

## RELATIONSHIP BETWEEN GENETIC DIVERSITY BASED ON SSRs MARKERS WITH HETEROSIS AND COMBINING ABILITY IN DIALLEL CROSS OF BREAD WHEAT (*Triticum aestivum* L.)

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**ABSTRACT:** *Combining ability and heterosis studies were performed for number of spikes per plant, spike weight, spike length, number of grains per spike, 1000-grain weight and grain yield per plant in a diallel crosses involving five spring wheat varieties. Genotypes, parents and the resultant ten hybrid combination mean squares were found to be highly significant for number of spikes per plant, spike length, 1000-grain weight and grain yield per plant except spike weight for parent mean square. Parent vs. crosses mean square estimates were found to be significant for all traits studied except number of grains per spike. Both general (GCA) and specific combining ability (SCA) variances were found to be highly significant for all traits studied. The GCA/SCA ratios were found to be greater than unity for all traits except spike weight and 1000 grain weight. Variety Gemmieza 3 was considered to be good general combiner for number of spikes per plant, 1000-grain weight and grain yield per plant. The simple sequence repeat (SSRs) markers identified 53 alleles with an average 3.12 alleles per locus. The number of alleles per locus ranged from two for Xgwm3, Xgwm186 and Xgwm408 to five for Xgwm513. Polymorphic information content (PIC), a measure of gene diversity, was ranged from 0.320 for the Xgwm186 to 0.800 for Xgwm513 with an average of 0.605. The correlation coefficient between gene diversity and number of alleles was highly significant,  $r = 0.899^{**}$  ( $P < 0.01$ ). Genetic distances were significantly positive associated with SCA and heterosis effects for spike weight. Genetic distances were found to be significantly negative associated with SCA and heterosis effects for number of grains per spike. These results indicate that the level of SCA and heterosis depends on the level of genetic diversity between the wheat genotypes examined. Microsatellite markers were effective in predicting the mean and the variance of SCA in various cultivars combinations. Information generated from this study can be useful to predict hybrid for selecting parents and hybrid development to maximize the grain yield and its components.*

**Key words:** *Wheat (*Triticum aestivum* L), Diallel cross, Heterosis Combining ability, Simple sequence repeats (SSRs), Genetic diversity.* •

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### INTRODUCTION

Bread wheat is the first important and strategic cereal crop for the majority of the world's populations as it is a major source of calories and protein for a large segment of the world population (Harlan, 1995). In Egypt, wheat is the most important cereal crops. Efforts have been made in the past decade to develop high yielding, early maturing and good quality wheat

varieties to meet the demands of a growing population. In order to improve productivity, one of the most important steps in a breeding programme is the choice of suitable parents. Diallel cross analysis leads to identify parents with additive and non-additive effects for specific characteristics. Most frequently diallel or line x tester crossing is applied (Marciniak *et al.* 2003; Ahuja and Dhayal, 2007). This in turn helps in choosing parents to be included in hybridization or population breeding programmes (Murtaza *et al.* 2005). Prediction of genetic diversity and GCA of parents before crossing reduces the number of crosses and progeny to be screened and leads to a reduction in cost and time (Kumar, 1999). In case of self-pollinated crops these methods require a large number of manual crossings, which make them time consuming and expensive (Sant *et al.* 1999; Shen *et al.* 2006). Heterosis effect has been used in breeding of open-pollinated plants, such as maize or rye. At present, hybrid breeding is also being focused on self-pollinated plants, including wheat (Liu *et al.* 1999; Pomaj, 2002; Weißmann and Weißmann 2002). The agronomic value of wheat hybrids appears to be promising (Oury *et al.* 2000). A few studies were carried out using molecular markers such as RFLP, RAPD or SSR markers, but no clear relationship between molecular diversity and heterosis was observed (Liu *et al.* 1999; Corbellini *et al.* 2002; Dreisigacker *et al.* 2005). Molecular markers based on DNA analysis are independent of environmental factors and exhibit a high degree of polymorphism. Moreover, they appear to be a promising tool in the prediction of heterosis in other species, for example in maize (Boppenmaier *et al.* 1992; Melchinger *et al.* 1992), rice (Zhang *et al.* 1996), wheat (Martin *et al.* 1995), rape (Sheng *et al.* 2002) or oat (Moser and Lee 1994). DNA markers are most suitable for genetic diversity estimations (Plaschke *et al.* 1995; Sun *et al.* 2003). In wheat, the initial studies used DNA molecular markers found a significant relationship between genetic distances (GD) and heterosis for grain weight Martin *et al.* (1995). Barbosa-Neto *et al.* (1996) showed the occurrence of a weak relationship between GD based on RFLP and heterosis effects. In turn, Corbellini *et al.* (2002) investigated the relationship between genetic similarity and GCA and SCA for yield and its components in wheat and found it unfeasible to apply these relationships to predict heterosis effects. Currently, simple sequence repeats (SSRs), is the most suitable marker system in wheat. They allow an even coverage of the genome, abundant, genome specific, co-dominant in nature and have been used to characterize genetic diversity in advanced wheat breeding materials (Dreisigacker *et al.* 2004, Röder *et al.* 2002). The objectives of this study were as follows to: (i) assess genetic diversity based on SSRs markers among some bread wheat genotypes; (ii) estimate GCA, SCA and heterosis effects and (iii) examine the relationship between genetic distance based on SSR markers with SCA and heterosis effects of all traits studied.

## MATERIALS and METHODS

### Plant materials

Five bread wheat varieties were used in this study Gemmieza 10, Gemmieza 3, Seds 4 from the Agriculture Research Center (ARC), Giza, Egypt, ATRI 9890 and ATRI 11712 from Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany. The name, origin and pedigree (if known) are presented in (Table 1). A 5 x 5 half diallel (without reciprocal) mating system by hand emasculation and pollination was followed to obtain ten hybrids.

**Table (1): Name, Origin and pedigree of five bread wheat varieties**

No	Name	Origin	Pedigree
1	Gemmieza 10	Egypt	Maya 74 "s"/On//1160-147/3/Bb/4/Chat"s"/5/Ctow
2	Gemmieza 3	Egypt	Bb/7C*2//Y50/Kal*3//Sakha8/4/Prv/WW/5/3/Bg"s"/On
3	Seds 4	Egypt	Maya"s"/Mons//Cmh74A-592/3/Giza157 <sup>2</sup>
4	ATRI 9890	Germany	No data
5	ATRI 11712	Pakistan	No data

### Field experiments

A half diallel set of crosses involving five bread wheat varieties was carried out in 2006/2007 growing season. The parents and ten F1 crosses were evaluated at the Agricultural Research Station, Faculty of Agriculture, Menoufiya University, Egypt during the wheat growing season 2007/2008. The experiment was arranged in a randomized complete block design (RCBD), with three replicates. Each plot comprised two rows, 3 meters long, with 30 cm between rows and 10 cm within rows. Ordinary cultural practices for bread wheat production were applied. At maturity, ten guarded plants were selected at random from each plot for subsequent character as follows: number of spikes per plant, spike length (cm), spike weight (gm), number of grains per spike, 1000-grain weight (gm) and grain yield per plant (gm).

### Molecular analysis

#### Genomic DNA isolation

Total genomic DNA was extracted from leaf tissue per each variety. Young leaves from eight-weeks-old plants were cut as tissue samples for DNA extraction. DNA was isolated from these genotypes according to (Plaschke *et al.*, 1995).

#### Microsatellite marker

Microsatellite name, chromosomal location, motif, annealing temperature (T<sub>m</sub> °C) and fragment size in CS (bp) were presented in Table (2). Since the information on allele sizes of 'Chinese Spring' (CS) is available (Huang *et al.* 2002), this cultivar has been used as a reference. Microsatellite amplifications were carried out as reported by Röder *et al.* (1998).

**Table (2): Description of 17 wheat microsatellite, their chromosomal location, motif, annealing temperature and fragment size**

No	Microsatellite	Chromosomal location	Motif	Annealing T <sub>m</sub> (°C)	Fragment size in CS (bp)
1	<i>Xgwm3</i>	3DL	(CA)18	55	79
2	<i>Xgwm18</i>	1BS	(CA)17GA(TA)4	50	183
3	<i>Xgwm46</i>	7B (C)	(GA)3GC(GA)33	60	179
4	<i>Xgwm95</i>	2AS	(AC)16	60	122
5	<i>Xgwm155</i>	3AL	(CT)19	60	144
6	<i>Xgwm160</i>	4AL	(GA)21	60	182
7	<i>Xgwm165</i>	4AS, 4BL, 4DL	(GA)20	60	190
8	<i>Xgwm186</i>	5AL	(GA)26	60	135
9	<i>Xgwm190</i>	5DS	(CT)22	60	209
10	<i>Xgwm261</i>	2DS	(CT)21	55	189
11	<i>Xgwm389</i>	3BS	(CT)14 (GT)16	60	129
12	<i>Xgwm408</i>	5BL	(CA)>22(TA)(CA)7(TA)9	55	173
13	<i>Xgwm437</i>	7DL	(CT)24	50	107
14	<i>Xgwm458</i>	1D	(C) (CA)13	60	112
15	<i>Xgwm513</i>	4BL	(CA)12	60	140
16	<i>Xgwm631</i>	7AS	(GT)23	60	196
17	<i>Xtaglgap</i>	1BS	(CAA)31	60	282

### SSRs marker analysis

Seventeen simple sequence repeats (SSRs) markers developed by Röder *et al.* (1998) were selected for genotyping on the basis of their known chromosomal location to give a uniform coverage for all three wheat genomes A, B and D (Table 2). Microsatellite name, chromosomal location, motif, annealing temperature (T<sub>m</sub>, °C) and fragment size in CS (bp) were presented in (Table 2). Microsatellite analysis was performed as described by Röder *et al.* (1998). Polymerase chain reactions (PCR) were performed according to Devos *et al.* (1995) and Röder *et al.* (1998).

### Statistical analysis

Better-parent heterosis (BPH) for each trait of individual cross was expressed as percentage increase of the F1 performance above the better parent (BP) performance (Mather 1949). The general (GCA) and specific combining ability (SCA) analysis were computed according to Griffing (1956) designated as Method 2, Model 1.

To measure the informativeness of the Gatersleben wheat microsatellite (*Xgwm*) markers, the polymorphic information content (PIC) for each *Xgwm* marker was calculated according to the formula of Nei (1973):

$$PIC = 1 - \sum_{i=1}^k P_i^2, \text{ where } k \text{ is the total number of alleles detected for a locus}$$

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of a marker and  $P_i$  is the frequency of the  $i$ th allele in the set of five varieties investigated (Botstein *et al.*, 1980). For genetic similarity estimates and cluster analysis, the allelic data were converted to a binary format, with the presence of a specific allele scored as unity and its absence as zero. Genetic similarities were estimated from the allele binary format dataset using the Dice method (Nei and Li 1979). The binary data were used to compute pair wise similarity coefficients and the similarity matrix obtained was subjected to cluster analysis using the unweighted pair group method of arithmetic average (UPGMA) algorithm on NTSYS-pc version 2.1 software package (Rohlf, 2002). The data were used to examine the relationships between the number of alleles Vs. the gene diversity. Correlation coefficient genetic distance (GD) with heterosis and SCA were calculated according to (Zar, 1999).

### Results and Discussion

The genotypes mean performances for the traits studied are given in Table (3). Genotypes, parents and the resultant ten hybrid combination mean squares were found to be highly significant for number of spikes per plant, spike length, 1000-grain weight and grain yield per plant except spike weight for parents mean square, which indicate overall differences among these populations (Table 4).

Table (3): Mean performances for yield and its components characters of parental genotypes and their hybrids evaluated in 2007/2008 growing season.

Genotypes	No. of spikes/ plant	Spike weight (gm)	Spike length (cm)	No. of grains/ spike	1000 grain weight (gm)	Grain yield/ plant (gm)
Gemmeiza10	16.07	3.91	12.47	70.00	37.15	63.77
Gemmeiza3	12.03	4.53	13.41	74.74	39.74	48.66
Seds 4	3.13	4.00	18.29	94.83	39.70	15.74
ATRI9890	10.03	4.52	12.38	74.70	39.23	39.77
ATRI11712	14.45	4.16	11.01	71.24	38.27	52.11
Gemmeiza10 x Gemmeiza3	18.87	4.39	15.51	77.70	41.93	74.88
Gemmeiza10 x Seds 4	15.15	5.18	15.53	79.55	40.82	69.00
Gemmeiza10 x ATRI9890	17.82	4.61	16.48	79.51	41.35	74.00
Gemmeiza10xATRI11712	16.00	4.34	13.15	75.88	40.60	63.00
Gemmieza 3 x Seds 4	16.15	5.12	16.41	80.66	41.77	76.33
Gemmieza 3 x ATRI9890	13.90	5.53	14.41	80.83	43.27	70.11
Gemmeiza3 x ATRI11712	15.25	5.61	13.43	78.22	42.54	76.22
Seds 4 x ATRI9890	9.47	6.03	17.05	80.47	41.80	55.97
Seds 4 x ATRI11712	9.57	5.57	14.72	77.14	41.67	48.02
ATRI9890 x ATRI11712	10.65	5.87	13.87	77.33	42.27	58.33
L.S.D at 0.05	2.84	0.58	2.22	5.11	0.64	14.05
L.S.D at 0.01	3.82	0.79	3.03	6.89	0.87	18.92

Table (4): Mean square estimates of ordinary and combining ability analysis for grain yield and its components characters of the diallel cross evaluated in 2007/2008 growing season.

S.O.V	d.f.	No. of spikes/ plant	Spike weight	Spike length	No. of grains/ spike	1000 grain weight	Grain yield/ plant
Rep.	2	0.004	0.10	0.36	3.65	0.002	18.24
Genotypes	14	50.30**	1.49**	11.98**	95.49**	8.59**	827.44**
Parents	4	76.13**	0.25	23.62**	307.83**	3.66**	971.04**
Crosses	9	33.46**	1.10**	5.50**	8.79	1.85**	289.39**
Heterosis	1	98.58**	10.01**	23.78**	26.47	88.99**	5095.55**
G.C.A	4	115.57**	1.35**	29.47**	222.53**	6.27**	1099.64**
S.C.A	10	24.19**	1.55**	4.99**	44.68**	9.52**	718.57**
Error	28	2.88	0.12	1.57	9.35	0.15	70.52
G.C.A/ S.C.A		4.78	0.87	5.90	4.98	0.66	1.53

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

Concerning number of grains per spike, the Genotypes, parents mean squares were found to be highly significant. Parent Vs. crosses mean square estimates were found to be significant for all traits studied except number of grains per spike.

### I. Heterosis:

Heterosis effects evaluated in relation to better-parent values are presented in Table (5). These effects were observed in all the traits studied but the degree of heterosis showed variation from trait to trait. High positive values of heterosis would be of interest in most traits under investigation from the wheat breeder's point of view.

Table (5): Percentages of heterosis over better parents for grain yield and its components characters.

Genotypes	No. of spikes/ plant	Spike weight	Spike length	No. of grain/ spike	1000 grain weight	Grain yield/ plant
Gemmeiza10 xGemmeiza3	17.42**	-3.16**	15.68**	3.96	5.51**	17.43*
Gemmeiza10 x Seds 4	-5.70**	29.74**	-15.09**	-16.11**	2.84**	8.20
Gemmeiza10 x ATRI9890	10.89**	1.92**	32.16**	6.46*	5.41**	16.04*
Gemmeiza10 x ATRI11712	-0.46	4.41**	5.43**	6.52*	6.10**	-1.21
Gemmeiza 3 x Seds 4	34.25**	12.95**	-10.28**	-14.94**	5.12**	56.86**
Gemmeiza 3 x ATRI9890	15.52**	22.08**	7.43**	8.14**	8.87**	44.07**
Gemmeiza3 x ATRI11712	5.54**	23.84**	0.15	4.66	7.05**	46.29**
Seds 4 x ATRI9890	-5.62**	33.33**	-6.80**	-15.14**	5.32**	40.74**
Seds 4 x ATRI11712	-33.75**	33.97**	-19.54**	-18.66**	5.00**	-7.86
ATRI9890 x ATRI11712	-26.27**	29.94**	12.10**	3.53	7.75**	11.94
L.S.D at 0.05	2.84	0.58	2.09	5.12	0.65	14.05
L.S.D at 0.01	3.82	0.79	2.82	6.89	0.87	18.92

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

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For number of spikes per plant, five hybrid combinations had significantly more spikes per plant than their respective better parents. This useful heterosis ranged from 5.54% to 34.25%. Also, for spike weight, nine out of the ten hybrid combinations investigated exhibited significant useful heterotic effects. This heterosis ranged from 1.92% to 33.97% over better parent. With regard to spike length, five crosses had significantly longer spikes than their respective better parents. This useful heterotic effects ranged from 5.43% to 32.16%. For number of grains per spike, three hybrid combinations showed significant heterosis in comparison with their respective better parent which ranged from 6.52% to 8.14% over better parent. Concerning 1000-grain weight, all hybrid combinations showed significant heterosis in comparison with their respective better parent which ranged from 2.84% to 8.87%. As for grain yield per plant, six out of the ten hybrid combinations studied exhibited significant useful heterotic effects which varied from 17.43% to 56.86% over better parent. Similar results were obtained by Hendawy *et al.* 1993.

### **II. Combining ability:**

Both general and specific combining ability variances were found to be highly significant for all traits studied (Table 4). This indicate the importance of both additive and non-additive genetic variances in determining the performance of these characters. The GCA/SCA ratios were found to be greater than unity, indicating that additive and additive x additive types of gene action were greater importance in the inheritance for number of spikes per plant, spike length, number of grains per spike and grain yield per plant. For the other two attributes, i.e. spike weight and 1000 grain weight, GCA/SCA ratios were found to be less than unity, indicating that non-additive genetic variances were of greater importance in the inheritance of these two traits. It is therefore could be concluded that selection procedures based on the accumulation of additive effect would be successful in improving these six characters. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variance are involved, would be preferred. The results are in accordance with Abul-Nass, *et al.*, 1986; Hendawy *et al.* 1993; El-Hennawy *et al.* 1991 and Rizwan and Khan, 2000.

Estimates of the general combining ability effects (gi) for the parental lines in each trait are presented in Table (6).

High positive general combining ability effects would be of interest in most traits under investigation. The two Egyptian wheat varieties Gemmieza 10 and Gemmieza 3, showed significantly positive GCA effects for number of spikes per plant, proving to be good combiner in this concern. With regard to spike weight, only the wheat variety ATRI 9890, showed significantly positive value of GCA effects, revealing that this wheat variety could be considered as good combiner for this trait. The Egyptian wheat variety Seds 4 exhibited

significantly positive GCA effects for spike length and number of grains per spike, proving to be excellent combiner for these trait. The two wheat varieties Gemmieza 3 and ATRI 9890 showed significantly positive GCA effects for 1000-grain weight, proving to be good combiners in this trait. For grain yield per plant, the two Egyptian wheat varieties Gemmieza 10 and Gemmieza 3 showed significantly positive general combining ability effects. The combining ability effects in wheat has been previously described (Perenzin *et al.* 1998, Esmail, 2002; Shoran *et al.* 2003; Topal *et al.* 2004; Esmail, 2007).

**Table (6): Estimates of general combining ability effect for the parental genotypes for grain yield and its components characters in diallel cross evaluated in 2007/2008 growing season.**

Genotypes	No. of spikes/ plant	Spike weight (gm)	Spike length (cm)	No. of grain/ spike	1000 grain weight (gm)	Grain yield/ plant (gm)
Gemmeiza10	8.81**	-1.29**	-0.70	-7.06**	-2.50**	23.17**
Gemmeiza3	3.77**	0.15	-0.28	-0.95	1.78**	17.36**
Seds 4	-9.78**	0.23	5.59**	16.44**	0.26*	-31.52**
ATRI9890	-3.22**	0.74*	-0.30	-0.68	0.99**	-7.03*
ATRI11712	0.41	0.16	-4.31**	-7.74**	-0.52	-1.97
L.S.D at 0.05	1.14	0.24	0.84	2.05	0.25	5.63
L.S.D at 0.01	1.53	0.87	1.13	2.76	0.35	7.59

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

Specific combining ability effects (Si) for the parental combinations in each trait are presented in Table (7). Four of the ten hybrid combinations studied showed significantly positive SCA effects for number of spikes per plant. Three of these superior four crosses was found to show useful heterosis (Table 5). It is of interest to mention that the two varieties Gemmieza 10 and Gemmieza 3 were found to be an excellent combiner for number of spikes per plant, therefore, the hybrid combination Gemmieza 10 x Gemmieza 3, Gemmieza 10 x Seds 4, Gemmieza 10 x ATRI 9890 and Gemmieza 3 x Seds 4 could be of practical importance in a breeding programme for developing either hybrid wheat or pure lines since it had significant SCA effect for the trait in view and contained a good combiners (Table 6).

For spike weight, six hybrid combinations exhibited highly significant SCA effects. The two hybrid combinations Gemmieza 3 x ARTI 9890 and ARTI 9890 x ATRI 11712 showed significant positive useful heterosis (Table 5). Also, the wheat variety ARTI 9890 proved to be a good combiner for spike weight. This cross could be of practical importance in a breeding programme since it had significant SCA effect for the trait in view and contained a good combiners. For spike length, three hybrid combinations (Gemmieza 10 x Gemmieza 3, Gemmieza 10 x ATRI 9890 and ATRI 9890 x ATRI 11712)



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exhibited significant SCA effects. The hybrid combination Gemmeiza 10 x ATRI 9890 showed useful heterosis (Table 5) and could be exploited in wheat breeding programme to obtained a long spike varieties.

**Table (7): Estimates of specific combining ability effects for the hybrids for grain yield and its components characters**

Genotypes	No. of spikes/ plant	Spike weigh t	Spike length	No. of grains/ spike	1000 grain weight	Grain yield/ plant
Gemmeiza10 x Gemmeiza3	4.31**	-0.38	3.90**	6.55*	4.09**	6.95
Gemmeiza10 x Seds 4	6.71**	1.92**	-1.93	-5.29	2.27**	38.17**
Gemmeiza10 x ATRI9890	8.16**	-0.30	6.81**	11.72**	3.15**	28.67**
Gemmeiza10 x ATRI11712	-0.95	-0.52	0.83	7.90**	2.41**	-9.39
Gemmeiza 3 x Seds 4	14.74**	0.29	0.30	-8.06**	0.86*	65.98**
Gemmeiza 3 x ATRI9890	1.43	1.02**	0.18	9.55**	4.61**	22.82**
Gemmeiza3 x ATRI11712	1.85	1.84**	1.27	8.80**	3.94**	36.08**
Seds 4 x ATRI9890	1.69	2.43**	2.22	-8.91**	1.73**	29.30**
Seds 4 x ATRI11712	-1.62	1.65**	-0.75	-11.85**	2.86**	0.36
ATRI9890 x ATRI11712	-4.94**	2.04**	2.59*	5.85*	3.92**	6.81
L.S.D at 0.05	3.12	0.64	2.30	5.63	0.71	15.45
L.S.D at 0.01	4.20	0.87	3.10	7.58	0.96	20.80

\* and \*\*, significant at 0.05 and 0.01 level of probability, respectively.

With regard to number of grains per spike, six hybrid combinations exhibited significant SCA effects. The best hybrid combinations were Gemmeiza 10 x ATRI 9890 and followed by Gemmeiza 3 x ATRI 9890 showed significantly SCA effects and high parent hetrotic effects (Table 5). Concerning 1000 grain weight, all hybrid combination showed significant SCA effects and useful heterosis. Also, three wheat varieties Gemmeiza 3, Seds 4 and ATRI 9890 proved to be good combiners for 1000 grain weight (Table 6). The crosses included these parents could be of practical importance in a breeding programme. As for grain yield per plant, six out of the ten hybrid combinations studied showed highly significant positive SCA effects. Also, five of these six superior crosses exhibited useful heterosis (Table 5). These hybrid combinations could be of practical importance in a breeding programme since it had significant SCA effect for the trait in view and contained a good combiners.

The result obtained here concerning GCA and SCA effects could indicate that the excellent hybrid combinations were obtained for crossing good by good, good by low and low by low combiners. Consequently, it could be concluded that GCA effects of the parental lines were generally unrelated to the SCA estimates of their respective crosses. This finding was also found by Hendawy, 1989; Esmail, 2002 & 2007.

### III. Genetic diversity and distances

A total of 53 alleles were detected by the 17 simple sequence repeats (SSRs) markers on the five bread wheat genotypes from different origin. The number of alleles per locus ranged from two for *Xgwm3*, *Xgwm186* and *Xgwm408* to five for *Xgwm513* with an average number of 3.12 alleles per locus (Table 8).

Table (8): Description of 17 wheat microsatellite, their position, size range of alleles, number of alleles and gene diversity.

No	SSRs	Chromosomal location	Fragment size		Number of alleles	Gene diversity
			Min Allele	Max Allele		
1.	<i>Xgwm3</i>	3DL	77	84	2	0.480
2.	<i>Xgwm18</i>	1BS	182	190	3	0.625
3.	<i>Xgwm46</i>	7B (C)	147	186	4	0.720
4.	<i>Xgwm95</i>	2AS	109	122	3	0.560
5.	<i>Xgwm155</i>	3AL	129	147	3	0.640
6.	<i>Xgwm160</i>	4AL	177	184	4	0.720
7.	<i>Xgwm165</i>	4AS, 4BL, 4DL	187	197	3	0.560
8.	<i>Xgwm186</i>	5AL	126	130	2	0.320
9.	<i>Xgwm190</i>	5DS	204	212	3	0.640
10.	<i>Xgwm261</i>	2DS	165	192	3	0.625
11.	<i>Xgwm389</i>	3BS	119	132	3	0.640
12.	<i>Xgwm408</i>	5BL	180	182	2	0.480
13.	<i>Xgwm437</i>	7DL	91	130	4	0.720
14.	<i>Xgwm458</i>	1D	109	122	3	0.560
15.	<i>Xgwm513</i>	4BL	141	149	5	0.800
16.	<i>Xgwm631</i>	7AS	190	200	3	0.560
17.	<i>Xtaglgap</i>	1BS	235	280	3	0.640
Total					53	10.29
Mean					3.12	0.605

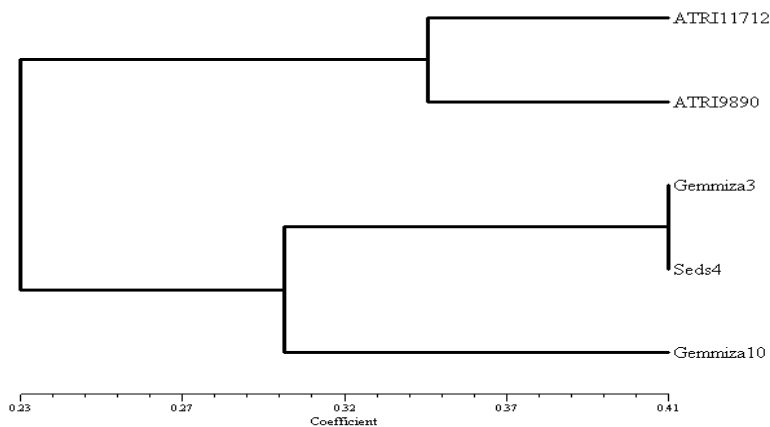
Different number of alleles has been detected in wheat using SSRs markers. Huang *et al.* (2002) reported an average allele number of 18.1 in 998 gene bank accessions of hexaploid wheat originated from 68 countries of five continents. Khlestkina *et al.* (2004) found an average allele number of 6.6 in 54 Siberian old and modern common spring wheat varieties. Roussel *et al.* (2005) reported an average allele number of 16.4 in 480 wheat varieties originating from 15 European geographical areas and released from 1840 to 2000. Salem *et al.* (2008) detected an average of 3.2 alleles in seven wheat

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varieties. Mattar (2009) detected an average of 4 alleles in eleven wheat varieties. In the present study, the average number of allele was 3.12 in five wheat varieties. The value obtained here was lower than most previous results, but it was comparable with results obtained by (Stachel *et al.* 2000), they found 4.8 alleles per locus in wheat varieties and close to results obtained by Salem *et al.* (2008) when studied the genetic diversity in seven bread wheat varieties (3.2 alleles per locus).

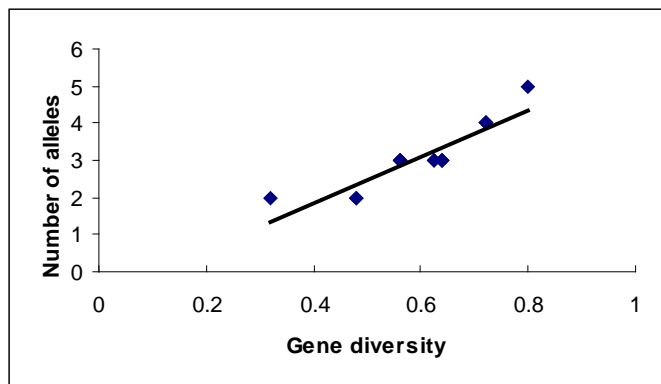
To assess the genetic diversity of wheat varieties, marker data were converted into binary matrix, which in turn allowed to calculate the genetic similarity index. A dendrogram was created with the use of these data (Fig. 1). The consensus tree showed that the five wheat varieties were divided into two main groups, the first group included the two exotic wheat varieties ATRI 11712 and ATRI 9890. The second main group included the three Egyptian wheat varieties and was divided into two sub-groups. The first sub-group included the two wheat varieties Gemmiza 3 and Seds 4. The second sub-group included Gemmiza 10.



**Fig. (1): Cluster analysis of genetic distance for five bread wheat varieties**

Polymorphic information content (PIC), a measure of gene diversity, for the 17 SSRs was ranged from 0.320 for the *Xgwm186* to 0.800 for *Xgwm513* with an average of 0.605 (Table 8). Results revealed that, the value of gene diversity increased with the increasing number of alleles at a given locus (Fig. 2). There was significant correlation between gene diversity and the number of alleles ( $r = 0.899^{**}$ ,  $P < 0.01$ ). Therefore the number of alleles can be used for the evaluation of genetic diversity. Our results agree with those of Huang *et al.* 2002; Salem *et al.* 2009; Salem and Mattar, 2009 and Mattar

2009 who reported that the PIC value was correlated with the number of alleles and did not agree with those of Prasad *et al.* (2000).



**Fig. (2): Relationship between gene diversity and the number of alleles detected at 17 microsatellite loci.**

A genetic distance (GD) matrix based on all possible pairs of lines ranged from 11.1% to 41.2% (Table 9). This result mean that the variation was high. The lowest pair wise GS value was between the German wheat variety ATRI 9890 and the Egyptian wheat variety Seds 4 (0.111), while the highest value (0.412) was between the two Egyptian wheat varieties Seds 4 and Gemmieza 3 (Table 9). Nei's genetic distance (GD) was measured using the 53 polymorphic SSR alleles. Genetic distance within the wheat varieties was significantly different.

**Table (9): Genetic similarity estimates for 5 wheat varieties based on 17 SSRs markers analysis**

Variety	ATRI 11712	ATRI 9890	Gemmieza 3	Seds 4	Gemmieza 10
ATRI 11712	1.00				
ATRI 9890	0.343	1.00			
Gemmieza 3	0.363	0.235	1.00		
Seds 4	0.228	0.111	0.412	1.00	
Gemmieza 10	0.182	0.235	0.250	0.353	1.00

### **III. Relationship of hybrid SCA and heterosis with genetic distance**

Correlation coefficients between GD and SCA effects are presented in Table (10). Genetic distance was significantly positive correlated with SCA for spike weight. GD was significantly negative correlated with SCA for

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number of grains per spike. No correlations were found between GD and SCA for number of spike per plant, spike length, 1000 grain weight and grain yield per plant.

Table (10): Correlation coefficient between genetic distance of the materials studied with specific combining ability and heterosis effects in grain yield and its components characters

	No. of spikes/ plant	Spike weight	Spike length	No. of grains/ spike	1000 grain weight	Grain yield/ plant
SCA	-0.06	0.47**	0.09	-0.44**	-0.26	0.05
Heterosis	-0.34**	0.31**	-0.19	-0.47**	-0.50**	-0.13

\* and \*\*, significant at 0.05 and 0.01 level of probability, respectively.

Similarly, heterosis effects was significantly positive correlated with GD only in the case of spike weight. GD was significantly negative with heterosis effects for number of spike per plant, number of grains per spike and 1000 grain weight. No correlation was found between GD and heterosis effects for spike length and grain yield per plant. Results recorded for yield and its components traits are promising for practical purposes. It is of interest that in heterosis breeding the effectiveness of choosing pairs of parental genotypes based on GD and SCA effects may be similar. The GD between cultivars may be defined on the basis of molecular markers (Shamsuddin 1985; Melchinger *et al.* 1990; Diers *et al.* 1996).

In conclusion, this study indicated that the SSRs are very effective molecular markers for genotype identification and for estimation the genetic diversity among Egyptian and exotic wheat varieties. It concludes that on the basis of microsatellite markers, diverse parents can be selected. Results recorded in this study may contribute to the development of an effective method to select components for heterosis, combining ability of both quantitative and molecular breeding.

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## تقدير العلاقة بين التنوع الوراثي باستخدام المعلم الجزيئي الميكروستاليت وقوة الهجين والقدرة على الائتلاف لبعض الهجن التبادلية في قمح الخبز

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### الملخص العربي

أجرى هذا البحث بمزرعة كلية الزراعة - شبين الكوم - جامعة المنوفية - مصر خلال موسمي ٢٠٠٦/٢٠٠٧، ٢٠٠٧/٢٠٠٨ وقد استخدم لتنفيذ هذا البحث خمسة أصناف من القمح ثلاثة منها مصرية هي جمييزة ١٠، جمييزة ٣، سدس ٤، وصنف ألماني ATRI9890 ، والأخر باكستاني المنشأ ATRI11712. أجرى التهجين التبادلي بينهما (ماعد العكسي) في الموسم ٢٠٠٦/٢٠٠٧ تم تقييم الأصناف والهجن في موسم ٢٠٠٧/٢٠٠٨ وقد تم تحليل البيانات باستخدام طريقة جرفنج (١٩٥٦) الطريقة الثانية الموديل الأول ولقد أجرى هذا البحث بهدف:

- (١) دراسة التنوع الوراثي بين أصناف القمح المستخدمة باستخدام المعلم الجزيئي الميكروستاليت.
- (٢) تقدير قوة الهجين والقدرة العامة والخاصة على الائتلاف.
- (٣) تقدير العلاقة بين قوة الهجين والقدرة الخاصة على الائتلاف و التباعد الوراثي باستخدام الميكروستاليت .

وكانت الصفات تحت الدراسة هي عدد السنابل على النبات، طول السنبل، وزن السنبل، عدد الحبوب في السنبل، وزن ١٠٠٠ حبة، محصول النبات الفردي وفيما يلي ملخص لأهم النتائج المتحصل عليها :

- ١- كانت قيم التباين الراجعة إلى التراكيب الوراثية والآباء والهجن عالية المعنوية لجميع الصفات تحت الدراسة ماعدا صفة وزن السنبل للآباء وعدد الحبوب على السنبل للهجن.
- ٢- كانت قيم التباين الراجع إلى قوة الهجين معنويا لكل الصفات المدروسة ماعدا صفة عدد الحبوب على السنبل.

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- ٣- تم الحصول على قوة هجين عالية المعنوية ومرغوبة بالنسبة لكل الصفات وقد وجد أن جميع الأصناف تحت الدراسة قد اشتركت في تكوين هجن متفوقة.
- ٤- كان التباين الوراثي الراجع لكل من القدرة العامة والخاصة على الانتلاف عالي المعنوية لجميع الصفات تحت الدراسة.
- ٥- أظهرت النسبة بين تبايني القدرة العامة والخاصة على الانتلاف تأثير أكبر للقدرة العامة على الانتلاف مما يشير الى أهمية كل من الفعل الوراثي المضيف، وأيضا التفاعل بين الفعل الوراثي المضيف x المضيف، وذلك في وراثة صفات عدد السنابل على النبات، عدد الحبوب على السنبل، محصول النبات الفردي فيما عدا صفتي وزن السنبل ووزن ١٠٠٠ حبة.
- ٦- تم الحصول على أفضل التأثيرات المرغوبة للقدرة الخاصة على الانتلاف لصفة محصول النبات الفردي وذلك في ستة هجن وهي  
(Gemmeiza10 x Seds 4), (Gemmeiza10 x ATRI9890), (Gemmeiza 3 x Seds 4),  
(Gemmeiza 3 x ATRI9890), (Gemmeiza3 x ATRI11712), (Seds 4 x ATRI9890) .  
وهذه الستة هجن المتميزة لها أهمية خاصة في برامج التربية سواء لإنتاج هجين أو إنتاج سلالات قمح جديدة حيث أنها تفوقت على أعلى آباءها لصفة المحصول وبعض مكوناته.
- ٧- باستخدام المعلمات الجزيئية الميكروستاليت لتقدير التنوع الوراثي تم الحصول على ثلاثة وخمسون أليل وراثي بمتوسط ٣.١٢ أليل لكل موقع وراثي وتراوح عدد الأليلات بين ٢ الى ٥ أليلات.
- ٨- تراوحت قيم PIC بين ٠.٣٢٠ للميكروساليت Xgwm186 الى ٠.٨٠٠ للميكروساليت Xgwm513 بمتوسط قدرة ٠.٦٠٥ .
- ٩- أظهرت العلاقة بين عدد الأليلات وقيمة التنوع الوراثي (المحتوى المعلوماتي) وجود ارتباط موجب عالي المعنوية قيمته ٠.٨٩٩ .
- ١٠- قسم الدندوجرام التراكيب الوراثية الى مجموعتين رئيسيتين وشملت المجموعة الأولى الصنفين الأجنبيين وهما الصنف ATRI11712، ARTE9890، بينما المجموعة الثانية شملت الأصناف المحلية وقسمت إلى تحت مجموعتان الأولى شملت الصنفين مميزة ٣، سدس ٤ والثانية الصنف مميزة ١٠ .

١١- أظهرت الدراسة وجود ارتباط موجب على المعنوية بين التباعد الوراثى والقدرة الخاصة على الائتلاف وقوة الهجين لصفة وزن السنبله، وجود ارتباط سالب على المعنوية بين التباعد الوراثى والقدرة الخاصة على الائتلاف وقوة الهجين لصفة عدد الحبوب على السنبله ووزن ١٠٠٠ حبة.

١٢- توضح هذه الدراسة أهمية استخدام المعلم الجزيئى الميكروستاليت فى تحديد الاختلافات الوراثية بين الأصناف فى التنبؤ بقوة الهجين والقدرة على الائتلاف لإنتاج هجين أو إنتاج سلالات قمح جديدة فى برامج التربية لصفة المحصول و مكوناته وتوفير الوقت والنفقات لاختيار الآباء الداخلة فى التهجين.