

GENETICAL ANALYSIS OF SDS-SEDIMENTATION VOLUME AND GRAIN PROTEIN CONTENT IN EGYPTIAN BREAD WHEAT VARIETIES

Sheren N. Nathan^{1*}, A.A. Swelam¹, E.M.I. Mahgoub² and
A.H. Fayed²

1- Wheat Dept., Field Crops Research Institute, ARC, Giza, Egypt

2- Genetics Dept., Fac. Agric., Zagazig Univ., Zagazig, Egypt

ABSTRACT

A line x tester set of crosses, involving five bread wheat genotypes, were used to investigate the nature and magnitude of gene effects controlling the inheritance of SDS-sedimentation volume, protein content and grain yield attributes and to determine their general combining ability (GCA) and specific combining ability (SCA) of these studied traits. The study revealed sufficient variation among the genotypes (parents and hybrids) for these traits. The data suggested that the expression of measured traits in the hybrids varied according to the parental combination. The F₁ hybrids exhibited no heterotic effects. The GCA and SCA variances showed that gene action was predominantly additive for all the studied quality traits and yield. The results suggested also that partial dominance is operating in the inheritance of these traits. Parents differed significantly for GCA effects. This study identifies Sakha 93 (P1) and Giza 168 (P2) as a good general combiner which showed significant desirable GCA effects for all studied traits. The differences for SCA effects of F₁ hybrids were not significant. The results were discussed in relation to their implications for the development of technologically superior wheat genotypes.

Keywords: Wheat (*Triticum aestivum* L), SDS-sedimentation volume, grain protein content, combining ability, gene effects.

*Corresponding author: Sheren N. Nathan, Tel.: + 0105223163

E-mail address: sherennathan@yahoo.com

INTRODUCTION

Bread wheat is the most important cereal crop. Due to its high adaptation and multiple uses, high nutritive value associated with high crop production it is used as staple food for more than third of the world population.

Information about combining ability of parents and nature of gene effects would be helpful in identifying suitable parents for hybridization, understanding the inheritance of traits and in isolating the promising hybrids for further exploitation in breeding program. Several investigators have studied these aspects for quality traits in various cereal crops (Shenoy *et al.*, 1991; Ramesh and Hudda, 1994; Nayeem, 1996; Barnard *et al.*, 2002 and Groos *et al.*, 2004).

Such information concerned with the genetic systems controlling nutritional and technological qualities of grain proteins in wheat are very important for the development of direct methods for genetic improvements in many aspects of protein quality. SDS-sedimentation volume (SV) is a biochemical index widely used to evaluate flour quality in durum and bread wheats. Significant association between SV and endosperm proteins (gliadin,

HMW- and LMW-glutenin subunits) have been reported. Protein loci, however, account for only a portion of the total genetic variability (Blanco *et al.*, 1998). The traits analyzed here, were grain components, which influence quality and are often used to predict bread-making ability. The main quality properties studied were protein content and SDS-sedimentation volume.

The present study, therefore, has been undertaken to determine the nature and magnitude of gene effects and the combining ability effects of parents and hybrids for SDS-sedimentation volume and protein content along with 1000-grain weight and grain yield per plant through line x tester analyses at the F₁ generation.

MATERIALS AND METHODS

The materials for the present study comprised five Egyptian bread wheat varieties and their F₁ hybrids. The five wheat genotypes were Sakha 93 (P1), Giza 168 (P2), Sids 1 (P3), Sids7 (P4) and Gemmeiza 9 (P5). The five wheat genotypes were grown at the Experimental Farm of Kafr El-Hamam Research Station in the winter season 2007/2008. P1 and P2 were used as males (testers) and

each was crossed with the other three genotypes which used as females (lines) in a line x tester mating design to obtain six F₁ hybrids.

The six F₁ hybrids along with the five parents were planted in a randomized complete block design with three replications during the winter of 2008/2009. Each entry in a replication had two rows and each row consisted of 20 plants.

The grains harvested from 10 F₁ plants and their parents were mixed and five randomly selected samples in each replication were used for biochemical analysis. Grain protein content was estimated according to the Micro-Kjeldahl method. Each sample was analyzed in duplicates. The SDS-sedimentation test (SDSS) was performed manually in a 100 ml cylinder filled with 50 ml water. A 3g sample of flour was mixed with water and shaken three times at regular intervals. A lactic acid mixture (containing SDS) was added to the mixture, and inverted at regular intervals. Ten minutes and thirty minutes after the third inversion, a reading of sedimentation volume was taken. The SDS-sedimentation test and protein content were performed as described by Martinez *et al.* (2004). The grain yield per plant

and 1000-kernel weight were recorded on 10 random individual plants for the studied genotypes in each replication.

The data were subjected to line x tester analysis on the basis of mean plot for estimating general and specific combining ability (GCA and SCA) effects and gene effects as described by Kempthorne (1957) and adopted by Singh and Chaudhary (1977). The average degree of dominance was measured as $(\sigma^2D/\sigma^2A)^{0.5}$.

RESULTS AND DISCUSSION

The problem in the genetic analysis of seed quality components is that a seed has tissues from two generations. Bourland and Bird (1985) indicated that the F₁ generation of seed related traits might be represented by seeds having parental seed coat and F₁ embryos or by seeds having F₁ seed coat and F₂ embryos. The grains analyzed in the present study were of the second type.

The mean performance of the studied wheat genotypes (parents and hybrids) for quality and yield characteristics is presented in Table 1 and graphically in Figures 1-3. The data, in general, revealed a wide range of variation for

Table 1. Mean performance for SDS-sedimentation volume, grain protein content, 1000 grain-weight and grain yield per plant of parents and F₁ hybrids

Parents & Hybrids	SDS-sedimentation		Protein content	1000 grain- weight	Grain yield per plant
	10 min.	30 min.			
Parents					
P1	39.00	36.33	11.56	45.07	48.67
P2	36.67	32.33	11.15	42.92	49.00
P3	31.00	29.00	12.15	45.22	41.12
P4	37.33	33.00	13.11	44.37	38.40
P5	49.00	39.00	12.88	52.81	38.10
F₁Hybrids					
P1 x P3	40.00	37.67	13.09	51.31	39.87
P1 x P4	37.00	34.33	13.32	55.81	39.98
P1 x P5	35.00	33.33	13.09	43.91	41.33
P2 x P3	31.00	29.00	11.78	49.40	42.95
P2 x P4	30.33	29.33	11.92	49.45	43.17
P2 x P5	27.00	24.33	11.85	52.13	44.92
LSD _{0.05}	3.86	2.63	0.97	4.55	3.14
LSD _{0.01}	5.27	3.59	1.33	6.21	4.29

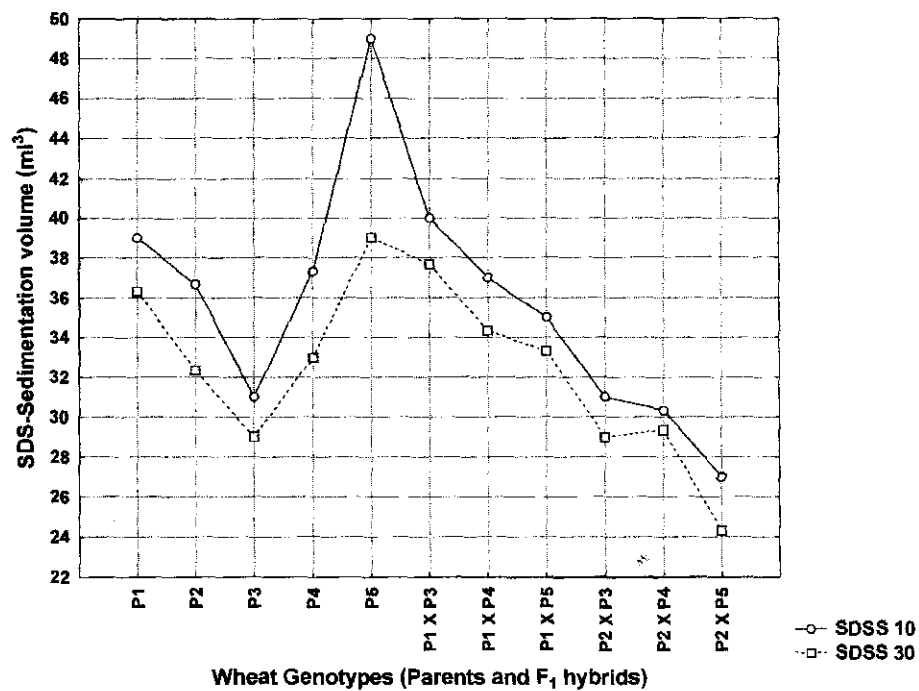


Figure 1. Mean performance for SDS-sedimentation (SDSS) volume of parental genotypes and their F₁ hybrids

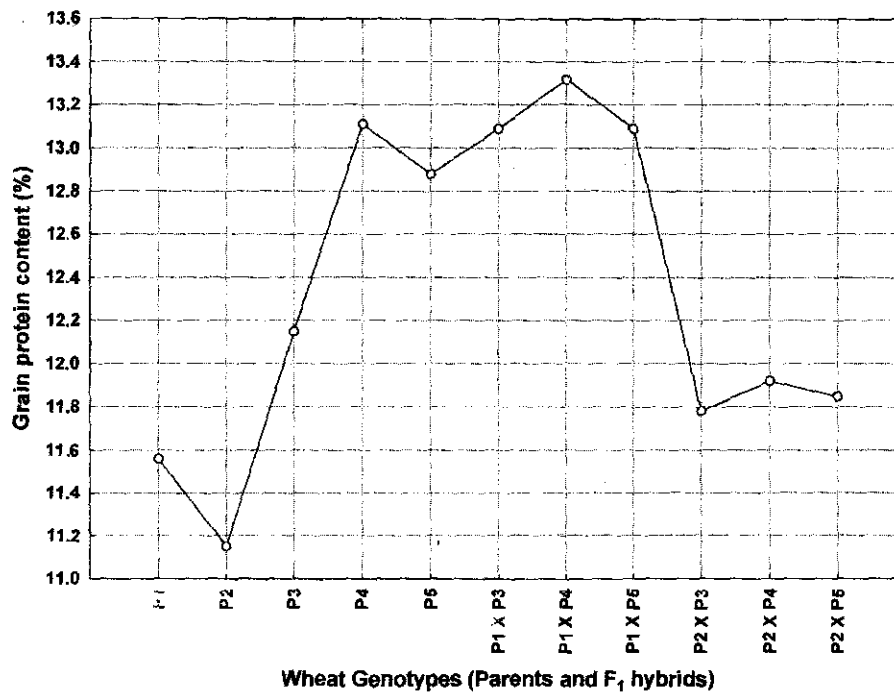


Figure 2. Mean performance for grain protein content in maturing endosperm of parental genotypes and their F₁ hybrids

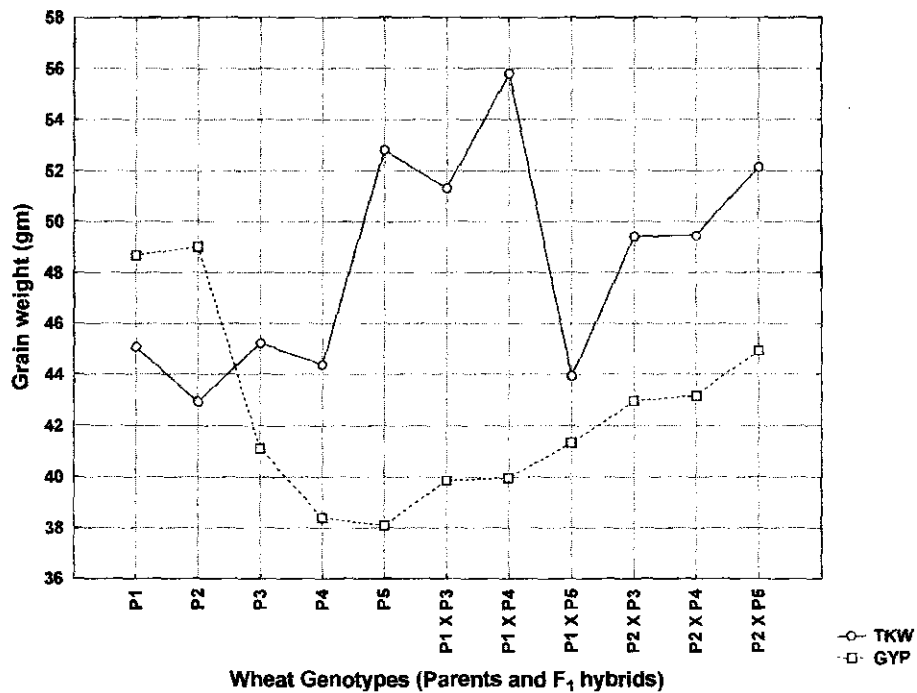


Figure 3. Mean performance for 1000-kernel weight (TKW) and grain yield per plant (GYP) of parental genotypes and their F₁ hybrids

protein content, SDS-sedimentation volume and grain yield among parents and their progenies. A consideration of the mean performance of parental genotypes and their progenies for grain yield and quality suggested that the expression of these characteristics in the hybrids varied according to the parental combination.

The parents P1 and P5 were superior for SDS-sedimentation volume, while P5 was the highest for grain yield. The cross P1 X P3 and P1 X P4 appeared to be a desirable combination as it gave high mean performance for 1000-kernel weight. The crosses P2 X P3 and P2 X P4 were significantly superior to the best parent for 1000-kernel weight. In the present study, none of the crosses have exhibited any moderate manifestation of heterosis, which was an indicative of high degree of additive gene effects.

The analysis of variance for quality and grain yield traits, summarized in Table 2, showed that differences among the genotypes were highly significant for SDS-sedimentation volumes, 1000-kernel weight and all grain yield characteristics. This trend was clearly detected in the parents, indicating greater genetic diversity

among the parents. Significant variances due to hybrids for SDS-sedimentation volumes, 1000-kernel weight and all grain yield characteristics, revealed high differences among the crosses. Variances due to parents vs. hybrids were also significant for SDS-sedimentation volumes, 1000-kernel weight and all grain yield components. Further, the partitioning of hybrid sum of squares revealed that variances due to testers were highly significant for all studied traits.

The analysis of variance for combining ability revealed that the estimates of variances due to specific combining ability (σ^2 SCA) were positive and considerably lower in magnitude than the variances of general combining ability (σ^2 GCA) for all traits (Table 2), indicating the predominant role of additive gene action including partial dominance in the expression of these quality traits and yield components.

The estimates of genetic components of variance and their ratios are also shown in Table (2). The ratio of a σ^2 A / σ^2 D which was higher than unity, implied that these traits were predominantly under the control of additive gene action (partial dominance). The important role of the additive

Table 2. Analysis of variance for means and combining ability of SDS-sedimentation volume, grain protein content, 1000 kernel-weight and grain yield per plant of the studied wheat genotypes

Item	d.f.	SDS-sedimentation		Protein content	1000 kernel-weight	Grain yield per plant
		10 min.	30 min.			
Mean Squares						
Replications	2	0.576	1.485	0.018	0.580	0.055
Genotypes	10	111.333**	50.285**	1.727	57.181**	41.843**
Parents (P)	4	140.567**	32.000**	2.099	49.052**	87.609**
P vs. H	1	205.456**	58.182**	0.929	116.878**	8.522*
Hybrids (H)	5	69.122**	63.333**	1.589	51.746**	11.895*
Lines(L)	2	30.722	45.500	0.060	21.808	5.377
Testers (T)	1	280.056**	213.556**	7.801	205.504**	48.511**
L x T	2	2.056	6.056	0.003	4.804	0.105
Error	20	5.142	2.385	0.326	11.077	3.404
Estimates of genetic components						
σ^2_{gca}	-	5.322	4.545	0.125	3.725	0.935
σ^2_A	-	10.645	9.092	0.250	7.451	1.871
σ^2_{sca}	-	1.028	1.223	0.104	2.091	1.099
σ^2_D	-	1.028	1.223	0.104	2.091	1.099
σ^2_A/σ^2_D	-	10.345	7.430	2.386	3.563	1.701
$(\sigma^2_D/\sigma^2_A)^{0.5}$	-	0.311	0.366	0.647	0.529	0.766
Contribution to hybrids (%)						
Due to lines	-	0.178	0.287	0.015	0.169	0.181
Due to testers	-	0.810	0.674	0.982	0.794	0.816
Due to L x T	-	0.012	0.038	0.003	0.037	0.004

portion of genetic variance was also observed through the average degree of dominance which was in the range of partial dominance (<1). This indicated that the inheritance of protein content, SDS-sedimentation volume and grain yield traits are controlled mainly through additive gene action. Similar findings were reported in bread wheat by Singh *et al.* (1986) and Barnard *et al.* (2002)

The data are in parallel to those mentioned on GCA and SCA variances. Thus, the results indicated that although most of the differences noted among crosses for the studied quality traits and yield were due to genes with primarily additive effects, the relatively negligible contributions of non-additive effects cannot be overlooked. This may be due to the fact that the parental materials included in this study were highly selected for yield and yield components.

The GCA and SCA effects of the parents and the hybrids, respectively, are presented in Table (3). It is evident that the parents possess significant GCA effects for the different quality and yield attributes. However, the estimates of GCA effects had definite pattern and two the

parents, Sakha 93 and Giza 168, were superior for all traits studied. The parents that proved to be good general combiners on the basis of their desirable GCA effects of grain protein content, SDS-sedimentation volumes and grain yield traits were P1 and P2. The parent P5 showed also significant negative GCA effects for SDS-sedimentation volumes. These parents were the most outstanding genotypes for protein quality and yield and they may be used for hybridization to obtain desirable segregates.

The data presented in Table (3) indicated that there no specific cross combinations exhibited desirable SCA effects. At least one of the parents in these crosses was good general combiner. However, these crosses had potential to give segregates in subsequent generations if the additive genetic system present in good combiner and the complementary epistatic effects acted in the same direction to maximize the desirable plant attribute (Andrus, 1963)

The SCA effects of different crosses indicated that high GCA effects of parents were no guarantee of high SCA effects in different crosses. Nearly all crosses, e.g. P1 x P3, P1 x P4 and P1 x P5 were found to be

Table 3. Estimates of general combining effects of parents and specific combining ability effects for cross combinations in the F₁ generation for SDS-sedimentation volume, grain protein content, 1000 grain-weight and grain yield per plant

Parents & Hybrids	SDS-sedimentation		Protein content	1000 grain- weight	Grain yield per plant
	10 min.	30 min.			
General combining ability effects of parents in the F₁ generation					
P1	3.944**	3.444**	0.658	-3.379**	-1.642**
P2	-3.944**	-3.444**	-0.658	3.379**	1.642**
P3	2.111	2.667	-0.075	0.296	-0.628
P4	0.278	0.167	0.113	1.741	-0.461
P5	-2.389**	-2.833**	-0.038	-2.037	1.089*
SE testers	0.756	0.630	0.190	1.109	0.615
SE lines	0.926	0.515	0.233	1.359	0.753
Specific combining ability effects of hybrids in the F₁ generation					
P1 x P3	0.556	-0.111	-0.002	0.997	0.100
P1 x P4	-0.611	-0.944	0.043	-0.264	0.050
P1 x P5	0.056	1.056	-0.042	-0.733	-0.150
P2 x P3	-0.556	0.111	0.002	-0.997	-0.100
P2 x P4	0.611	0.944	-0.043	0.264	-0.050
P2 x P5	-0.056	-1.056	0.042	0.733	0.150
SE	1.309	0.892	0.329	1.922	1.065

outstanding in showing low SCA effects where one of the parents showed high GCA effects. This suggested that the crosses showing poor SCA effects involving one poor and one good or both poor general combiners could have been due to lack of complementation of genes. The SCA analysis of the crosses revealed that none of the crosses combined high SCA effects for all studied quality and yield traits. This suggests a prominent role for additive genetic effects. Similar results have also been reported in wheat by other workers (Ahmad *et al.*, 1991; Mou and Kronstad, 1994; Sharma *et al.*, 1996 and Sharma and Pawar, 2000). In contrast to this, Paroda and Joshi (1970) reported a significant SCA for 1000-kernel weight, and Jain and Singh (1978) and Kamaluddin *et al.* (2007) reported a significant SCA for grain yield. The results revealed that gene effects and combining ability estimates can be used to design a selection strategy to improve quality traits. This information can assist in choosing new bread wheat lines with favourable genetic combinations for improved quality.

REFERENCES

- Ahmad, Z., K.N. Singh and V.K. Srivastava (1991). Grain quality characters in wheat. *Indian J. Genet.*, 51:84-89.
- Andrus, C.F. (1963). Plant breeding systems. *Euphytica*, 12: 205-228.
- Barnard, A.D., M.T. Labuschagne and H.A. van Niekerk (2002). Heritability estimates of bread wheat quality traits in the Western Cape province of South Africa. *Euphytica*, 127: 115-122.
- Blanco, A., M. P. Bellomo, C. Lotti, T. Maniglio, A. Pasqualone, R. Simeone, A. Troccoli and N. Di Fonzo (1998). Genetic mapping of sedimentation volume across environments using recombinant inbred lines of durum wheat. *Plant Breeding*, 117: 413-417.
- Bourland, F.M. and L.S. Bird (1985). A diallel analysis of seedling growth in cotton. *Field Crops Res.*, 10: 197-203.
- Groos, C., E. Bervas and G. Charne (2004). Genetic analysis of grain protein content, grain hardness and dough rheology in a hard \times hard bread wheat progeny. *J. Cereal Sci.*, 40: 93-110.

- Jain, K.B.L. and G. Singh (1978). Estimates of additive, dominance and additive x additive genetic variances in common wheat. In: S. Ramanujam (Ed.), Fifth Int Wheat Genetics Symp.,: 606-612. New Delhi, India.
- Kamaluddin, R.M.S., L.C. Prasad, M.Z. Abdin and A.K. Joshi (2007). Combining ability analysis for grain filling duration and yield traits in spring wheat (*Triticum aestivum* L em. Thell). Genetics and Molecular Biology, 30: 411-416.
- Kempthorne, O. (1957). An introduction to genetical statistics. John Wiley and Sons, Inc. New York.
- Martinez, M.C., M. Ruiz and J.M. Carrillo (2004). New B low Mr glutenin subunit alleles at the Glu-A3, Glu-B2 and Glu-B3 loci and their relationship with gluten strength in durum wheat. J. Cereal Sci., 40: 101-107.
- Mou, B. and W.E. Kronstad (1994). Duration and rate of grain filling in selected winter populations. I. Inheritance Crop Sci., 34:833-837.
- Nayeem, K.A. (1996). Genetic architecture of protein, lysine and sugar contents in grain sorghum. Indian J. Genet., 56: 447-451.
- Paroda, R.S. and A.B. Joshi (1970). Combining ability in wheat. Ind. J. Genet. & Plant Breed., 30: 630-637
- Ramesh, B. and M.P.S. Hudda (1994). Study on variability and associations involving protein content, amino acids and grain yield in sorghum. Indian J. Genet., 54: 37-44.
- Sharma, P.K., D.K. Garg and P.C. Sharma (1996). Genetic characterization of some quantitative characters in wheat. Indian J. Genet., 56: 281-284.
- Sharma, P.K. and I.S. Pawar (2000). Genetic architecture of some wheat crosses through triple test cross method. Indian J. Genet. & Plant Breed., 48: 45-48.
- Shenoy, V.V., D.V. Seshu and J.K.S. Sachan (1991). Inheritance of protein per grain in rice. Indian J. Genet., 51: 214-220.
- Singh, R.K. and B.D. Chaudhary (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, :205-214.

- Singh, N., R.S. Paroda and R.K. Behl (1986). Diallel analysis for combining ability over environments in wheat. Wheat Information Service, 61/62: 74-76.

التحليل الوراثى لصفات حجم الترسيب فى وجود SDS ومحتوى الحبوب من البروتين فى أصناف قمح الخبز المصرية

شبرين نبيل ناثان^١ - عبد الله عبد المحسن سويلم^١
السيد محمود إبراهيم محجوب^٢ - أحمد حسن فايد^٢

^١ قسم القمح - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية - الجيزة
^٢ قسم الوراثة - كلية الزراعة - جامعة الزقازيق

استخدمت مجموعة هجن سلالة X كشاف تشمل خمسة أصناف قمح خبز مصرية لدراسة طبيعة و مقدار التأثيرات الجينية التى تتحكم فى توارث صفات حجم الترسيب فى وجود SDS ومحتوى الحبوب من البروتين وكذلك تعيين قدرة الانتلاف العامة والخاصة. وقد أظهرت الدراسة وجود مقدار كبير من الأختلافات بين التراكيب الوراثية (أباء و هجن) لهذه الصفات. وتقترح النتائج ان تعبير الصفات المدروسة فى الهجن قد اختلف على حسب توليفة الأباء الداخلة فى الهجن. لم تظهر هجن الجيل الأول تأثيرات قوة الهجين. وقد أظهرت التباينات الرجعة الى قدرة الانتلاف العامة والخاصة ان الفعل الجينى كان اساساً من الفعل المضيف لكل الصفات المدروسة. وتقترح النتائج ان السيادة الجزئية كانت فعالة فى توارث هذه الصفات. وقد اختلفت الأباء معنوياً فى تأثيرات قدرة الانتلاف العامة. وقد أظهرت الدراسة بأن الأباء سخا ٩٣ و جيزة ١٦٨ كانت الأفضل بالنسبة لقدرة الانتلاف العامة حيث بينت تأثيرات مرغوبة لكل الصفات المدروسة ماعدا محتوى الحبوب من البروتين. الفروق فى تأثيرات قدرة الانتلاف الخاصة لم تكن معنوية بين الهجن. وقد نوقشت النتائج فيما يتعلق بإمكانية الحصول على تراكيب وراثية من قمح الخبز عالية الجودة.