توصيف وتقييم بعض التراكيب الوراثية في القمح تحت ظروف بيئية متباينة
٢ – التحليل البياني

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الملخص العربى

أجريت هذه الدراسة خلال موسمين متتالين ٢٠٠٨/ ٢٠٠٩ و ٢٠١٠/٢٠٠٩ حيث استخدم لهذه الدراسة ثمانية تراكيب وراثية من قمح الخبز متباعدة المصدر منه خمسة سلالات بلدية قديمة وثلاث أصناف محلية، تم التهجين بين هذه التراكيب الوراثية في موسم ٢٠٠٩/٢٠٠٨ باستخدام طريقة التهجين التبادلي في اتجاه واحد وفي موسم ٢٠٠٩ / ٢٠١٠ تم تقييم الآباء والهجن الناتجة منها في تجربتين مستقلتين ذات قطاعات كاملة العشوائية في ثلاث مكررات بكل من محطتي الجميزة والمطاعنة. تم تحليل البيانات باستخدام طريقة الهجن التبادلية (هيمن ١٩٥٤) وتم التحليل البياني بطريقة Johanson and Aksel. لعام ١٩٥٩ م .

ولقد أجري هذا البحث بهدف : تقدير مكونات التباين الوراثي باستخدام طريقة هيمن ١٩٥٤

وكانت الصفات المدروسة ميعاد طرد السنابل ، ميعاد النضج ، فترة امتلاء الحبوب ، طول النبات ، عدد السنابل في النبات، عدد السنيبلات في السنبلة، وزن الألف حبة ، عدد الحبوب في السنبلة ، محصول النبات الفردي من الحبوب و نسبة البروتين . وفيما يلي ملخص لأهم النتائج المتحصل عليها :

١- كان التباين الوراثي المضيف ($\widehat{D}$) عالي المعنوية لمعظم الصفات المدروسة في موقعي الجميزة والمطاعنة عدا صفة عدد السنابل بالنبات لموقعي الجميزة والمطاعنة، و كلا ٍمن صفتي عدد السنيبلات بالسنبلة و محصول النبات من الحبوب لموقع الجميزة كما كان التباين الوراثي السيادي $\widehat{H}_1$ و $\widehat{H}_2$ معنويا ومرتفعا في قيمته عن الجزء المضيف وذلك لمعظم الصفات المدروسة وذلك في موقعي الجميزة والمطاعنة.

٢- أظهرت قيم متوسط السيادة ($\widehat{H1}/\widehat{D}$)$^{1/2}$ إلي وجود السيادة الفائقة لجميع الصفات تحت الدراسة لموقعي الجميزة والمطاعنة.

٣- كانت قيم التوريث (الكفاءة الوراثية) بمعناها الضيق مرتفعة لكل من طول النبات، وزن الألف حبة ،عدد الحبوب بالسنبلة لموقعي الجميزة والمطاعنة بينما كانت عالية لصفة فترة امتلاء الحبوب ونسبة البروتين لموقع الجميزة.

٤- أوضح التحليل البياني أن السيادة التامة كانت متحكمة في وراثة كل من ميعاد طرد السنابل لموقع المطاعنة وعدد السنابل بالنبات ، نسبة البروتين لموقع الجميزة . بينما كانت السيادة الجزئية في وراثة صفات فترة امتلاء الحبوب ، عدد السنيبلات بالسنبلة لموقع الجميزة وصفة طول النبات ، عدد الحبوب بالسنبلة لموقع المطاعنة . وكذلك السيادة الفائقة في صفات ميعاد طرد السنابل وطول النبات وعدد الحبوب بالسنبلة لموقع الجميزة بالإضافة إلي فترة امتلاء الحبوب وعدد السنابل بالنبات وعدد السنيبلات بالسنبلة ونسبة البروتين بالنسبة لموقع المطاعنة بينما كانت السيادة فائقة في وراثة صفات ميعاد النضج ووزن الألف حبة، محصول النبات الفردي من الحبوب لموقعي الجميزة والمطاعنة.

CHARACTERIZATION AND EVALUATION OF SOME WHEAT GENOTYPES UNDER DIFFERENT ENVIRONMENTAL CONDITIONS 2- GRAPHICAL ANALYSIS

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ABSTRACT: *Gene action and heritability were studied in a 8 x 8 diallel set of bread wheat for heading date, maturity date, grain filling period, plant height, number of spikes per plant, number spikelets per spike, 1000-grain weight, number of kernels per spike, grain yield per plant and protein percentages under Gemmeiza location (normal temperature) and Mataana location (high temperature). The additive genetic variance ($\hat{D}$) was found to be highly significant for traits studied at the two different locations except number of spikes per plant at the two locations, however number of spikelets per spike and grain yield per plant at Gemmeiza location. The dominance genetic variation $\hat{H}_1$ and $\hat{H}_2$ were found to be highly significant for most traits studied at the two different locations. Moreover, the estimated values dominance components $\hat{H}_1$ and $\hat{H}_2$ were found to be greater in their magnitude than the corresponding additive genetic variations ($\hat{D}$) for most traits under investigation. The average degree of dominance ($\hat{H}1/\hat{D}$)1/2 was greater than unity at the two locations for all traits under investigations. High to moderate heritability values were detected for; plant height, 1000-grain weight and number. of kernels per spike at the two locations as well as grain filling period and protein percentage at Gemmeiza location. The graphical analysis demonstrated the existence of complete dominance for heading date at Mataana location as well as number of spikes per plant and protein percentage at Gemmeiza location. Partial dominance was also found for grain filling period, number of spikelets per spike at Gemmeiza location as well as plant height and number of kernels per spike at Mataana location. Over dominance was detected for heading date, plant height and number of kernels per spike at Gemmeiza location as well as grain filling period, number of spikes per plant, number of spikelets per spike and protein percentage at Mataana location., also maturity date, 1000-grain weight, grain yield per plant at Gemmeiza and Mataana locations.*

Key words: Wheat, Diallel cross, Gene action, Heritability and Graphical analysis.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the first important and strategic cereal crop for the majority of world's populations. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. Old bread wheat (landrace) an important genetic resource that can be used to improve modern varieties (Feldman and Sears 1981) by introducing new alleles or combinations of genes. This heterogeneity has not been analysed systematically (Nevo and Payne 1987) and such landraces may include genetic sources of biotic and a biotic stress resistance, especially in environments not tested in major breeding programmes, and also quality, yield and resistance genes. Heat stress is an important constraint to wheat productivity affecting different growth stages specially anthesis and grain filling. It has already been established that heat stress can be a significant factor in reducing the yield and quality of wheat (Stone and Nicolas 1995). Hayman (1954) suggested certain assumptions which need to be fulfilled for valid diallel analysis. These include homozygous parents, diploid segregation, no reciprocal differences, no genotype environmental interaction, no epistasis, no multiple alleles and uncorrelated gene distribution. Failure of any one or any combinations of the assumptions invalidates to some degree the conclusion obtained by means of analysis. The objective of the present study is to establish the different genetic components according to Hayman (1954).

MATERIALS AND METHODS
Plant materials

Five promising landraces for heat tolerance were collected from diverse areas of Egypt as well as three cultivars used to establish the experimental materials for this investigation. The names, pedigree and source of these varieties and lines are presented in Table (1).

Filed experiments

A diallel cross set was carried out among the eight parents in 2008/2009 growing season. The parental genotypes and their possible 28 crosses were sown in 2009/2010 under two location , which would be mentioned in the text as Gemmeiza location (L1) and Mataana location (L2), respectively. The two experiments were arranged in a randomized complete block design with three replicates per each location. Each plot comprised single rows 3 meters long with 30 cm. between rows, plants within rows were 10 cm. apart allowing a total of 30 plants per plot. Normal agricultural practices were applied as usual for the ordinary wheat fields in the area. Ten guarded plants were randomly selected from each plot for subsequent measurements as follows heading date, maturity date, grain filling period, plant height, number of spikes per plant, number spikelets per spike, 1000-grain weight, number of kernels per spike, grain yield per plant and protein percentage.

Statistical procedures

The obtained data were statistically analyzed for analysis of variance by using Hayman (1954).

Point of regression analysis for Wr and Vr:

Different types of gene action were interpreted strictly from the visual inspection of the Wr/Vr of each trait as outlined by (Mather and Jinks, 1971).

The standardized deviation graphical analysis:

The relationship of Wr with Vr provides some very useful informations. The analytical methods were based largely on Hayman (1954) i.e. the regression of parent – offspring (array) covariance (Wr) on parental array variances (Vr) and were supplemented by plotted (Yr) and the sum (Wr + Vr). (Johanson and Aksel 1959).

Table (1). Name, pedigree and source of the studied bread wheat genotypes.

Code	Name	pedigree	Source

No.			
1	Line 1	Landraces	New valley
2	Line 2	Landraces	Sohag
3	Line 3	Landraces	Sohag
4	Line 4	Landraces	Sohag
5	Line 5	Landraces	Qena
6	Sahel 1	NS732/PIMA//Veery"S"#5	Local variety
7	Sids 1	HD2172/Pavon "S" // 158-57 Maya 74 "S" Sd 46-45d-2Sd-1Sd-0Sd	Local variety
8	Gemmeiza 9	ALD"s"/HUAC//CMH74A-630/SX	Local variety

RESULTS AND DISCUSSION

The mean values of each cross were used to estimate the different genetic components of variation $\hat{D}$, $\hat{F}, \hat{H}_1, \hat{H}_2$, $\hat{h}^2$ and $\hat{F}$ as defined by Hayman (1954). The different genetic components of variation and their portions for all traits studied at Gemmeiza location (L2) and Mataana location (L2) are given in Table (2).

The additive genetic variance ($\hat{D}$) was found to be significant for all traits studied at the two different locations except number of spikes per plant at the two locations, and number of spikelets per spike and grain yield per plant at L1, revealing that the importance of additive effects in the inheritance of most traits studied. These results are in harmony with those previously obtained from the combining ability analysis. These results are in agreement with those obtained by Ahmad *et al.* (2011).

The dominance genetic variation $\hat{H}_1$ and $\hat{H}_2$ were found to be significant for all traits studied at the two different locations. Moreover, the estimated values dominance components $\hat{H}_1$ and $\hat{H}_2$ were found to be greater in their magnitude than the corresponding additive genetic component ($\hat{D}$) for most traits under investigation. These results indicated that the dominance genetic variations had greater role in the inheritance of most traits under studied. This contradiction between the two different approaches could be due to the presence of the non – allelic interactions, Mather and Jinks (1982) stated that the additive genetic variations ($\hat{D}$) would be affected by the presence of the non – allelic interactions. Similar results were previously obtained by Ullah *et al.* (2010) and Ahmad *et al.* (2011).

A positive $\hat{F}$ value indicates an excess of dominant genes while a negative value indicates an excess of recessive genes. In the present investigation, the positive values of $\hat{F}$ showed that there were more dominant genes present in the parents than recessive alleles, irrespective of whether these dominant alleles are increasing or decreasing in their effects for all traits studied under the two different locations except plant height under L2 and number of spikes per plant and grain yield per plant at L1 . The estimated F values were found to have different signs at the two different locations respectively. Consequently, the excess of genes either dominant or recessive controlling these three traits were not consistent at the two different locations, susceptible to environmental changes and the degree of dominance or recessiveness may be determined by growing conditions.

The overall dominance effects, as the algebra sum over all loci in heterozygotes in all crosses symbolized as ($\hat{h}^2$) were found to be significant for plant height at the two different locations, 1000- grain weigh , number of kernels per spike at L1, indicating the prevalence of dominant effect over all loci in all crosses. Insignificant estimates of ($\hat{h}^2$) were detected for heading date, maturity date, grain filling period, number of spikes per plant, number of spikelets per spike , grain yield per plant and protein percentage at the two different locations and 1000- grain weight and number of kernels

per spike at L2, and that would indicate the absence of the dominance effect over all loci in the heterozygotes in all crosses and that could be due to presence of a considerable amount of canceling dominance effects in the parental varieties. Similar results were previously obtained by Okan (2009).

The average degree of dominance $(\hat{H}1/\hat{D})^{1/2}$ was found be greater than unity at the two locations for all traits under investigations, indicating the presence of over dominance for these traits. Similar results were previously obtained by Seleem and Koumber (2011).

When positive and negative genes are equally distributed in the parental varieties, the proportion $(\hat{H}2/4\hat{H}1)$ is expected to be 0.25. The estimated values of $(\hat{H}2/4\hat{H}1)$ were found to be close to this value (0.25) for most traits under study The estimated values of $(\hat{H}2/4\hat{H}1)$ however, were found to be below (0.25) for the remainder of the characters studied, indicating that positive and negative alleles were not equally distributed among the parents in these traits Similar results were previously obtained by Seleem and Koumber (2011).

Table 2

Table 2

Table 2

Estimates of the ratio of dominant to recessive alleles in the parents (K_D / K_R) were found to be more than unity for all traits studied at the two different locations, except plant height at L2 and number of spikes per plant and grain yield per plant at L1 confirming the existence of more dominant than recessive genes in the parents as previously discussed concerning the positive values of ($\widehat{F}$) parameter. The degree of dominance or recessiveness may be determined by growing conditions.

The correlation coefficient (r) between the parental values (Y_r) and the parental order of dominance (Wr + Vr) for all characters studied at the two different locations are presented in Table (2). If the correlation is negative, it means the parents containing most increasing genes have the lowest values of (Wr + Vr) and thus contain most dominant genes, and the correlation would be positive if the case is reverse. Thus, on this basis, it could be concluded whether or not the increasing or decreasing genes are the dominant ones. Also, when the correlation between parental mean values and (Wr + Vr) is small, it suggests that the dominant genes with positive and negative effects in the parental line could be in equal proportions. If the correlation coefficient is high, the most dominant alleles will act in one direction and most recessive alleles will act in the opposite one (Hayman, 1954). In the present study, the correlation coefficients were found to be negative for most traits studied except grain filling period, however number of kernels per spike and protein percentage at L1 also number of spikes per plant , number of spikelets per

spike and grain yield per plant at L2, only two of these values were found to be significant, and that would indicate the prevalence of dominant genes. It is of interest to mention that the sign of the correlation coefficient values for number of spikes per plant, number of kernels per spike, grain yield per plant and protein percentage were found to be different at the two different locations which would ascertain that dominant genes could be increases of decreases according to the growing environmental conditions. The estimated values of correlation coefficient were found to be low for grain filling period, number of spikelets per spike and protein percentage at L2 and number of kernels per spike and grain yield per plant at L1 and L2 which would indicate that the dominant genes of positive and negative effects in the parents could be in equal proportion.

Heritability

Heritability is one of the most important parameter for determination the genetic behavior of a metric character. It is expressed as the proportion of the variance attributed to the average effect of genes. However, the most important function of the heritability in the genetic study of quantitative character as its predictive role. It expresses the reliability of phenotypic value as a guide to the breeding value. The possible advance through selection based on phenotypic value can therefore, be predicted only from knowledge of the degree of correspondence is measured by heritability estimates. The heritability estimates enter into almost every formula connected with breeding methods and many practical decisions about

the techniques followed depends on its magnitude.

Heritability in narrow sense was estimated for all traits studied at the two different locations are presented in Table (2). High to moderate heritability values were detected for heading date, plant height, 1000-grain weight and number. of kernels per spike at the two different locations, and grain filling period and protein percentage date at L1. Therefore, the genetic system controlling these traits might be attributed to additive effects of genes. Consequently, pedigree selection program for these traits might be quite promising. For other traits, low heritability in narrow sense was detected. Therefore, breeding programs towards pure line selections seemed to be meaningless (Allard and Bradshaw 1964). However, the bulk method program for these traits might be quite promising.

Graphical analysis:
Heading date:-

The graphical analysis of heading date at the two different locations are presented in Figures (1a and 1b). The Wr on Vr regression lines cut the Wr axis below the origin points at Gemmeiza location (L1) and nearly the origin points at Mataana location (L2), which would indicate the presence of over and complete dominance in the inheritance of this trait at L1 and L2 respectively. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-allelic interaction in the performance of this character. Standardized deviation of Yr and of (Wr + Vr) are plotted in Figs. (1c and 1d) for both L1 and L2 respectively. The correlation coefficients between these variables were found to be negative but not significant at the two different locations, suggesting a tendency (not significant) of recessiveness to be associated with high numbers of days to heading (lateness) and dominance to be associated with low number of days to heading (earliness). It is obvious from these two figures that the parental 2,6 and 5 had the lowest number of days to start heading and first two parents possessed more recessive genes, however,

the third parent possessed more recessive gene at Gemmeiza and more dominant gene at L2. Over dominance was found by El-Borhamy *et al.* (2008).

Maturity date:

The position of actual regression line was found to be shifted to the right of the unit slope line and below the origin point at the two different locations indicating that F_1 arrays on the average express over dominance. The regression coefficient at the two different locations were found to be highly significant deviate from the unity which might indicate the involvement of non-allelic interaction in the performance of this character. Standardized deviation of Yr and of (Wr + Vr) are plotted in Figs. (2c and 2d) for both L1 location and L2, respectively. The correlation coefficients between these variables were found to be negative but not significant at the two locations, suggesting a tendency (not significant) of recessiveness to be associated with high numbers of days to maturity (lateness) and dominance to be associated with low number of days to maturity (earliness). The parental 2, 5 and 6 were found to have the lowest values of days to maturity at the two locations, with different excess of dominant and recessive genes. Over dominance was found for earliness by El-Borhamy *et al.* (2008).

Grain filling period :

The graphical analysis of grain filling period is given in Figures (3a and 3b). Both partial dominance and over dominance apparently influenced no. of days of grain filling period at L1 and L2 respectively. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-allelic interaction in the performance of this character. Standardized deviation of Yr and of (Wr + Vr) are plotted in Figs. (3c and 3d). The correlation coefficients between these variables were found to be insignificant at the two locations. The parental 1, 4, and 6 have the lowest values of days to grain filling period at the two locations, with different excess of dominant and recessive genes. Partial and over dominance were also obtained by Menshawy (2005).

Plant height:

The graphical analysis of plant height is given in Figures (4a and 4b). The Wr on Vr regression lines were found to be shifted to the right of unit slope line and cut Wr axis below the origin point at L1 and it shifted to the left of unit slope line and cut Wr axis above the origin point at L2, revealing the existence of both over and partial dominance controlling this character, at L1 and L2 respectively. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-allelic interaction in the performance of this trait at two locations. The standardized deviation of given points is illustrated graphically in Figs. (4c and 4d). The correlation coefficients between these variables were found to be insignificant at the two locations. In spite of insignificancy it is obvious from these two figures that parental varieties 1,5 and 6 were found to have the desirable expression of plant height with different excess of dominant and recessive genes. Partial dominance was obtained by Seleem and Koumber (2011). However, over dominance was found by El-Borhamy *et al.* (2008) .

$b= 0.502 \pm 0.061$
$b0= 8.275^{**}$
$b1= 8.222^{**}$

Fig. (1 - a) Heading date (days) - L1.

$r= -0.584$

Fig. (1 - c) Heading date (days) - L1.

$b= o.705 \pm 0.014$
$b0= 50.788^{**}$
$b1= 21.215^{**}$

Fig. (1 - b). Heading date (days) – L2.

$r= -387$
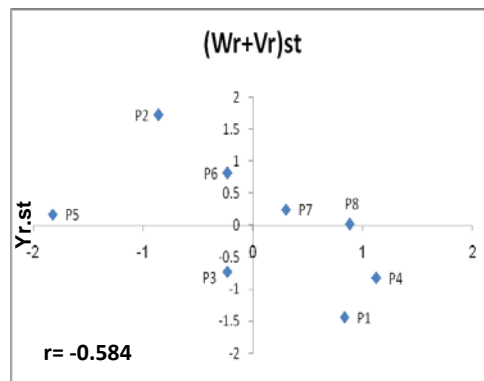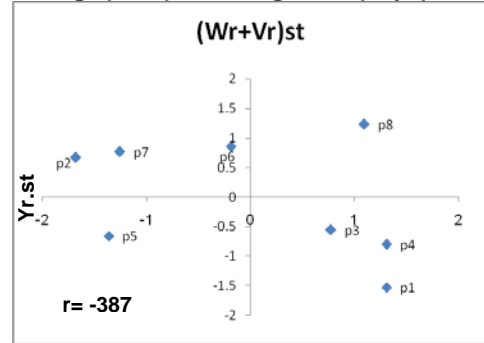
Fig. (1 - d). Heading date (days) – L2.
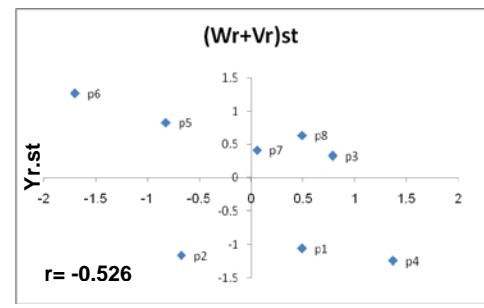
$b= 0.560 \pm 0.057$
$b0= 9.785^{**}$
$b1= 7.687^{**}$

Fig. (2 - a). Maturity date (days) – L1.

$r= -0.526$

Fig. (2 - b). Maturity date (days) – L1.

Fig. (2- b). Maturity date (days) – L2.

b= 0.535 ± 0.007
b0= 73.387**
b1= 63.754**
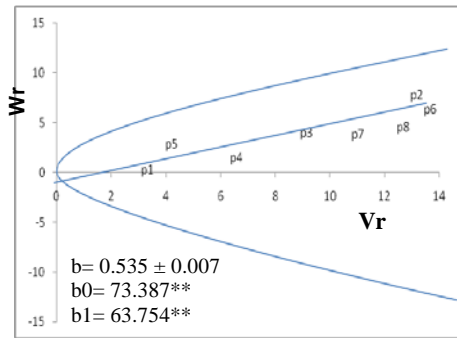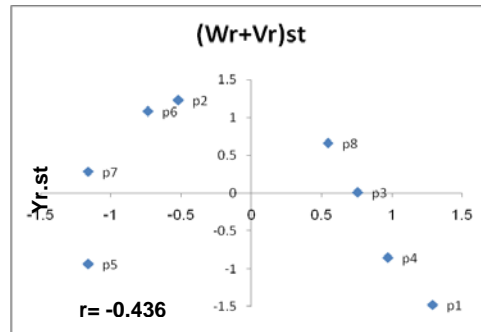
Fig. (2 -d). Maturity date (days) – L2.

r= -0.436

Fig. (3- a) Grain filling period (days)– L1.

b= 0.332 ± 0.041
b0= 8.081**
b1= 16.227 **
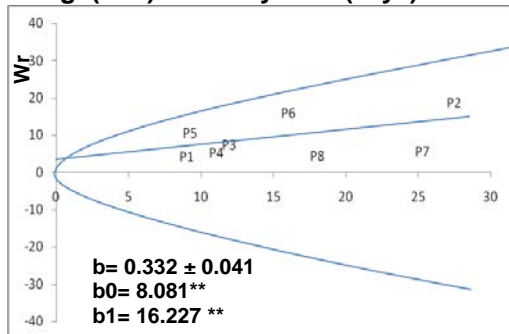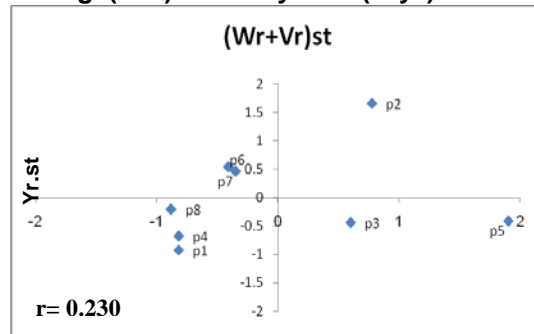
Fig. (3 - c) Grain filling period (days) – L1.

r= 0.230

Fig. (3 - b) Grain filling period (days) – L2.

b= 0.575 ± 0.056
b0= 10.358**
b1= 7.644**

Fig. (3 - d) Grain filling period (days) – L2.

r= -0.034

Fig. (4 - a) Plant height (cm) – L1

b= 0.506 ± 0.017
b0= 29.172**
b1= 28.450**

Fig. (4 - c) Plant height (cm) – L1

r= -0.616

Fig. (4 - b) Plant height (cm) – L2

Fig. (4 - d) Plant height (cm) – L2

Number of spikes per plant:

The Wr and Vr graph of number of spikes per plant is presented in Figures (5a and 5b). Both complete dominance and over dominance apparently influenced no. of number of spikes per plant at L1 and L2 respectively. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-allelic interaction in the performance of this trait at two locations. Standardized deviation of Yr and of (Wr + Vr) are plotted in Figs. (5c and 5d). The correlation coefficients between these variables were found to be insignificant at the two locations. Its is obvious from these two figures that parents 1, 3, 5 and 6 had higher number of spikes per plant with different excess of recessive and dominant genes at the two locations. Over dominance was found by Seleem and Koumber (2011).

Number of spikelets per spike:

The graphical analysis of number of spikelets per spike is given in Figures (6a and 6b). Both partial and over dominance apparently influenced number of spikelets per spike at L1 and L2 respectively. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-allelic interaction in the performance of this character. The standardized deviation of given points is illustrated graphically in Figs. (6c and 6d). The correlation coefficients between these variables were found to be insignificant at L1 and L2. It is observed from Figs. (6c and 6d) that the wheat
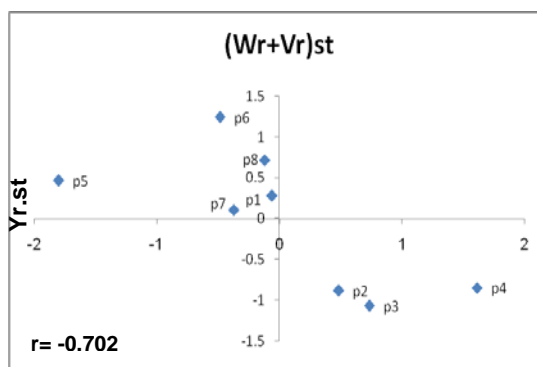
parents 3,2 and 5 had higher number of spikelets per spike with different excess of recessive and dominant genes at the two locations. Over dominance was found by Irshad *et al* (2012) However, partial dominance was previously found by Ullah *et al.* (2010).

1000-grain weight:

The actual regression lines were found to be below the origin points indicating the existence of over dominance in the inheritance of 1000-grain weight under the two different locations. The regression coefficient at the two different locations were found to be significantly deviated from zero but not from unity, indicating that gene system controlling this character could deduced to be additive without the complication of non-allelic interactions. The standardized deviation of given points is illustrated graphically in Figs. (7c and 7d). The correlation coefficients between these variables were found to be negative significant at L1(-0.770*) but not significant at L2 which reflected the consistent association of increasing 1000-grain weight with the excess of dominant genes at L1 . It is observed from Figs. (8c and 8d) that the wheat parents 3, 7 and 8 had higher 1000-grain weight with different excess of recessive and dominant genes at the two locations. Over dominance was previously found by Seleem and Koumber (2011).

Number of kernels per spike:

The graphical analysis of number kernels per spike is presented in Figures (8a and 8b) under the two locations. The regression

lines indicated the existence of partial dominance and over dominance in the inheritance of this trait L1 and L2, respectively. The regression coefficient at L1 were found to deviate significantly from zero at the two different locations and from the value of unity at L2 which would indicate the presence of both additive and non-allelic interactions at L1 and non-allelic interactions at L2. Standardized deviation of Yr and of (Wr + Vr) are plotted in Figs. (8c and 8d). The correlation coefficients between these variables were found to be insignificant at the two locations. It is obvious from these two figures that parents 3 and 6 had the highest desirable expression of number kernels per spike and possessed more dominant genes at the two locations. Over dominance was obtained by Seleem and Koumber (2011). However, partial dominance was obtained by El-Borhamy *et al.* (2008).

Grain yield per plant:

The graphical analysis of grain yield per plant is given in Figures (9a and 9b). The position of actual regression line was found to be shifted to the right of the unit slope line and below the origin point at the two different locations indicating that F_1 arrays on the average express over dominance. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-

allelic interaction in the performance of this character. The standardized deviation of given points is illustrated graphically in Figs. (9c and 9d). The correlation coefficients between these variables were found to be insignificant at the two locations. It is observed from It is obvious from these two figures that parents 1,3 and 6 had higher grain yield per plant with different excess of recessive and dominant genes at the two locations. Over dominance was previously found by Heidari *et al.* (2006). However, partial dominance was previously found by Ullah *et al.* (2010) and Irshad *et al* (2012).

Protein percentage

The graphical analysis of protein percentage is given in Figures (10a and 10b). Both complete dominance and over dominance apparently influenced of protein percentage at L1 and L2 respectively. The regression coefficient at the two different locations were found to be highly significant deviate from the value of unity which might indicate the involvement of non-allelic interaction in the performance of this character. Standardized deviation of Yr and of (Wr + Vr) are plotted in Figs. (10c and 10d). The correlation coefficients between these variables were found to be insignificant at the two locations. It could be reported from these two figures that parents 4and 6 had higher protein percentage with different excess of recessive and dominant genes at the two locations. Over dominance was found by Bebyakin *et al.* (1998).
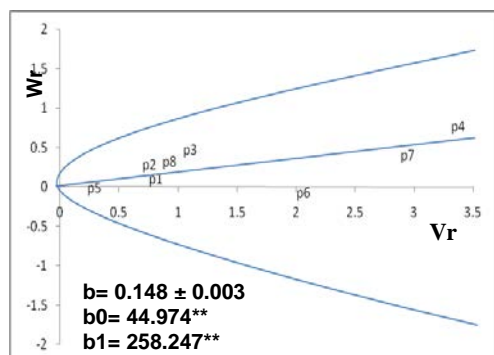

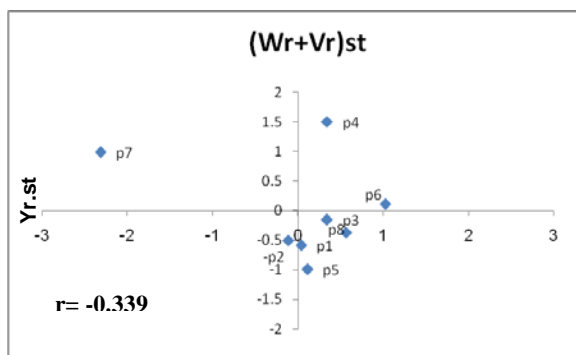**Fig.(5-a) Number of spikes per plant-L1.**

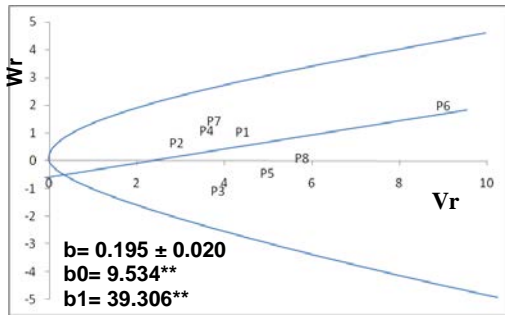**Fig. (5 - c) Number of spikes per plant - L1.**
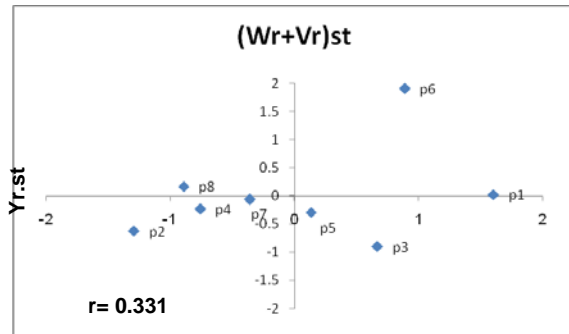
Fig.(5-b) Number of spikes per plant-L2.

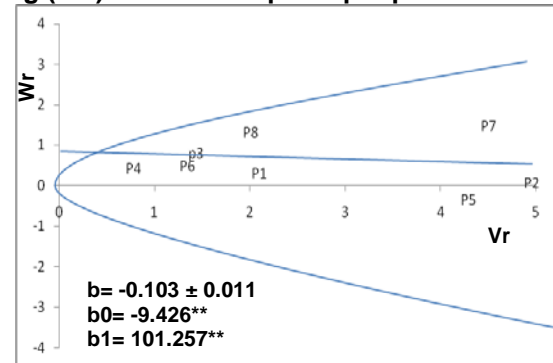Fig. (5 - d) Number of spikes per plant - L2.
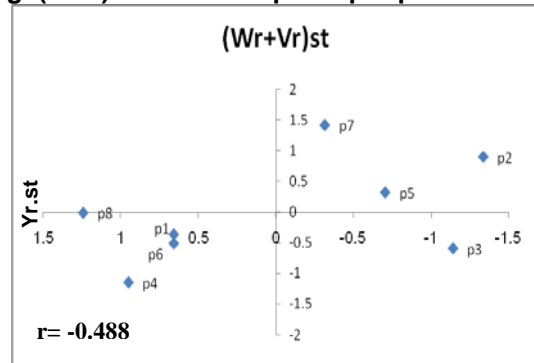

Fig.(6-a) Number of spikelets per spike-L1.

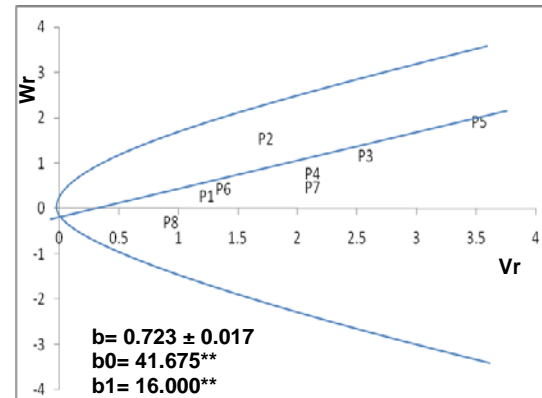Fig.(6-c) Number of spikelets per spike-L1

Fig.(6-b) Number of spikelets per spike-L2.

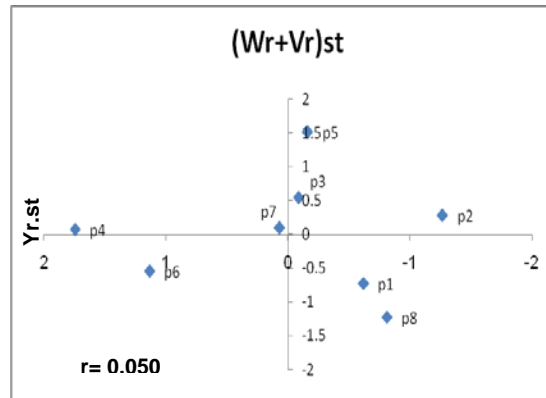Fig.(6-d) Number of spikelets per spike-L2.

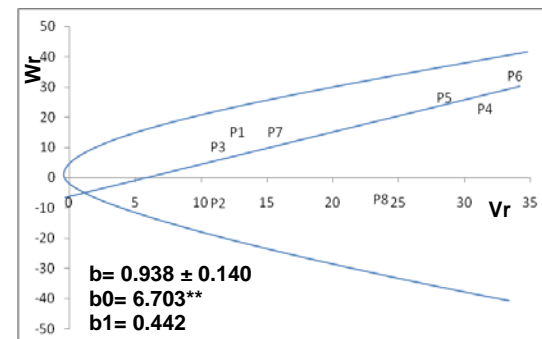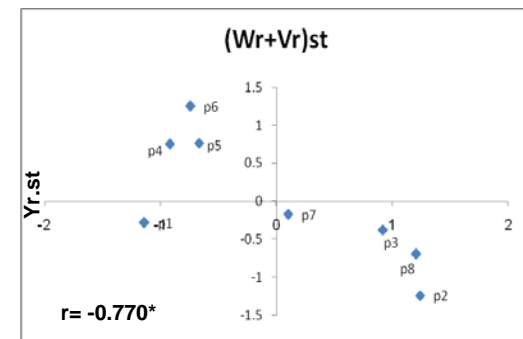Fig. (7 - a) 1000-grain weight (gm) – L1.

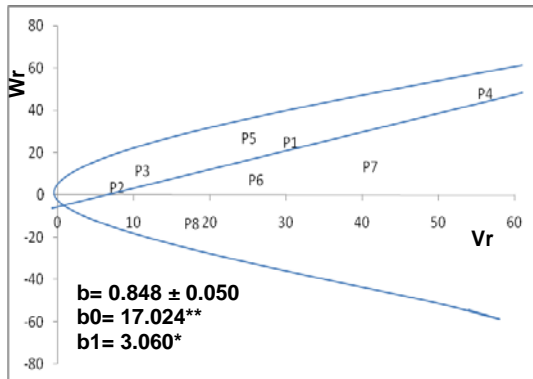Fig. (7 - c) 1000-grain weight (gm) – L1.

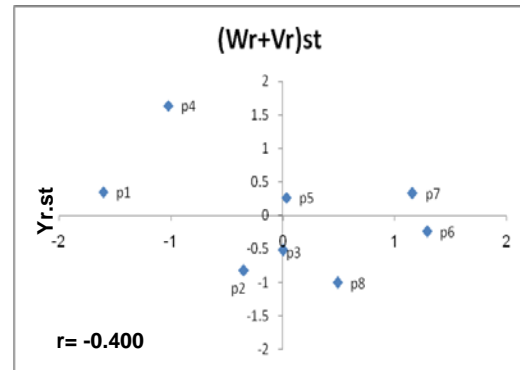**Fig. (7 - b) 1000-grain weight (gm) – L2.**

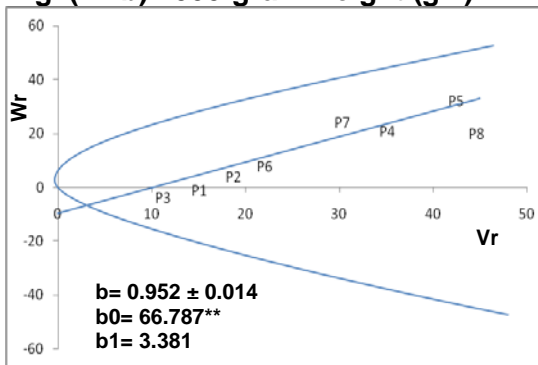**Fig. (7 - d) 1000-grain weight (gm) – L2.**

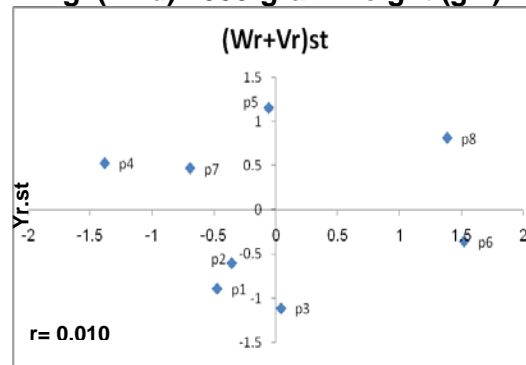**Fig.(8- a) Number of kernels per spike – L1.**

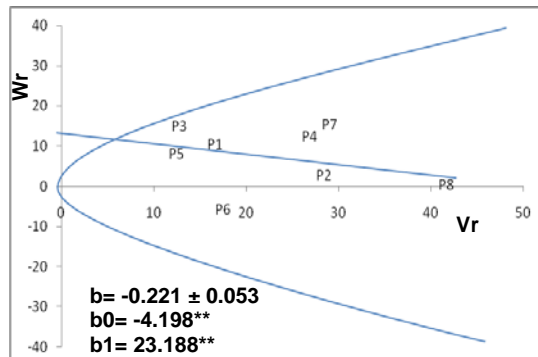**Fig. (8 - c) Number of kernels per spike – L1.**

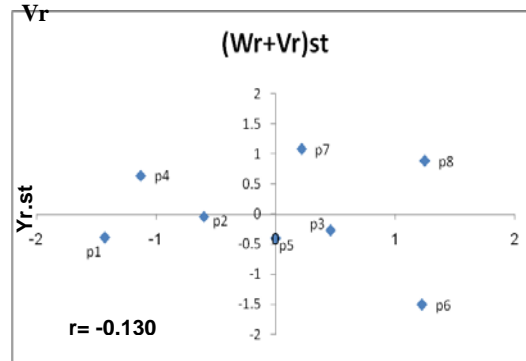**Fig.(8- b) Number of kernels per spike – L2.**

Fig. (8-d) Number of kernels per spike – L2.
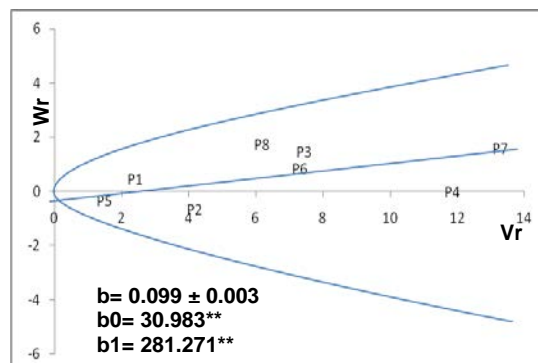

Fig. (9 – a) Grain yield per plant (gm) – L1
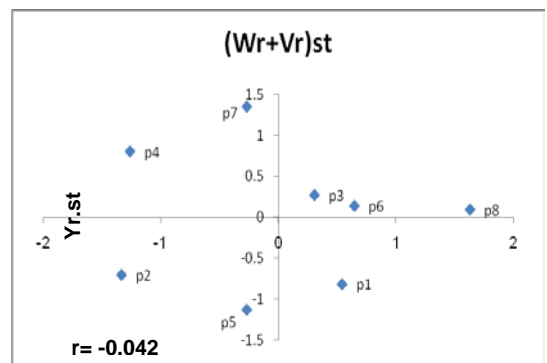
Fig. (9 - c) Grain yield per plant (gm) – L1
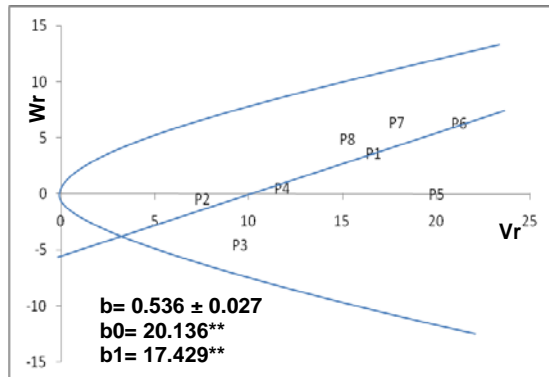
Fig. (9 – b) Grain yield per plant (gm) – L2
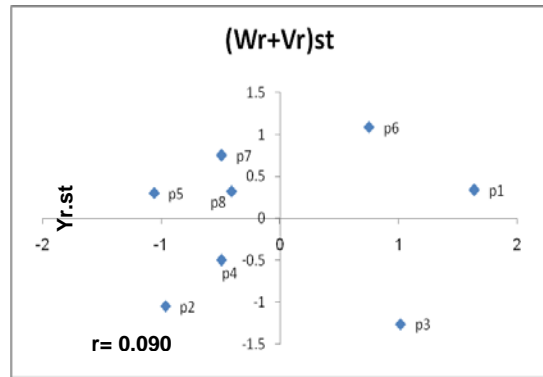
Fig. (9 - d) Grain yield per plant (gm) – L2
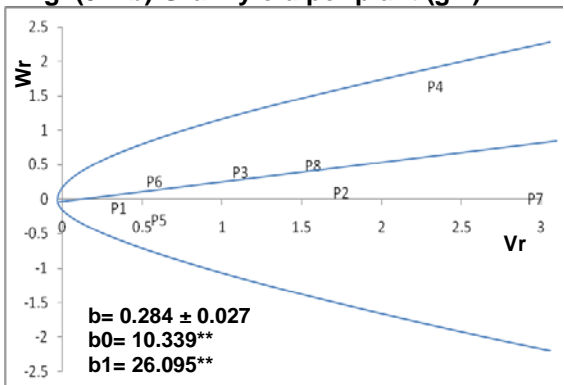
Fig. (10 - a) Protein percentage - L1.
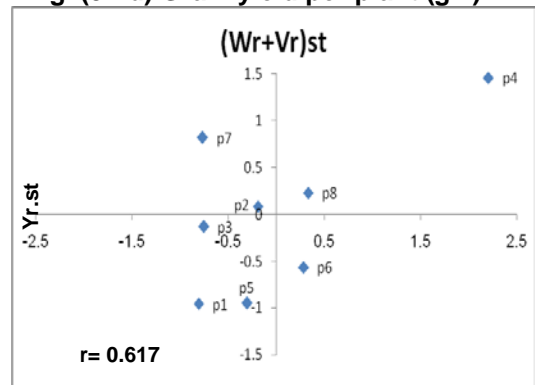
Fig. (10 - c) Protein percentage - L1.
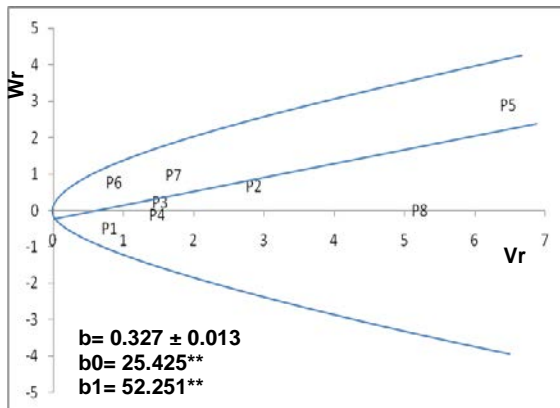
Fig. (10 - b) Protein percentage – L2
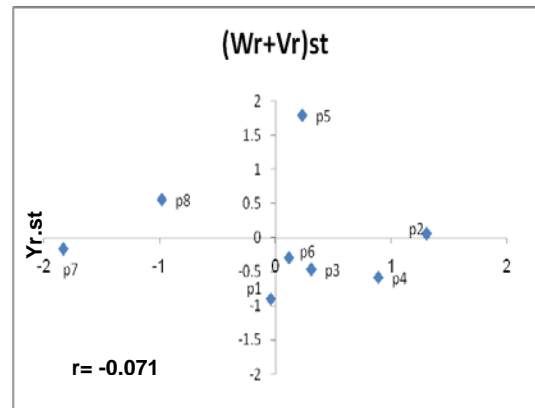
Fig. (10 - d) Protein percentage – L2

In generally, complete dominance for heading date at Maatana location as well as number of spikes per plant and protein percentage at Gemmeiza location. Partial dominance was also found for grain filling period and number of spikelets per spike at Gemmeiza location as well as plant height and number of kernels per spike at Maatana location. Over dominance was detected for heading date, plant height and number of kernels per spike at Gemmeiza location as well as grain filling period, number of spikes per plant , number of spikelets per spike and protein percentage at Maatana location, also maturity date, 1000-grain weight and grain yield per plant at Gemmeiza and Maatana locations. These contradictions could be due the presence of non – allelic interactions.

It could be concluded that the Line 1 and line 3 which contain a high proportion of dominance alleles recorded the best parents for grain yield per plant and some of the contributory yield characters i.e. number of spikes per plant , number of spikelets per spike , 1000-grain weight and number of kernels per spike. While, Line 2 and Sahel 1 which contain a high proportion of recessive alleles were found to be the best parental for earliness .

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توصيف وتقييم بعض التراكيب الوراثية في القمح تحت ظروف بيئية متباينة

٢ – التحليل البياني

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الملخص العربي

أجريت هذه الدراسة خلال موسمين متتالين ٢٠٠٨ / ٢٠٠٩ و ٢٠٠٩/٢٠١٠ حيث استخدم لهذه الدراسة ثمانية تراكيب وراثية من قمح الخبز متباعدة المصدر منه خمسة سلالات بلدية قديمة وثلاث أصناف محلية، تم التهجين بين هذه التراكيب الوراثية في موسم ٢٠٠٨/٢٠٠٩ باستخدام طريقة التهجين التبادلي في اتجاه واحد وفي موسم ٢٠٠٩ / ٢٠١٠ تم تقييم الآباء والهجن الناتجة منها في تجربتين مستقلتين ذات قطاعات كاملة العشوائية في ثلاث مكررات بكل من محطتي الجميزة والمطاعنة. تم تحليل البيانات باستخدام طريقة الهجن التبادلية (هيمن ١٩٥٤) وتم التحليل البياني بطريقة Johanson and Aksel . لعام ١٩٥٩ م .

ولقد أجري هذا البحث بهدف : تقدير مكونات التباين الوراثي باستخدام طريقة هيمن ١٩٥٤

وكانت الصفات المدروسة ميعاد طرد السنابل ، ميعاد النضج ، فترة امتلاء الحبوب ، طول النبات ، عدد السنابل في النبات، عدد السنيبلات في السنبلة، وزن الألف حبة ، عدد الحبوب في السنبلة ، محصول النبات الفردي من الحبوب و نسبة البروتين . وفيما يلي ملخص لأهم النتائج المتحصل عليها :

٥- كان التباين الوراثي المضيف ($\widehat{D}$) عالي المعنوية لمعظم الصفات المدروسة في موقعي الجميزة والمطاعنة عدا صفة عدد السنابل بالنبات لموقعي الجميزة والمطاعنة، و كلا من صفتي عدد السنيبلات بالسنبلة و محصول النبات من الحبوب لموقع الجميزة كما كان التباين الوراثي السيادي $\widehat{H}_1$ و $\widehat{H}_2$ معنويا ومرتفعا في قيمته عن الجزء المضيف وذلك لمعظم الصفات المدروسة وذلك في موقعي الجميزة والمطاعنة.

٦- أظهرت قيم متوسط السيادة $(\widehat{H1}/\widehat{D})^{1/2}$ إلي وجود السيادة الفائقة لجميع الصفات تحت الدراسة لموقعي الجميزة والمطاعنة.

٧- كانت قيم التوريث (الكفاءة الوراثية) بمعناها الضيق مرتفعة لكل من طول النبات، وزن الآلف حبة ،عدد الحبوب بالسنبلة لموقعي الجميزة والمطاعنة بينما كانت عالية لصفة فترة امتلاء الحبوب ونسبة البروتين لموقع الجميزة.

٨- أوضح التحليل البياني أن السيادة التامة كانت متحكمة في وراثة كل من ميعاد طرد السنابل لموقع المطاعنة وعدد السنابل بالنبات ، نسبة البروتين لموقع الجميزة . بينما كانت السيادة الجزئية في وراثة صفات فترة امتلاء الحبوب ، عدد السنيبلات بالسنبلة لموقع الجميزة وصفة طول النبات ، عدد الحبوب بالسنبلة لموقع المطاعنة . وكذلك السيادة الفائقة في صفات ميعاد طرد السنابل وطول النبات وعدد

الحبوب بالسنبلة لموقع الجميزة بالإضافة إلى فترة امتلاء الحبوب وعدد السنابل بالنبات وعدد السنيبلات بالسنبلة ونسبة البروتين بالنسبة لموقع المطاعنة بينما كانت السيادة فائقة في وراثة صفات ميعاد النضج ووزن الآلف حبة، محصول النبات الفردي من الحبوب لموقعي الجميزة والمطاعنة.

Table (2): Estimates of genetic components of variation and their ratios for all traits studied under the two different locations.

Genetic component	Heading date (days)		Maturity date (days)		Grain filling period (days)	
	L1	**L2**	**L1**	**L2**	**L1**	**L2**
$\widehat{D}$	46.34** ± 5.79	15.47** ± 2.13	4.43** ± 0.86	8.20** ± 1.69	29.93** ± 5.19	6.06* ± 2.71
$\widehat{H}1$	66.46** ± 13.31	29.10** ± 4.90	8.89** ± 1.97	24.27** ± 3.89	49.32** ± 11.94	51.52** ± 6.23
$\widehat{H}2$	42.86** ± 11.58	25.68** ± 4.26	*7.44*** ± 1.71	21.87** ± 3.39	33.88** ± 10.39	45.95** ± 5.42
$\hat{h}^2$	0.20 ± 7.77	-0.09 ± 2.86	0.77 ± 1.15	-0.68 ± 2.27	-0.72 ± 6.97	-0.08 ± 3.63
$\widehat{F}$	40.83** ± 13.68	1.96 ± 5.04	4.47* ± 2.03	1.56 ± 4.00	24.22 ± 12.27	4.09 ± 6.40
$\widehat{E}$	1.20 ± 1.93	0.56 ± 0.71	0.77** ± 0.29	1.56** ± 0.56	1.73 ± 1.73	0.92 ± 0.90
$(\widehat{H}1/\widehat{D})^{1/2}$	1.20	1.37	1.42	1.72	1.28	2.91
$(\widehat{H}2/4\widehat{H}1)$	0.16	0.22	0.21	0.23	0.17	0.22
KD/Kr	2.16	1.10	2.10	1.12	1.92	1.26
$\hat{h}^2/\widehat{H}2$	0.0047	-0.0035	0.1035	-0.0311	-0.0212	-0.0011
Hn	0.55	0.55	0.21	0.39	0.51	0.23
R	-0.55	-0.39	-0.52	-0.44	0.23	0.09

Table (2). Cont.

Genetic component	Plant height (cm)		No. of spikes per plant		No. of spikelets per spike	
	L1	L2	L1	L2	L1	L2
$\widehat{D}$	95.96** ± 19.35	136.19** ± 48.28	0.43 ± 0.74	1.60 ± 1.36	1.24 ± 1.41	2.31** ± 0.33
$\widehat{H}1$	339.08** ± 44.49	426.21** ± 111.00	4.23* ± 1.69	15.53** ± 3.13	7.43* ± 3.24	4.82** ± 0.77
$\widehat{H}2$	215.11** ± 38.70	320.83** ± 96.57	3.48* ± 1.47	13.51** ± 2.72	7.13* ± 2.82	4.53** ± 0.67
$\hat{h}^2$	255.43** ± 25.96	305.44** ± 64.76	-0.13 ± 0.99	-0.12 ± 1.83	3.25 ± 1.89	-0.18 ± 0.45
$\widehat{F}$	14.57 ± 45.73	-100.32 ± 114.09	-0.10 ± 1.74	1.10 ± 3.22	0.16 ± 3.33	1.68* ± 0.79
$\widehat{E}$	2.83* ± 6.45	2.20 ± 16.09	0.34 ± 0.25	0.63 ± 0.45	0.64 ± 0.47	0.76** ± 0.11
$(\widehat{H}1/\widehat{D})^{1/2}$	1.88	1.77	3.14	3.11	2.45	1.45
$(\widehat{H}2/4\widehat{H}1)$	0.16	0.19	0.21	0.22	0.24	0.24
KD/Kr	1.08	0.66	0.93	1.25	1.05	1.67
$\hat{h}^2/\widehat{H}2$	1.1874	0.9520	-0.0373	-0,0089	0.4558	-0.0397
Hn	0.64	0.67	0.35	0.24	0.22	0.20
R	-0.62	-0.70	-0.34	0.33	-0.49	0.05

L1= Gemmeiza , L2 = Mataana
*and ** significant at 0.05 and 0.01 levels of probability, respectively

Table (2). Cont.

Genetic component	1000 grain weight (gm)		No. of kernels per spike		Grain yield-plant (gm)		Protein percentage	
	L1	L2	L1	L2	L1	L2	L1	L2
$\widehat{D}$	41.42** ± 9.11	53.55** ± 9.41	48.94** ± 3.93	26.86** ± 9.71	0.72 ± 2.90	6.06* ± 2.71	1.63* ± 0.64	2.48* ± 1.21
$\widehat{H}1$	59.28** ± 20.93	82.03** ± 21.63	88.70** ± 9.03	79.17** ± 22.32	21.19** ± 6.67	51.52** ± 6.23	5.44** ± 1.47	9.42** ± 2.77
$\widehat{H}2$	47.94* ± 18.21	59.28** ± 18.82	58.07** ± 7.86	63.37** ± 19.42	17.08** ± 5.80	45.95** ± 5.42	3.52** ± 1.28	8.51** ± 2.41
$\hat{h}^2$	32.34* ± 12.21	-0.61 ± 12.62	15.71** ± 5.27	5.51 ± 13.02	0.65 ± 3.89	-0.08 ± 3.63	0.19 ± 0.86	2.49 ± 1.62
$\widehat{F}$	28.52 ± 21.52	47.55* ± 22.24	47.74** ± 9.28	25.76 ± 22.94	-0.67 ± 6.85	4.09 ± 6.40	2.02 ± 1.52	2.36 ± 2.85
$\widehat{E}$	2.98 ± 3.04	4.04 ± 3.14	4.90** ± 1.31	3.93 ± 3.24	0.95 ± 0.97	0.92 ± 0.90	0.01 ± 0.21	0.01 ± 0.40
$(\widehat{H}1/\widehat{D})^{1/2}$	1.20	1.24	1.35	1.72	5.41	2.91	1.82	1.95
$(\widehat{H}2/4\widehat{H}1)$	0.20	0.18	0.16	0.20	0.20	0.22	0.16	0.23
KD/Kr	1.81	2.12	2.14	1.78	0.84	1.26	2.03	1.65
$\hat{h}^2/\widehat{H}2$	0.6746	-0.0103	0.2705	0.0813	0.0380	0.0017	0.0540	0.2926
Hn	0.45	0.43	0.45	0.30	0.35	0.23	0.46	0.19
R	-0.77*	-0.40	0.01	-0.13	-0.04	0.09	0.62	-0.07

L1= Gemmeiza , L2 = Mataana
 *and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (2). Cont.

Genetic component	Protein percentage	
	L1	L2
$\widehat{D}$		
$\widehat{H}1$		
$\widehat{H}2$		
$\hat{h}^2$		
$\widehat{F}$		
$\widehat{E}$		
$(\widehat{H}1/\widehat{D})^{1/2}$		
$(\widehat{H}2/4\widehat{H}1)$		
KD/Kr		
$\hat{h}^2/\widehat{H}2$		
Hn		
R		

L1= Gemmeiza , L2 = Mataana

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