

GENE ACTION AND RELATIVE IMPORTANCE OF SOME AGRONOMIC AND BIOTIC STRESS TRAITS AFFECTING GENETIC DIVERGENCE IN RICE

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ABSTRACT

Egypt has the world's highest rice productivity from unit area, yet yield was constrained by biotic stresses being targeted by breeders. This work was carried out at the experimental Farm of Rice Research and Training Center, Sakha Kafer El-Sheik, Egypt, during 2011 and 2012 rice growing seasons. Five parents and their 10 hybrids were used to study gene action, combining ability and heterosis for certain agronomic traits and biotic stresses. Giza177 and M101 rice varieties were resistant to rice blast, while GZ6214 and M202 were resistant to stem borer, and both M201 and M202 to white tip nematode. General combining ability (GCA) and specific combining ability (SCA) were highly significant for all studied traits. M202 gave highly significant and negative estimates of GCA effects desired for plant height, vegetative stage, reproductive stage and days to heading. Significant and highly significant negative estimates of SCA effects were found for plant height, vegetative stage and days to heading. The best crosses for yield and its components were Giza177 x GZ6214, Giza177 x M201, Giza177 x M202, GZ6214 x M201 and GZ6214 x M202. Regarding stem borer infestation, the crosses M101 x M201, M101 x M202 and Giza177 x GZ6214 gave highly significant and desirable negative estimates of SCA. For blast reaction, stem borer infestation and white tip nematode two hybrid combinations, Giza177 x GZ6214 and GZ6214 x M201 recorded highly significant negative desirable heterosis and showed highly significant negative SCA effects. M202 was a good resource for resistance to white tip nematode, with all crosses with this cultivar having low levels of infection. Principal component analysis as one of Multivariate analysis components was used to study the genetic dissimilarity and relative importance of agronomic and biotic traits as a source of variation among the five parents and their hybrids. The first three principal components were significant and accounted about 80.4 % of the total variance of all characters. The 15 rice genotypes were grouped into three major clusters based on relative dissimilarity among them with significant differences among these groups for most characters, the progeny produced from crossing between Egyptian and US parents which are distantly related showed divergent distance and gave values surpassed their parents in most characters. The results of all multivariate analysis showed that US parent M202 is the most divergent parent. Grain yield plant⁻¹, filled grains panicle⁻¹ and blast reaction were the most important source of variation among all genotypes with largest coefficients on the first PC axis. However, the second axis PC2 deals with the most earliness characters; vegetative stage and days to heading. On the other side, PC3 was dominated by white tip nematode. Finally, crossing among more genetic divergent Egyptian rice varieties Giza 177, GZ6214 and US parents created new suitable combinations in breeding program. Rice breeder can maximize genetic diversity among new cultivars, meanwhile at the same time maintaining the level of desired agronomic traits present in current popular cultivars.

Keywords: General combining ability, specific combining ability, blast, white tip nematode, genetic divergence, multivariate and principal component analysis

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most important crops and is the staple food for nearly half of the global population (FAO, 2004). In Egypt, where rice is considered the second most important cereal crop after wheat (Bastawisi et al., 2003) and also constitutes one of the country's main agricultural exports, the cultivated area under rice was 0.7 million hectares in 2006 with an average yield of 9.84 ton/ ha giving the highest productivity in the world (RRTC, 2006). Despite this high average yield, biotic stresses such as blast, stem borers and white tip nematodes constrain rice production in Egypt. Blast disease affects rice production in all rice growing regions and it can reduce annual rice production by about 5% in normal or mildly-affected seasons. In epidemic seasons, yield losses may reach as high as 30 –50 % Sehly, et al., (2002) and El-Shafey, (2007). Several blast-resistant varieties have been released by rice breeding programs and adopted by farmers only to lose their resistance within a few years due to adaptation and race shifting of blast pathogen. The loss of resistance has been striking and well documented (Kiyosawa, 1982; Koizumi, 2007). The variable nature of the pathogen often leads to breakdown of host resistance and consequent widespread epidemics. Thus, breeding for durable blast resistance is one of the major challenges faced by rice breeders (Ou, 1985). Changes in prevalence of specific races of blast pathogen meant that the highly susceptible old rice cultivars Giza159 and Reiho appeared to be resistant and escaped from the disease in some locations in Egypt in the 2005 season. In addition, the resistance of the cultivars Sakha 101 and Sakha 104 was broken down due to the appearance of specific virulent races: IB-45 specific to Sakha 104, while IG-1 was specific to Sakha 101 during 2004 season (El-Shafey, 2002 and Sehly, et al., 2008). The extensive variability of the blast fungus pathogen means that breeding for greater cultivar diversity must be targeted at inducing changes in the genetic background of promising lines through the introduction of new genes of resistance. Giza177 proved to be a good resource for blast resistance, demonstrating under different tests for blast that it remained resistant from its release in 1995 to the present (Sehly et al., 2008). White tip disease of rice leaves caused by the rice leaf nematode *Aphelenchoides besseyi* (Christie, 1942) is widespread and present in nearly all rice ecosystems worldwide (Ou, 1985), and has recently been found in Egypt where the response of rice cultivars has been significantly different in terms of infection level and yield losses. The sensitive older rice cultivars Giza171 and Reiho, and some newer cultivars, were suffered extensive losses of up to 47%. Others are resistant: Giza178, Giza182, hybrid1 and hybrid2, Giza159 and Giza176, while Sakha101 and Giza177 are moderately susceptible and Giza171 and Reiho highly susceptible (El-Shafey, 2007). Some varieties, such as M201 and M202, originating in the USA are resistant to white tip nematode.

Genetic diversity among parents is considered an important factor for obtaining heterotic hybrids. Genetic diversity and relationships among breeding materials is essential to the rice breeder in the efficient improvement

of rice crop. Crosses between genetically divergent parents are expected to have a large genetic variance among progenies than crosses between closely related parents (Cox *et al.* 1985 and Melchinger *et al.* 1990). According to Cruz and Carneiro (2003), this distance is essential to increase the chance of recovering superior genotypes. In rice breeding program, it is possible to estimate the genetic divergence by using multivariate methods. This divergence is based on physiological, morphological and agricultural characters of a group of genotypes. To make advances in rice breeding it is important to understand the relatedness and ancestry of introduced rice accessions, and identify SSR markers associated with agronomically important phenotypic traits, for example yield, Agrama *et al.*, 2007. The efficacy of the genetic divergence as a criterion for choosing parents to be crossed has been reported by several authors (Cox *et al.* 1985; Dias and Kageyama, 1997; Machado *et al.*, 2002 and Menshawy 2008). Moreover, the Principal Component Analysis and the Canonical Variable Analysis have analogous efficacy to determine the most suitable combinations for a breeding program (Machado *et al.*, 2002; Suinaga *et al.*, 2005). Estimation of genetic diversity is an important step for any breeding program, but not the last one. Another helpful issue to be evaluated is the relative importance of the characters, though plant breeders often measure several characters simultaneously in rice breeding program, then it is possible to estimate the genetic divergence by using multivariate methods (Agrama and Eizenga, 2007). It is desirable for breeder to have much information as possible on the genetic control of the important agronomic and yield characters of the crop. Thus knowledge of the nature and extent of variability, particularly genetic variability, present in any crop is essential for further improvement. In theory, mating of distantly-related parents will produce a greater number of transgressive segregates than mating of closely-related parents. Cornelius and Sneller (2002) reported that a lack of genetic diversity may limit breeding progress. Information of genetic diversity is important when working to improve crop and develop new varieties. Also, characterizing genetic diversity and/or degree of association between and within varieties would be the first step toward developing germplasm and crop cultivars. Successful crop improvement depends on genetic variability that arises from genetic diversity (Rana and Bhat, 2005). Multivariate technique could resolve several phenotypic measurements into fewer, more interpretable and more easily visualized dimensions such an analysis which used principle components (Hair *et al.*, 1987) seemed to elucidate pattern of variation in agronomic attributes and to obtain the initial factor solution using eigen values. These values measure the explained variance associated with variable and refer to its contribution to the whole divergence. Principal component analysis and factor analysis have analogous efficacy to determine the most suitable combinations and grouping the varied genotypes into varied groups. Principal component and cluster analysis can be used to create genetic variability, also multivariate technique to determine the relative contribution of characters of variation and grouping the genotypes into varied

clusters, (El-Mansy, 2009 and Abdel-Salam *et al.*, 2010)

The scope of the present investigation was to examine the divergence among two Egyptian and three US parents and their 10 crosses by using multivariate analysis on the basis of agronomic and yield characters to give graphical presentation of genotypes as well as to investigate the relative importance of the evaluated characters. Also, select the most suitable combinations for crossing programmes and resistant to all biotic stresses. In addition, our current investigation studied the inheritance of rice blast, stem borer infestation and white tip nematode disease.

MATERIALS AND METHODS

The present investigation was carried out at the Experimental Farm of the Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt during the rice seasons in 2011 and 2012. The five rice genotypes, i.e. Giza177, GZ6214 (Egyptian rice varieties, resistance to blast), M101, M201 and M202 (originating from the USA, and possess the Pi-k^s gene and all cultivars which have this ineffective gene were highly susceptible to the prevalent races; IG-1, ID-13, IC-15 and IB-63 but M101 resistant to blast under Egyptian conditions). Those genotypes were grown at three successive sowing dates in the 2011 growing season with 15-day intervals to overcome their differences in heading date, and a half diallel crossing was carried out among them (without reciprocals). Bulk emasculation was practiced using the hot water technique according to Jodon (1938) and modified by Butany (1961). A total of 10 F₁ generations were made and after 30 days F₁ plants were transplanted to the field in 2012 using a spacing of 20 x 20 cm. The experimental plots were grown in a Randomized Complete Block Design (RCBD), with three replications. Each variety in a replication was represented by three rows with 20cm spacing and 25 plants in each row. Plot samples were taken at 7-day intervals to determine panicle initiation stage. Plant height, tillers plant⁻¹, 1000-grain weight, filled grains panicle⁻¹ and grain yield plant⁻¹ were measured at harvest. Each variety in a replication was represented by three rows with 20-cm spacing and 25 plants in each row. Total chlorophyll content in the flag leaf was recorded at heading stage using a chlorophyll meter (5 SPAD-502, Minolta Camera Co. Ltd., Japan). Panicle primordium initiation character (3 mm length approximately) was recorded by dissecting the main culm of five plants randomly taken from each variety per replication. The five parents; Giza177, GZ6214, M101, M201 and M202, were crossed in half diallel analysis in 2011 according to Griffing (1956) Method 2 model 1. The parents and their F₁ crosses were grown as individual plants in a Randomized Complete Block design with their replications with spacing of 20 cm between rows and 20 cm between plants. All recommended cultural practices were followed. Extent of heterosis was measured as percentage deviation of F₁ mean values from better-parent (Heterobeltiosis). The significance of the heterobeltiosis was tested using "t" test according to the formula suggested by Wynne *et al.*, (1970).

Evaluation of blast infection: All genotypes were tested for blast reaction at adult stage in Sakha Experimental Farm. Blast reaction was recorded according to the IRRI Standard Evaluation System using a 0–9 scale (IRRI, 1996).

White tip nematode infection: The resistance of different varieties was evaluated according to infection percentage with 0–less than 1% = resistant, 1–30 = moderately susceptible, > 30–50 = susceptible, and 51–100 = highly susceptible, El-Shafey, (2007).

Percentage of white tip nematode infection: To estimate the resistance of rice varieties, all rice hills were examined to record the infected hills and calculate the infection percentage using the following formula:

$$\text{Percentage of infection} = \frac{\text{No. of infected hills}}{\text{Total no. of rice hills}} \times 100$$

Rice stem borer evaluation: Parents and their F₁ genotypes were evaluated for rice stem borer infestation. The reaction of evaluated genotypes was classified into five categories according to the standard evaluation of the Rice Research and Training Center (RRTC), Sakha, Egypt (2006) as follows:

Resistant (R): 0–3% whiteheads (WH), Moderately resistant (MR): > 3–6% WH, Moderately susceptible (MS): > 6–9%, Susceptible (S): > 9–12%, and Highly susceptible (HS) > 12%.

Statistical Analysis: The statistical analysis for estimation of combining ability was done using method 2, model 1 of Griffing (1956).

The dissimilarity among rice genotypes was estimated by using multivariate analysis (Johnson and Wichern, 1988). Therefore hierarchical clustering procedure using Ward's minimum variance methods, which minimize within cluster of sum of square across all partitions was applied to determine genetic divergence and distance. This procedure used a method performing a disjoint cluster analysis on the basis on Euclidean distance as described by Hair *et al.*, (1987). The dendrogram is constructed on Euclidean distance basis. On order to study the relative importance of the studied characters towards genetic divergence, principal components analysis was performed according to Hair *et al.*, 1987. This analysis was calculated from a matrix based on correlation between the contributed characters for all genotypes. The principal components associated with all genotypes were expressed as eigen values and manifested in eigen vector for all studied characters in each principal component axis. The genotypes were grouped as diagram on principal component axis.

RESULTS AND DISCUSSION

A- Physiological traits

A.1: Mean performance:

Mean performance of all physiological traits for the five parents and their 10 crosses are presented in Table 1. The data indicated that all studied traits had a wide range of variability, reflected in the variation among parents

and their crosses. Data in Table 1 shows that GZ6214, M101 and M201 and the two crosses, GZ6214 x M101 and M201 x M202, gave the highest mean values for flag leaf area (38.1, 37.6, 37, 45.8 and 45.03 cm², respectively). While M201 (51 SPAD) and M202 (49 SPAD) showed the highest chlorophyll content of the five parents, the crosses M101 x M202 and M201 x M202 also exhibited the highest mean values of chlorophyll content (54.33 and 52.33 SPAD, respectively). For plant height, M201 and M202 and the hybrid combination M201 x M202 recorded the shortest plants (94, 98 and 69 cm) compared with other genotypes. With regard to vegetative stage, M101 and M202 and the hybrid combinations Giza 177 x M101, GZ6214 x M101 and M201 x M202 recorded the lowest days to reach maximum tillering (60, 61, 62 and 63 days) and were also the earliest in heading compared with the other rice genotypes with the mean values (81, 83.33, 91.33 and 88 days, respectively).

Table1. Mean performance of parents and their crosses for physiological studied traits.

Genotype	Flag leaf area (cm ²)	Chlorophyll content	Plant height (cm)	Vegetative Stage (day)	Reproductive Stage (day)	Days to heading (day)	Panicle length (cm)
Giza177	24.50	44.90	101.00	72.00	21.67	93.67	20.00
GZ6214	38.10	41.27	97.00	72.00	29.33	101.33	18.30
M101	37.6	46.00	124.00	60.00	23.33	83.33	21.00
M201	37.00	51.00	94.00	67.30	19.00	87.00	20.00
M202	35.8	49.00	98.00	61.00	20.00	81.00	21.30
Giza177x GZ6214	32.27	42.00	96.00	84.00	21.00	105.00	17.00
Giza177 x M101	38.23	51.33	116.67	62.00	29.00	91.00	23.00
Giza177 x M201	41.63	48.00	116.00	84.33	20.67	105.00	23.33
Giza177 x M202	41.80	45.00	112.00	78.00	23.00	101.33	22.17
GZ6214 x M101	45.80	51.00	124.00	62.00	29.00	91.33	26.00
GZ 6214 x M201	32.80	42.00	94.00	85.00	20.00	105.00	20.00
GZ6214 x M202	36.17	43.00	95.00	88.00	19.00	107.00	21.33
M101 x M201	39.20	51.00	121.67	72.00	24.33	96.33	25.00
M101 x M202	41.53	52.33	103.00	67.00	25.33	92.33	22.00
M201 x M202	45.03	54.33	69.00	63.00	25.00	88.00	19.00
LSD at 0.05	1.14	8.44	1.18	1.21	1.08	1.18	1.05
LSD at 0.01	1.53	11.27	1.57	1.62	1.45	2.42	1.40

A.2: Analysis of combining ability:

Estimates of both general (GCA) and specific combining ability (SCA) variance for physiological traits are presented in Table 2. Both general and specific combining ability variance were found to be highly significant for all physiological studied traits except chlorophyll content, indicating the importance of both additive and non-additive genetic variance in determining the inheritance of the studied traits. The relative importance of each variance was determined using GCA/SCA; the GCA/SCA variances were found to be greater than unity for all studied traits except panicle length, suggesting greater importance of additive genetic variance in the inheritance of these traits. Therefore, it could be concluded that selection procedures based on the accumulation of additive effects would be successful in improving these traits. These findings agree with those of Hammoud (1996); Ammar (1997); El-Malky (1997); Abd El-Aty (2001); El-Mowafi and Abou Shousha (2003); Hammoud (2004); Sedeek *et al.*, (2007) and Hammoud *et al.* (2008).

Table 2. Analysis variance and mean square for physiological traits.

S.V.	d.f.	Flag leaf area (cm ²)	Chlorophyll content	Plant height (cm)	Vegetative Stage (day)	Reproductive Stage (day)	Days to heading (day)	Panicle length (cm)
Replications	2	5.74**	40.07 ^{ns}	2.96 ^{ns}	0.16 ^{ns}	2.22 ^{ns}	2.29 ^{ns}	2.32 ^{ns}
Genotypes	14	86.30**	116.80*	413.79**	289.18**	39.26**	216.12**	17.53**
Parents	4	97.94**	211.33 ^{ns}	440.10**	100.27**	49.83**	205.23**	4.10*
Crosses	9	64.76**	64.67**	424.23**	332.98**	37.89**	155.63**	22.04**
P vs. F1	1	233.61**	207.94*	214.68**	650.71**	9.34**	804.01**	30.63**
Error	28	0.86	46.71	0.91	0.97	0.77	2.15	0.72
G.C.A.	4	31.38**	37.45 ^{ns}	310.04**	143.43**	17.00**	124.25**	5.58**
S.C.A.	10	27.72**	10.91 ^{ns}	69.09**	77.58**	11.52**	51.15**	5.95**
Error	28	0.29	15.57	0.30	0.32	0.26	0.72	0.24
G.C.A./S.C.A		1.13	3.43	4.49	1.85	1.48	2.43	0.94

*, **: significant at 5% and 1% level, respectively; ns: not significant.

A.2.1 : General combining ability (GCA) effect:

Estimates of general combining ability effects of individual parental lines for physiological traits are given in Table 3. Highly significant and positive GCA effects were observed for flag leaf area, chlorophyll content and panicle length, while highly significant and negative values were recorded for plant height, vegetative phase, reproductive phase and days to heading which are desirable for improvement of these traits in breeding programs since breeders target low mean values. For flag leaf area and chlorophyll content, varieties M101 and M201 showed significant and highly significant positive general combining ability effects, indicating that these varieties could be used as good combiners for improvement of these traits. In relation to plant height, vegetative stage, reproductive stage and days to heading, the M202 gave highly significant and desirable negative GCA effects. The negative values of GCA effects for these traits are required from a breeding perspective since they refer to short stature plant types and earliness.

A.2.2: Specific combining ability (SCA) effect:

Estimates of specific combining ability effects for the five parental varieties are shown in Table 4. Regarding flag leaf area and chlorophyll content, the two crosses GZ6214 x M101 and M201 x M202 exhibited highly significant and positive estimates of SCA effects, so these combinations may be useful in exploitation of heterosis due to their desirable increase in flag leaf area and chlorophyll content. For plant height, vegetative stage and days to heading, two further crosses Giza177 x M101 and M201 x M202 gave highly significant and negative estimates of SCA effects. These crosses could be utilized in rice breeding programs due to their desirable stature and earliness.

Table 3. Estimation of general combining ability effect for physiological traits.

Parents	Flag leaf area (cm ²)	Chlorophyll content	Plant height (cm)	Vegetative Stage (day)	Reproductive Stage (day)	Days to heading (day)	Panicle length (cm)
Giza177	-3.44**	-1.25 ^{ns}	1.05**	3.04**	-0.41**	2.60**	-0.33**
GZ6214	-0.54**	-3.48**	-4.62**	4.56**	1.11**	5.65**	-0.97**
M101	1.84**	1.83*	11.14**	-6.87**	2.07**	-4.83**	1.46**
M201	0.82**	1.78*	-2.81**	1.13**	-1.70	-0.45**	-0.07 ^{ns}
M202	1.32**	1.11 ^{ns}	-4.76**	-1.87**	-1.08**	-2.97**	-0.09 ^{ns}
LSD at 0.05	0.18	1.33	0.19	0.19	0.17	0.29	0.17
LSD at 0.01	0.29	2.11	0.29	0.30	0.27	0.45	0.26

*, **: significant at 5% and 1% level, respectively; ns: not significant.

Table 4. Estimates of specific combining ability effect for physiological traits.

Crosses	Flag leaf area (cm ²)	Chlorophyll content	Plant height (cm)	Vegetative Stage (day)	Reproductive Stage (day)	Days to heading (day)	Panicle length (cm)
Giza177x GZ6214	-1.59**	-0.75 ^{ns}	-6.32**	4.56**	-3.02**	1.51**	-3.00**
Giza177 x M101	2.00**	3.27 ^{ns}	-1.41**	-6.02**	4.03**	-2.02**	0.57**
Giza177 x M201	6.42**	-0.01 ^{ns}	11.87**	8.32**	-0.54**	7.60**	2.43**
Giza177 x M202	6.08**	-2.34 ^{ns}	9.83**	4.98**	1.17**	6.46**	1.29**
GZ6214 x M101	6.66**	5.17**	11.59**	-7.54**	2.51**	-4.73**	4.21**
GZ6214 x M201	-5.31**	-3.78**	-4.46**	7.46**	-2.73**	4.56**	-0.26 ^{ns}
GZ6214 x M202	-2.45**	-2.12 ^{ns}	-1.51**	13.46**	-4.35**	9.08**	1.10**
M101 x M201	-1.29**	-0.09 ^{ns}	7.44**	5.89**	0.65**	6.37**	2.31**
M101 x M202	0.53**	1.91 ^{ns}	-9.27**	3.89**	1.03**	4.89**	-0.67**
M201 x M202	5.06**	3.96**	-2.32**	-8.11**	4.46**	-3.83**	-2.14**
LSD at 0.05	0.47	3.44	0.48	0.50	0.44	0.74	0.43
LSD at 0.01	0.49	3.65	0.51	0.53	0.47	0.78	0.45

B-Yield and its components and some biotic stress traits.

B.1: Mean performance:

The mean performance of yield and its components and some biotic stress traits for the five parents and their ten F₁ are presented in Table 5. For grain yield plant⁻¹ and panicles plant⁻¹ the cross M101 x M201 gave the highest values, Giza177 x M202 and GZ6214 x M101 hybrid combinations showed the highest mean values for the same trends. Additionally, GZ6214 x M101 and M101 x M201 were resistant to blast, stem borer infestation and white tip nematode; therefore these combinations are useable in plant breeding programs as donors for transfer of genes conferring such resistances. However, the parental variety M201 and the cross M201 x M202 exhibited the lowest values of yield and its components, and were susceptible to blast, stem borer with resulting reduced grain yield.

Table 5. Mean performance of parents and their crosses for yeild and its components and biotic stress traits.

Genotype	panicles plant ⁻¹	filled grains panicle ⁻¹	1000-grain weight (g)	grain yield plant ⁻¹ (g)	Blast reaction	Stem borer	White tip nematode
Giza177	20	125	28.10	42.67	2	5.90	60.00
GZ6214	19	117	27.00	46.67	3	4.20	51.00
M101	17	125	30.70	46.00	2	31.00	61.00
M201	18	101	22.20	36.00	7	8.30	0.00
M202	17	142	24.50	32.200	7	5.0	0.00
Giza177x GZ6214	24	122	26.63	70.00	1	2.13	2.33
Giza177 x M101	21	177	31.30	55.00	2	28.13	0.17
Giza177 x M201	25	193	28.10	70.00	1	2.87	10.00
Giza177 x M202	24	206	27.50	77.67	1	2.13	5.00
GZ6214 x M101	20	184	32.20	79.67	1	13.10	0.13
GZ6214 x M201	24	136	26.10	64.33	1	3.23	1.33
GZ6214 x M202	22	144	27.10	67.67	1	4.50	0.17
M101 x M201	26	160	28.13	82.33	1	3.80	0.13
M101 x M202	22	108	27.87	37.67	2	4.67	0.17
M201 x M202	25	95	18.50	27.67	6	2.63	0.13
LSD at 0.05	1.47	5.24	0.32	3.92	0.80	0.71	0.73
LSD at 0.01	1.96	7.00	0.42	5.24	1.07	0.95	0.98

B.2: Analysis of combining ability:

Highly significant differences among genotypes (parents and their F₁) for all yield and its components, blast resistance, stem borer and white tip nematode are shown in Table 6, indicating the wide range of genetic variation among the parents which used in this study. Both general and specific combining ability variance was found to be highly significant for yield and its components, blast resistance, stem borer and white tip nematode, indicating the importance of both additive and non-additive genetic variance in determine the inheritance of all studied traits. General combining ability/specific combining ability ratio was used to clarify the nature of genetic variance involved; GCA/SCA ratios were found to be greater than unity for

1000-grain weight, blast resistance, stem borer and white tip nematode, indicating that the additive and additive x additive types of the gene action were more important in the inheritance of these traits. It could be concluded that selection procedures based on the accumulation of additive effect would be successful in improving these traits. While, GCA/SCA ratios were found to be lower than unity for panicles plant⁻¹, filled grains panicle⁻¹ and grain yield plant⁻¹, indicating that non-additive genetic variance (dominance or epistasis) was more important in the inheritance of these traits. This concurs with the findings of Bansal *et al.* (2000) and Sharma and Mani (2001) who reported on the importance of non-additive genetic variance (dominance or epistasis) in inheritance of yield and its components traits.

Table 6. Analysis variance and mean square estimates for yield and its components and biotic stress traits.

S.V.	d.f.	panicles plant ⁻¹	filled grains panicle ⁻¹	1000-grain weight (g)	grain yield plant ⁻¹ (g)	Blast reaction	Stem borer	White tip nematode
Replications	2	1.16 ^{ns}	31.40 ^{ns}	0.13 ^{ns}	3.76 ^{ns}	0.42 ^{ns}	0.35 ^{ns}	1.32 ^{ns}
Genotypes	14	26.78**	3589.76**	35.69**	1028.55**	12.75**	252.02**	1874.63**
Parents	4	5.10*	653.07**	32.33**	124.00**	19.57**	386.81**	1911.75**
Crosses	9	10.87**	4253.42**	40.35**	980.68**	6.39**	200.90**	31.36**
P vs. F ₁	1	256.71**	9363.60**	7.11**	5077.51**	42.71**	173.06**	18315.55**
Error	28	1.42	18.02	0.07	10.09	0.42	0.33	0.35
G.C.A.	4	3.85**	557.51**	30.74**	223.21**	8.06**	188.14**	390.21**
S.C.A.	10	10.96**	1452.22**	4.36**	390.70**	2.73**	42.35**	718.74**
Error	28	0.47	6.01	0.02	3.36	0.14	0.11	0.12
G.C.A./S.C.A.		0.35	0.38	7.05	0.57	2.96	4.44	0.54

*, **: significant at 5% and 1% level, respectively; ns: not significant

B.2.1: General combining ability (GCA) effect:

Estimates of the general combining ability effects of individual parental lines for yield and its components traits and biotic stress are given in Table 7. Highly significant and positive GCA were observed for panicles plant⁻¹, filled grains panicle⁻¹, 1000-grain weight and grain yield plant⁻¹, while highly significant and negative values were recorded for blast resistance, stem borer and white tip nematode; these being desirable for improvement of these traits in breeding programs since breeders target low mean values. Giza177 and M101 showed highly significant and positive estimates of general combining ability effects for filled grains panicle⁻¹, 1000-grain weight and grain yield plant⁻¹, indicating that these varieties could be used in breeding programs as good combiners for these traits. Along with GZ6214, Giza177 also appeared to be good parental combiners in rice for blast resistance and stem borer, having exhibited highly significant and negative estimates of GCA effects for these traits. Regarding white tip nematode, M202 gave highly significant and negative values of GCA effects, indicating that this rice variety could be used as a good combiner for improving resistance to white tip nematode in Egyptian rice varieties through a hybridization program to transfer the genes responsible for resistance from M202.

B.2.2: Specific combining ability (SCA) effect:

Estimates of specific combining ability effects for F₁ crosses in relation to agronomic traits and biotic stress are presented in Table 8. The hybrid combination M101 x M201 gave highly significant and positive estimate of SCA effects for panicles plant⁻¹ and grain yield plant⁻¹, the crosses Giza177 x M202 and Giza177 x M201 recorded the highest values of SCA effects for filled grains panicle⁻¹ and 1000-grain weight, respectively.

Table 7. Estimates of general combining ability effect for yield and its components and biotic stress traits.

Source of variance	panicles plant ⁻¹	filled grains panicle ⁻¹	1000-grain weight (g)	grain yield plant ⁻¹ (g)	Blast reaction	Stem borer	White tip nematode
Giza177	0.65**	13.48**	1.05**	3.41**	-0.90**	-0.22**	5.83**
GZ6214	-0.26*	-4.90**	0.53**	5.84**	-0.57**	-2.48**	1.23**
M101	-0.88**	3.62**	2.65**	1.79**	-0.86**	9.01**	3.61**
M201	0.89**	-9.67**	-2.45**	-2.54**	1.14**	-2.78**	2.32**
M202	-0.40**	-2.52**	-1.78**	-8.50**	1.19**	-3.53**	-13.00*
LSD at 0.05	0.23	0.83	0.05	0.62	0.13	0.11	0.12
LSD at 0.01	0.37	1.31	0.08	0.98	0.20	0.18	0.18

*, **: significant at 5% and 1% level, respectively

Table 8. Estimates of specific combining ability effect for yield and its components traits and biotic stress.

Crosses	panicles plant ⁻¹	filled grains panicle ⁻¹	1000-grain weight (g)	grain yield plant ⁻¹ (g)	Blast reaction	Stem borer	White tip nematode
Giza177x GZ6214	2.03**	-29.24**	-2.01**	5.06**	0.25ns	-3.27**	-20.96**
Giza177 x M101	-0.35 ^{ns}	17.90**	0.54**	-5.89**	0.87**	11.24**	-25.50**
Giza177 x M201	1.89**	47.19**	2.43**	13.44**	-1.46**	-2.24**	-14.38**
Giza177 x M202	2.17**	52.71**	1.17**	27.06**	-1.51**	-2.22**	-4.06**
GZ6214 x M101	-0.11 ^{ns}	43.29**	1.96**	16.35**	0.21ns	-1.54**	-20.93**
GZ6214 x M201	1.46**	8.24**	0.95**	5.35**	-1.79**	0.38**	-18.45**
GZ6214 x M202	0.75**	8.76**	1.29**	14.63**	-1.84**	2.40**	-4.29**
M101 x M201	4.41**	23.38**	0.87**	27.40**	-1.51**	-10.54**	-22.02**
M101 x M202	1.70**	-35.43**	-0.06ns	-11.32**	-1.22**	-8.92**	-6.67**
M201 x M202	2.94**	-34.81**	-4.33**	-16.98**	1.11**	0.83**	-5.41**
LSD at 0.05	0.60	2.14	0.13	1.60	0.33	0.29	0.30
LSD at 0.01	0.64	2.27	0.14	1.70	0.35	0.31	0.32

*, **: significant at 5% and 1% level, respectively; ns: not significant.

For blast resistance, six crosses exhibited highly significant and negative values of SCA. The best crosses were GZ6214 x M202, GZ6214 x M201 and Giza177 x M202, indicating that these crosses could be used in breeding programs to improve this trait. A further set of six rice crosses showed highly significant and desirable negative SCA effects for stem borer. The best combinations giving the highest values were M101 x M201, M101 x M202 and Giza177 x GZ6214, indicating that these crosses could be used in breeding programs and their parents used as good donors for resistance genes to counteract stem borer. Table 8 reveals that all crosses gave highly

significant and negative estimates of SCA effects for white tip nematode. The best crosses were Giza177 x M101, M101 x M201, Giza177 x GZ6214 and GZ6214 x M101, indicating that these could be used for crossing to improve resistance to this nematode.

C: Heterosis:

Useful heterosis expressed as the percentage deviation of F_1 mean values from their respective better parent estimates for physiological traits, yield and yield components, together with some for biotic stress, are presented in Tables 9 and 10. Significant positive heterotic effect relative to better parent values would be of interest for flag leaf area, chlorophyll content, panicle length, panicles plant⁻¹, filled grains panicle⁻¹, 1000-grain weight and grain yield plant⁻¹. Breeders would also find it useful to have significant negative heterotic effect relative to better parent values for plant height, vegetative stage, reproductive stage, days-to-heading, blast reaction, stem borer and white tip nematode. Table 9 shows that significant and highly significant positive estimates of heterosis over better parent for flag leaf area were recorded for six crosses. Moreover, since these significant and highly significant positive heterotic effects were computed on the basis of specific combining ability, it seems that dominance effect plays a major role in the inheritance of this trait. The best crosses were M201 x M202, GZ6214 x M101 and Giza177 x M202. Highly significant negative heterosis for plant height and reproductive stage was exhibited by the cross GZ6214 x M202. Of the four crosses showing highly significant and positive heterosis for panicle length, the best crosses were GZ6214 x M101 and M101 x M201.

Table 9. Estimates of heterosis over better-parent for physiological traits.

Crosses	Flag leaf area (cm ²)	Chlorophyll content	Plant height (cm)	Vegetative Stage (day)	Reproductive Stage (day)	Days-to-heading (day)	Panicle length (cm)
Giza177x GZ6214	- 15.30**	-6.46 ^{ns}	-1.03 ^{ns}	16.66**	-2.77**	12.10**	-15.00**
Giza177 x M101	1.76 ^{ns}	11.59 ^{ns}	15.51**	3.33**	34.25**	9.20**	9.52**
Giza177 x M201	12.42**	-5.88 ^{ns}	23.40**	25.26**	8.42**	20.69**	16.65**
Giza177 x M202	16.53**	-8.16 ^{ns}	14.29**	27.86**	15.00**	25.10**	3.94 ^{ns}
GZ6214 x M101	20.21**	10.87 ^{ns}	27.84**	3.33**	24.46**	9.60**	23.81**
GZ6214 x M201	-13.91**	-17.65 ^{ns}	0.00 ^{ns}	26.3**	5.26**	20.69**	0.00 ^{ns}
GZ6214 x M202	-5.07**	-12.24 ^{ns}	-2.06**	44.26**	-5.00**	32.10**	0.00 ^{ns}
M101 x M201	4.34*	0.00 ^{ns}	29.43**	20.00**	27.89**	15.60**	19.05**
M101 x M202	10.54**	6.80 ^{ns}	5.10**	11.66**	26.5**	13.99**	3.14 ^{ns}
M201 x M202	21.60**	6.53 ^{ns}	2.13**	3.27**	31.57**	8.64**	-10.92**
LSD at 0.05	1.32	9.74	1.36	1.65	1.47	2.09	1.21
LSD at 0.01	1.76	13.01	1.81	2.22	1.98	2.79	1.62

*, **: significant at 5% and 1% level, respectively; ns: not significant.

In respect of panicles plant⁻¹, filled grains panicle⁻¹ and grain yield plant⁻¹, the crosses Giza177 x M202, M101 x M201, Giza177 x M201 and GZ6214 x M201 exhibited highly significant positive heterosis and recorded highly significant and positive specific combining ability effects, indicating that

dominance plays a major role in the inheritance of these traits which appears as high heterosis over the better parent. For blast reaction, the hybrid combinations GZ6214 x M201 and GZ6214 x M202 recorded highly significant negative at both heterosis and specific combining ability effects, indicating that dominance plays a major role in the inheritance of this trait; It can be concluded that these crosses could be used in a hybridization breeding program for improving this trait. Likewise, the major role of dominance in the inheritance of resistance traits for stem borer infestation and white tip nematode was identified through four crosses, Giza177 x GZ6214, Giza177 x M201, GZ6214 x M201 and M101 x M201, which showed negative combining ability effects.

Table 10. Estimates of heterosis over better-parent for agronomic and biotic stress traits.

Crosses	panicles plant ⁻¹	filled grains panicle ⁻¹	1000-grain weight	grain yield plant ⁻¹ (g)	Blast reaction	Stem borer	White tip nematode
Giza177x GZ6214	20.00**	-2.66 ^{ns}	-5.23**	50.21**	-20.36**	-50.00**	-96.00
Giza177 x M101	5.00 ^{ns}	41.86**	1.95**	19.56**	0.00 ^{ns}	376.30**	-99.60
Giza177 x M201	25.00**	54.66**	0.00 ^{ns}	64.31**	-20.36 ^{ns}	-52.50**	-80.40
Giza177 x M202	20.00**	45.41**	-2.14**	82.15**	-20.36 ^{ns}	-58.00**	4900.0
GZ6214 x M101	7.00 ^{ns}	47.46**	4.89**	18.02**	-20.36 ^{ns}	211.90**	-99.80
GZ 6214 x M201	24.58**	16.24**	-3.44**	37.98**	-55.67**	-23.80**	-98.00
GZ6214 x M202	14.05**	1.41 ^{ns}	0.26 ^{ns}	45.06**	-55.67**	7.10**	0.00
M101 x M201	44.44**	27.74**	-8.37**	78.91**	-20.36 ^{ns}	-54.20**	-99.80
M101 x M202	29.41**	-23.77**	-9.22**	-18.26**	0.00 ^{ns}	-8.00**	0.00
M201 x M202	38.89**	-32.71**	-24.40**	-23.33**	-10.04 ^{ns}	-48.00**	0.00
LSD at 0.05	1.70	6.05	0.37	4.53	0.93	0.96	0.99
LSD at 0.01	2.27	8.08	0.49	6.05	1.24	1.30	1.33

*, **: significant at 5% and 1% level, respectively; ns: not significant.

Genetic divergence among rice genotypes:

Genetic divergence studies in rice have been revealed some interesting feature of differentiation and adaptability importance. Such an analysis could provide useful additional information, studying interrelation ship of genotypes and giving graphical assessment of genetic variability.

Cluster analysis:

A cluster analysis was used to group the varieties and to construct a dendrogram (Figure 1). The 15 genotypes (Five parents and their 10 F₁ hybrids) were grouped into three major clusters.

The first cluster: Included most genotypes which characterized by the highest values for flag leaf area , high values of chlorophyll content and the lowest for days to reach maximum tillering such as crosses of M101with GZ6214 and Giza 177. For grain yield plant⁻¹ and panicles plant⁻¹ the cross Giza177 x M202 and GZ6214 xM101 gave the highest value. Additionally, GZ6214 x M101 and Giza 177 x M101 were resistant to blast, and white tip nematode disease.

The second cluster: Included all Parents, the three American parents each

components were significant and accounted for about 80.4% of the total variance of all characters, (Table 11 and Fig. 2B). While PC1, PC2 and PC3 explained 34.3, 62.9 and 17.5%, of the multivariate variation among genotypes showing the highest eigen values 4.78, 4.00 and 2.44, this values could measure the explained variance associated with variable, Table 11. The relative magnitude of the coefficient of each character relating to the first three principal components can often provide an agronomic interpretation for each component axis, table 11. The sign of the coefficient is irrelevant and is in fact arbitrary, though negatively correlated characters will generally opposite sings on a given axis. PC1 gave higher loading to grain yield plant⁻¹, filled grains panicle⁻¹ and blast, while PC2 gave higher to vegetative stage, stem borer, days to heading and panicle length. On the other side, PC3 was dominated by white tip nematode, flag leaf area and chlorophyll content. The most important evaluated characters in divergence of genotypes were: filled grains panicle⁻¹; grain yield plant⁻¹; panicle length; 1000-grain weight; plant height; blast and white tip nematode. Thus it is possible to include the corresponding amount of variance in the two dimensional plot of the components. Each genotype is plotted at it is principal component score on each axis, Brown, 1991.

Table 11: Principal component (PC) analysis of characters associated with 15 rice genotypes showing eigen values and proportion variation associated with the first PC axes and eigen vector of characters.

Eigen value	4.7993	4.0003	2.4443	11.2439
%	34.3	28.6	17.5	80.3
Cumulative Percentage	34.3	62.9	80.4	
Eigen vector				
	PC1	PC2	PC3	Communality
FLA (Flag leaf Area)	0.165	0.462	-0.686	0.711
Ch. Cont. (Chlorophyll content)	-0.262	0.613	-0.648	0.865
PH (Plant height)	0.640	0.623	0.325	0.904
Veg st (Vegetative Stage)	0.518	-0.826	0.068	0.956
Rep st (Reproductive Stage)	0.142	0.611	-0.095	0.403
DH (Days to heading)	0.656	-0.692	0.036	0.910
PL (Panicle length)	0.568	0.646	-0.268	0.812
NOP (panicles plant ⁻¹)	0.528	-0.435	-0.575	0.799
NOF (filled grains panicle ⁻¹)	0.810	0.274	-0.086	0.738
1000-GW (1000-grain weight)	0.676	0.494	0.494	0.944
GY (grain yield plant ⁻¹)	0.942	-0.076	-0.013	0.893
BLS (Blast)	-0.888	0.091	-0.251	0.860
SB (stem borer)	-0.04	0.736	0.438	0.735
WTN (white tip nematode)	-0.428	0.073	0.725	0.714

Construction of scatter diagram based on the values of principal component score I and II obtained from the principal component analysis, a two dimensional scatter diagram using component score I as X axis and component score II as Y axis was constructed (Figure 2 A). The positions of the genotypes in the scatter diagram were apparently distributed into four

groups, which indicated that considerable diversity existed among all genotypes.

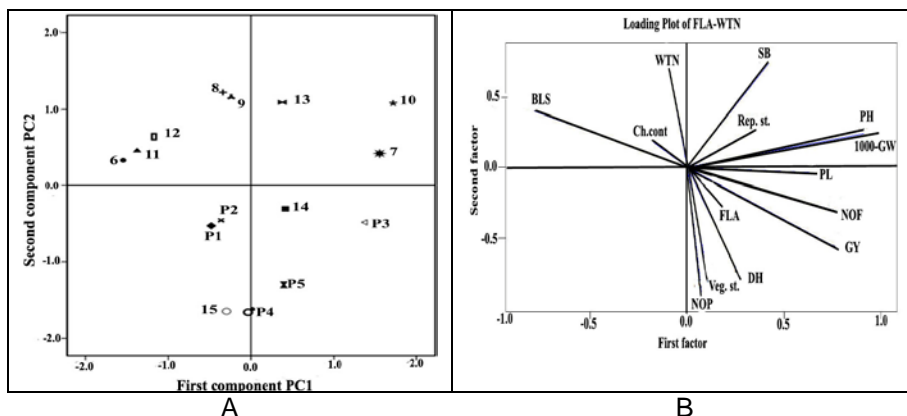


Fig. 2. Loading plot of 15 genotypes (A) and their 14 characters (B) contributed towards genetic divergence based on their principal component scores.

The scattered diagram for rice genotypes of different clusters revealed that the Egyptian parents, Giza 177 and GZ 6214 were clustered and clearly assigned to distinct group in the PCA separated from all genotypes which suggesting more diverged from the American genotypes (Figure 2 A). All completely resistant genotypes for both blast and white tip nematode such as, line 7, 10 and 13 were distributed in the same group, while the genotypes which blast resistant and moderately resistant to white tip nematode; 6, 8, 9, 11 and 12 were strongly concentrated together. The best crosses for yield and its components were Giza177 x GZ6214, Giza177 x M201, Giza177 x M202, GZ6214 x M201 and GZ6214 x M202. Also, the Egyptian parents which resistant to blast but susceptible to nematode, were distributed with genotype 15, conversely, the American parents; P3, P4 and P5. The genotypes are most distinctly separated. Some lines were densely aggregated, such as L6, L8, L9, L11 and L12 formed a more closely related group. Hence, PCA (Fig. 2A) agreed well with the UPGMA cluster. It is worthily to note that, Egyptian parents; Giza 177 and GZ6214 and US parents; M101, M201 and M2012 were presented in two divergent groups and other lines distributed in a unique group and also wide distance from each. **Cox et al., (1985)** suggested crossing distantly related lines in an inbred improvement. Thus high heterotic response and good segregants could obtain from crossing among Egyptian and US parents.

Principal coordinate analysis (PCoA):

The PCoA is one of the multivariate approaches of grouping based on the similarity coefficients or variance-covariance values of the component traits of the entities. It is expected to be more informative about differentiation among major groups, while the cluster-analysis provides higher resolution among

closely related populations (Liu *et al.*, 2000). In our PCoA analysis, more than 90.98% of the variation in the estimates of similarity was explained by the first three components, indicating the suitability of clustering based on agronomic traits and biotic stresses. This analysis could provide useful additional information about relationships of genotypes. Such information could be useful in identifying optimal breeding strategies of rice improvement.

The actual values of Euclidean distance corresponding to possible comparisons among all parents and crosses and represented divergence, Table 12. These estimates which treated as chi-square values showed that 92 % of the value were significant squared Euclidean distance ranged from 10.59 between line 12 and line 11 to 125.46 between line 9 (Giza177 x M202) and P4 (M201). Euclidean distance among Egyptian parent Giza 177 and its crosses with US parents ranged from 87.10 to 106.60, while, with GZ6214 it ranged from 58.99 to 97.05. While, Euclidean distance among Giza 177 and US parents ranged from 32.97 to 66.98, while among GZ6214 ranged from 29.47 to 64.49. M202 exhibited wide range of divergence with other parents. Euclidean distance among M202 and all parents ranged from 64.49 and 75.14. Giza 177 and GZ6214 were appeared to be nearly related with Euclidean distance 22.39. So, based on Euclidean Distance, the most divergent cultivars were M202 and Giza 177.

Based on eigenvalues of all multivariate analyses associated with parents, the most divergent parent was M202 (Table13). The Egyptian parents created suitable combinations with US parents due to wide range of variability among them. So, the divergence based on morphological, agronomical and biotic stress traits has a good efficacy as a criterion for choosing parents to be crossed, in agreement with Cox *et al.* 1985 and Menshawy 2008.

The multivariate methods were congruent in their results. Also, they have analogous efficacy to determine the most suitable combinations and grouping the varied genotypes into varied groups. Principal component and cluster analysis can be used to create genetic variability, also multivariate techniques to determine the relative contribution of characters of variation and grouping the genotypes into varied clusters in agreement with (El-Mansy, 2009 and Abdel-Salam *et al.*, 2010)

Finally, rice breeders desire to increase genetic diversity among new cultivar, while at the same time maintaining the complex of desired agronomic and quality traits present in existing popular cultivars. Developing such a combination can be difficult, as the introgression of new genetic material is expected to disturb genetic complex responsible for desirable traits. The use of crosses among divergent cultivars could be a mean to achieve both ends. So, chose parents which have greatest genetic divergence in order to obtain the best combination. However, not only genetic divergence might be used to choose parents for crossing but also their performance.

It is evident to note that crossing of distantly related parents may give best hybrids which surpassed their parents in most characters and should produce higher variances for most characters in segregating generation rather than crossing between closed related parents which agree with Suinaga *et al.*, (2005).

From a plant breeding principal component analysis is useful in identifying the most influential characters affecting genetic variation of plant population. The loading of morphological, agronomic and biotic stresses characters of individual genotypes indicate the magnitude of genetic variation.

Machado *et al.*, (2002), in order to obtain the best combinations, choose parents which have the greatest genetic divergence. However, not only the genetic divergence might be used to choose parents for crossing, but also their performance. As reported by Abreu *et al.*, (1999) the best hybrids to be tested in a breeding program might involve both divergent and highly productive parents.

REFERENCES

- Abd El-Aty, M.S.M. (2001). Heterosis and combining ability for grain yield and some related characters in rice (*Oryza sativa* L.). *J. Agric. Res., Tanta Univ.*, 27(3):436–449.
- Abdel-Salam, M.E.; Y.M. El-mansy and Rokia, M. Hassan (2010). The relative importance of characters affecting genetic divergence in cotton. *J.Agric. Kafer El-Sheikh Univ.*, 36(1):44-63.
- Abreu, A. de F. B.; M. A. P. Ramalho; D. F. Ferreira, (1999). Selection potential for seed yield from intra and inter-racial populations in common bean. *Euphytica*, 108 (2): 121-127.
- Agrama, H. A. and G. C. Eizenga (2007). Molecular diversity and genome-wide linkage disequilibrium patterns in a worldwide collection of *Oryza sativa* L. and its wild relatives. *Euphytica*, DOI 10.1007/s10681-007-9535-y.
- Agrama, H. A., G. C. Eizenga and W. Yan (2007). Association mapping of yield and its components in rice cultivars. *Mol. Breeding*, 19:341–356.
- Ammar, M.H.M. (1997). Breeding studies on rice through anther culture. M.Sc. Thesis, Agronomy Department, Fac. of Agric., Minufiya Univ., Shibin El-Kom, Egypt..
- Bansal, U.K.; R.G. Saini and N.S. Rani. (2000). Heterosis and combining ability for yield, its components and quality traits in some scented rices (*Oryza sativa* L.). *Tropical Agriculture* 77, 3:180–187.
- Bastawisi, A.O.; H.F. El-Mowafi; M.A. Maximos and M.F. Sobaa. (2003). Hybrid rice production technology in Egypt. Proceeding: workshop on rice integrated crop management system for food security in the near east countries. 27–29 July, 2003. Alexandria, Egypt.
- Brown, J.S. (1991). Principal component and cluster analysis of cotton cultivars variability a cross the US cotton Belt. *Crop Sci.* 31: 913-922.

- Butany, W.T. (1961). Mass emasculation in rice. Intern. Rice Com. Newsletter, 9:9–13.
- Cornelius, B.K. and C.H. Sneller (2002). Yield and molecular diversity of soybean lines derived from crosses between Northern and Southern elite parents, Crop Sci., 20: 187-190.
- Cox, T.S.; J.L. Lookhart ; D.E. Walker ; L.G. Harrel ; L.D. Albers and D.M. Rodgers (1985). Genetic relationship among hard red winter wheat cultivar. Crop Sci., 25:1058-1063.
- Cruz, C. D. and Carneiro, P. C. S. (2003). Modelos biométricos aplicados ao melhoramento genético. Viçosa: Imprensa Universitária,. 585p. Vol. 2.
- Dias, L. A. and Kageyama, P. Y. (1997). Multivariate genetic divergence and hybrid performance of Cacao (*Theobroma cacao* L.). Revista Brasileira de Genética, 20 (1): 63-70.
- El-Malky, M.M. (1997). Studies on some genetic characters in rice using tissue culture techniques. MSc. Genetics Department, Fac. of Agric., Minufiya Univ., Shibin El-Kom, Egypt.
- El-Mansy Y.M. (2009). Cluster analysis with selection index for improvement some characters in some cotton genotypes. 1st Nile Delta Conf. Fac. of Agric. Minufiya , Uni., 135-155.
- El-Mowafi, H.F. and A.A. Abou Shousha. (2003). Combining ability and heterosis analysis of diverse CMS lines in hybrid rice. J. Agric. Res. Tanta Univ., 29(1):106–127.
- El-Shafey, R.A.S. (2002). Studies on *Pyricularia oryzae* the causal organism of rice blast disease and its control. M.Sc. Thesis, Fac. of Agric., Minufiya Univ., Egypt.
- El-Shafey, R.A.S. (2007). Biological and ecological studies on white tip nematode in rice with special reference to its control. Ph.D. Thesis, Fac. of Agric., Kafrelsheikh Univ., Egypt.
- FAO, (Food and Agriculture Organisation of the United Nations). (2004). The state of food and agriculture 2003–2004. Agricultural Biotechnology. Meeting the needs of the poor.
- Griffing, J.B. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Austr. J. Biol. Sci. 9, 463–493.
- Hair, J.F.; Jr.R.E. Anderson and R.L.Tatham (1987). Multivariate data analysis. McMillan Pub., Co. New York.
- Hammoud, S.A.A. (1996). Breeding studies on some rice characters. M.Sc. Thesis, Agronomy Department, Fac. of Agric., Minufiya Univ., Shibin El-Kom, Egypt.
- Hammoud, S.A.A. (2004). Inheritance of some quantitative characters in rice (*Oryza sativa* L.). Ph.D. Thesis Agronomy Department, Fac. of Agric., Minufiya Univ., Shibin El-Kom, Egypt.
- Hammoud, S.A.A., M.M. El-Habashy, A. El-Gohary and A.S.M. Abd El-Latif. (2008). Combining ability, heterosis and correlation coefficient of some rice genotypes for yield and yield components and stem borer infestation. The Second Field Crops Conference, Field Crops Research Institute, Agricultural Research Center.

- IRRI (International Rice Research Institute) (1996). Standard Evaluation System for Rice. Manila, Philippines: IRRI.
- Jodon, N.E. (1938). Experiments on artificial hybridization of rice. *J. Amer. Soc. Agron.* 30:249–305.
- Johnson, R.A. and D.W. Wichern (1988). Applied Multivariate Statistical Analysis 2nd ed. Prentice-Hall. Englewood Cliffs, N.J. USA.
- Kiyosawa, S. (1982). Genetic and epidemiological modeling of breakdown of plant disease resistance. *Ann. Rev. Phytopathol.*, 20:93–117
- Koizumi, S. (2007). Durability of resistance to rice blast disease. In: JIRCAS (Japan International Research Center for Agricultural Sciences, Tsukuba, Japan) Working Report No. 53, 1–10
- Liu, D., S. Coloe; R. Baird and J. Pedersen (2000). Rapid mini-preparation of fungal DNA for PCR. *J. Clin. Microbiol.* 38: 471.
- Machado, G.F.; G.H.S. Nunes, and D.F. Ferreria (2002). Genetic divergence among genotypes using multivariate technique. *Ciencia Rural.* V32(2): 251-258.
- Melchinger, A.E., M. Lee, K.R. Lamkey and W.W. Woodman, (1990). Genetic diversity for Restriction Fragment Length Polymorphism: Relation to estimated genetic effects in maize inbreds. *Crop Sci.* 30: 1033-1040.
- Menshawy, A.M.M. (2008). Estimation of gene action and predicting new recombination lines in bread wheat cross using F₂ triple test cross analysis. *Egypt J. Agric. Res.*, 86(5). 1905-1920.
- Ou, S.H. (1985). Rice Diseases II edition. CMI, Kew, England. pp. 337–364.
- Rana, M.K and Bhat, K.V (2005). RAPD marker for genetic diversity study among Indian cotton cultivars. *Current Sci.* 88 : 1956-1961.
- RRTC (Rice Research and Training Center). (2006). Annual rice national campaign report of rice program. Field Crops Research, Agric. Research Center, Ministry of Agriculture, Egypt.
- Sedeek, S.E.M.; S.A.A. Hammoud; A.B. El-Abd and I.O.M. Rewainy. (2007). Generation mean analysis of some agronomic traits, blast disease and stem borer resistance in two rice crosses under two N-levels. *Egypt. J. Plant Breed.*, 11: 563–583.
- Sehly, M.R., Z.H. Osman, and E.A. Salem. (2002). Rice diseases. In: Rice in Egypt, pp. 301.
- Sehly, M.R., S.M. El-Wahsh, E.A.S. Badr, M.M.H. El-Malkey, R.A.S. El-Shafey and I.R. Aidy. (2008). Evaluation of certain Egyptian rice cultivars to blast disease incidence during fourteen years in Egypt. *J. Agric. Sci. Mansoura Univ.*, 33 (4):2533–2547.
- Sharma, D.K. and S.C. Mani. (2001). Combining ability studies for grain yield and other associated characters in Basmati rice (*Oryza sativa* L.). *Crop Improv.*, 28(2):236–243.
- Suinaga, A.F. ;E.C. Freire and L.E.P. Rangel (2005). Multivariate analysis of genetic divergence in cotton. *Revista Brasileira de Al Godao.*
- Wynne, J.C., D.A. Emery and P.W. Rice (1970). Combining ability estimates in (*Arachis hypogea* L.): II- Field performance of F₁ hybrids. *Crop Sci.* 10(15): 713-715.

**الفعل الجيني والأهمية النسبية لبعض الصفات المحصولية والمرضية المؤثرة في
التباين الوراثي في الأرز**
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تحقق مصر أعلى إنتاجية للأرز في العالم لوحده المساحة ومازال محصول الأرز يتعرض للأمراض وتعد التربية لمقاومة الأمراض أحد أهم أهداف المربي. أجري هذا البحث في مزرعة مركز البحوث والتدريب في الأرز في موسمي 2011، 2012. تم استخدام خمسة أباء وعشرة هجن ناتجة منها لدراسة الفعل الجيني والقدرة علي التآلف وقوة الهجين لمعظم الصفات المحصولية والمرضية. حيث كانت الأصناف جيزة 177 والصنف M101 مقاومة لمرض اللفحة بينما السلالة 6214 و M202 مقاومة لتأقيات الأرز بينما الصنفين M201 و M202 مقاومة لنيماتودا القمة البيضاء. كانت كلاً من القدرة العامة والخاصة علي التآلف شديدة المعنوية لكل الصفات المدروسة. أظهر الصنف M202 قدرة عامة علي التآلف ذات معنوية سالبة ومرغوبة لصفة طول النبات وفترة النمو الخضري والتمري وعدد الأيام حتي التزهير كما أظهر ذات الصنف قدرة خاصة علي التآلف معنوية إلي عالية المعنوية وسالبة لنفس الصفات. وكانت أفضل الهجن لصفتي المحصول ومكوناته هي جيزة 177 × السلالة 6214 و جيزة 177 × M201 ، جيزة 177 × M202 و السلالة 6214 × M201 و السلالة 6214 × M202. أما بالنسبة لتأقيات الأرز، أعطت الهجن M201 × M202 ، M101 × M202 ، جيزة 177 × السلالة 6214 قيمة عالية المعنوية سالبة ومرغوبة مع القدرة الخاصة علي التآلف. بالنسبة لمرض لفحة الأرز، وتأقيات الأرز ونيماتودا القمة البيضاء سجل كلاً من الهجينين جيزة 177 × السلالة 6214 والصنف M201 × السلالة 6214 قوة هجين عالية المعنوية سالبة ومرغوبة بينما أظهرت قدرة خاصة عالية المعنوية. كان الصنف M202 من الطراز الياباني مصدراً من مصادر المقاومة لمرض نيماتودا القمة البيضاء حيث حققت كل الهجن الناتجة منه مستويات أصابة منخفضة. تم استخدام التحليل المتعدد Multivariate analysis باستعمال تحليل المكونات الأساسية Principal component analysis وتحليل التباين الوراثي Genetic divergence علي أساس عدم التشابه النسبي بين المجموعات وذلك لدراسة الأهمية النسبية للصفات المختلفة ومدى مساهمتها في التباين الوراثي وكذلك أهميتها في التباين الوراثي وتوزيع التراكيب الوراثية المختلفة في مجاميع مختلفة. أظهر تحليل المكونات الأساسية Principal component analysis أن الثلاث مكونات كانت معنوية تحصر حوالي 80,4% من التباين الكلي لكل الصفات. وباستخدام تحليل المجموعات المتباعدة Hierarchical clustering analysis تم توزيع التراكيب الوراثية الخمسة عشرة إلي 3 مجموعات رئيسية علي أساس عدم التشابه النسبي بينهما مع وجود معنوية بين هذه المجموعات لمعظم الصفات. أظهر النسل الناتج من التهجين بين الأباء المصرية والأمريكية المتباعدة درجة كبيرة من عدم التشابه النسبي كما أعطي قيماً تفوق أباؤها لمعظم الصفات. أظهرت نتائج التحليل المتعدد أن الصنف M202 كان أكثر الأصناف من حيث عدم التشابه والأختلاف. كانت صفات المحصول / نبات وعدد الحبوب الممتلئة / سنبللة ومرض اللفحة الأكثر أهمية في التباين بين التراكيب الوراثية علي المحور الأول First axis PC1. بينما تعامل المحور الثاني مع صفات التبرير وهي فترة النمو الخضري وعدد الأيام حتي التزهير وشغل مرض نيماتودا القمة البيضاء المحور الثالث. وتوصي هذه الدراسة بأن التهجين بين الأصناف المصرية والأمريكية المتباعدة وراثياً يخلق تراكيب وراثية جديدة مناسبة في برنامج التربية. ومن ثم فإن مربي الأرز يستطيع تعظيم التباين الوراثي في الأصناف الجديدة مع الحفاظ علي الصفات المحصولية المرغوبة والموجودة أصلاً في الأرز المصري.

قام بتحكيم هذا البحث

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Table 12: Euclidean dissimilarity coefficients among studies 15 rice genotypes in matrix form.

		Euclidean Distance														
	P1- Giza177	P2- GZ6214	P3- M101	P4- M201	P5- M202	L6- Giza177x GZ6214	L7- G177 x M101	L8- G177 x M201	L9- G177 x M202	L10- GZ6214 x M101	L11- GZ6214 x M201	L12- GZ6214 x M202	L13- M101 x M201	L14- M101 x M202	L15- M201 x M202	
P1	0.0	22.39	40.18	32.97	66.98	67.01	87.10	93.42	106.60	98.59	66.98	72.06	84.52	65.52	80.70	
P2		0.00	46.52	29.47	64.49	56.88	86.98	93.43	106.66	97.05	58.99	64.67	81.01	55.34	69.52	
P3			0.00	49.00	75.14	82.60	81.80	99.11	111.38	94.18	83.10	86.53	86.26	73.60	95.72	
P4				0.00	66.43	69.42	99.50	112.22	125.46	112.73	73.11	80.14	96.46	53.83	59.55	
P5					0.00	55.88	53.96	75.71	85.15	71.96	48.87	52.74	62.71	38.85	58.09	
L6						0.00	72.75	75.28	86.94	77.29	15.68	23.75	51.89	44.65	66.42	
L7							0.00	45.06	50.52	31.73	62.23	58.36	42.94	76.58	103.38	
L8								0.00	18.44	35.65	63.02	55.10	40.38	95.14	121.05	
L9									0.00	35.68	74.73	66.71	48.74	107.62	131.59	
L10										0.00	68.37	62.36	30.31	90.28	118.69	
L11											0.00	10.59	45.67	47.82	69.54	
L12												0.00	41.05	55.45	77.61	
L13													0.00	71.58	101.69	
L14														0.00	40.03	
L15															0.00	

Table 13: Eigen values and proportion variation associated with the first PC axes and eigen vector of different parents based on three multivariate analysis.

	Principal component analysis (PCA)			Principal coordinate analysis (PCoA)			correspondence analysis (CA)		
	Axis 1	Axis 2	Axis 3	Axis 1	Axis 2	Axis 3	Axis 1	Axis 2	Axis 3
Eigenvalues	4.799	4.000	2.444	23500.53	7963.73	3666.05	0.060	0.014	0.010
Percentage	34.281	28.573	17.459	61.535	20.853	9.599	65.665	15.864	10.525
Cumulative Percentage	34.281	62.854	80.313	61.535	82.387	91.987	65.665	81.53	92.055
	Axis 1	Axis 2	Axis 3	Axis 1	Axis 2	Axis 3	Axis 1	Axis 2	Axis 3
Giza177	-0.310	-0.257	-0.673	35.209	31.871	-12.173	1.738	-0.796	-0.764
GZ6214	-0.267	-0.192	-0.389	37.167	19.748	-14.202	1.367	-0.997	-0.241
M101	-0.284	0.738	-0.767	29.808	48.877	10.448	1.899	1.855	0.010
M201	-0.970	-0.018	-0.029	57.010	16.11	-1.439	1.629	-0.725	0.873
M202	-0.758	0.211	0.127	7.685	-14.219	25.924	-0.566	0.027	1.485