Relationship between genetic and phenotypic diversity of parental genotypes and specific combining ability and heterosis in tetraploid wheat

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Abstract

The purpose of the study was to evaluate the relationship between the genetic (GD) and phenotypic (PD) distance of parents and the specific combining ability (SCA) and mid – parent, heterosis, (MP).

The experiment comprised (8) cultivers of tetraploid wheat (*Triticum durum* Desf.) and (15) hybrids obtained by crossing in a (line× tester) scheme. Parents and hybrids were planted in the botanic experimental station, in the Agricultural and Forestry Collage of Mosul University, conducted in a randomized complete block design (R. C. B. D.) with three replications during the growing season (2010 – 2011), (2011 – 2012). SCA as well as at mid parent heterosis (MP) were estimated for quantitative characters, GD and PD values were investigated between pairs of parental genotypes. GD was evaluated by using randomly amplified polymorphic DNA markers. The ratio between the general combining ability components to that of the specific one revealed that the non-additive genes effects were more important in the inheritance of all the studied characters. Most of hybrids showed desirable or highly significant (SCA) and heterotic values at (MP) for most studied characters. As well as, a highest genetic distance determined between cultivars; 3(Azeghar– 1) and 6 (Acsad– 65) and the lowest between cvs. 2(Leeds) and 4(Doma– 1) by using (Nei and Li 1979). (Non-significant correlations were observed between genetic distance (GD) as well as (PD) with both: the amount of SCA and heterosis for grain yield, wherase the correlation coefficient between(GD) and heterosis for these characters had apositive and significant value.

Keywords:, Mid – Parents Heterosis, RAPD – DNA Marker

Introduction

Wheat is one of the most important and strategic crop all over the worlds. It is the most widely grown and consumed food crop of the world cultivated on alarger area. And produce more tonnage of food. (KrystKowiak *et a l*2009) reported that wheat contributes more calories and protein to the diet than any other cereal food crop, (Subhaschandra B.,2007).

However, total wheat consumption has drastically increased due to over population

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growth by about (2.5%) a year. This reflects the size of the problems and the efforts needed to increase wheat production. Thus, increasing production per unit area appears to one of the important factors for narrowing the gap between wheat production and consumption, (Gad, 2010). The choice of appropriate components for crossing is the first and foremost step in the creation of new crop cultivars. Knowledge on the effects of general combining ability (GCA) and specific combining ability (SCA) is useful in the selection of parental genotypes. The main goal of hybrid wheat breeding is the identification of parents with high SCA for technological quality and agronomic traits. Such data facilitate the choice of pairs of parental genotypes with high probability of heterosis in their F_1 progeny which having phenotype character appearance than mean of both parents, (Brieger,1950).The breading value of genotypes, including combining ability is evaluated on the basis of the analysis of hybrids produced in appropriate crossing schemes(line x tester) is most frequently applied,(Marciniak *et al.*, 2003); (Ahuja and Dhayal, 2007). In case of self-pollinated crops, these methods require a large number of manual crossings, which make time consuming and expensive; (Shen *et al.* ,2006). Thus the selection of parental genotypes in wheat breeding based on combining ability is seldom used. Heterosis effects has been used in breeding of self-pollinated plants, including wheat (Weibmann and Weibmann ,2002). The agronomic value of wheat hybrids appears to be promising, (Oury *et al.* ,2000). However knowledge about heterosis the relative importance of GCA, SCA genetic background of parental materials for exploitation of heterosis in wheat remains limited.

Molecular marker technology was effective in learning phenomena as heterosis, specific combining abilities and parental genotypes interaction with environment. The initial studies were associated with the search for a relationship between the genetic diversity of parents evaluated with molecular techniques and their hybrids performance. DNA markers are most suitable for genetic diversity estimates, Sun *et al.* (2003). Randomly amplified polymorphic DNA($RAPD_S$) has been widely employed because of il's simplicity and ability to detect genetic variation among very closely related genotypes in a number of genotypes. (Jain *et al.*, 1994); (Kuczynska*et al.*, 2007). RAPD has been attemped to develop a method to select crossing components based on genetic distance (GD) between genotypes among sun flower, wheat and maiz,(Corbellini *et al.* ,2002). In heterosis breeding this approach was found on the simultaneous evaluation of both GCA and SCA as well as GD. (Burkhamer*et al.*, 1998); (Corbellini *et al.* ,2002).

The aims of this research were:

1. To estimate the general combining ability(GCA) for eight varieties of tetraploid wheat.
2. To estimate the specific combining ability(SCA)for hybrids obtained by (line x tester) scheme according to Kempthorn (1957).

3. To determine the hybried performance at mid – parent .
4. Determination of genetic and phenotypic diversity(GD and PD) between parents.
5. Examining the relationship between (GD,PD) with the magnitude of specific combining ability (SCA) and Heterotic effects.

Materials and Methods

Plant material:

Eight varieties of tetraploid wheat (*Triticum durum* Desf.) Um –Rabie 3, Leeds, Azeghar– 1, Acsad– 65, Buhoth– 7, Doma– 1, Korfela and Um –Rabie 5, (Table 1).

Table(1): Source of (8) varieties of tetraploid wheat.

Code	Genotype	Source
1	Um –Rabie– 3	ICARDA
2	Leeds	ICARDA
3	Azeghar– 1	Department field crop college of Agriculture and forestry – University of Mosul
4	ACSAD– 65	ACSAD
5	Buhoth– 7	The general organization for agricultural research in Syria
6	Doma– 1	Shared program between The general state for scientific and agricultural research in Syria and ICARDA and ACSAD
7	Korfela	ICARDA
8	Um –Rabie– 5	ICARDA

Field experiments:

Grains of these varieties were planted at botanic experimental field of agricultural and forestory college,Mosul University during the growing season(2010-2011).Fifteen hybrids (F1)have been obtained after crossing using (linextester) scheme (3) testers and (5) lines. All genotypes (8 parents and 15 hybrids grains were planted at growing

season (2011 – 2012) at the same field with three replications using randomized complete block design (R.C. B. D.).

1. Statistical Analysis:

Data for all characters had been subjected to an analysis of variance (ANOVA) according to(Kempthorn, 1957). General and specific combining ability (GCA and SCA) effects for (line x tester). Heterosis was calculated as a deviation of F_1 mean from themean of mid – parent (MP) according to following formula:

$H(\overline{M.P}) = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}}$

H(M.P)= Hetrosis over mid parents.

$\overline{F_1}$= value of F_1.

$\overline{MP}$= mean of parents.

DNA – extraction and RAPD Amplification :

The DNA samples were extracted from dried grains of tetraploid wheat varieties ground to afine powder (1 gm) by CTAB method [cetyltrimethyl ammonium bromide] (Weigand*et al.* ,1993). With some modified followed by an RNase– treatment

(promege com.) for 30 min at 37 ^{o}c., (Sambrook*et al.*, 1989).

The DNA quality was tested using (1%) agarose gel electrophotometer (UV – 1800shimadzu) at 260 – 280 nm. The concentration of DNA was calculated according to the following formula:

DNA concentration ($\mu g/\mu l$)= [OD 260 × 100(dilution factor) × 50 $\mu g/\mu l$] / 1000 the DNA samples are adjusted to concentration of 50 ng/μl with TE buffer and subjected to

polymerase chain Reaction (PCR) amplification, (Gyulai *et al.* ,2000).

PCR Amplification and Data analysis:

The reaction of RAPD – PCR were performed in a thin – walled 96 – well thermal cycler (model: Multi GENE Optimax, Lab net, USA) according to(Williams*et al.* ,1990) with 10meroligo nucleotides from by Biooner as mentioned previously (Abdulla *et al.*, 2013). The final volume of 20 μl contained 5μl of PCR premix from Bioneer Accu power, [each tube in PCR premix contain: 1U DNA polymerase, 250 μm dNTP'S (dAtP, dCtP, dGtP, dTtP), 10 m μtris–HCl (pH 9), 30 mμ KCl, 1.5 m$\mu$$MgCl_2$], 3$\mu$l of 10 pmol of each primer, 5μl of 50 ng of DNA template and 7 μl of dH_2O. The reaction tubes were treated to the following temperature cycles: 94 ^{o}c.for 4 minute (denaturation), followed by 36 cycles of annealing, 94 ^{o}c. for30 sec, 35 ^{o}c.for 45 sec and 72 ^{o}c. for secand final extension of 5 min at 72 ^{o}c.

The PCR products were analyzed on (2%) a garose gel at 40 volt for 3h. then the gel were stand in 0.5 $\mu g/\mu l$of ethidiumbromid and DNA fragments visualized under UV trans-illuminator. the fragments were estimated based on a DNA ladder of 100pb (Tahir,2008).

RAPD Data analysis:

Clear and distinct amplification products were scored for presence (1), absence(0). The dissimilarity matrix (GS) between genotypes was estimated using Nie and Li dissimilarity coefficient, (Nei and Li, 1979). Dendrogram was concetructed from dissimilarity matrices using the un weighted pair group method with Arithmetic mean (UPGMA).

Clustering procedure, based on the dissimilarity matrices for RAPD data which obtained using the software NTSYS –pc numerical taxonomy system. ver 2.21c (Applied Biostatics Inc. Setaukett: (New york USA) (Rohlf ,2000)

Differences between studied varieties for all characters treated simultaneously were assessed by using Mahalanobis distance (D). Which was treated as a measure of phenotypic distance (PD) between parents, the analyzed data obtained by software PASW Statistics 18Mahalanobis(1936)

the correlation between genetic diversity (GD) evaluated on the basis of RAPD markers and phenotypic distance (PD) of parental forms, , SCA and heterosis at mid – parents. for grain – yield are obtained using Mantel test, (Mantel, 1967).

Result and Discussion

1. Field experiment (Genetic Analysis of Tetraploid Wheat Characters)

a. Analysis of variance:

(Table 2) revealed that mean squares of genotypes, parents and crosses (line x tester) were highly significant for all studied characters. Indicating wide diversity among the parents. The ratio of GCA/SCA variances was less than unity for all the studied characters suggesting that non – additive gene effects in the expression of these characters. In addition, the magnitude of SCA mean squares was greater than GCA mean squares, suggesting that non – additive genes effects were predominant and played a major role in the inheritance of all characters. These result are also in line with those obtained by (AL – Hamadany and yousif ,2006); (Srivastaval et al. ,2012); (Ayoob and Hazim ,2005).

Table (2):Analysis of variance (ANOVA)for studied characters of tetraploid wheat using (line x testers) scheme according to Kempthorne (1957).

Sources of variance	Means square										
	d. f.	Flag leaf area (cm^2)	Plant height(cm)	No. spike $plant^{-1}$	No. spikelet's $spike^{-1}$	Spike length (cm)	No. grains $spike^{-1}$	100 grains weight (gm)	Grain yield $plant^{-1}$ (gm)	Biological yield (gm)	Harvest index %
Replications	٢	١٠,٢٠٠	١٨,١٥٢	٠,٠٤٢	٠,٠٥٨	٠,١٩٢	٣,٨٤٧	٠,٠١١	٠,٦٢١	١,٨٥٤	٥,٥١٤
Genotypes	٢٢	**١٣٢,٠٥٠	**٥٨,٣٥٦	**١,٠١٩	**١,٢١٢	**٥,٣١٣	**١٤١,٨٩٩	**٠,٣١٣	**٩,٣٧٥	**١٨,٠١٩	**٥٢,٥٩٣
Parents	٧	**١٠٣,٩٦٠	**٣٠,٢٤٠	**٠,٩٥٦	**١,٠٣٤	**١,٣١٧	**١٤٥,١٤٦	**٠,٣٩٨	**٦,٥٠٥	**١٨,٧٥٢	**٤٣,٧٤٩
Parents vs. crosses	١	**١٦٠,٨٧٠	٢٥,٢٤٥	٠,٣٣٠	٠,٠٢١	*١,١٢٠	*٣٨,٠٣٧	٠,٠٤٩	٠,٢٧٦	٢,٤٤٢	٤,٣٣٣
Crosses	١٤	**١٣٦,٦١٠	**٧٢,٦١٩	**١,٠٣٢	**١,٣١٣	**٧,٥١٦	**١٣٧,٣٢٧	**٠,٢٦١	**١٠,٩٩٥	**١٧,٤٢٥	**٥٧,٣٣٧
Line	٤	٩,١٨٦	٠,٧٥٥	٠,٢٥٠	٠,١٣٩	٠,٥٢٣	٣٧,٢٥٥	٠,٠٤٥	٢,٠٦٨	٤,٥٢٥	١٣,١٤٦
Tester	٢	٦٦,٩٥٨	٥١,٥٩٠	٠,١٤٧	٠,٠٢٨	٣,٤١٠	١٥,٣٩٩	٠,٠٣٤	١,٣١٥	٠,٦١٤	٥,٥٥٧
Line x tester	٨	**٢١٧,٧٣٥	**١١٣,٨٠٩	**١,٦٤٤	**٢,٢٢١	**١٢,٠٤٠	**٢١٧,٨٤٦	**٠,٤٢٥	**١٧,٨٧٩	**٢٨,٠٧٨	**٩٢,٣٧٨
Error	٤٤	٤,٦٩٧	٧,٥٢٨	٠,٢٠٦	٠,١٦٠	٠,٢٠٨	٦,٧١٦	٠,٠٥٣	١,١١٧	٢,٥١٢	٦,١٩٢
σ^2 G. C. A.		٠,٠٩٧	٠,٠٨٠	٠,١٤٢	٠,١٤٥	٠,١٠٠	٠,١٣١	٠,١٤٣	٠,١٣٥	٠,١٤٧	٠,١٣٧
σ^2 S. C. A.											

* and ** Level 5% and 1% respectively.
G. C. A.= General combining ability.
S. C. A.= Specific combining ability.

b. Combining abilities:

It is often desirable to select lines as parents of crosses, most studies on wheat revealed that general combining ability (GCA) was found to be more important than specific combining ability(SCA) for most characters. From table (3) several parents showed appositive significant(GCA)such as:

parent (3)(Line):for flag leaf area, no.of spikes$plant^{-1}$, 100 – grains weight, grains – yield and harvest index.

Parent(4)(line): For flag leaf area, spike length and biological yield.

Parent(2)(line): For flag leaf area, no. of spikes $plant^{-1}$ and spike length.

Parent(6)(Tester): For flag leaf area, no. of spikelet's $spike^{-1}$, spike length, no .of grains $spike^{-1}$and 100 – grains weight.

So thereforep_6 considered as the best general combiner.

Parent(8)(Tester): For plant height, no. of spikes$plant^{-1}$, no. of grains $spike^{-1}$,grian yield $plant^{-1}$ and harvest index.

All these parents considered as a good sources of genes for improving these traits by hybridization and selection programs.

From table(3) also several hybrids show appositive significant values of (SCA) as in:

(3×7): For no. of grains $spike^{-1}$, 100 – grains weight, grains – yield and biological yield.

(4×6): For flag leaf area, no. of spikes $plant^{-1}$, no. of spikletes per spike, length and no. of grains $spike^{-1}$.

(5×8): For flag leaf area, no. of grains $spike^{-1}$, spike length and biological yield.

These crosses can be considered as the best combinations for increasing such characters aggregate selection.

These highest (SCA)significant values of these hybrids due to their highest performance in combination, and that refers to the non-additive effects of genes controlling those characters similar results of wheat were obtained in (Saeed 2005;Saeed 2001;and Anwar 2011).

Table (3):Estimates of general combining ability and specific combining ability:

Genotype and hybrids		Flag leaf area (cm^2)	Plant hight(cm)	No. spike $plant^{-1}$	No. spikelet's $spike^{-1}$	Spike length (cm)	No. grains $spike^{-1}$	100 grains weight (gm)	Grain yield $plant^{-1}$ (gm)	Biological yield (gm)	Harvest index %
Line	1	٠,٨٦٤١	٠,٩٢٠٠	٠,٢٨٠٠	-٠,١٤٢٢	-٠,٧٦٥٨	-٠,٦٠٨٩	٠,١٠٤٢	-٠,٠٦٠٨	٣,١٤٢٢	-٢,٠٦١٥
	2	١,٩٥٧٩	٠,٤٧٥٦	٠,٥٤٦٧	-٠,٠٣١١	٠,٥٦٣١	-٤,٠٠٨٩	-٠,٠٣٢٨	-٠,٥٢٧٥	-١,٠٨٠٠	-٠,٦٦٥٠
	3	١,٤٩٤٨	-١,٣٩١١	-٠,٠٥٣٣	٠,٥٤٦٧	٠,٤٣٢٠	١٠,٦٨٠٠	٠,٢٣٨٤	٢,٤٥٥٨	-٠,٥٩١١	٦,٤٠٩٢
	4	١,٠٥١٩	٠,٠٧٥٦	٠,٠١٣٣	٠,١٠٢٢	٠,٥٨٣١	-٢,٧٦٤٤	٠,٠٢٣٩	-٠,٦٠٤٢	٠,٩٤٢٢	-١,٩٧٤٤
	5	-٥,٣٦٨٦	-٠,٠٨٠٠	-٠,٧٨٦٧	-٠,٤٧٥٦	-٠,٨١٢٤	-٣,٢٩٧٨	-٠,٣٣٣٦	-١,٢٦٣٣	-٢,٤١٣٣	-١,٧٠٨٣
$S.E.(\hat{g}_i - \hat{g}_j)$		١,٠٢١٦	١,٢٩٣٤	٠,٢١٤١	٠,١٨٨٥	٠,٢١٥١	١,٢٢١٦	٠,١٠٨٠	٠,٤٩٨١	٠,٧٤٧١	١,١٧٣٠
Tester	6	٦,٩٣٦٣	-٦,٣٠٦٧	-٠,١١٥٦	٠,٠٥٣٣	١,٦٤٧٦	١,٩٥١١	٠,١٥٥٠	٠,٢٣١٩	٠,١٤٦٧	٠,٤٢٥٠
	7	-١,٤٤٥٥	٢,٠٩٣٣	-٠,٢٢٢٢	٠,٠٩٣٣	-٠,٧٢٣١	-٣,٥٠٢٢	-٠,١٢٤٩	-٠,٩٨١٣	-٠,٦٦٦٧	-٢,٠٠١٠
	8	-٥,٤٩٠٨	٤,٢١٣٣	٠,٣٣٧٨	-٠,١٤٦٧	-٠,٩٢٤٤	١,٥٥١١	-٠,٠٣٠١	٠,٧٤٩٤	٠,٥٢٠٠	١,٥٧٦٠
$S.E.(\hat{g}_i - \hat{g}_j)$		٠,٧٩١٣	١,٠٠١٩	٠,١٦٥٨	٠,١٤٦٠	٠,١٦٦٦	٠,٩٤٦٣	٠,٠٨٣٧	٠,٣٨٥٩	٠,٥٧٨٧	٠,٩٠٨٦
١×٦		٠,٦٧٤	-١,٨٢٧	-٠,٢٤٠	٠,٢٣٦	-١,٠٩٤	٢,٣٨٢	٠,١٥٠	٢,١١٧	٠,٨٩٨	٤,٣٤٩
٢×٦		-٥,٢٣٢	٠,٦٨٤	٠,٠٩٣	-٠,٨٧٦	٠,٧٥٠	-١,٨٨٤	٠,٢٠٧	-٠,٠٤٣	٠,٢٥٣	-٠,١٥٦
٣×٦		٢٣٦٨	-٠,٢٤٩	-٠,١٧٣	-٠,٣٨٧	٠,٦٤٨	-٢,٥٧٣	-٠,٣٧٠	-٢,٢٤٣	-١,٧٠٢	-٤,٢٥١
٤×٦		٥,٥٥٦	-٠,٨٤٩	٠,٤٢٧	١,١٢٤	١,١٣٠	٣,٦٧١	-٠,٢٠٩	٠,٧٧٠	١,٠٣١	١,١٩٢
5×٦		-٣,٣٦٥	٢,٢٤٠	-٠,١٠٧	-٠,٠٩٨	-١,٤٣٤	-١,٥٩٦	٠,٢٢٣	-٠,٦٠١	-٠,٤٨٠	-١,١٣٤
١×٧		٠,٩٩١	٠,٩٠٧	٠,٢٦٧	-٠,٢٠٤	٠,٦١٦	-١,٤٣١	-٠,٠٨٣	-٠,٨٥٦	-١,٠٨٩	-١,٣٠٠
٢×٧		١,٣٥٧	-١,٦٤٩	٠,١٣٣	٠,٠١٨	٠,٤٥٩-	٠,٤٣٦	-٠,١٧٤	-٠,٢٩٠	-٠,٨٠٠	-٠,٣١٣
٣×٧		-١,٠٨٧	١,٢١٨	-٠,١٣٣	٠,١٠٧	-٠,١٩٥	٥,٦٨٠	٠,٢٨١	٢,٠٨٧	١,٦٤٤	٣,٩٩٢
٤×٧		-١,٧٠٤	٠,٦١٨	-٠,٥٣٣	-٠,٠٤٩	-٠,٥٩٢	-٣,١٤٢	٠,٠٨٨	-٠,٧٤٠	١,٥١١	-٢,٥٧٣
٥×٧		٠,٤٤٣	-١,٠٩٣	٠,٢٦٧	٠,١٢٩	٠,٦٣٠	-١,٥٤٢	-٠,١١٢	-٠,٢٠١	-١,٢٦٧	٠,١٩٣
١×٨		-١,٦٦٤	٠,٩٢٠	-٠,٠٢٧	-٠,٠٣١	٠,٤٧٨	-٠,٩٥١	-٠,٠٦٧	-١,٢٦٠	٠,١٩١	-٣,٠٥٠
٢×٨		٣,٨٧٥	٠,٩٦٤	-٠,٢٢٧	٠,٨٥٨	-٠,٢٩١	١,٤٤٩	-٠,٠٣٣	٠,٣٣٣	٠,٥٤٧	٠,٤٦٩
٣×٨		-١,٢٨١	-٠,٩٦٩	٠,٣٠٧	٠,٢٨٠	-٠,٤٥٣	-٣,١٠٧	٠,٠٨٩	٠,١٥٦	٠,٠٥٨	٠,٢٥٩
٤×٨		-٣,٨٥٢	٠,٢٣١	٠,١٠٧	-١,٠٧٦	-٠,٥٣٨	-٠,٥٢٩	٠,١٢٢	-٠,٠٣٠	-٢,٥٤٢	١,٣٨١
٥×٨		٢,٩٢٢	-١,١٤٧	-٠,١٦٠	-٠,٠٣١	٠,٨٠٤	٣,١٣٨	-٠,١١١	٠,٨٠٢	١,٧٤٧	٠,٩٤١
$S.E.(\hat{g}_i - \hat{g}_j)$		١,٧٦٩٥	٢,٢٤٠٣	٠,٣٧٠٨	٠,٣٢٦٦	٠,٣٧٢٦	٢,١١٦٠	٠,١٨٧١	٠,٨٦٢٨	١,٢٩٤٠	٢,٠٣١٧

1,2,3,4,5,6,7,8 Symblos of parents

c. Heterosis:

Heterosis effects evaluated in relation to mid – parent value are presented in table (4), these effects were observed in all the analyzed characters but the heterotic for value showed a significant variation from character to character and from hybrid to another among the same character according to (t) test from table (4): A hybrid(1×6) showed a highly significant values for flag leaf area (11.422) cm^2.,plant height(-9.367) cm; no. of grains$spike^{-1}$(8.183),100- grain weight(2.699) gm.,and harvest index (5.378)% from hybrid (4×6); flag leaf area (21.163) cm^2 plant height (-8.233) cm spike length (1.183) cm, no. of spikelet's$spike^{-1}$(3.188), no. of grain (8.083) while (3x7) showed from parents

Table (4): Heterosis from mid parents by (line x tester) for studied characters:

hybrid	Flag leaf area (cm^2)	Plant height (cm)	No. spike $plant^{-1}$	No. spikelet's $spike^{-1}$	Spike length (cm)	No. grains $spike^{-1}$	100 grains weight (gm)	Grain yield $plant^{-1}$ (gm)	Biological yield (gm)	Harvest index %
١×٦	**١١,٤٢٢	-**٩,٣٦٧	-٠,٠٦٧	٠,١٧٢	٠,١٦٧	**٨,١٨٣	**٢,٦٩٩	١,٤٠٠	**٥,٣٧٨	٠,١٨١
٢×٦	**٤,٤٧٢	-٢,٧١٧	**٠,٩١٧	**٢,٥٧٥	-**١,٢٨٣	١,٥١٧	٠,٨١٤	٠,٤٣٣	١,٧٢٦	-٠,٠٣٣
٣×٦	**١٥,٩٥٣	-**٧,٨٣٣	-٠,٢٣٣	**٢,٢٢٧	-٠,٣٦٧	*٤,٧٦٧	-٠,٥٦٨	-١,٧٨٣	-٠,٤٠١	-٠,٢٦٠
٤×٦	**٢١,١٦٣	-**٨,٢٣٣	٠,٦٠٠	**٣,١٨٨	**١,١٨٣	**٨,٠٨٣	١,١٣١	١,٠٣٣	٢,١٤٦	-٠,٠٩٢
5×٦	**٨,٣٢٧	-٣,١٠٠	-٠,٢٦٧	-**٠,٨٩٠	-٠,٥١٧	٠,٣١٧	-٠,٢٤٩	-١,٤٦٧	٠,٢٤٨	-٠,١١١
١×٧	-٠,٥٩١	٠,٧٥٠	-٠,٢٥٠	-٠,٠٣٨	٠,٣٠٠	٠,٢١٧	-١,٥٠٨	-١,٦١٧	-٢,٦٢٢	٠,٢٧١
٢×٧	-١,٢٦٨	٢,٣٣٣	٠,٢٦٧	-٠,٥٥٥	٠,١٨٣	-٠,٣١٧	-٠,٦٦٧	-١,٦٥٠	-٠,٧٨٢	-٠,٠٩٢
٣×٧	٠,١٦٨	١,٠١٧	-*٠,٨٨٣	-٠,٥٣٧	*٠,٧٠٠	**٨,٨٦٧	**٢,٥٢٨	٠,٥٣٣	**٥,٤٩١	**٠,٧١٤
٤×٧	١,٥٧٤	٠,٦١٧	-**١,٠٥٠	-٠,٤٥٥	٠,٥٨٣	-٢,٨٨٣	-١,٦١٣	٠,٤٨٣	-*٣,٩٧٠	**٠,٥٢٨
٥×٧	-٠,١٩٤	٠,٩٥٠	-٠,٥٨٣	-*٠,٧٤٧	٠,٢٨٣	-٣,٧٨٣	-١,٠٨٣	-**٣,٢٨٣	-٠,٧٧٦	-٠,١٢٣
١×٨	-**٧,٠٢٢	٠,٤٣٣	-٠,١٥٠	٠,٠٦٣	٠,١٨٣	٠,٧٥٠	-١,٠٧٠	٠,٣٦٧	-٢,٦٢٣	٠,٠٩٣
٢×٨	-٢,٥٢٦	*٤,٦١٧	٠,٣٠٠	-٠,١٤٧	*٠,٧٣٣	٠,٧٥٠	٠,٧٩٨	٠,٤٠٠	١,٧٤٩	-٠,١٤٣
٣×٨	-*٣,٨٠٣	-١,٥٠٠	-٠,٠٥٠	-٠,٥٥٥	٠,٥٨٣	٠,١٣٣	١,٤٤٠	-٠,٣٥٠	٣,٥٠٧	٠,٣٢٩
٤×٨	-**٤,٣٥٠	-٠,١٠٠	-٠,٠١٧	-٠,١٦٠	-*٠,٧٣٣	-٠,٢١٧	-٠,٠٦٢	-*٢,٨٦٧	١,٧٣٤	*٠,٣٦٩
٥×٨	-١,٤٩٢	٠,٥٦٧	-٠,٦١٧	-٠,٣٣٢	-٠,١٦٧	٠,٩٥٠	٠,٧٦٢	٠,٤٣٣	١,٧٢١	-٠,٣١٥

* and ** Level 5% and 1% respectively.

ahighly significant heterosis value at no. of grains spike^{-1}(8.867), 100-grains – weight (2.528) gm., biological yield(5.491)gm.and harvest index (0.714%).It was concluded that most of these hybrid have the same parent (6) which was much superior than any other parents as well as it played an important role in transferring the genes that controlled such characters above to it's hybrids, such results corresponding with (Abdullah et al. , 2002); (Chowdhry et al., 2005);(Aknincl 2009),(Beche et al. ,2013).

d. Genetic and Phenotypic distances between parents

From the 24 RAPD decamer primers used in the PCR amplification the total number of the amplified bands (141 bands) are obtained, 101 of which were polymorphic, the DNA fragment size are ranged between 120 - 1500 bp, the polymorphism of RAPD markers are high (70.18%) and it was adequate to discriminate each variety, this gave an average of 26.740 bands for each primer combination. The dissimilarity matrix table (5)are obtained based on Nei and Li coefficient.. Genetic distances among the (8) parents ranged from the lowest value of(0.167) which was between p_2 and p_4 to the highest(0.629),between p_3 and p_6 .Theaverage value was (0.350) table (5).Estimated values of PD for morphological characters varied from (0.000604) between p_7 and1 The highest value (0.0227) between p 2 and p4.

Table (5): Genetic and phenotypic distances between 8 varieties of Tetraploid wheat on RAPD analysis:

GD								
Parents	1	2	3	4	5	6	7	8
1	0.00							
2	0.199	0.00						
3	0.177	٠.208	0.00					
4	0.222	0.167	0.218	0.00				
5	0.278	0.221	0.345	0.179	0.00			
6	0.504	0.337	0.629	0.389	0.214	0.00		
7	0.380	0.315	0.385	0.246	0.263	0.301	0.00	
8	0.416	0.388	0.499	0.314	0.328	0.314	0.180	0.00

PD								
Parents	1	2	3	4	5	6	7	8
1	0.00							
2	0.00279	0.00						
3	0.0193	0.00896	0.00					
4	0.00321	0.0227	0.0154	0.00				
5	0.00985	0.00408	0.00846	0.00298	0.00			
6	0.00277	0.00324	0.0157	0.00842	0.0139	0.00		
7	0.000604	0.00313	0.0196	0.00516	0.0118	0.00136	0.00	
8	0.0022	0.00202	0.0118	0.00365	0.00569	0.00393	0.0024	0.00

e.Correlation analysis:

One of the most important aims of this work was to determine the relationship between genetic diversity GD evaluated on the basis of RAPD marker and phenotypic distance PD of parental forms for grain yield, SCA and heterosis at mid – parents,(table6).

Table (6): Correlation coefficient between genetic (GD) and phenotypic distances (PD) of parents and specific combining ability as well as heterosis in grain yield.

Parameters		
GD	SCA	
	Heterosis	
PD	SCA	
	Heterosis	

*. Correlation is significant at the 0.05 level.

ns. No significant correlation.

Table (6) Demonstrate that (GD) as well as (PD)were not significantly correlated with SCA, (PD) also show no significant correlation with heterosis, wherase, the correlation coefficient between (GD) and heterosis for this character had apositive and significant value. The GD between varieties may be defined on the basis of molecular and morphological (phenotypic) markers (Shamsulddin, 1985); (Melchinger*et al.* 1990);(Diers*et al.* 1996). The investigation of distance based on phenotypic characters may be burdened with an error resulting from the dependence of the expression of these characters on environmental conditions. Molecular marker 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 wheat, (Martine *et al.* 1995). Other studies in maize did not showed any association between combining ability and (GD),(Melchinger*et al.*, 1990);(Dudley *et al.*, 1991). In turn (Corbellini *et al.*, 2002) found statically significant correlation between (GD) based on molecular markers and mid – parents heterosis value for grain yield, but (Krystkowiak K. *et al.*, 2009)noticed that these correlations were too low to be of predictive value.

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علاقة البعد الوراثي والمظهري مع المقدرة الاتحادية الخاصة وقوة الهجين للتراكيب الوراثية الأبوية في الحنطة الرباعية

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الخلاصة

تهدف الدراسة إلى تقييم العلاقة بين البعد الوراثي والمظهري للآباء والمقدرة الاتحادية الخاصة وقوة الهجين عن متوسط الابوين. استخدم في هذه الدراسة ثمانية آباء للحنطة الرباعية (*Triticum durum* Desf.) وخمسة عشر هجيناً استحصلت من النظام التزاوجي (السلالة × الفاحص) .زرعت الآباء والهجن في محطة التجارب النباتية لكلية الزراعة والغابات في جامعة الموصل بثلاث مكررات وبموجب تصميم القطاعات العشوائية الكاملة (R. C. B. D) خلال موسمي النمو (2010 – 2011) و (2011 – 2012).

قدرت المقدرة الاتحادية الخاصة وقوة الهجين عن متوسط الابوين للصفات الكمية المدروسة. وقدرالبعد الوراثي باستخدام المؤشرات بالأعتماد على طريقة التضاعف العشوائي المتعدد الاشكال للحامض النووي الرايبي منقوص الاوكسجين (RAPD).كانت النسبة بين مكونات التباين للمقدرة الاتحادية العامة إلى مكونات التباين للمقدرة الاتحادية الخاصة أقل من الواحد الصحيح ولجميع الصفات المدروسة مما يشير إلى ان الفعل غير الاضافي للجينات هو المسيطر على وراثة الصفات المدروسة جميعها . أظهرت معظم الهجن قيماً معنوية عالية بالاتجاه المرغوب للمقدرة الاتحادية الخاصة ولقوة الهجين عن متوسط الابوين لمعظم الصفات المدروسة . بيّن التحليل العنقودي (Abdullah et al.,2013) الذي تم تشكيله بين الآباء الثمانية باستخدام طريقة المجموعات الزوجية غير المزانة (UPGMA) أعلى قيمة للبعد الوراثي بين الابوين3(1–Azeghar) 6 (1– Doma) وأقل قيمة بين الابوين2 (Leeds) و 4(65 –Acsad) استناداً إلى معاملات التشابه المحسوبة بطريقة Nei and Li (1979). أما قيمة البعد المظهري (PD) فتم احتسابها بطريقة(1936) Mahalanobis .لم يظهر ارتباط معنوي بين قيم كل من البعد الوراثي (GD) والبعد المظهري (PD) مع المقدرة الاتحادية الخاصة للهجن ، وتبين انعدام الارتباط المعنوي للبعد المظهري مع قوة الهجين عن متوسط

الابوين . في حين أظهر البعد الوراثي ارتباطاً موجباً معنوياً مع قوة الهجين عن متوسط الابوين.

الكلمات المفتاحية: قوة الهجين عن متوسط الأبوين ،مؤشرات التضاعف العشوائي للحامض النووي منقوص الأوكسجينRAPD ،معلمات الDNA.

البحث مستل من اطروحة الدكتوراه للباحث الثاني