

GENETIC SYSTEM CONTROLLING THE YIELD AND ITS COMPONENTS IN THREE BREAD WHEAT (TRITICUM AESTIVUM, L.) CROSSES

MOHAMED A. I.KHALED

Wheat Research Dept. Field Crops Research Institute, ARC, Egypt.

(Manuscript received 10 February 2013)

Abstract

This investigation was carried out at El. Gemmeiza Agric. Res. Station , A.R.C, Egypt, during the three successive seasons, 2009/2010, 2010/2011 and 2011/2012 to study genetic variance, gene action, heterosis, inbreeding depression, heritability and genetic advance for grain yield and its components and some agronomic characters. Six populations (P1, P2, F1, F2, Bc1 and Bc2) for three crosses were used in this study coming from (P1x P3), (P2 x P4) and (P3 x P4). Analysis of variance showed significant differences among the studied generations' means for all studied traits. Scaling test showed that most studied characters were significant indicating the presence of non-allelic interaction.. Additive type of gene effect was significant either positive or negative for no .of spikes / plant, 100-kernel weight and grain yield /plant in the first and second crosses. Meantime, dominance gene effects was significantly positive for all studied traits except plant height, no. of spikes /plant and grain yield /plant in the second cross .Additive x additive and additive x dominance type of gene actions were significantly positive or negative for all studied traits in the three crosses except for no .of spikes / plant in the first and second crosses and 100- kernel weight in the second and third crosses. On the other hand dominance x dominance type gene effect was found to be significant for all studied traits except plant height and 100-kernel weight in the first and third crosses, respectively. Heritability for days to heading in narrow sense was high and nearly equal to its corresponding in broad sense. High estimates for heritability in broad sense were accompanied by moderate value of narrow sense for no. of kernels /spike, 100 –kernel weight and grain yield plant in the three crosses.

The third cross gave the highest heterotic effect towards earliness for number of days to heading and number of days to maturity with moderate heritability in narrow sense and with genetic advance being 1.59 and 1.98 days for both characters , respectively .Significant positive heterotic effects relative to better parent was obtained for no . of kernels / spike , 100 kernel weight and grain yield in the second and third crosses .

INTRODUCTION

In Egypt, wheat (*Triticum aestivum* L.) is the most important cereal crop. However, the gap between the local production and consumption is continuously increasing due to increasing the country population with limited cultivated area. It has become necessary to develop genotypes which characterized by superior performance (Shehab EL- Din 1993).

Wheat breeders are interested in estimating the relative magnitude of the genetic variance and types of gene action involved in expression of characters. Therefore, breeders need information about the nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for different characters related to grain yield and its components. Many investigators studied the type of gene effect in wheat and reported that dominance was relatively more important than additive for grain yield, while additive genetic effect was predominated in the expression of plant height and days to heading. Abul- Nass *et al* (1993) reported that, dominance component of gene action played an important rule in the genetic control for, number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant. In addition, concerning the heritability as narrow sense, Hendawy (2003) and El-Sayed and El.Shaarawy (2006) reported that heritability estimates for yield and its components were medium to high. However, Hamada (2003), Tammam (2005) and Abd El-Majeed (2005) reported that, additive and dominance components of gene actions were detected for most studied traits.

The objective of the current study was to estimate gene effects, genetic advance, inbreeding depression and genetic coefficient of variation for seven traits in three bread wheat crosses by using their six populations i.e., P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 .

MATERIALS AND METHODS

The present study was carried out at El-Gemmiza Agric. Res. Station, A.R.C., Egypt, during the three successive seasons of 2009/2010, 2010/2011 and 2011/2012. Four bread wheat genotypes (*Triticum aestivum*L.) were chosen for this study on the basis of their genetic diversity and origin (Table 1).

In the first season of 2009/2010, three crosses were made among the parents to produce F_1 hybrid grains. The three crosses were $P_1 \times P_3$ (cross 1), $P_2 \times P_4$ (Cross 2) and $P_3 \times P_4$ (cross 3). In 2010/2011 season, some of F_1 plants for each cross were backcrossed to produce the (Bc_1 and Bc_2). At the same time, some other F_1 plants were selfed to produce F_2 seeds. In 2011/2012, the six population seeds, i.e. P_1 , P_2 , F_1 , F_2 , Bc_1 and Bc_2 of the three crosses were sown in a randomized complete block design with four replications. Each plot consisted of 20 rows, i.e., eight rows for F_2 seeds, two rows for each of P_1 and P_2 or F_1 and three rows for Bc_1 or Bc_2 . The rows were 3.0m long, 30cm apart and seeds were spaced 10cm within rows.

Data were recorded on 25 individual guarded plants for P_1 , P_2 or F_1 and 60 plants for each of Bc_1 or Bc_2 and 75 plants for F_2 in each replicate for the studied characters, i.e., number of days to heading, number of days to maturity, plant height (cm), number of spikes/plant, number of kernels/spike, 100-kernel weight (gm) and grain yield/plant (gm). All recommended field practices for wheat production were applied in all growing seasons.

Table 1. The pedigree of the four parents of bread wheat genotypes

Parents	Pedigree	C.B 2009/10
P ₁	KAUZ/BAV CM103329-10M -030M -020M -010M -Y -010Y - 0M-0SY-0AP	Mexico
P ₂	PL//CM1170 A-955*2 /CNO79/3/BOW "S" 4 Sids #6 CGM 7851 -3GM -1GM -0GM	Egypt
P ₃	KAUZ/PASTOR CMSS93BOOO 25 S-484 -010M -010Y -010M -4Y -0M	Mexico
P ₄ Sids 12	BUC//7C/ALD/ 5MAYA74/ON //1160 -147//3/BB/G/4/ Chat,s, /6MYA/VUL//CMH 74a-630/4*SX-SD7096-4SD-ISD-OSD	Egypt

Statistical and genetic analysis

To determine the presence or absence of non-allelic interactions, scaling test as outlined by Mather (1949) was used. The scalls A, B, C and D and their variance were calculated to test the presence of inter allelic interaction.

The standard error of A, B, C and D was obtained by taking the square root of their respective variances. T-test was calculated by dividing the effects, of A, B, C and D by their respective standard error.

Type of gene effects estimated according to Gamble (1962) six parameter's model as follows:

M = Mean = F₂, additive (a), dominance (d), additive x additive (a a), additive x dominance (a d), dominance x dominance (d d). The amount of heterosis was expressed as the percentage deviation of F₁ mean performance forms the better-parent values. Inbreeding depression was calculated as the difference between the F₁ and F₂ means expressed as percentage of the F₁ mean, Wynn *et al* (1970). T-test was used to determine the significance of these deviations where the standard error (S.E) was calculated as follows:

$$F_1 - B_p / (\overline{VF_1} + \overline{VB_p})^{1/2}$$

And S-E for inbreeding depression was estimated as following $F_1 - F_2 = (\overline{VF_1} + \overline{VF_2})^{1/2}$

Heritability in both broad and narrow sense were estimated according to Mather (1949) and the predicted genetic gain from selection (Δg) was calculated according to Johanson *et. al.* (1955).

RESULTS AND DISCUSSION

Means and variances of the seven traits in the three studied crosses of the six populations i.e. P₁, P₂, F₁, F₂, BC₁ and BC₂ are presented in Table (2).

. All studied characters showed significant genetic variance in F₂ plants in the three crosses, therefore other needed parameters were estimated i.e., simple scaling test as outlined by Mather (1949) and the test of the presence of non-allelic interaction was estimated.

In general, the mean performance values of P₂ and F₂ in cross1 and F₂ in cross2 and F₁, P₁ and F₂ in cross3 were the earliest in days to heading. At the same time P₂, BC₁ and (P₁ and F₂) were the best as early maturing for the three crosses 1, 2 and 3, respectively.

For plant height, P_1 in crosses 1, 2 and 3 had the highest values. For number of spikes/plant, BC_1 , P_2 and P_1 had the highest values for the crosses 1, 2 and 3, respectively. On the other hand, P_1 , P_2 and F_1 were the highest in number of kernels/spike in the crosses 1, 2 and 3. BC_2 , F_2 and F_1 have the heaviest kernel weight for the crosses 1, 2 and 3, respectively. Meanwhile, BC_1 in cross 1 and P_2 in cross 2 and BC_2 in cross 3 recorded the highest grain yield / plant.

The choice of the most efficient breeding procedures depends, to a large extent, on the knowledge of the genetic system controlling the characters to be selected. The estimates of various types of gene effects contributing to the genetic variability are presented in Table (3).

Scaling test A, B, C and D in Table (3) showed that all the studied characters in the three crosses were significant except six out of eighty four estimates. These results in general, indicated the presence of non-allelic interaction. On the other hand, if scaling test A, B and C were significant, this may indicate the inadequacy of the simple model in computing the differences between populations. Also, the scaling test for the excepted traits (insignificant ones) indicated the absence of non-allelic interactions and have the additive-dominance model is adequate. These results are in agreement with those of Hamada (2003), Tammam (2005) Abd El-Majeed (2005), and Hendawy *et al.*(2009).

The estimated mean effect of F_2 (m), which reflects the contribution due to the overall mean plus the locus effects and interactions of the fixed loci, was found to be highly significant.

Additive gene effect (a) was positive and significant for plant height and 100-kernel weight in the second cross and no. of spikes/plant and grain yield/plant in the first cross and no. of kernels/spike in the third cross. On the other hand, it was negative and significant for days to heading, no. of spikes/plant and no. of kernels/spike in the second cross and days to maturity and grain yield/plant in the second and third crosses and plant height in the first and third crosses and 100-kernel weight in the first cross. These results indicated that the potentiality of improving the performance of these traits using the pedigree selection program may be more effective, Abul-Nass *et. al.* (1993) and Hendawy (2003).

In autogamous crops, i.e., wheat and barley, the breeder is usually aiming to isolate parental combinations that are likely to produce desirable homozygous segregates. The utility of attempts in identifying such pure lines is facilitated by the preponderance of additive genetic effects in self pollinating crops, (Joshi and Dhawan, 1966).

The estimates of dominance (d) effects were significant for all studied traits. The estimates of dominance were positive and significant for days to heading and no. of kernels/spike in the three crosses, days to maturity, 100-kernel weight and grain yield/plant in the first and third crosses, plant height in the second cross and no. of spikes/plant in the first cross. They were negative and significant for days to maturity, 100-kernel weight and grain yield/plant in the second cross, plant height in the first and third crosses and no. of spikes/plant in the second and third crosses.

These results indicate the importance of dominance gene effects in the inheritance of these traits. On the other hand, significance of additive (a) and dominance (d) components indicated that both additive and dominance gene effects were important in the inheritance of these traits. Also, selecting desirable characters

may be practiced in the early generations but it would be effective in the late ones. Similar results were obtained by Hendawy (2003) and Moussa (2010).

Estimates of epistatic gene effects, additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd) are presented in Table (3). Significant estimates of epistatic gene effects for one or more of these three types of epistatic gene effects in the three crosses for all studied traits were detected.

Additive x additive (aa) gene effects were positive and highly significant in days to heading and no. of kernels/spike in the three crosses, for days to maturity, 100-kernel weight and grain yield/plant in the first and third crosses, plant height in the second cross and no. of spikes/plant in the first cross. Meanwhile, it was negative and significant in case of days to maturity, 100-kernel weight and grain yield/plant in the second cross, plant height in the first and third crosses and no. of spikes/plant in the second and third crosses. These results indicated that the materials used in this study to detect and investigate inheritance of these characters could not be effective except in the case of days to maturity and plant height in which selection will be effective in identifying early dwarf lines. Similar trends were obtained by Hendawy (2003) and Moussa (2010).

Data concerning the epistatic gene effects, additive x dominance (ad) revealed different positive and significant estimates in the second and third crosses for heading date, plant height and 100-kernel weight, and in the third cross for days to maturity and no. of kernels/spike and for grain yield/plant in the first and third crosses. They also were negative and significant in the first cross for all studied characters and in the second cross for grain yield / plant. These results indicated that the inheritance of these traits was affected by the type of epistatic genes.

The dominance x dominance (dd) gene effect differed according to crosses and characters. Number of spikes/plant, number of kernels/spike and 100-kernel weight were positive and significant in the second and third crosses, and negative and significant in the first cross. Maturity date and plant height were positive and significant in the second and third crosses, respectively. Days to heading and grain yield/plant were negative and significant in the three crosses. Positive and significant results confirm the important role of dominance x dominance gene interactions in the genetic system controlling these characters. Similar results were reported by Singh *et al.* (1985), Tamm am (2005) and Hendawy *et al.* (2009).

The absolute relative magnitude of the epistatic gene effects to the mean effects was somewhat variable depending on the cross and the studied trait. Generally, the absolute magnitude of the epistatic effects was larger than additive or dominance effects. Therefore, it could be concluded that homozygous x homozygous and heterozygous x homozygous non-allelic interactions were more important than the heterozygous x heterozygous interaction in the inheritance of most studied traits. The study further revealed that epistatic gene effects were as important as additive and dominance gene effects for most of the traits. Thus, the system of inbreeding employed in exploiting any character depends on the gene action involved in its expression for predicted gain in selection progress (Abul-Naas *et al.* 1993).

Heterosis

In self pollinated crops, such as wheat, plant breeders have been investigating the possibility of developing hybrid cultivars. Thus, the utilization of heterosis in various crops through the world has tremendously increased the production either for human food or livestock feed. Heterosis is a complex

phenomenon which depends on the balance of different combinations of genotypic effect as well as the distribution of plus and minus alleles in the parents. Heterosis is expressed as the percentage deviation of F_1 mean performance from the better or mid parent of the traits. Better-parent for plant height was the short one and heterosis relative to the mid-parent value may be also effective. On the other hand, early heading and maturity may be preferable for developing genotypes characterized by early maturing and high grain yield.

In this concern, percentage of heterosis over better parent values is presented in table (4). Negative significant heterosis was obtained for days to heading in the third cross. Therefore, this cross can be utilized in breeding for early heading. Plant height heterosis value in the third cross was also negative and significant, so they were suitable for breeding dwarf plant. The second cross had positive and significant heterosis values for no. of spikes/plant, no. of kernels/spike and grain yield/plant being 14.45% , 12.26% and 5.31% , respectively . Also, positive and significant heterosis was obtained for 100-kernel weight in the first and second crosses. These results are in agreement with those obtained by Hamada (2003), Hendawy (2003) and Moussa (2010). Significant and positive better parent heterosis effects for grain yield/plant which was obtained in the third cross, could be considered as a promising one in wheat breeding program when planning for producing a hybrid wheat.

Inbreeding depression

Inbreeding depression measures the reduction in performance of the F_2 generation due to inbreeding. The results in Table (4) showed significant positive values for days to heading in the first and second crosses. Days to maturity in the third cross, no. of spikes/plant in the second cross, no. of kernels/spike in the second and third crosses, 100-kernel weight in the first and second crosses and for grain yield/plant in the second crosses. On the other hand, significant negative inbreeding depression values were detected for days to heading and plant height in the third cross, no. of spikes/plant and grain yield/plant in the first and third crosses, no. of kernels/spike in the first cross and for 100-kernel weight in the second cross.

Significant effects for both heterosis and inbreeding depression were associated with days to heading, maturity and plant height in the third cross, no . of spikes/plant and kernels/spike in the three crosses, 100-kernel weight in the first cross and for grain yield/plant in the first cross. Significant effects for both heterosis and inbreeding depression seems logic since the expression of heterosis in F_1 was followed by considerable reduction in the F_2 performance. Also, reduction in values of non-additive genetic components is logically caused by means of inbreeding depression. These results were in agreements with those obtained by Abul-Naas *et. al.* (1993) , Hendawy (2003) , El-Sayed and El-Shaarwy(2006) and Moussa (2010).

Heritability

Assessment of heritability of various traits is of considerable importance in crop improvement program, for example, to predict the response to selection, Nyquist (1991) and to identify optimum environment for selection, Allen *et. al.* (1978), Heritability has been estimated in several experimental situations in literature.

Heritability estimates depending on magnitudes of its genetic variance components of additive and dominance are presented in Table (4). The highest broad sense heritability values were obtained for days to heading (84.66%), kernel weight (77.9%) and grain yield (41.52%) in the second cross. Meanwhile, the lowest

estimate was resultant for no. of kernels/spike in second cross (27.97%). Heritability in narrow sense as estimated by using F_2 and backcrosses data, were low for plant height, no. of spikes/plant, 100-kernel weight and grain yield in the first cross with values 8.84% , 23.28% ,36.67% and 14.6% , respectively , and high in the third cross for days to maturity (70.87%) , medium for no. of spikes/plant (59.1%) ,and low for no. of kernels/spike (20.92%) and 100-kernel weight(46.79%).

The results revealed also that the genetic variance was mostly attributed to the additive effects of genes for the other studied traits. This confirms the previous results found by means of gene action estimates of additive genetic portion, which was mostly predominant. These results are in harmony with those obtained by El-Hosry *et. al.* (1997), Hendawy (2003), and Moussa (2010).

Genetic advance

The genetic advance as percentage of the F_2 mean for the studied characters is presented in Table (4). Moderate to high genetic advance ($\Delta g\%$) was detected for number of spikes/plant, number of kernels/spike, 100-kernel weight and grain yield/plant for the three crosses, however, low genetic advance was obtained for days to heading , days to maturity and plant height for the three crosses .

In the present work, high genetic advance was found to be associated with high heritability estimates for no. of spikes / plant , 100-kernel weight and grain yield / plant in the three crosses. Therefore, selection in that particular population should be effective and satisfactory in the early generations for successful breeding purposes. Also, moderate and low genetic advance was found to be associated with moderate or low heritability estimates.

As it is well known, expected improvement via selection is directly proportional to heritability. This figure is a measure of low total variability in these traits and therefore reflects the total response that could be realized by breeding techniques. It is possible to visualize a situation where the heritability is high but little response can be expected, El-Hosary *et. al.* (1997), El-Sayed and El-Shaarawy (2006), and Moussa (2010).

REFERENCES

1. Abd El-Majeed, S.A. 2005 . Estimation of epistasis additive and dominance variation in some bread wheat (*Triticum aestivum* L) cross. J. Agric. Sci., Mansoura Univ., 30 (6) : 2999 – 3011.
2. Abul – Nass, A.A., M.A. Mahrous and A.A. El Hoseary 1993. Genetical studies on grain yield and some of its components in barley (*Hordeum vulgare* L.) Egypt. J. Agron., 18 (1-2) 33-46.
3. Allen, F.L., R.E. Comstock and O.C. Resumes 1978. Optimal environment for yield testing. Crop. Sci., 18 : 747-751.
El-Hosary, A., M.B. Habeeb and A.I. Fahmi 1997. Genetic studies of some quantities characters in soybean (*Glycine max* L.). Menufiya J. Agric Rec., 22 (2) : 405 – 419.
4. El-Sayed, E.A. M and G.A. El. Shaarawy 2006. Genetical studies on yield and some agronomic characters in some bread wheat (*Triticum aestivum* L.) crosses. J. Agric. Sci., Mansoura Univ., 30 (8) : 4901-4914.
5. Gamble, E.E. 1962. Gene effects in corn (*Zea mays* L.) separation and relative importance of gene effects for yield. Canadian J. Plant Sci., 42: 339-348.
6. Hamada, A.A. 2003. Gene effect for some agronomic traits in three bread wheat crosses. Annals Agric. Sci., Ain Shams Univ., Cairo 48 (1): 131-146.
7. Hendawy, F.A., H.A. Dawwam, M.A. Abo Sheriff and E. L. El- Massry (2009). Detection of epistasis in the inheritance of grain yield and its components in bread wheat (*Triticum aestivum* L.) using triple test cross analysis. Menufiya J. Agric. Res., 34 (2) : 625- 640.
8. Hendawy. H.. 2003. Genetic architecture of yield and its components and some other agronomic traits in bread wheat. Menufiya J. of Agric. Res., 28 (1) : 71-86.
9. Johanson, H.W., F. Robinson and R.E. Comstock 1955. Estimation of genetic and environmental variability in soybeans. Agro. J., 47 : 314.
10. Joshi., A.B. and N.L. Dhawan 1966. Genetic improvement in yield and special reference to self -fertilized crop. India J. Genet and plant breed., 26-101.
11. Mather, K. 1949. Biometrical Genetics, Dover publ. Inc. London.
12. Mousaa, A.M. 2010. Estimation of epistasis, additive and dominance variation in certain bread wheat (*Triticum aestivum* L.) crosses. J. plant prod., Mansoura Univ, Vol. (12): 1707-1719.
13. Nyquist. W.E. 1991. Estimation of heritability and prediction of response in plant populations CRC Critical Reviews in plant science, 10 (3) : 235- 322.
14. Shehab El- Din, T.M. 1993. Response of two spring wheat cultivars (*Triticum aestivum* L. em . *Thell*) to ten seeding rates in sandy soil. J. Agric. Sci., Mansoura Univ., 18: 2235 – 3240.
15. Singh. G., G. S. Bhullar and K.S. Gill 1985. Inheritance of some plant characters in an intervarietal cross of bread wheat. Crop improve., 12 (2) : 179-183.
16. Tammam, A. M. 2005. Generation mean analysis in bread wheat under different environmental conditions, Menufiya J. Agric. Res., 30 (3) : 937-956.
17. Wynn, J.C., T.A. Emery and P.W. Rice 1970. Combining ability in archis hypogaeaen. Field performance of filhybrids. Crops., 10 713-715.

النظام الوراثي المتحكم في المحصول ومكوناته في ثلاث هجن من قمح الخبز

محمد عبد الكريم اسماعيل خالد

قسم بحوث القمح - معهد بحوث المحاصيل - مركز البحوث الزراعية - الجيزة - مصر

أجرى هذا البحث في محطة البحوث الزراعية بالجميزة في ثلاث مواسم زراعية متتالية وهي 2010/2009 ، 2011/2010 و 2012/2011 لدراسة قوة الهجين و نوع الفعل الجيني ودرجة التورث والتحسن الوراثي المتوقع للصفات الآتية (عدد الأيام إلي طرد السنابل وإلي النضج الفسيولوجي - ارتفاع النبات - عدد الحبوب / السنبله وعدد السنابل/ النبات - وزن 100 حبة ومحصول الحبوب/ النبات) لثلاثة هجن من قمح الخبز وهي (P1 X P3) و (P2 X P4) و (P3 X P4).

وتم تقييم العشائر الست لكل هجين في تجربة قطاعات كاملة العشوائية في أربعة مكررات :
وفيما يلي أهم النتائج المتحصل عليها :

أظهر تأثير الفعل الجيني المضيف معنوية لمعظم الصفات عدا عدد الأيام إلي طرد السنابل والنضج وعدد الحبوب/ النبات في الهجين الأول ، عدد الأيام إلي طرد السنابل وعدد السنابل/ النبات ووزن الألف حبة في الهجين الثالث.

أظهر الفعل الجيني السياتي تأثير أعلى من الفعل الجيني المضيف بدرجة معنوية موجبة لمعظم الصفات عدد الأيام إلي طرد السنابل والنضج وعدد الحبوب / السنبله ووزن الألف حبة ومحصول الحبوب/ النبات في الهجين الأول والثالث ، عدد أيام النضج وعدد السنابل/النبات ووزن الألف جنيه ومحصول الحبوب ذات تأثير معنوي سالب في الهجين الثاني.

التفاعل الجيني من النوع (المضيف × المضيف) أظهر معنوية موجبة للصفات عدد الأيام إلي طرد السنابل و النضج وعدد الحبوب/السنبله ووزن الألف حبة ومحصول الحبوب/النبات في الهجين الأول والثالث، وتأثير معنوي سالب في الهجين الثاني لصفات تاريخ النضج وعدد السنابل/ النبات ووزن الألف حبة ومحصول الحبوب/النبات.

التفاعل الجيني من النوع (المضيف×السيادي) أظهر معنوية عالية لكل الصفات فيما عدا عدد الأيام إلي طرد السنابل وعدد السنابل/النبات ووزن الألف جنيه في الهجين الثاني حيث أظهر معنوية موجبة لجميع الصفات فيما عدا وزن الألف حبة فكان غير معنوياً في الهجين الثالث، كما أظهر الهجين الأول معنوية سالبة بكل الصفات فيما عدا عدد السنابل/النبات فكان غير معنوي.

التفاعل الجيني من النوع (السيادي×السيادي) أظهر معنوية لكل الصفات فيما عدا طول النبات ووزن الألف حبة في الهجين الأول والثالث على التوالي، أظهرت عدد السنابل/ النبات وعدد الحبوب/ السنبله معنوية موجبة في كلا من الهجين الثاني والثالث مما يشير إلى أن التراكيب الوراثية والمستعملة في هذه الدراسة بها آليات ذات تأثيرات موجبة مما يجعل تحسين هذه الصفات بالانتخاب في الأجيال المبكرة فعال ومفيد.

قوة الهجين أظهرت معنوية سالبة عالية لصفة عدد الأيام إلي طرد السنابل وطول النبات في الهجين الثالث، كما أظهرت قوة الهجين معنوية موجبة لصفات عدد السنابل/النبات وعدد

الحبوب/السنبلة ووزن الألف جنيه ومحصول الحبوب فى الهجين الثاني والثالث بينما كان وزن الألف حبة غير معنوي فى الهجين الثالث.

وجدت تأثيرات سالبة ومعنوية بين قوة الهجين والتربية الداخلية ومتلازمة بين عدد الأيام إلى طرد السنابل وطول النبات وعدد السنابل/النبات فى الهجين الثالث وبينما وجد عدد أيام النضج وعدد الحبوب/السنبلة ووزن الألف حبة فى الهجين الثالث تلازماً موجباً، وتلازماً سالباً ومعنوياً لكل من عدد السنابل/النبات وعدد الحبوب/السنبلة ومحصول الحبوب/النبات فى الهجين الأول وكذلك أظهر عدد السنابل وعدد الحبوب ومحصول الحبوب/النبات تلازماً موجباً فى الهجين الثاني. أظهرت درجة التوريث بمعناها الضيق قيماً تقترب من قيم درجة التوريث بمعناها الواسع لصفات عدد الأيام إلى طرد السنابل والنضج وهذا له أهمية فى وراثة تلك الصفات وامكانية الانتخاب لها فى الأجيال المبكرة وتراوحت هذه القيم بين (84.66%)، (70.87%) على الترتيب. كما أظهرت درجة التوريث بمعناها الواسع قيم مرتفعة ومنخفضة لمعظم الصفات ما بين (27.97% إلى 84.66%).

أظهرت النتائج وجود تلازم بين صفتي وزن 100 حبة ومحصول الحبوب وبين درجة التوريث بمعناها الواسع وبدرجة التوريث بمعناها الضيق وهذا راجع إلى أهمية الفعل الجيني المضيف بالإضافة إلى الفعل الجيني غير المضيف فى وراثة تلك الصفات.

كما أظهرت النتائج وجود قيم مرتفعة للتحسين الوراثي المتوقع لصفة ارتفاع النبات ومحصول الحبوب/النبات ومحصول الحبوب/النبات فى الهجين الثاني والثالث بينما كان التحسين الوراثي المتوقع ذو قيم متوسطة لصفة عدد السنابل/النبات وعدد الحبوب/النبات وزن 100 حبة فى الهجين الأول.

يمكن الاستفادة من هذا البحث من خلال الانتخاب فى الأجيال الانعزالية المبكرة لصفة التبيكر والمحصول وذلك للحصول على سلالات مبكرة النضج وعالية المحصول.