COMBINING ABILITY FOR GRAIN ꞏYIELD AND BROWN SPOT DISEASE RESISTANCE TRAITS IN RICE (*Oryza sativa* L.) UNDER SALINE SOIL CONDITIONS

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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 brown spot disease infection traits, at Rice Breeding Salinity Program, Sirw Agricultural Research Station, during 2007 and 2008 summer seasons. The ratio of variances due to general combining ability and specific combining ability ($\delta 2$ GCA / $\delta 2$ SCA) was more than unity, indicating the preponderance of additive genes in controlling, chlorophyll content, plant height, number of days to heading, number of panicles/plant, both percentage and severity of brown spot infection, and grain yield/plant. Moreover, additive x additive type of gene interaction was played an important role in the inheritance of proline 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. 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 infection. The genotypes Sakha 102 and Sakha 103 were good general combiners for earliness, chlorophyll content, and both percentage and severity of brown spot infection, and Sakha 104 for panicle length, 1000-grain weight, grain yield, proline content, osmotic pressure and both percentage and severity of brown spot infection, 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 infection and 3 hybrids for plant height and number of days to 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, 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, number of days to 50% heading, panicle length and proline content indicating that dominant genes were more than recessive genes 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 infection. In addition, high estimates of heritability in narrow sense were recorded for proline content, osmotic pressure and both percentage and severity brown spot disease infection.

Keywords: rice, salinity, grain yield, brown spot infection, combining ability, heritability, gene action, heterosis and degree of dominance.

INTRODUCTION

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, 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. Salt tolerance is considered to be a polygenic trait, and its expression is affected by various genetic, development, and physiological interactions within the plant, and in addition between genotypes and external environments, Salt tolerance is a complex character controlled by a number of genes or groups of genes, and involves a number of component traits which are likely to be quantitative in nature, and the importance of salinity as a breeding objective is likely to increase in future, Flowers and Yeo (1995).

In various studies of different species, tests for salt tolerance have suggested that both additive and 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. 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. Diallel analysis for grain yield and brown spot disease was investigated to estimate the general and specific combining ability and nature of gene action for grain yield and its components traits, and resistance to brown spot disease infection. In addition, heterosis, heritability and degree of dominance were appraised.

MATERIALS AND METHODS

The present investigation was carried out at the Farm of Sirw Research Station, during 2007 and 2008 summer seasons. Six Egyptian rice cultivars with a wide rang in same quantitative characters, were 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 brown spot disease infection in rice. 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
1	Giza 177	Giza 177 / Yomji No.1 // Pi No. 4	Japonica	Sensitive
2	Giza 178	Giza 175 / Milyang 49	Ind. /Jap.	Tolerant
3	Sakha 101	Giza 176 / Milyang 79	Japonica	Moderate
4	Sakha 102	Gz 4096-7-1 / Giza 177	Japonica	Sensitive
5	Sakha 103	Giza 177 / Suweon 349	Japonica	susceptible
6	Sakha 104	Gz 4096-8-1 / Gz 4100-9-1	Japonica	Tolerant

The six rice cultivars were raised thrice at an interval of 15 days to ensure synchronization in flowering for the purpose of hybridization during 2007 summer season at Sirw Research Station. Thirty days old seedlings from fifteen cross combinations along with their parents were transplanted in a randomized complete block design experiment with three replications during 2008 summer season. In each replicate, the plot consisted of 4 rows with a length of 5 meters/ row. The two central rows were used for collecting data and observation. A spacing of 15 x 15 cm was considered between and within rows. Doses of recommended fertilizer were given and also recommended agronomic practices were adopted. Twenty plants/ replicate were randomly taken from each parent and each F1 cross for collecting data 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 both percentage and severity of brown spot disease.

Statistical and Genetical 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 (1954), 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 including 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 greater 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 deviation of the F_1 mean from better parent mean and expressed as percentage. Heterosis over better-parent % was estimated as follows:

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

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).

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

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). Some chemical characteristics of experimental soil and water at Sirw location in 2008 season are given in Table (2).

Table (2): Some chemical characteristics of experimental soil, irrigation, drainage and ground water at El-Sirw location in season 2008

Samples soil and water	EC ds/m	Anions meq/L			Cations meq/L				PH 1:2.5	O.M %	C.E.C	ESP	Soil text.
		HCO^{-3}	CL^-	SO^-_4	Ca^{++}	Mg^{++}	Na^+	K^+					
Soil	8.8	18	70	2.24	23.1	2.74	63.0	1.4	8.06	1.64	42.0	19.6	Clay
Mixed water	1.9	5	11	11.9	9.34	7.08	11.2	0.3	-	-	-	-	-
Drainage water	3.8	9.5	28	24.1	15.4	17.2	28.4	0.6	-	-	-	-	-

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 a 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 variances 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 study 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. These results 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. The obtained results are in harmony with those previously observed by El Abd (1995), Annadurai and Nadarajan (2001), Sao and Motiramani (2004), Singh and Kumar (2004), 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 brown spot infection 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. Sakha 103 followed by Sakha 102 and Giza 177 were the earliest rice cultivars, otherwise, Sakha 101, Sakha 104 and Giza 178 were the latest comparing with other rice cultivars. In addition, Sakha 101 has a longest panicle (24.21cm), more filled grains /panicle (160 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 (26.35) 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 selecting 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 for 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 for cross Giza 178 X Sakha 104. Moreover, the largest number of filled grains /panicle was detected for the crosses; 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) respectively. The heaviest 1000 grain weight was obtained for the crosses; Giza 177 X Sakha 102, Giza 178 X Sakha 103, Giza 177 X Sakha 104 and Giza 177 X Sakha 101. 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 the possibility of increasing grain yield through exploring hybrid vigor in F1 plants.

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 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 their leaves, opposite, the lowest estimated values were exhibited for Giza 178 and Sakha 101. From another point of view, Sakha 103, Giza 178 and Sakha 102 were highly resistance for both percentage and severity of rice brown spot disease, while, Sakha 104 and Sakha 101 were moderately resistance. In addition, Giza 177 was found to by highly susceptible 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 Sakha 101 X Sakha 103 and Giza 177 X Sakha 103 crosses; 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) which 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 combination were found to be resistance to rice brown spot disease when it investigated as a percentage or severity.

Table (5): Mean performance of the six parents and their F$_1$ hybrieds for some 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

Estimates of general (GCA) and specific (SCA) combining ability effects

Obviously, estimates of GCA effects 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 stature. Moreover, Sakha 103 and Sakha 102 were the best general combiners for earliness.

Table (7): Estimates of general combining ability (GCA) effects for grain 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.

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. 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.

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 its component traits and other studied traits in this investigation. 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 resistance to brown spot disease. Similar results were obviously recorded by El Abd (1995), Iftekharuddauta *et al.* (2004), Shehata (2004), Satish and Seetharamaiah (2005), Sharma *et al.* (2005) and Dhakar

and vinit (2006). According to the results of the osmotic pressure and proline content, all the studied genotypes were good combiners for salt tolerance, consequently successful breeding program could be conducted for salinity tolerance depending on 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.

Table (8): Estimates of general combining ability (GCA) effects for some physiological and brown spot infection traits

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	0.02	0.09	0.30	0.11	0.13
S.E. at 0.01	0.04	0.14	0.47	0.17	0.21

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

The estimates of specific combining ability of 15 crosses for 12 agronomic yield and its component; physiological and brown spot disease 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 least 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 resulted from low / high or high / low or high / high or low / low combining parents. But very few crosses including low / low general combiners gave high SCA.

The cross combinations showing high negative SCA for number of 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 best specific combinations 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.

Table (9): Estimates of specific combining ability (SCA) effects for some agronomic, yield and its components 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	1.45	1.01	0.39	0.33	3.60	0.46	1.81
S.E. at 0.01	1.63	1.13	0.40	0.31	4.06	0.51	2.04

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

Table (10): Estimates of specific combining ability (SCA) effects for some physiological and brown spot infection 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.

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 the best specific combinations for panicle length. While, the best specific combination 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. Among the fifteen hybrids, almost half of them recorded negative significant SCA effects favoring resistance of brown spot disease. The results revealed that 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 Singh and Kumar (2004), Yu *et al.* (2004), Bagheri *et al.* (2005), Rosamma and Vijayakumar (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 vigor 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 x Sakha 103 exhibited highest negative heterosis (-7.9%) for days to 50% heading followed by Sakha 101 X Sakha 104 (-4.1%), Sakha 101 X Sakha 102 (-3.2%). Appearance of significant and negative heterosis for number of days to 50% heading indicated the possibility of exploiting heterosis for earliness. For plant height, further, only one cross, Giza 177 X Giza 178 (-4.4%) was recorded significant heterosis in a desirable negative direction. Three crosses, Giza 177 X sakha 101, 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 was 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): Estimate 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 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. 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), Verma and Sirvastara (2004), Zhen *et al.* (2004), Jin *et al.* (2005), Khoyumthem *et al.* (2005), Raju *et al.* (2005), Chitra *et al.* (2006), Saravanan *et al.* (2006), Senguttuvel *et al.* (2006) and Shanthala *et al.* (2006).

Table (12): Estimate 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.

Genetic variance component analysis

The results of the regression analysis for F_1 generations for agronomic, yield and its component traits were presented in (Table 13). 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 alleles 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 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).

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 genetic components and relative proportion of various components and broad and narrow-sense heretability for agronomic, yield and its component traits are furnished in (Table 14). 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. 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, number of 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.

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) yr¹	-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.

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 heritability were recorded for all the studied traits, while high and moderately high estimates of narrow sense heritability for plant height, number of days to 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 brown spot disease traits (Table 15) 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 of 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.

Table (15): Validity of hypothesis through homogeneity tests for some physiological and brown spot disease 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 genetic components estimated by the diallel analysis (Table 16), 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 that excess of dominant alleles were present in the genetic material.

Table (16): Estimates of genetic components of variation with their standard errors and various ratios between the components for some physiological and brown spot disease 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.

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 were 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).

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القدرة على التآلف والتحليل الوراثى لصفات محصول الحبــوب وبعــض صــفات مقاومة الأمراض في الأرزتحت ظروف الاراضى الملحية.

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تمت دراسة القدرة على التآلف والتحليل الوراثى لصفات محصول الحبــوب ومقاومــة الاصابة بمرض التبقع البنى باستخدام نظام الهجن التبادلية بين ستة تراكيب وراثية مختلفة وذلك بدون الهجن العكسية ببرنامج الملوحة بمحطة البحوث الزراعية بالسرو وذلك أثناء موسمى ٢٠٠٧ و٢٠٠٨.

أوضحت النتائج أن:

النسبة بين كل من تباين القدرة العامة على التآلف الى تباين القدرة الخاصة على التآلف أعلى مــن الواحد الصحيح مشيرة إلى أهمية الفعل المضيف للجين فى التحكم فى صفات محتوى الكلوروفيـل، ارتفــاع النبات، عدد الأيام الى ٥٠ % تزهير، عدد النورات الدالية / نبات، كل من نسبة وشــدة الإصــابة بمــرض التبقع البنى و محصول الحبوب / نبات .إضافة الى ذلك فقد لعب التفاعل الجينى المضيف X المضيف دورا هاما فى وراثة كل من محتوى البرولين و الضغط الاسموزى .على النقيض من ذلك، أكــدت النتــائج علــى اهمية الفعل الجينى السيادى فى التحكم في السلوك الوراثى لصفات طول النورة الدالية، عدد الحبوب الممتلئة / النورة الدالية ووزن الألف حبة . بين الآباء، كان الصنف سخا ١٠١ أكثر الآباء قدرة عامة علــى التــآلف لجميع الصفات المدروسة عدا التبكير ، محتوى الكلوروفيل وكل من نسبة وشدة الإصابة بمرض التبقع البنى . وكانت التراكيب الوراثية سخا١٠٢ و سخا ١٠٣ أفضل الآباء قدرة عامة علــى التــآلف لــصفات التبكيــر، محتوى الكلوروفيل وكل من نسبة وشدة الإصابة بمرض التبقع البنى، والصنف سخا ١٠٤ لــصفات طــول النورة الدالية، وزن الالف حبة، محصول الحبوب، محتوى البرولين، الضغط الاسموزى وكل من نسبة وشدة الإصابة بمرض التبقع البنى .كما اظهر الصنفين جيزة ١٧٧و جيزة ١٧٨ قدرة فائقة علــى التــآلف لــصفة التبكير . هذا وقد أعطت التراكيب الوراثية جيزة ١٧٧ X سخا ١٠٣، جيزة ١٧٨ X ســخا ١٠٣ و ســخا ١٠٣ X . سخا ١٠٤ أعلى قدرة خاصة على التآلف لصفتى عــدد الحبــوب الممتلئــة / النــورة الداليــة و محصول النبات / نبات .أظهرت سبعة هجن قدرة خاصة على التآلف مرغوبة وعاليــة المعنويــة وســالبة لصفتى نسبة وشدة الإصابة بمرض التبقع البنى، وثلاثة هجن لصفات طول النبات، وعدد الأيام الــى ٥٠% تزهير. إضافة الى ذلك كانت التراكيب الوراثية جيزة ١٧٧ X سخا ١٠١ وجيزة ١٧٨ X سخا١٠١ أفــضل الهجن قدرة خاصة على التآلف لصفات طول النورة الدالية ووزن الألف حبة ومحتوى الكلوروفيل .والهجين سخا ١٠١ X سخا ١٠٤ لصفتى محتوى البرولين والضغط الاسموزي .كما أوضحت النتائج أن قيم درجــة السيادة كانت اعلى من الواحد الصحيح لجميع الصفات الزراعية والمحصول ومكوناته ومحتوي الكلوروفيـل مشيرة الي تحكم السيادة القائقة في وراثة هذه الصفات بينما تحكمت السيادة الجزئية في وراثة باقي الصفات، كما كانت النسبة بين كل من الجينات السائدة والمتحية في الآباء اعلى من الواحد لجميع الصفات المدروســة عدا طول النبات، عدد الأيام الى ٥٠% تزهير، طول النورة الدالية ومحتوى البرولين مبينة تفــوق الــسلوك السائد للجين في السلالات الأبوية عن السلوك المتنحي للجين .كما سجلت النتائج أن درجة التوريث بالمعني الواسع كانت عالية لجميع الصفات المدروسة حيث تراوحت بين٩٤،٤ % الي ٩٨،٧ % لــصفتي الــضغط الاسموزي والنسبة المئوية للإصابة بمرض التبقع البنى . إضافة إلي ذلك كانت درجة التوريــث بــالمعني الضيق عالية لصفات محتوي البرولين والضغط الاسموزي وكلا من نسبة وشدة الإصابة بمــرض التبقــع البنى.