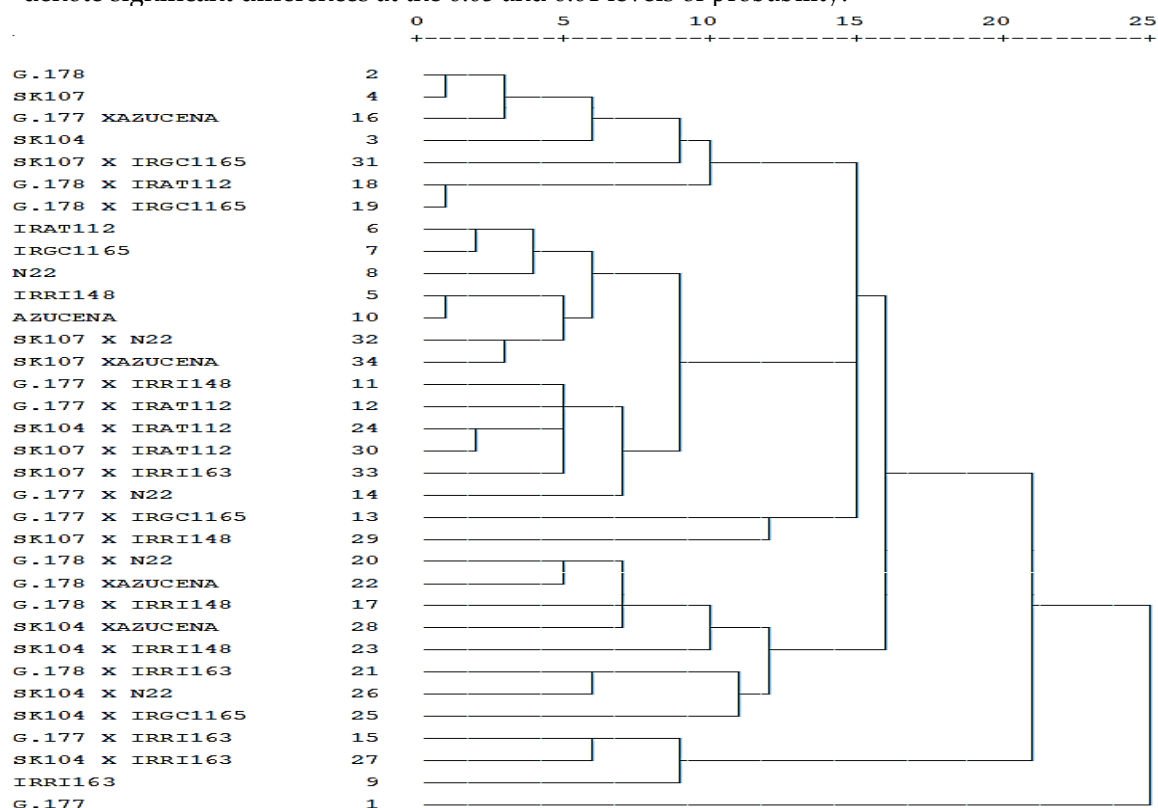
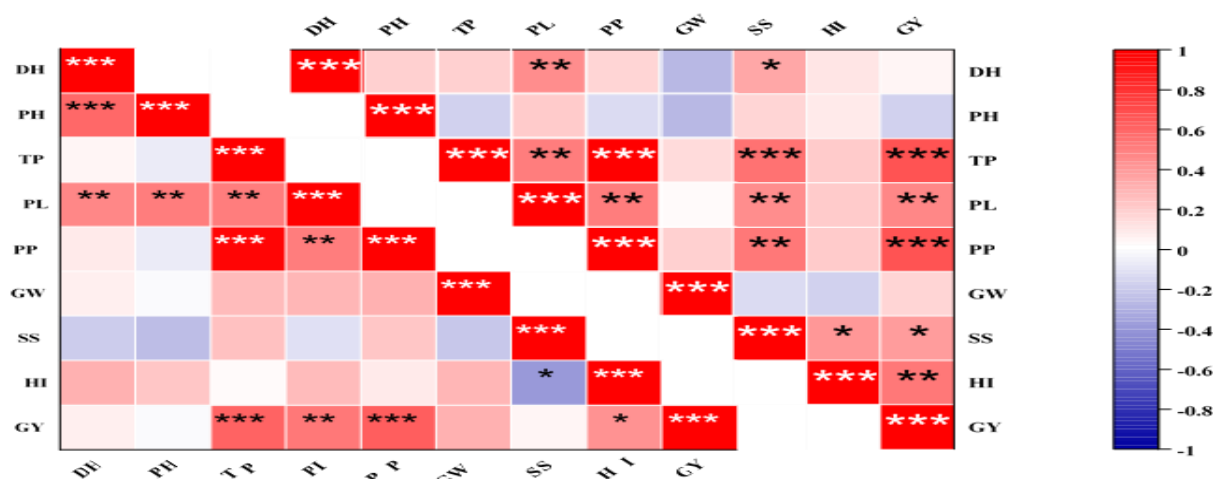
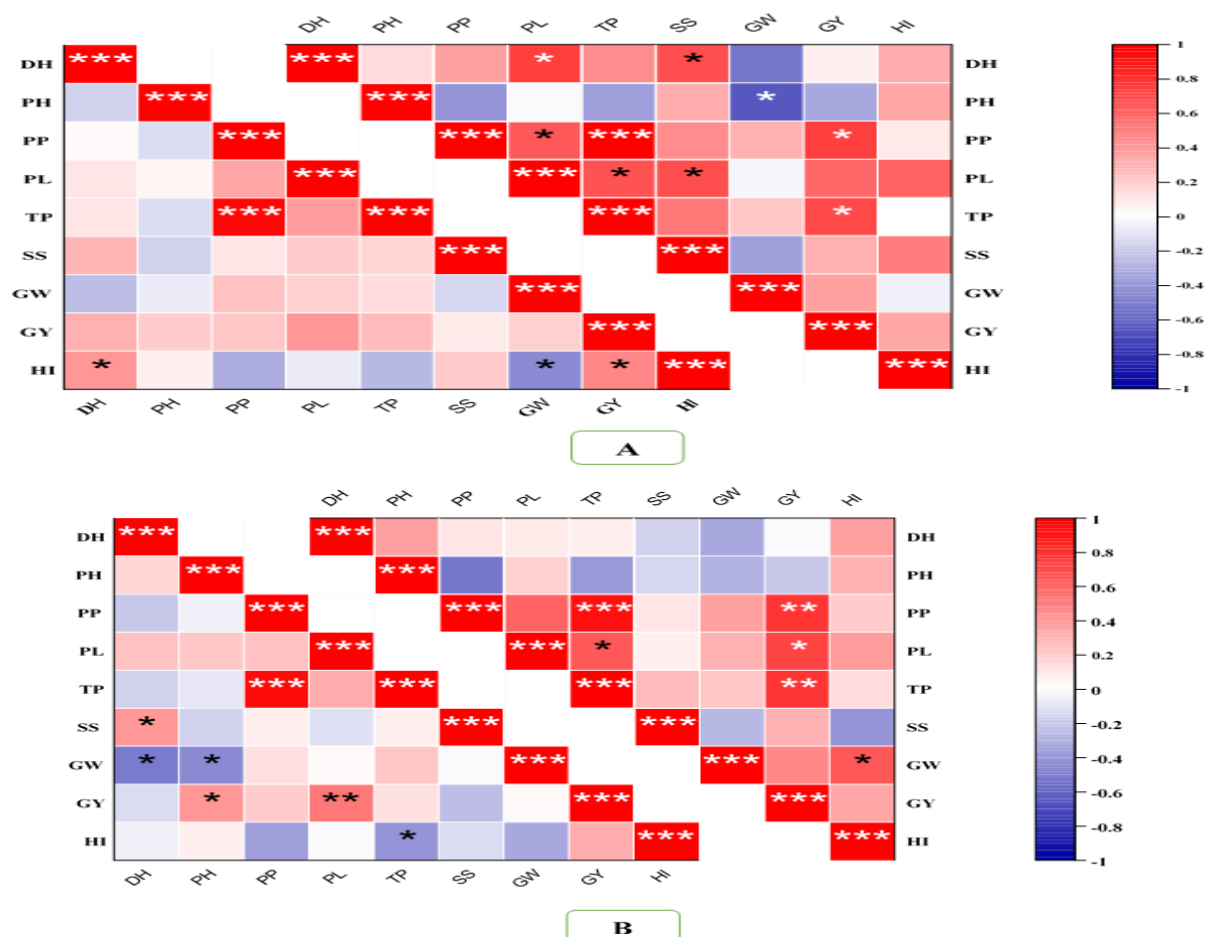


Figure 1: On the basis of morphological data for their yield component qualities, UPGMA dendrogram analysis was performed on ten parents and their crosses.



**Figure 2:** Corplot depicts the Pearson correlation between nine yield traits across 34 genotypes under normal (upper triangle) and water stress (lower triangle) conditions. Red squares indicate a positive; Blue squares indicate a negative correlation; the white boxes indicate no correlation. Asterisks indicate significant correlation using a two-tailed t-test (\* and \*\*p < 0.05; \*\*\*p < 0.01).



**Figure 3:** Corplot depicts the Pearson correlation between general and specific combining ability for nine yield traits across 34 genotypes. Blue squares indicate a negative correlation; Red squares indicate a positive correlation; the white boxes indicate no correlation. (A) GCAs (upper triangle) and SCAs (lower triangle) under normal growth conditions. (B) GCAs (upper triangle) and SCAs (lower triangle) under water stress conditions. Asterisks indicate significant correlations using a two-tailed t-test (\* and \*\*p < 0.05; \*\*\*p < 0.01).

## تقدير القدرة على التألف وطبيعة الفعل الجيني للمحصول في الأرز تحت ظروف الإجهاد المائي

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## الملخص العربي

أجرى هذا البحث بهدف دراسة القدرة على التألف والفعل الجيني المتحكم في وراثته المحصول ومكوناته في الأرز تحت ظروف الإجهاد المائي وذلك لتحديد أفضل الآباء التي تتمتع بأعلى قدرة على التألف كأداة فعالة لزيادة إنتاج الأرز. وذلك باستخدام عشرة تراكيب وراثية (أربع سلالات وست كشافات) من الأرز وتم عمل التهجينات بين الآباء باستخدام نظام التزاوج (السلالة × الكشاف) للحصول على أربعة وعشرين هجيناً. تم تقييم الآباء والهجن الناتجة منها تحت ظروف الري العادي وتحت ظروف الجفاف. تشير النتائج إلى وجود اختلافات معنوية بين التراكيب الوراثية تحت الدراسة. وأظهرت النتائج أن تأثير نقص المياه على صفة المحصول ومكوناته كانت معنوية. وكان الفعل الغير المضيف للجين (السيادي) هو المتحكم في وراثته لصفة محصول الحبوب تحت ظروف الري العادية وظروف الجفاف. وسجلت السلالتين الابويتين جيزة G.178 و SK104 أفضل قدرة عامه على التألف لصفة محصول الحبوب وكذلك العديد من الصفات الأخرى تحت ظروف الري العادية والجفاف. وأظهرت الهجن G.178 × N22 و SK107 × IRAT112 و SK104 و AZUCENA × أفضل التأثيرات المرغوبة للقدرة الخاصة على التألف حيث أعطت تأثيرات موجبة ومعنوية لصفة محصول الحبوب تحت كل من الظروف العادية للري وظروف الجفاف. وأظهرت نتائج هذه الدراسة أهمية كل من القدرة العامة للتألف والقدرة الخاصة على التألف لفهم طبيعة الفعل الجيني لصفة المحصول ومكوناته في الأرز. لذلك، نوصي بانتخاب أفضل الآباء لتطوير أصناف أرز متفوقة تحت ظروف الإجهاد المائي.

الكلمات الاسترشادية: الفعل الجيني و القدرة على التألف، ودرجة التوريث، إجهاد الجفاف، الأرز.