COMBINING ABILITY FOR GRAIN YIELD AND SOME DISEASES RESISTANCE TRAITS IN RICE (*Oryza sativa* L.) UNDER SALINE SOILS CONDITIONS.

Shehata, S. M.*; A. B. El Abd* and E. A. S. Badr**
* Rice Res. Section, Filed Crops Res. Inst., ARC, Giza, Egypt.
** Rice Plant Pathology Section, Plant Pathology Res. Inst., ARC, Giza, Egypt.

ABSTRACT

Combining ability analysis was carried out in rice through A 6 x 6 diallel set analysis excluding reciprocals involving 6 diverse parents for grain yield and some diseases resistance traits, at Rice Salinity Program at Serw farm, during 2007 and 2008 summer seasons. The ratio of variances due to general combining ability and specific combining ability ($\acute{o}2$ GCA / $\acute{o}2$ SCA) was more than unity, indicating the preponderance of additive genes in controlling, chlorophyll content, plant height, days to 50% heading, number of panicles/plant, both percentage and severity of brown spot, and grain yield/plant. Moreover, additive x additive type of gene interaction was played an important role in the inheritance of praline content and osmotic pressure. On the contrary, Predominance of non-additive gene action chiefly controlled the expression of panicle length; number of filled grains/panicle and 1000-grain weight traits. Among the parents, Sakha 101 was found to be significantly superior general combiner for all the studied traits except, earliness, chlorophyll content and both percentage and severity of brown spot. The genotypes Sakha 102 and Sakha 103 were good general combiners for earliness, chlorophyll content, and both percentage and severity of brown spot, and Sakha 104 for panicle length, 1000-grain weight, grain yield /plant , proline content, osmotic pressure and both percentage and severity of brown spot, Giza 177 and Giza 178 for earliness. Cross combinations, Giza 177 x Sakha 103, Giza 178 x Sakha 102 and Sakha 103 x Sakha 104 gave high SCA effects for number of filled grains/panicle and grain yield/plant. Seven hybrids for both percentage and severity of brown spot and 3 hybrids for plant height and days to 50% heading expressed desired significant negative SCA effects. In addition, Giza 177 x Sakha101 and Giza 178 x Sakha101 were found to be the superior cross combinations for panicle length, 1000-grain weight and chlorophyll content; and Sakha 101 X Sakha 104 for proline content and osmotic pressure. The values of mean degree of dominance $(H_1/D)^{0.5}$ exhibited over dominance with a value above the unity for all agronomic, yield and its component traits; and chlorophyll content while the other remaining traits were controlled by partial dominance. The ratio of dominant and recessive genes (K_D/K_R) in the parents was high than unity for all the studied traits except plant height, days to 50% heading, panicle length and proline content indicating more of dominant genes in the parental lines than recessive genes. High estimates of broad sense heritability was recorded for all the traits, it was ranged between 94.4% and 98.7% for osmotic pressure and percentage of brown spot disease. In addition, high estimates of heritability in narrow sense were recorded for proline content, osmotic pressure and both percentage and severity brown spot disease.Results of field tests revealed that 12 entries were resistant to blast,four moderately resistant,four susceptible,and only one highly susceptible,three inbred varieties were completely free from false smut,inaddition to five hybrids For white tip nematode,ten hybrids were not infected,but three inbred varieties had considerable infection.for brown spot the highest infected varieties were sakha 101 and Giza 177,while the lowest were Sakha 103 and Sakha104.However,the hybrids had generally lower infection than inbreeds. Results of greenhouse test showed that nine entries performed resistance to both races, while six entries were moderately resistant

to RaceIG1,and four entries were moderately resistant to Race IB45.On the other hand, three and four entries were susceptible to the first and second races respectively.

INTRODUCTION

Rice is life and princes among the cereals. More than half of the world's population depends on rice for calories and protein, especially in developing countries. The world population, particularly in that of the rice consuming countries is increasing at a faster rate. By the year 2025, about 756 million tonnes of paddy, which is 70 percent, more than the current production, Rice is one of the most important crops in Egypt and its production plays a significant part in the strategy to overcome food shortage and improve self sufficiency. It is grown on about one million feddans (about 0.42 million ha). Because of the limited land available for cultivation in Egypt, further increase in rice production from increased yield per unit area is needed. This can be achieved through varietal improvement. will be needed to meet the growing demand. Crop improvement in rice depends on the magnitude of genetic variability and the extent to which the desirable genes are heritable. Rice diseases are one of the most limiting factors of rice production in Egypt, as well as in other rice producing countries. Blast disease caused by Pyricularia grisea (cooke.) scc. is considered the most important disease affecting rice crop in Egypt (Abde-Hak, *et al.,* 1981). The second important one is brown spot caused by *Helminthosporium oryzae* (Breada de Hann). In addition to false smut, disease caused by Ustilaginoidea virens (Cke.) as a new rice disease in Egypt since 1997.sehly *et al.* (1999) and white tip Nematode caused by *Aplenchiodes bessyi* badr and El-Habashy (2007)

Brown spot disease caused by *Helminthosporium oryzae* (Breada de Hann) (*Cochliobolus miyabeanus*) is considered one of the most common diseases of rice and it is widely spread in salt affected soils. The disease can adversely affect the yield and milling quality of the grains. However, the nutritional disorders promote the disease outbreak (Ou, (1985), and Chakrabarti and Chaudhuri (1992). Heavy leaf spotting is an indication of some unfavorable growth factors, usually a soil problem (Kauraw and Samantaray, 1982). Oku (1967) reported that brown spot disease has been known to be associated with soils deficient in nutritional elements or with soils in a much-reduced condition. In breeding rice for saline environments, multiple stress tolerance traits must be considered. Some degree of cultivar tolerance for these stresses is in rice germplasm. However, understanding the physiological mechanisms of these traits, their biochemical basis, inheritance and efficient screening techniques are needed to hasten breeding progress.The deficiency of some elements like potassium, phosphorous and zinc increases severity of brown spot (Ou, 1985; Fompa & Singh, 1991). Sehly *et al.* (2001) mentioned that disease incidence was higher in case of leaching of nutrients from soil and lower oxidation- reduction potential (Eh) value.The successes of rice breeding will be limited if rice selection is only based on breeders' practices under field conditions without biometrical analysis. Quantitative genetic analysis should be dealt to have more effect in

rice selection.Combining ability has been extensively used for choosing suitable parents in crossing programs to combine traits of interest in high-yielding background. Combining ability analysis also provides estimates of genotypic variance components, useful for genetic enhancement of crops. Considering that hybrids offer good opportunity to improve yield levels, as evident from several other self-pollinated crops such as rice. GCA (general combining ability) and SCA (specific combining ability) values would be need for good combiners and proper choice of male and female parent in hybridization programs and rice selection. Heterosis may be positive or negative. Depending upon breeding objectives, both positive and negative heterosis are useful for crop improvement. In general, positive heterosis is desired for yield, and negative heterosis for early maturity. Heterosis is expressed in three ways, depending on the criteria used to compare the performance of a hybrid. The three ways are: mid-parent, standard variety and better parent heterosis. However, from the plant breeder's viewpoint, better parent and/or standard variety is more effective. The former is designated as heterobeltiosis (Fanseco and Peterson, 1968). Heritability determines the degree of resemblance between relatives and it expresses the proportion of the total variance that is attributable to differences of breeding values. The term heritability has been further divided into two different concepts, broad sense and narrow sense heritability. The broad sense heritability is defined as the ratio of total genetic variance to phenotypic variance h_2 b=VG/VP. The narrow sense heritability is the ratio of additive genetic variance to phenotypic variance h_2 n=VD/VP (Dudley and Moll, 1969).

The present investigation aimed to estimate the general and specific combining ability and nature of gene action for grain yield and its components traits, and some diseasing resistance in rice under saline soil. In addition, heterosis and heritability were appraised. Diallel analysis for grain yield and some diseasing resistance could furnish interesting information about type of gene action, which would be helpful in particular situations to understand the type of gene action involved in the expression of a trait. It can identify genotypes possessing the most dominant and recessive alleles responsible for the expression of certain trait, and also, provide information on narrow and broad sense heritability associated with the traits. This enables breeders to carry out efficient selection in the segregating generations, leading to the improvement of certain traits in breeding populations and Develop field techniques for mass screening of rice cultivars for salinity tolerance.

MATERIALS AND METHODS

The present investigation was carried out at Farm of Serw Agricultural Research Station, during 2007 and 2008 summer seasons. Six Egyptian genetically diverse rice cultivars, namely, Giza 177, Giza 178, Sakha 101, Sakha 102, Sakha 103 and Sakha 104 employed in half diallel crossing to estimate the general and specific combining ability and type of gene action for grain yield and its components, and some diseasing traits in rice. In addition, heterosis and heritability were appraised. Parentage and Type of Planting Group of these rice cultivars are given in Table (1)

Table (1): Parentage and Type of Planting Group of rice cultivars

No	Cultivar	Parentage	Type	Salinity tolerance	Disease resistance	
					Brown spot	Blast
1	**Giza 177**	Giza 177 / Yomji No.1 // Pi No. 4	Japonica	Sensitive	S	R
2	**Giza 178**	Giza 175 / Milyang 49	Ind. /Jap.	Tolerant	R	R
3	**Sakha 101**	Giza 176 / Milyang 79	Japonica	Moderate	R	S
4	**Sakha 102**	Gz 4096-7-1 / Giza 177	Japonica	Sensitive	R	R
5	**Sakha 103**	Giza 177 / Suweon 349	Japonica	susceptible	MR	R
6	**Sakha 104**	Gz 4096-8-1 / Gz 4100-9-1	Japonica	Tolerant	R	S

Six Egyptian rice cultivars chosen based on their considerable level of variability in yield and yield component characters and their resistances to diseases were raised at an interval of 15 days to ensure synchronization in flowering for the purpose of hybridization during 2007 summer season at Sakha Agricultural Research Station. Thirty days old seedlings from fifteen cross combination along with six parents were transplanted in randomized complete block design with three replications during 2008 summer season. In each replication the size of the plot consisted of 4 rows with a length of 5 meters. The two central rows were used for data collection and observation. A spacing of 15 x 15 cm and a dose of recommended fertilizer were given and also recommended agronomic practices were adopted. Each hybrid was raised in 5m length plot size. Twenty plants were randomly taken from each parent and each F1 cross, from each replicate. Data were collected on eleven rice traits, viz; plant height (cm), days to 50% heading, panicle length (cm), number of panicles / plant, number of filled grains / panicle, 1000-grain weight, grain yield /plant (g), proline content, osmotic pressure, chlorophyll content (ppm) and somedisease.

1. Blast infection:

1.1. Greenhouse test:

The seven cultivars in addition to eight international differential cvs. (Atkins *et al.*, 1967) were evaluated for blast reaction under greenhouse conditions using two blast isolates collected from Sakha 104 and Sakha 101 rice cultivars. All the materials were seeded in plastic trays (30 x 20 x 15 cm). Each tray (as one replicate) comprised 20 rows having seven cultivars, eight international differential varieties and Giza 159 as a rice susceptible check to blast. The trays were kept in the greenhouse at 25-30 OC and fertilized with urea 46.5 % nitrogen (5 g/tray). The isolates were grown and multiplied on banana medium and incubated at 28 OC. The spores were harvested at a density of at least 25 spores / microscopic field. Rice seedlings of 20 days old were inoculated by spraying with the spore suspension (5×10^4 spores / ml) of each isolate in the evening to avoid the retarding effect of sunlight on both spore germination and germ tube growth. The reaction of the tested entries to blast infection was estimated according to IRRI scale (1996) seven days after inoculation.

1.2. Blast infection determination under field conditions:

Samples of rice leaves were taken four times at 15-day intervals starting from thirty days after transplanting. Each sample consisted of one hundred leaves randomly collected from each plot. Percentage of the infected leaves was calculated, while severity of infection was estimated by counting the total number of type (4) blast lesions / 100 leaves. Neck rot infection was

estimated by collecting one hundred panicles from each plot, and the severity was calculated using the formula adopted by Townsend and Huberger (1943).

2. White tip nematode:

Severity of white tip nematode infection was evaluated by counting number of infected leaves per m2 in each plot, just before heading or at late booting to count larvae, 10 seedlings (just before transplanting) were collected from each nursery treatment, washed, cut into small pieces and placed with water in a watch glass. Twenty-four hours later, the number of nematode larvae was counted using the stereoscopic microscope. At maturity stage, five infected and five healthy panicles were collected from each plot to count the harboured nematode larvae as previously mentioned.

3-Estimation of brown spot:

Samples of rice leaves were taken after thirty days of transplanting. Total number of brown spot lesions was counted in a sample of one hundred leaves collected randomly from each plot during vegetative stage. After harvest, samples of one hundred grains were taken for estimating the discolored grain percentage.

4--Estimation of false smut:

Number of infected panicles/m2 was taken as disease incidence. While number of smut, balls/ m2 was considered as severity.

Statistical analysis:

The mean data was subjected could be identified if selection is postponed to later to ANOVA and combining ability studies using Diallel generations due to the presence of non additive gene analysis, Method 2 and Model 2 (Griffings, 1956). The data for each measurement was tabulated and analyzed by Fisher's analysis of variance (Steel and Torrie, 1980). The diallel analysis was used to evaluate traits that had significant variation among the parents. Significant differences in phenotypes were assumed to imply that genetic differences were present. Simple additive – dominance model approach of Hayman (1954a), (1954b), Jinks (1954) and Singh and Chaudhary (1979) as modified by Mather and Jinks (1982) was followed for genetic analysis and for the estimation of components of genetic variation. The significance of components of variation in F_1 generation was tested by Jinks (1956), Hayman (1958) and Mather and Jink (1971). When the value of a parameter divided by its standard error, exceeds 1.96 then it was significant.

Calculation for the analysis of (Wr-Vr) and the following genetic components, ratios, and estimators were include in the program.

(Wr + Vr) = an estimator of the order of dominance of the parents as indicated by the relative values of each parent. Low values of (Wr + Vr) indicate high levels of dominance while high values indicate low dominance.

D = component of variation due to additive effects of genes.

F = an indicator of excess of dominant or recessive genes in the parent. A positive sign indicates an excess of dominant alleles of dominant effects on the parents while a negative sign indicates the same of recessive alleles. A value of F = 0 indicates that either no genes exhibited

dominance or that the dominant and recessive alleles of each gene are distributed equally among the parents.

H_1 and H_2 = components of variation due to the dominance effects of genes.

h^2 = the summation of dominance deviation over all loci. When the frequency of dominant and recessive alleles is equal, then $H_1 = H_2 = h^2$. Significance of h^2 confirms that dominance is unidirectional.

E=environmental component as estimated by the error mean square from the analysis of variance.

$(H_1/D)^{0.5}$ = a weighted measure of the average degree of dominance at each locus with a value of zero indicating no dominance, a value of 1 indicating complete dominance and a value grater than 1 indicating over-dominance. Partial dominance results in a value between 0 and 1. The dominance component H_1 is used in this ratio because it has the same coefficient as D, Hayman (1954a).

$H_2/4H_1$ = an estimator of the average frequency of negative versus positive alleles at loci exhibiting dominance. It has a maximum value of 0.25 when $p = q = 0.5$. Value less than 0.25 indicate that the additive components do not contain all dominance effects. Therefore, the above ratio of average degree of dominance would not be accurate Mather & Jinks (1971).

$K_D/D_R = (4DH_1)^{0.5} + F/ (4DH_1)^{0.5} -F$. A ratio of the total number of dominates genes to recessive genes in all the parents.

Heritability = $(1/4D)/ (1/4D+ 1/4H_1 -1/4F + F)$.

The above estimators were calculated only when the genetic components in the respective ratios were significantly different from zero.

Estimation of heterosis:

Useful heterosis for each trait of individual cross was calculated as the percentage increase F1, performance above the better parent performance. Heterosis over better-parent % was estimated as follows:

$$H (\%) = \frac{F1-BP}{BP} \times 100$$

Where, F1 = Mean value of the first generation BP= Mean value of the better-parent. Appropriate LS.D value was calculated to test the significance of the heterotic effects, according to the following formula, suggested by Wynne *et al.* (1970).

L.S.d. for better parent heterosis = $t \frac{(\sqrt{2Mse})}{r}$

Where: t = tabulated "t" value at the specified level of probability for the experimental error degrees of freedom. MSE = the experimental error mean squares of the analysis of variance, and r = number of replications.

Soil analysis:

Four sites (from1-4) were chosen within El-Sirw farm to represent the area under study. Before conducting the experiments, Soil samples of each site were taken from a depth of 0-30 cm .All samples were then air dried and prepared for chemical analysis .The chemical analysis was carried out using the soil extract 1:5 to estimate the soluble anions, cations and total dissolved salts (TDS). Soil saturation extract was measured according to Jakson (1967). The electrical conductivity (Ec) was measured in the extract of the soil

saturated past. The procedure for preparation and measurements of soil extract was taken according to the method of Blank et al (1965). The method of Chapman and Parker (1961). Some chemical characteristics of experimental soil and water at El-Serw location in 2001season are given in Table (2) .

Table (2): Some chemical characteristics of experimental soil irrigation ,drainage and ground water at El-Sirw location in season 2002.

Samples soil and water	EC ds/m	Anions meq/L				Cations meq/L				PH 1:2.5	O.M %	SAR	C.E.C	ESP	Soil texture
		CO^{-3}	HCO^{-3}	CL^-	SO^-_4	Ca^{++}	Mg^{++}	Na^+	K^+						
Soil	8.75	-	18	70	2.24	23.10	2.74	63.0	1.40	8.06	1.64		42.02	19.64	Clay
Mixed water	1.96	-	5	11	11.97	9.34	7.08	11.2	0.35						
Drainage water	3.82	-	9.5	28	24.18	15.40	17.24	28.4	0.64						

RESULTS AND DISCUSSION

Analysis of variance

Analyses of variance for the studied traits under investigation are presented in Table (3 and 4). The genotype mean square exhibited highly significant for all the studied traits indicating wide range of genetic variability among the studied genotypes and this is a primary requirement for further computation**.** Mean square values of parents and crosses were found to be highly significant for all traits except parents for panicle length which was significant. Parents Vs crosses mean squares were highly significant for all agronomic, yield and its component traits, and Chlorophyll content, while, such estimates were insignificant for other remaining traits. Both general and specific combining ability variance were found to be highly significant for all traits, indicating the importance of both additive and non-additive genetic variance in determining the performance of these eleven traits. General combining ability/specific combining ability ratio was used to clarify the nature of the genetic variance involved. With the exception of all traits under investigation, GCA/SCA ratios were found to be greater than unity for all characters under studied except Panicle length, number of filled grains/panicle and 1000-grain weight, indicating that the additive and additive x additive types of gene action were of greater importance in the inheritance of all the studied characters except these three mentioned traits which has been controlled by non-additive genetic variance. It is therefore could be concluded that the presence of large amounts of additive effects suggests the potentiality for obtaining further to improved these characters studied. Also, selection procedure based on the accumulation of additive effects would be very successful in improving these characters. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variation are involved. The obtained results are in harmony with those previously observed by El Abd (1995), Vaithiyalingan and Nadarajan (2005) and Sinha *et al.* (2006).

Table (3): Mean square estimates of ordinary and combining ability analysis for some agronomic, yield and its component traits.

S.O.V.	d.f	Plant height (cm)	Days to heading (days)	Panicle length (cm)	No. of panicles /plant	No. of filled grains /panicle	1000-grain weight(g)	Grain yield/plant
Replications	3	14.46	7.49	1.1914	0.73112	81.70834	0.7708	24.90
Genotypes	20	210.72**	281.74**	19.0283**	15.3619**	1326.5188**	17.7885**	383.60**
Parents (P)	5	225.07**	268.07**	2.30*	45.585**	847.37**	15.13**	586.08**
Crosses (Cr)	14	208.10**	284.97**	22.61**	2.58**	136.124**	18.79**	180.74**
P. vs Cr.	1	175.54**	304.80**	52.50**	43.20**	3209.73**	17.14**	2211.31**
Error	60	10.700	5.170	0.7759	0.5811	66.09792	1.07604	16.640
G.C.A	5	126.29**	180.94**	2.898**	7.33**	126.963**	2.109**	199.89**
S.C.A	15	28.14**	33.60**	5.377**	2.677**	399.850**	5.226**	61.24**
Error	60	2.670	1.290	0.194	0.145	16.524	0.269	4.160
GCA / SCA		4.490	5.390	0.539	2.738	0.318	0.400	3.260

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Table (4): Mean square estimates of ordinary and combining ability analysis for some physiological and diseases traits.

S.O.V.	d.f	Proline content	Osmotic pressure	Chlorophyll content	Brown spot percentage	Brown spot severity
Replications	3	0.017	0.152	2.82	0.222	0.583
Genotypes	20	1.194**	5.629**	80.34**	42.332**	55.089**
Parents (P)	5	1.668**	9.890**	139.223**	80.941**	109.775**
Crosses (Cr)	14	1.11**	4.40**	58.04**	19.480**	24.278**
P. vs Cr.	1	0.06	0.99	97.97**	169.20	213.01
Error	60	0.024	0.338	3.536	0.497	0.708
G.C.A	5	0.99**	4.772**	34.10**	26.431**	35.188**
S.C.A	15	0.07**	0.286**	15.41**	5.300**	6.634**
Error	60	0.01	0.085	0.88	0.124	0.177
GCA / SCA		14.143	16.685	2.213	4.987	6.304

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Mean performance of parents and their F_1 generation

Evidently, Table 5 shows that the shortest plants were observed in Sakha 103 followed by Sakha 101 and Giza 177, while, the tallest ones were exhibited in Sakha 104 and Sakha 102 rice varieties. Sakha 103 followed by Sakha 102 and Giza 177 were the earlier rice cultivars, otherwise, Sakha 101, Sakha 104 and Giza 178 were the latest rice cultivars comparing with other rice cultivars. In addition, Sakha 101 has a longest panicle (24.21cm), more filled grains /panicle (160.5 fertile grains), heaviest grains (25.40 g /1000 grains) and superior grain yield (46.61 g /plant) comparing with the other cultivated parents, while, the highest estimated value for number of panicles /plant was observed for Giza 178 rice cultivar. The parental mean

values of grain yield were ranged between 4.22 and 4.89 t. /fed., for Giza 177 and Sakha 101, respectively.

The F_1 mean values of plant height were ranged between 74.5 for (Giza 177 X Giza 178) and 100 cm for (Sakha 103 X Sakha 104) rice crosses, which agree with the target of rice breeders for selected short stature rice genotypes, resistance to lodging and suitable for mechanical harvesting. Moreover, all rice crosses were earlier than the late rice cultivar, Sakha 101 from almost 1 to 22 days. Six rice crosses, Giza 177 X Sakha 103 (88.5), Giza 178 X Sakha 102 (90.2), Giza 178 X Sakha 103 (84.2), Sakha 101 X Sakha 102 (90.2), Sakha 101 X Sakha 103 (91) and Sakha 102 X Sakha 103 (88.5 days) were earlier than the earliest rice cultivar, Sakha 103 (91.5 days). The highest estimated values of panicle length and number of panicles /plant were recorded on Giza 178 X Sakha 104 rice cross. Moreover, the largest number of filled grains /panicle was detected for Sakha 101 X Sakha 104 (167 grains) followed by Sakha 101 X Sakha 103 (162.75 grains) and Giza 177 X Sakha 103 (158.25 grains). The heaviest 1000 grain weight was obtained for Giza 177 X Sakha 102, Giza 178 X Sakha 103, Giza 177 X Sakha 104 and Giza 177 X Sakha 101 rice crosses. Maximum grain yield /plant was observed for Sakha 101 X Sakha 102 (66.25 g), followed by Sakha 102 X Sakha 103 (63.25 g) and Sakha 101 X Sakha 104 (59.25 g), almost it was ranged between 12.12 and 16.56 ton / ha., indicating possibility of increasing grain yield through hybridization followed by selection in any traditional breeding programme.

It is clear from Table (6) that the highest estimated mean values of both proline content and osmotic pressure traits were recorded for Sakha 104 followed by Sakha 101, while, the lowest mean values of proline content and osmotic pressure were observed for Sakha 103 and Sakha 102, respectively. Giza 177 followed by Sakha 102 and Sakha 104 had the highest concentration value of chlorophyll in its leafs, opposite, the lowest estimated values were exhibited for Giza 178 and Sakha 101 rice cultivars. Sakha 103, Giza 178 and Sakha 102 were highly resistance for both percentage and severity of rice brown spot disease, while, each of Sakha 104 and Sakha 101 were moderately resistance, in addition, Giza 177 was found to by highly susceptible rice variety for both traits.Regarding the F1 mean values of physiological and diseases resistance traits (Table 6) shows that Sakha 101 X Sakha 104 and Giza 178 X Sakha 104 had the highest estimated values of proline content (3.45) and osmotic pressure comparing with their parental values. The highest estimated values of chlorophyll content were observed for Giza 177 X Sakha 101 followed by Giza 177 X Sakha 103 and Sakha 101 X Sakha 103, there estimated values were (43.98, 42.98 and 42.23), respectively. On the contrary, the lowest chlorophyll content values were detected for Sakha 101 X Sakha 104 (29.55), Sakha 102 X Sakha 104 (33.35) and Giza 177 X Sakha 104 (34.58) all of them included Sakha 104 as a male parent. On the other hand, Giza 178 X Sakha 102, Giza 178 X Sakha 103, Sakha 101 X Sakha 103 and Sakha 102 X Sakha 103 were found to be resistance to rice brown spot disease when it investigated as a percentage or severity. Estimates of general (GCA) and specific (SCA) combining ability Obviously, estimate of GCA showed that the parents Giza 178, Sakha 101

and Sakha 104 were found to be good general combiners for grain yield/plant (Table 7). High GCA effect of Sakha 101 was associated with its high GCA effect for panicle length, number of panicles /plant, number of filled grains /panicle and 1000 grain weight. The good combining ability of cultivar Sakha 104 was due to high elongation of its panicle and its heavies grains, while the high estimates of general combining ability of cultivar Giza 178 for grain yield /plant was due to its highest estimates of panicle length and number of panicles /plant. The results also revealed that among the studied parents, Sakha 103 followed by Giza 177, Sakha 101 and Giza 178 were the best general combiners for short plant height. Moreover, Sakha 103 and Sakha 102 were the best general combiners for earliness.

In addition, Table (8) shows that Sakha 102, Sakha 103 and Sakha 104 were good combiners for both percentage and severity of brown spot rice disease. However, Sakha 101 and Sakha 104 were the best combiners for proline content and osmotic pressure. Highly significant and positive estimates of general combining ability of chlorophyll content were recorded for Giza 177, Sakha 102 and Sakha 103, indicating that these three parents were the greatest combiners for improving chlorophyll content in any rice breeding program. Giza 178 was found to be the best combiner for osmotic pressure. Generally, Sakha 101, Sakha 104 and Giza 178. were the best at of all, since they possessed significant and desirable GCA effects for most of the studied traits.

Table (5): Mean performance of the six parents and their F_1 generation of 6 x 6 diallel cross for some agronomic, yield and its component traits.

Entry	Plant height (cm)	Days to 50 % heading	Panicle length (cm)	No. of panicles /plant	No. of filled grains /panicle	1000-grain weight (g)	Grain yield /plant (g)
Giza 177	78	94.5	21.45	20.25	115.25	25.00	40.15
Giza 178	80.75	107	23.75	26.35	131.75	21.28	44.5
Sakha 101	77.25	112.2	24.21	23.00	160.5	25.40	46.61
Sakha 102	86	93.2	20.18	20.00	142.5	24.30	42.75
Sakha 103	74.5	91.5	21.38	19.70	139.75	23.50	41.25
Sakha 104	95	104	20.75	21.28	151.75	25.33	45.34
Giza 177 / Giza 178	74.5	104	20.00	33.68	134.5	25.50	52.5
Giza 177 / Sakha 101	82.25	110.7	27.00	29.60	150.75	26.25	49.25
Giza 177 / Sakha 102	92.5	92.5	19.75	25.28	146.5	27.00	53.75
Giza 177 / Sakha 103	76	88.5	21.25	34.63	158.25	23.00	65
Giza 177 / Sakha 104	92	105.7	24.25	39.35	110.5	26.75	59
Giza 178 / Sakha 101	86.2	111.2	24.00	44.95	150.5	24.25	48.5
Giza 178 / Sakha 102	80	90.2	24.50	31.88	149.5	20.75	55.25
Giza 178 / Sakha 103	80	84.2	20.50	31.10	121.5	27.00	50
Giza 178 / Sakha 104	92.5	100.7	27.00	44.95	111	21.00	50.5
Sakha 101 / Sakha 102	78.5	90.2	19.50	33.25	153.75	26.00	66.25
Sakha 101 / Sakha 103	82.7	91	22.50	44.43	162.75	25.00	63.25
Sakha 101 / Sakha 104	90.2	99.7	22.00	39.65	167	26.00	59.25
Sakha 102 / Sakha 103	81.7	88.5	22.50	35.00	143.5	21.50	50.75
Sakha 102 / Sakha 104	87.5	98	21.63	27.88	146.5	22.00	48.5
Sakha 103 / Sakha 104	100	95	22.88	36.20	142.5	25.00	52.25

Table (6): Mean performance of the six parents and their F$_1$ generation of 6 x 6 diallel cross for some physiological and diseases traits.

Entry	Proline content	Osmotic pressure	Chlorophyll content	Brown spot (percentage)	Brown spot (severity)
Giza 177	1.56	4.81	46.63	12.75	15.25
Giza 178	1.86	8.23	30.70	6.2	5
Sakha 101	2.74	6.08	35.35	7.75	9.5
Sakha 102	1.90	4.31	43.50	4.5	5.5
Sakha 103	1.35	4.69	41.93	2.5	3.5
Sakha 104	2.95	7.22	42.48	8.65	7
Giza 177 / Giza 178	1.72	5.95	38.13	10.25	11.75
Giza 177 / Sakha 101	2.63	5.22	43.98	10.5	12
Giza 177 / Sakha 102	2.01	4.68	38.90	12.75	10.5
Giza 177 / Sakha 103	1.58	4.54	42.23	9.5	11
Giza 177 / Sakha 104	2.84	5.45	34.58	13.25	17.75
Giza 178 / Sakha 101	2.15	6.69	35.65	6.25	6
Giza 178 / Sakha 102	1.70	5.45	38.63	3.5	4.25
Giza 178 / Sakha 103	1.59	4.56	39.60	2.75	4.1
Giza 178 / Sakha 104	2.20	8.36	35.20	2.25	8
Sakha 101 / Sakha 102	1.85	5.44	39.20	5	6
Sakha 101 / Sakha 103	2.13	5.32	42.98	4.5	5
Sakha 101 / Sakha 104	3.45	7.09	29.55	9.5	7.25
Sakha 102 / Sakha 103	1.59	4.57	36.85	3.5	4
Sakha 102 / Sakha 104	2.08	5.58	33.35	10.25	8.75
Sakha 103 / Sakha 104	2.30	5.83	36.78	9.5	7.25

Table (7): Estimates of general combining ability (GCA) effects for some agronomic, yield and its component traits.

Parents	Plant height (cm)	Days to 50 % heading	Panicle length (cm)	No of panicles /plant	No. of filled grains /panicle	1000-grain weight (g)	Grain yield /plant (g)
Giza 177	-2.021**	1.396**	0.042	-0.901**	-2.438**	-0.188*	-3.721**
Giza 178	-1.833**	2.396**	0.335**	1.255**	0.500	-0.594**	1.557**
Sakha 101	-1.865**	5.271**	0.523**	1.130**	7.281**	0.563**	7.885**
Sakha 102	0.354	-5.417**	-0.899**	-0.167*	0.781	-0.469**	-5.940**
Sakha 103	-2.490**	-6.385**	-0.555**	-0.557**	-2.438**	0.063	-2.255**
Sakha 104	7.854**	2.740**	0.554**	-0.760**	-3.688**	0.625**	2.473**
S.E. at 0.05	0.528	0.367	0.142	0.123	1.312	0.167	0.658
S.E. at 0.01	0.818	0.568	0.220	0.191	2.033	0.259	1.020

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Table (8): Estimates of general combining ability (GCA) effects for some

Parents	Proline content	Osmotic pressure	Chlorophyll content	Brown spot (percentage)	Brown spot (severity)
Giza 177	-0.11**	-0.57**	2.79**	2.094**	2.531**
Giza 178	-0.20**	0.93**	-2.52**	1.625**	1.656**
Sakha 101	0.37**	0.24**	-0.83**	1.031**	1.250**
Sakha 102	-0.21**	-0.71**	0.65**	-0.875**	-0.969**
Sakha 103	-0.36**	-0.73**	1.70**	-1.656**	-1.813**
Sakha 104	0.51**	0.84**	-1.79**	-2.219**	-2.656**
S.E. at 0.05	0.025	0.094	0.303	0.114	0.136
S.E. at 0.01	0.039	0.145	0.470	0.176	0.210

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Therefore, it may be concluded that crosses involving these parents would result in the identification of superior sergeants with favorable genes for grain yield and component traits and other studied traits. High GCA effects are related to additive and additive X additive components for genetic variation, the parents with higher positive significant GCA effects are considered as good combiners, while those with negative GCA effects are poor general combiners except in case of plant height, earliness and diseases. Similar results were obviously recorded by El Abd (1995), Shehata (2004), Satish and Seetharamaiah (2005) and Dhakar and vinit (2006). All the studied genotypes were good combiners for salt tolerance, consequently successful breeding program could be conducted for salinity depended on shuttle breeding involving pyramiding of gene specific to these characters and selection must be done in a later generation and under controlled conditions in order to minimize environmental effects. Modified bulk and single seed descent would be suitable breeding methods (Gregorio and Senadhira, 1993)

The estimates of specific combining ability of 15 crosses for 12 agronomic, yield and its component; physiological and diseases traits are presented in (Tables 9 and 10). It is observed that a total of 9 crosses exhibited positive and significant SCA for grain yield /plant The promising combinations for grain yield along with at lest two of yield component traits were Sakha 103 X Sakha 104, Giza 178 X Sakha 101, Giza 178 X Sakha 102, Giza 177 X Sakha 102, Giza 177 X Sakha 103 and Giza 177 X Giza 178. It is observed that majority of the crosses with high SCA for grain yield were involved with low / high or high / low or High / high or low / low combining parents. But very few crosses showing low / low general combiners showed high SCA. The cross combinations showing high negative SCA for days to 50% heading (earliness) were Giza 177 X Sakha 102, Giza 177 X Sakha 103, Giza 178 X Sakha 102, Giza 178 X Sakha 103, Giza178 X Sakha 104, Sakha 101 X Sakha 102, Sakha 101 X Sakha 103 and Sakha 101 X Sakha 104. For plant height, negative estimates of SCA are desirable and the good specific combiners were Giza 177 X Giza 178, Giza 177 X Sakha 103, Giza 178 X Sakha 102, Sakha 101 X

Sakha 102, Sakha 102 X Sakha 103 and Sakha 102 X Sakha 104. The cross combinations viz., Giza 177 X Sakha 101, Giza 177 X Sakha 104, Giza 178 X Sakha 101, Giza 178 X Sakha 102, Giza 178 X Sakha 104, Sakha 101 X Sakha 103, Sakha 102 X Sakha 103 and Sakha 103 X Sakha 104 were good specific combiners for panicle length.

The best specific combiners for number of panicles /plant were Giza 177 X Sakha 103, Giza 177 X Sakha 104, Sakha 102 X Sakha 104 and Sakha 103 X Sakha 104. The cross combinations, Giza 177 X Giza 178, Giza 177 X Sakha 101, Giza 178 X Sakha 101 and Sakha 103 X Sakha 104 showed higher SCA for number of filled grains / panicles and 1000 grain weight.

Four crosses namely, Giza 177 X Sakha 101 , Giza 177 X Sakha 102, Giza 177 X Sakha 104 and Sakha 101 x Sakha 104 exhibited highly significant and positive SCA effects for proline content, while, Giza 178 X Sakha 104, Sakha 101 X Sakha 103, Sakha 101 X Sakha 104 and Sakha 102 X Sakha 103 rice crosses were the best cross combinations for Osmotic pressure. The crosses, Giza 177 X Sakha 101, Giza 178 X Sakha 102, Giza 178 X Sakha 103, Giza 178 X Sakha 104, Sakha 101 X Sakha 102 and Sakha 101 X Sakha 103 showed desirable SCA effects for Chlorophyll content. Moreover, these cross combinations also included the parents which recorded either good or poor GCA for this trait.

Table (9): Estimates of specific combining ability (SCA) effects for some agronomic, yield and its component traits.

Cross	Plant height (cm)	Days to 50 % heading	Panicle length (cm)	No. of panicles /plant	No. of filled grains /panicle	1000-grain weight (g)	Grain yield /plant (g)
Giza 177 / Giza 178	-5.85**	2.30**	-2.49**	-1.16**	4.08**	2.00**	4.30**
Giza 177 / Sakha 101	1.93**	6.18**	4.32**	0.259	13.55**	1.59**	-6.11**
Giza 177 / Sakha 102	9.96**	-1.38**	-1.51**	-0.44**	15.80**	-0.63**	3.39**
Giza 177 / Sakha 103	-3.69**	-4.42**	-0.353	1.45**	30.77**	-3.16**	9.06**
Giza 177 / Sakha 104	1.95**	3.71**	1.54**	0.53**	-15.73**	-1.97**	9.06**
Giza 178 / Sakha 101	5.75**	5.68**	1.03**	-2.65**	10.36**	1.00**	3.97**
Giza 178 / Sakha 102	-2.72**	-4.64**	2.95**	0.275	15.86**	-1.47**	4.72**
Giza 178 / Sakha 103	0.121	-9.67**	-1.40**	-1.34**	-8.92**	4.25**	0.256
Giza 178 / Sakha 104	2.28**	-2.29**	3.99**	-1.13**	-34.17**	-2.32**	9.38**
Sakha 101 / Sakha 102	-4.19**	-7.51**	-2.24**	-1.10**	13.33**	-0.379	-0.237
Sakha 101 / Sakha 103	2.90**	-5.79**	0.416*	-2.09**	2.549	-2.91**	7.25**
Sakha 101 / Sakha 104	0.058	-6.17**	-1.19**	-0.132	-4.95**	1.53**	-2.25**
Sakha 102 / Sakha 103	-0.317	2.40**	1.83**	-0.79**	-17.20**	-1.38**	1.653
Sakha 102 / Sakha 104	-4.91**	2.77**	-0.147	0.42**	17.05**	-1.44**	-0.200
Sakha 103 / Sakha 104	10.43**	0.741	0.759**	1.06**	16.27**	1.03**	4.44**
S. E. at 0.05	1.450	1.007	0.390	0.338	3.603	0.460	1.808
S.E. at 0.01	1.635	1.137	0.440	0.381	4.065	0.519	2.040

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Table (10): Estimates of specific combining ability (SCA) effects for some physiological and diseases traits.

Cross	Proline content	Osmotic pressure	Chlorophyll content	Brown spot (percentage)	Brown spot (severity)
Giza 177 / Giza 178	-0.078**	-0.126	-0.540	1.817**	1.955**
Giza 177 / Sakha 101	0.259**	-0.165	3.629**	-2.339**	-2.388**
Giza 177 / Sakha 102	0.226**	0.244	-2.931**	-2.183**	-2.670**
Giza 177 / Sakha 103	-0.066	0.123	-0.650	-2.652**	-3.326**
Giza 177 / Sakha 104	0.334**	-0.540**	-4.815**	-2.339**	-2.732**
Giza 178 / Sakha 101	-0.119**	-0.193	0.610	-2.121**	-2.513**
Giza 178 / Sakha 102	0.016	-0.492**	2.100**	-1.964**	2.045**
Giza 178 / Sakha 103	0.046	-1.360**	2.032**	-1.933**	-1.951**
Giza 178 / Sakha 104	-0.204**	0.870**	1.116**	-1.871**	-1.607**
Sakha 101 / Sakha 102	-0.412**	0.199	0.994**	0.129	0.112
Sakha 101 / Sakha 103	0.008	0.960**	3.725**	0.411**	-0.045
Sakha 101 / Sakha 104	0.471**	0.295**	-6.215**	-0.027	0.049
Sakha 102 / Sakha 103	0.053	0.290*	-3.884**	1.317**	1.174**
Sakha 102 / Sakha 104	-0.322**	-0.266*	-3.900**	-0.371**	-0.323
Sakha 103 / Sakha 104	0.048	-0.001	-1.518**	0.661**	1.112**
S. E. at 0.05	0.069	0.258	0.833	0.313	0.373
S.E. at 0.01	0.078	0.291	0.940	0.353	0.421

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Among the fifteen hybrids, almost half of them recorded negative significant SCA effects favoring resistance of brown spot disease. Through there is a preponderance of non additive gene action for grain yield and most of the yield components in the hybrids resulted in high amount of vigor in F_1, selection can be postponed to later generation. These findings were in agreement with those of), Yu *et al.* (2004), Bagheri *et al.* (2005), , Allahgholipour and Ali (2006) and Soni *et al.* (2006).

Estimates of better parent heterosis

A large number of crosses exhibited high estimates of heterosis in a desirable direction for different traits under study. The estimates of heterosis for different traits are presented in (Tables 11 and 12). A greater magnitude of heterosis ranged between (11.3 and 57.5%) was observed in twelve crosses for grain yield /plant. The availability of sufficient hybrid vigour in several crosses in respect of grain yield suggests that a hybrid breeding programme could profitably be undertaken in rice under salinity conditions. The cross Giza 178 / Sakha 103 exhibited highest negative heterosis (-7.9%) for days to 50% heading followed by Sakha 101 X Sakha 104 (-4.1%), Giza 178 X Sakha 101 (-3.9%), Sakha 101 X Sakha 102 (-3.2%). Appearance of significant and negative heterosis for days to 50% heading indicated the possibility of exploiting heterosis for earliness. For plant height, only one cross, Giza 177 X Giza 178 (-4.4%) recorded significant heterosis in a

desirable negative direction. Three crosses, Giza 177 X Giza 178, Giza 177 X Sakha 104 and Giza 178 X Sakha 104 exhibited highly significant and positive estimates of heterosis for panicle length, their estimated values were (11.5, 13.0 and 13.6%), respectively. Moreover, highly significant and positive estimates of heterosis were observed for number of panicles /plant in all the studied crosses , the highest estimated value was recorded for Sakha 101 X Sakha 103 (93.1%), while, the lowest estimated value was detected for Giza 178 X Sakha 103 (18.0%). On the other hand, no desirable heterosis were found among all the studied crosses for 1000 grain weight, which exhibited either non-significant or highly significant estimates in negative direction. Out of fifteen studied crosses, three of them, Giza 177 X Sakha 103, Giza 178 X Sakha 102 and Sakha 101 X Sakha 104 exhibited highly significant and positive estimates of heterosis for number of filled grains /panicle, while the most of other remaining crosses recorded highly significant heterosis in negative direction for such trait.

Table (11): Estimates of heterosis as a deviation from better parent of the fifteen rice crosses for some agronomic, yield and its component traits.

Genotype	Plant height	Days to 50 % Heading	Panicle length (cm)	No of panicles /plant	No. filled grains /panicle	1000-grain weight (g)	Grain yield /plant (g)
Giza 177 / Giza 178	-4.4*	10.0**	-15.7**	27.8**	2.0	-2	17.9**
Giza 177 / Sakha 101	6.4**	17.1**	11.5**	28.6**	-6.0*	-0.5	5.6
Giza 177 / Sakha 102	18.5**	-1.0	-7.9*	24.8**	2.8	-12**	25.7**
Giza 177 / Sakha 103	3.40*	-3.2*	-0.9	71.0**	13.2**	-13.0**	57.5**
Giza 177 / Sakha 104	17.9**	11.8**	13.0**	84.9**	-27.1**	-14.1**	30.1**
Giza 178 / Sakha 101	11.5**	3.9*	-0.8	70.5**	-6.2*	-4.5*	4.0
Giza 178 / Sakha 102	-0.9	-3.2*	3.1	20.9**	4.9*	-14.6**	24.1**
Giza 178 / Sakha 103	7.3**	-7.9**	-13.6**	18.0**	-13.0**	14.8**	12.3*
Giza 178 / Sakha 104	14.5**	-3.1*	13.6**	70.5**	-26.8**	-17.0**	11.3*
Sakha 101 / Sakha 102	1.61	-3.2*	-19.4**	44.5**	-4.2*	-9.4*	42.1**
Sakha 101 / Sakha 103	11.0**	-0.5	-7.0*	93.1**	1.4	-17.3**	35.7**
Sakha 101 / Sakha 104	16.7**	-4.1*	-9.1**	72.3**	4.0*	2.3	27.1**
Sakha 102 / Sakha 103	9.6**	-3.2*	5.2	75**	0.7	-11.5**	18.7**
Sakha 102 / Sakha 104	1.74	5.1*	4.3	31.0**	-3.4	-13.1**	6.9
Sakha 103 / Sakha 104	34.2**	3.8*	7.0*	70.1**	-4.3	-1.3	15.2**

*and ** significant at 0.05 and 0.01 probability levels, respectively.

As shown in Table (12), Among the crosses, the estimated heterosis values for proline content varied from –32.4% (Sakha 101 X Sakha 102) to 16.9% (Sakha 101 X Sakha 104). Giza 177 X Sakha 102 showed highly significant and positive desirable heterosis (5.7%) for proline content, otherwise, most of other remaining crosses exhibited highly significant and negative estimates of heterosis for such trait. Five crosses, Sakha 101 X Sakha 103 followed by Giza 177 X Sakha 104, Giza 178 X Sakha 104 and Sakha 101 X Sakha 102 recorded highly significant and positive heterosis for osmotic pressure. Only one cross, Sakha 102 X Sakha 103 had desirable significant and positive heterosis (7.7%) for Chlorophyll content.

Table (12): Estimates of heterosis as a deviation from better parent of the fifteen rice crosses for some physiological and diseases traits.

Genotype	Proline content	Osmotic pressure	Chlorophyll content	Brown spot (percentage)	Brown spot (severity)
Giza 177 / Giza 178	-7.5*	-3.4	-18.2**	65.3**	135**
Giza 177 / Sakha 101	-4.0	-14.1**	-5.6	35.4**	26.3*
Giza 177 / Sakha 102	5.7*	-2.7	4.8	183.3**	90.9**
Giza 177 / Sakha 103	1.2	-5.6*	-9.4*	280**	214.2**
Giza 177 / Sakha 104	-3.7	17.0**	-54.8**	53.1*	153.5**
Giza 178 / Sakha 101	-21.5**	5.5*	0.8	0.8	20*
Giza 178 / Sakha 102	-10.5**	2.6	-11.1**	-22.2*	-15
Giza 178 / Sakha 103	-14.5**	4.0	-5.5	10	17.1
Giza 178 / Sakha 104	-25.4**	13.7**	-17.1**	-63.7*	60*
Sakha 101 / Sakha 102	-32.4**	5.9*	-9.8*	11.1	9.0
Sakha 101 / Sakha 103	-22.2**	20.3**	2.5	80*	42.8*
Sakha 101 / Sakha 104	16.9**	-1.8	-6.8*	22.5*	3.5
Sakha 102 / Sakha 103	-16.3**	-2.5	7.7*	40*	14.2
Sakha 102 / Sakha 104	-29.4**	-22.7**	-0.3	127.7**	59.0*
Sakha 103 / Sakha 104	-22.0**	-19.2**	-13.4**	280**	107.1**

*and ** significant at 0.05 and 0.01 probability levels, respectively.

For brown spot (percentage), only two crosses among the studied crosses, Giza 178 X Sakha 104 (-63.7%) and Giza 178 X Sakha 102 (-22.2%) exhibited highly significant with favorable direction. Furthermore, none of the crosses had negative heterosis values for severity of brown spot disease. From the foregoing discussion, it may be concluded that the crosses, Giza 178 X Sakha 104 and Sakha 101 X Sakha 104 can be rated as the best crosses based on their heterosis in most of the studied traits included grain yield. Thus, it can be exploited in subsequent generations to improve most of the studied traits. Similar results were reported by several scientists like, Kumer *et al.* (2004), Zhen *et al.* (2004), Jin *et al.* (2005), Khoyumthem *et al.* (2005), , Chitra *et al.* (2006)and Saravanan *et al.* (2006

Genetic component analysis

The results of the regression analysis for F_1 generations for agronomic, yield and its component traits were presented in (Table 12). The appropriateness of the model data analysis was also shown by the analysis of variance of (Wr + Vr) Which elaborated that there was no evidence of dominance effects as the mean square between arrays for Wr + Vr was non-significant for F_1 of all the studied traits except panicle length. Thus emphasizing partial adequacy of additive dominance hypothesis in F_1 generation The regression coefficient (b = 0.141±0.135) regarding panicle length depart significantly from unity but not from zero, which indicated, non-additive variation included epistasis or multiple allelism and correlated genes distribution among the parents. Therefore, the data did not fulfill the diallel assumptions; hence, additive dominance model was partially inadequate. On the other hand the regression analysis of F_1 generation (b=0.906±52) for plant height and days to 50%heading indicated that the

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regression coefficient depart significantly from zero and not from unity, suggesting no non-allelic interaction and an independence of genes distribution among the parents. Thus, the additive-dominance model did provide fair basis for interpreting the results. This property of the regression coefficient indicated intra-allelic interaction, meaning thereby, that genes were distributed independently among the parental lines, and was independent in action. The unit slope of the regression lines suggested that all the diallel assumptions have been met Mather and Jinks (1982).

The genetic components and relative proportion of various components and broad and narrow-sense for agronomic, yield and its component traits are furnished in (Table 13). The component of variance analysis revealed that both additive (D) and dominant (H_1 and H_2) components were positive and significant for all agronomic, yield and its component traits except panicle length, 1000 grain weight and number of filled grains /panicle for the additive component.

Table (13): Validity of hypothesis through homogeneity tests for some agronomic, yield and its component traits.

Statistics	Plant height (cm)	Days to 50% heading	Panicle length (cm)	No. of panicles /plant	No. of filled grains /panicle	1000 grain weight (g)	Grain yield /plant (g)
Uniformity test Vr and Wr (t^2)	0.283 [ns]	1.887 [ns]	3.346 [*]	0.359 [ns]	0.910 [ns]	0.154 [ns]	0.381 [ns]
Regression coefficient (b)	0.906 [**]	0.750 [**]	0.141 [ns]	0.753 [**]	0.146 [ns]	-0.186 [ns]	0.643 [ns]
S.E. (b)	0.152 [ns]	0.104 [ns]	0.135 [ns]	0.251 [ns]	0.317 [ns]	0.454 [ns]	0.489 [ns]
Ho: b = 0	5.941 [**]	7.202 [**]	1.037 [ns]	2.999 [ns]	0.460 [ns]	-0.410 [ns]	1.314 [ns]
Ho: b = 1	0.616 [ns]	2.394 [ns]	6.343 [*]	0.983 [ns]	2.659 [ns]	2.611 [ns]	0.728 [ns]

*and ** significant at 0.05 and 0.01 probability levels, respectively.

The non-significance D for these three mentioned traits was further attested by low values of narrow-sense Heritability (16.6, 10.7 and 13.8%) respectively. However, estimates of dominant components were higher than additive components suggesting that dominance variances were more important. The important of dominance variances has also been reported earlier by Mishra and Singh (1998) for plant height and grain yield. The estimate of H_2 component was smaller than H_1 for all the traits reflecting unequal proportion of positive and negative alleles at loci governing these agronomic, yield and its component traits in parents. This was further confirmed by the ratio ($h^2 /4H_1$). High h^2 estimates were observed for plant height, days to 50% heading, number of filled grains /panicle and grain yield /plant, these high estimates were due to greater contribution of additive genetic component and thus these traits could be improved by adopting progeny selection. The positive and significant values of h^2 and F for number of panicles /plant indicated that dominant genes were frequently distributed than the recessive ones for this trait. The values of mean degree of dominance $(H_1/D)^{0.5}$ exhibited over dominance with a value above the unity for all the traits except number of panicles /plant, which controlled by partial

or incomplete dominance. Moreover, the non-significant component (E) indicated the least influence of environment in the expression of these traits. The proportion of positive and negative alleles in the parents was found to be symmetrical for panicle length, 1000 grain weight and number of panicles /plant traits as evident by their close approach to theoretical value (0.25). The ratio of dominant and recessive genes (K_D/K_R) in the parents was less than unity indicating more of recessive genes in the parental lines than dominant genes. The magnitude of (h^2 /H_2) was found to be depressed for all traits suggesting the presence of at least one major group of genes controlling the inheritance of these traits. The negative values of coefficient of correlation between parental order of dominance and parental measurement was observed for plant height, number of filled grains / panicle and 1000 grain weight. These are in close agreement with those of Mohapatra and Debjani (2000) and Acharya *et al.* (2000) on estimates of various components and related statistics for grain yield. High estimates of broad sense were recorded for all the studied traits, while high and moderately high estimates of narrow sense heritability for plant height, days t o 50% heading and grain yield /plant indicated the presence of additive gene effects. The magnitude of narrow sense heritability was low for panicle length, 1000 grain weight, number of filled grains /panicle and number of panicles /plant suggesting the importance of non-additive gene effects in the inheritance of these traits. These results were in conformity with the findings of many rice workers such as Punitha *et al.* (2004), Gholipour *et al.* (2005), Hosseini *et al.* (2005), Mao *et al.* (2005), Hariprasanna *et al.* (2006), Murugan and Ganesan (2006).

Analysis of a diallel cross gives information on the proportion of dominant and recessive genes in individual parents. The analysis of test of homogeneity (t^2) was non significant for physiological and diseases resistance traits (Table 14) and thus indicated that the data fulfilled the basic assumptions for diallel analysis (Natarajan, 1994). The regression coefficient (b) was significantly deviant from zero for all traits. This revealed the presence no non-allelic interaction and an independence of genes distribution among the parents. Thus, the additive-dominance model did provide fair basis for interpreting the results.

The genetic components estimated by the diallel analysis (Table 15), illustrated that the additive component (D) was highly significant for osmotic pressure, chlorophyll content and both percentage and severity brown spot disease. This confirmed the additive effects of the genes for the inheritance of these traits. Dominance components (H_1 and H_2) were highly significant for all the traits except H1 of osmotic pressure, which showed dominance effects of genes. It's worthy to mention that value h^2 as a measure of over all dominance effects of heterozygous loci, was significant and positive estimates for chlorophyll content and both percentage and severity brown spot disease. These results indicated that the mean direction of dominance was positive for these traits. The non-significant values of h^2 for proline content and osmotic pressure did not indicate any direction of dominance. The positive values of the F component for osmotic pressure, chlorophyll content and both percentage and severity brown spot disease, indicated excess of dominant alleles were present in the genetic material.

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Table (15): Validity of hypothesis through homogeneity tests for some physiological and diseases traits.

Statistics	Proline content	Osmotic pressure	Chlorophyll content	Brown spot (percentage)	Brown spot (severity)
Uniformity test Vr and Wr (t^2)	1.135^{ns}	1.077^{ns}	0.254^{ns}	0.365^{ns}	0.487^{ns}
Regression coefficient (b)	0.647^{**}	0.804^{**}	0.462^{ns}	0.985^{**}	0.967^{**}
S.E. (b)	0.192^{ns}	0.132^{ns}	0.384^{ns}	0.035^{ns}	5.445^{ns}
Ho: b = 0	3.375^{**}	6.081^{**}	1.203^{ns}	28.330^{**}	17.758^{**}
Ho: b = 1	1.844^{ns}	1.487^{ns}	1.399^{ns}	0.438^{ns}	0.606^{ns}

*and ** significant at 0.05 and 0.01 probability levels, respectively.

The significance of the component h^2 in chlorophyll content and both percentage and severity brown spot disease confirmed that dominance was unidirectional. The ratio $(H_1/D)^{0.5}$ measured the overall degree of dominance, which was in the range of over dominance for chlorophyll content, while it was in the range of partial dominance in praline content, osmotic pressure and both percentage and severity brown spot disease. However, the non-significant component (E) indicated the least influence of environment in the expression of all traits, except praline content trait, which affected by environmental in its expression. The ratio $(H_2/4 H_1)$ proportion of genes with positive effects in the parents was much less than 0.25 indicated sharp asymmetry in the proportion of positive and negative genes for all the traits. The ratio K_D/K_R which equal $[(4 DH_1) + F/(4DH_1)-F]$ and gives the relative estimates of dominant and recessive genes greater than unity for all the traits indicating more of dominant genes in the parental lines than recessive genes except for proline content trait. Non-significant values for all traits, suggested the existence of equal proportion of dominant and recessive alleles in the parental lines. High estimates of broad sense heritability was recorded for all the traits, it was ranged between 94.4% and 98.7% for osmotic pressure and percentage of brown spot disease. In addition, high estimates of heritability in narrow sense were recorded for proline content, osmotic pressure and both percentage and severity brown spot disease represents fixable, additive heritable variation, which indicated that response to selection, should be rapid for these characters. This offers a lot of scope for improvement of the characters through individual plant selection. According to Hayman (1957), epistasis can decrease or increase degree of dominance, which also effect on heritability estimates. On the other hand, low estimates of narrow sense heritability was observed for chlorophyll content. Same findings were recorded earlier by Annadurai and Nadarajan (2001), Panwar (2005), Sivakumar and Bapu (2005), Sharma (2006), Verma *et al.* (2006), Zhang *et al.* (2006) and Zong *et al.* (2006).

Data presented in table (17) show the reaction of six rice varieties and their combined hybrids to infection of blast, false smut, white tip nematode and brown spot disease.

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The varieties Giza 177, Giza 178, Sakha 103 were resistance to blast. In addition, the hybrids of Giza 177/ Giza 178, Giza 177/Sakha 101, Giza177/ Sakha 102, Giza177/ Sakha 103, Giza 177/Sakha104, Giza 178/Sakha101, Giza 178/Sakha102, Giza178/Sakha103, and Giza178/Sakha104 performed as ones resistant to the blast disease. The moderately resistance were Sakha 102 and the hybrids Sakha 102/Sakha 103, Sakha 102/ sakha 104and Sakha 103/sakha 104. Two hybrids were susceptible to the blast; Sakha 101/Sakha102and Sakha 101/ Sakha 103, but only one hybrid Sakha101/ Sakha104 performed as highly susceptible Abo-yossef and El-wahsh (2005)

As for false smut, three varieties (Giza 177, Sakha103 and Sakha 104) were completely free from the infection in addition to the hybrids; Giza 177/Sakha 103, Giza 177/Sakha 104, Giza 178/Sakha 104, sakha 102/Sakha 103 and Sakha 103/ sakha 104. The other varieties and hybrids had very slight infection with false smut, but relatively Giza 178 and Sakha 101 were higher infected.

For white tip nematode infection, percentage in table (17) showed that ten hybrids were not effected while the high varieties infected were Giza 177, Giza 178 and Sakha 101 on the other hand the lower infected were Sakha 104 and hybrid Giza 178/ Sakha 102 Giza 178/Sakha103 and Giza 178/ Sakha 101, similar results were recorded by Badr and El-Habashy (2007)Brown spot disease is higher in saline environment data in Table(17) show that the highest infected varieties were Giza 177 and Sakha 101 while the lowest were Sakha 104 and Sakha 103. also lower infections were detected on Sakha 102/Sakha104 and Sakha 103/Sakha 104,this phenomenon is agreement with that of EL-wahash *et al.* (2005)

Six rice varieties, well as fifteen hybrids were evaluated to two Races of blast infection(Table18).Results of entries reaction showed that nine entries preformed resistance to both races, while six entries were moderately resistance to race IG1, and four entries were moderately resistant to race IB45. On the other hand, three and four entries were susceptible to the first and second races, respectively. Abo-Youssef and EL-Wahsh (2005) found that, out of 30 entries, nineteen and twenty-one entries were resistant to rice. Blast races, ID-7 and IA1o7, respectively. On the other hand, eight and five entries were susceptible, while three and four entries were moderately, resistant for the same races.

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Table (17): Evaluation the specific combining ability effects of hybrids revealed of rice diseases ie. Blast, false smut, white tip nematode and brown spot diseases at mean seasons(2007,2008)

no	varietiy/ Cross	Blast	False smut		White tip nematode %	Brown spot	
			%	S		%	Severity
1	Giza 177	R	0.0-	0.0	2.79	12.75	15.25
2	Giza 178	R	0.75	1.36	1.24	4	5
3	Sakha 101	S	0. 61	1.07	1.80	7.75	9.5
4	Sakha 102	MR	0.11	0.47	0.8	4.5	5.5
5	Sakha 103	R	0.0	0.0	0.6	2.5	3.5
6	Sakha 104	S	0.0	0.0	0.1	2.	2.25
8	Giza 177 / Giza 178	R	0.15	0.46	0.79	10.25	11.75
9	Giza 177 / Sakha 101	R	0.11	0.26	0.89	5.5	7
10	Giza 177 / Sakha 102	R	0.06	0.08	0.0	3.75	4.5
11	Giza 177 / Sakha 103	R	0.0	0.0	0.0	2.5	3
12	Giza 177 / Sakha 104	R	0.0	0.0	0.0	2.25	2.75
14	Giza 178 / Sakha 101	R	0.25	0.48	0.39	5.25	6
15	Giza 178 / Sakha 102	R	0.37	0.37	0.28	3.5	4.25
16	Giza 178 / Sakha 103	R	0.04	0.05	0.38	2.75	3.5
17	Giza 178 / Sakha 104	R	0.0	0.0	0.0	2.25	3
19	Sakha 101 / Sakha 102	S	0.05	0.05	0.0	5	6
20	Sakha 101 / Sakha 103	S	0.07	0.08	0.o	4.5	5
21	Sakha 101 / Sakha 104	HS	0.01	0.01	0.o	3.5	4.25
23	Sakha 102 / Sakha 103	MR	0.0	0.0	0.0	3.5	4
24	Sakha 102 / Sakha 104	MR	0.02	0.02	0.0	1.25	1.75
25	Sakha 103 / Sakha 104	MR	0.0	0.0	0.0	1.5	2.25

R(1-2)Resistant   MR(3)Modrately resistant   S(4-5)Susceptible

Table (18): Blast reaction of rice entries under artificial infection in greenhouse test for tow race, IG-1 (Sakha101 and race IB 45 (Sakha 104).

No	varietiy/ Cross	Race IG-1 (Sakha101)	Race IB-45 (Sakha 104)
1	Giza 177	MR	R
2	Giza 178	R	MR
3	Sakha 101	S	MR
4	Sakha 102	R	R
5	Sakha 103	R	R
6	Sakha 104	MR	S
8	Giza 177 / Giza 178	R	R
9	Giza 177 / Sakha 101	MR	R
10	Giza 177 / Sakha 102	R	R
11	Giza 177 / Sakha 103	R	R
12	Giza 177 / Sakha 104	R	S
14	Giza 178 / Sakha 101	R	R
15	Giza 178 / Sakha 102	R	R
16	Giza 178 / Sakha 103	R	R
17	Giza 178 / Sakha 104	R	S
19	Sakha 101 / Sakha 102	S	MR
20	Sakha 101 / Sakha 103	MR	R
21	Sakha 101 / Sakha 104	S	R
23	Sakha 102 / Sakha 103	R	R
24	Sakha 102 / Sakha 104	MR	MR
26	Sakha 103 / Sakha 104	MR	S

R(1-2)Resistant   MR(3)Modrately resistant   S(4-5)Susceptible

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القدرة على التآلف لمحصول الحبوب وبعض صفات مقاومة الأمراض في الأرز.

سعيد محمد شحاتة*- عبدالمعطى بسيونى العبد*- السيد علاء سعد بدر**

* قسم بحوث الأرز ـمعهد بحوث المحاصيل الحقلية ـمركز البحوث الزراعية ـالجـ

** قسم بحوث أمراض الأرز ـمعهد بحوث أمراض النباتات ـ -مركز البحوث الزراعية الجيزة

تمت دراسة القدرة على التآلف لمحصول الحبوب وبعض صفات مقاومة الأمراض باستخدام نظام الهجن التبادلية بين ستة تراكيب وراثية مختلفة وذلك بدون الهجن العكسية، بمحطة البحوث الزراعية بسخا وذلك أثناء موسمى 2007و 2008. أوضحت النتائج أن النسبة بين كل من تباين القدرة العامة على التآلف الى تباين القدرة الخاصة على التآلف أعلى من الواحد مشيرة إلى أهمية الفعل المضيف للجين فى التحكم فى صفات محتوى الكلوروفيل، ارتفاع النبات، عدد الأيام إلى التزهير، عدد النورات الدالية /نبات، كل من نسبة وشدة الإصابة بمرض التبقع البنى و محصول الحبوب /نبات. إضافة الى ذلك فقد لعب التفاعل الجينى المضيف Xالمضيف دورا هاماً فى وراثة كل من محتوى البرولين و الضغط الاسموزى .على النقيض من ذلك، أكدت النتائج على اهمية الفعل الجينى السيادى فى التحكم فى السلوك الوراثى لصفات طول النورة الدالية، عدد الحبوب الممتلئة /النورة الدالية ووزن الألف حبة .بين الآباء، كان الصنف سخا 101 أكثر الآباء قدرة عامة على التآلف لجميع الصفات المدروسة عدا التبكير ، محتوى الكلوروفيل وكل من نسبة وشدة الإصابة بمرض التبقع البنى .وكانت التراكيب الوراثية سخا 102و سخا 103أفضل الآباء قدرة عامة على التآلف لصفات التبكير، محتوى الكلوروفيل وكل من نسبة وشدة الإصابة بمرض التبقع البنى، والصنف سخا 104لصفات طول النورة الدالية، وزن الالف حبة، محتوى البرولين، الضغط الاسموزى وكل من نسبة وشدة الإصابة بمرض التبقع البنى .كما اظهر الصنفين جيزة 177و جيزة 178 قدرة فائقة على التآلف لصفة التبكير .هذا وقد أعطت التراكيب الوراثية جيزة 177 X سخا 103، جيزة 178 X سخا 102و سخا 103 X سخا 104 أعلى قدرة خاصة على التآلف لصفتى عدد الحبوب الممتلئة /النورة الدالية و محصول النبات /نبات .أظهرت سبعة هجن قدرة خاصة على التآلف مرغوبة وعالية المعنوية وسالبة لصفتى نسبة وشدة الإصابة بمرض التبقع البنى، وثلاثة هجن لصفات طول النبات، وعدد الأيام الى التزهير. إضافة الى ذلك كانت التراكيب الوراثية جيزة 177 X سخا 101وجيزة 177 X سخا 101أفضل الهجن قدرة خاصة على التآلف لصفات طول النورة الدالية ,وزن الألف حبة ومحتوى الكلوروفيل .والهجين سخا 101 X سخا 104 لصفتى محتوى البرولين والضغط الاسموزى .كما أوضحت النتائج أن قيم درجة السيادة كانت اعلى من الواحد لجميع الصفات الزراعية والمحصول ومكوناته ومحتوى الكلوروفيل مشيرة الى تحكم السيادة القائمة فى وراثة هذه الصفات بينما تحكمت السيادة الجزئية فى وراثة باقى الصفات، كما كانت النسبة بين كل من الجينات السائدة والمتنحية فى الآباء اعلى من الواحد لجميع الصفات المدروسة عدا ارتفاع النبات، عدد الأيام للتزهير، طول النورة الدالية ومحتوى البرولين مبينة تفوق السلوك السائد للجين فى السلالات الأبوية عن السلوك المتنحى للجين .كما سجلت النتائج أن درجة التوريث بالمعنى الواسع كانت عالية لجميع الصفات المدروسة حيث تراوحت بين 94.4% الى 98.7%لصفتى الضغط الاسموزى والنسبة المئوية للإصابة بمرض التبقع البنى .إضافة إلى ذلك كانت درجة التوريث بالمعنى الضيق عالية لصفات محتوى البرولين والضغط الاسموزى وكلا من نسبة وشدة الإصابة بمرض التبقع البنى فالحقل تم اختيار الاصناف والهجن لبعض الامراض وكانت النتائج كالآتى:اثنى عشرمقاومين لمرض اللفحة واربعة متوسط المقاومة واربعة قابلين للاصابة وواحد فقط كان عالى الاصابة اما بالنسبة لمرض التفحم الكازب فوجد ثلاثة اصناف وخمسة هجن غير قابلة للاصابة كذلك مرض القمة البيضاء لم يلاحظ فى عشرة هجن بل كانت الاصابةعالية فى ثلاث اصناف دون الاخرى.اما بالنسبة لمرض التبقع البنى فكانت الاصابةعالية على الاصناف سخا ١٠١،جيزة ١٧٧ بينما كانت منخفضة علسخا ١٠٣ ،سخا ١٠٤ واتلاحظ ان الاصابة عالية على الاصناف ومنخفضة على الهجن.

اما بالنسبة لاختبارات الصوبة فوجد تسعة مقاومين تحت العدوى الصناعية لسلالتين من فطر اللفحة بينما ستة متوسطى المقاومة للسلالة 1-IGاواربعة متوسطى المقاومة للسلالة 45-IB كذلك ثلاثة قابلين نلاصابة للعزلة 1-IG واربعة قابلين للاصابة بالعزلة 45-IB .

Table (16): Estimates of genetic components of variation with their standard errors and various ratios between the components for some physiological and diseases traits in 6 x 6 diallel crosses in rice.

Genetic parameters	Proline content	Osmotic pressure	Chlorophyll content	Brown spot (percentage)	Brown spot (severity)
(D) Additive gene effects	0.411 ± 5.214 ns	2.390 ± 0.208 **	33.931 ± 5.663 **	20.114 ± 0.438 **	27.268 ± 0.909 **
(H1) Dominance effect	0.296 ± 0.132 *	0.991 ± 0.528 ns	69.362 ± 14.376 **	17.096 ± 1.113 **	21.345 ± 2.307 **
(H2) Dominance effect	0.222 ± 0.118 *	0.858 ± 0.471 *	44.416 ± 12.842 **	15.342 ± 0.994 **	19.073 ± 2.061 **
(h^2) Dominance effect	6.971 ± 7.958 ns	0.114 ± 0.317 ns	15.392 ± 8.644 *	27.350 ± 0.669 **	34.418 ± 1.387 **
(F) Gene distribution	-5.233 ± 0.127 ns	0.147 ± 0.508 ns	41.657 ± 13.835 **	10.575 ± 1.071 **	14.691 ± 2.220 **
(E) Environmental effect	6.006 ± 1.971 **	8.243 ± 7.856 ns	0.875 ± 2.140 ns	0.121 ± 0.166 ns	0.176 ± 0.343 ns
$(H_1/D)^{0.5}$ Mean degree of dom.	0.848	0.644	1.430	0.922	0.885
$(H_2/4H_1)$ Gene asymmetry	0.187	0.216	0.160	0.224	0.223
(KD/KR) Ratio of dom. & recessive genes	0.860	1.100	2.505	1.798	1.875
$(r (Wr + Vr) yr^1$	0.874	1.010	-0.208	0.255	0.231
(h bs) Heritability broad sense	0.982	0.944	0.957	0.987	0.986
(h ns) Heritability narrow sense	0.814	0.800	0.418	0.588	0.600

*and ** significant at 0.05 and 0.01 probability levels, respectively.

Table (14): Estimates of genetic components of variation with their standard errors and various ratios between the components for some agronomic, yield and its component traits in 6 x 6 diallel crosses in rice.

Genetic parameters	Plant height (cm)	Days to 50% heading	Panicle length (cm)	No. of panicles /plant	No. of filled grains /panicle	1000 grain weight (g)	Grain yield /plant (g)
(D) Additive gene effects	53.547±6.285 **	65.697±11.463 **	0.337±1.768 ns	11.249±1.077 **	195.132±109.935 ns	3.516±2.451 ns	142.261±17.11 **
(H1) Dominance effect	106.012±15.954 **	136.025±29.099 **	20.125±4.487 **	11.061±2.735 **	1663.819±279.08 **	21.856±6.24 **	187.482±43.43 **
(H2) Dominance effect	96.672±14.252 **	109.672±25.995 **	19.044±4.009 **	7.270±2.443 **	1278.672±249.31 **	17.764±5.58 **	159.690±38.79 **
(h²) Dominance effect	26.934±9.593 **	48.657±17.497 **	8.396±2.698 **	6.919±1.644 **	510.810±167.80 **	2.630±3.757 **	355.948±26.45 **
(F) Gene distribution	-4.435±15.353 ns	-12.604±28.004 ns	0.520±4.318 ns	13.029±2.632 **	472.749±268.57 **	6.484±6.013 ns	79.392±41.797 ns
(E) Environmental effect	2.719±2.375 ns	1.319±4.333 ns	0.199±0.668 ns	0.147±0.407 ns	16.710±41.552 **	0.265±0.930 ns	4.258±6.467 ns
$(H_1/D)^{0.5}$ Mean degree of dom.	1.407	1.439	7.311	0.992	2.920	2.493	1.148
$(H_2/4H_1)$ Gene asymmetry	0.228	0.202	0.240	0.160	0.190	0.200	0.213
(KD/KR) Ratio of dom. & recessive genes	0.943	0.875	0.827	3.808	2.418	2.174	1.642
(r (Wr + Vr) yr[1]	-0.120	0.073	0.182	0.647	-0.478	-0.173	-0.109
(h bs) Heritability broad sense	0.955	0.984	0.966	0.950	0.957	0.950	0.952
(h ns) Heritability narrow sense	0.556	0.645	0.166	0.339	0.138	0.107	0.506

*and ** significant at 0.05 and 0.01 probability levels, respectively.

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