Genetic Analysis of Yield, Yield Components and Earliness in Two Soybean Crosses

Mansour, S.H.
Food Legumes Res. Section, Field Crops Res. Inst., ARC.

ABSTRACT

Performance of the parents; F_1's, F_2's and backcross generations of two soybean (*Glycine max* (L.) Merrill) crosses was evaluated in the summer season of 2001. The evaluated parameters were: (1) Heterosis in F_1, which exhibited positive significant effect over the mid parent for most of the studied characters, however, negative significant heterosis were observed for other characters. (2) Inbreeding depression in F_2, this was highly significant for all characters studied in both crosses. (3) F_2 deviation (E_1) and backcross deviation (E_2) were significant for most of the studied traits. (4) Gene action effects were highly significant for the mean, additive, dominance and epistatic values, for most of the studied characters. (5) Broad sense heritability estimates for all of the studied characters ranged from 66.32 to 94.06% in both crosses. (6) Narrow sense heritability ranged from 23.6% for plant height to 62.9% for the number of branches. Therefore, these crosses can be used in selection programs (pedigree selection, modified single seed or single pod descent) for improving seed yield in soybean crop.

INTRODUCTION

The plant breeder usually has in mind an ideal plant that combines maximum number of desirable characteristics. One of the aims of virtually every breeding project is to increase yield. Early maturity is another important character since it frees land quickly, often allowing an additional planting of the same crop or other crop in the same year. The plant breeder is interested in the determination of gene effects to establish the most advantageous breeding programs for the improvement of the desired characters (Tawar *et al.*, 1989), especially for soybean because it is an important source of protein and oil, its seeds contain about 14 to 24% or more oil and about 45 to 48% protein (Brim and Burton, 1979). It is widely used in Egypt for human and poultry consumption. Moreover in Egypt, the quantity of oil seeds produced, including main oil crops; i.e., cotton, sesame, flax seeds and peanut, is far from being sufficient for excessive demand. Therefore, Egyptian plant breeders have intensified their efforts to increase soybean yield and yield components to meet the increasing demand for oil and protein production. Such improvement is strongly dependent upon the genetic improvement of soybean germplasm (Mansour, 1991; Ibrahim *et al.*, 1996; Bastawisy *et al.*, 1997; Ragaa Eissa *et al.*, 1998; Fahmi *et al.*, 1999 and El-Hosary *et al.*, 2001).

To achieve such goals, it is important to study the type and mode of gene actions that influence agronomic traits. The aim of the present study is to evaluate some genetic parameters in three soybean genotypes involved in two crosses and their six populations; i.e., P_1, P_2, F_1, F_2, BC_1 and BC_2. In order to achieve such genetic evaluation, the heterotic effect, inbreeding depression, broad and narrow senses heritability, five types of gene action, potency ratio and the genetic advance for selection were estimated.

MATERIALS AND METHODS

The present study was carried out in the summer seasons of 1999, 2000 and 2001 at Zarzura Agricultural Research Station.

In the first season, two soybean crosses were carried out between genotype $D_{89-8940}$ as a male parent and H_2L_{20}, H_1L_{68} as female parents. The cultivar $D_{89-8940}$ belongs to the maturity group VI; i.e., it requires 157 days from sowing to the maturity, the genotype H_2L_{20} belongs to the maturity group IV it requires 120 days to maturity, while the genotype H_1L_{68} belongs to the maturity group III which requires 110 days to maturity.

In the second season, the hybrid seeds were planted, F_1 plants from each cross were self-pollinated and backcrossed to both parents to obtain the F_2's and the backcross seeds, at the same time crosses between the parental varieties were repeated to obtain F_1 hybrid seeds.

In the third season, the six populations of each cross (P_1, P_2, F_1, F_2, BC_1 and BC_2) were planted in a randomized complete block design experiment with three replications. Each plot consisted of two rows for non-segregating generations; i.e., P_1, P_2 and F_1, four rows for backcrosses and eight rows for F_2 generations, each row was 4 m long, 60 cm width and 20 cm between hills. One seed was planted per hill at one side of the ridge. Before flowering, 10, 30 and 50 plants were kept with caution for non-segregating generations, backcross and F_2 and were tagged in each one of the three plots. A total tagged plants for each cross was 30 P_1, 30 P_2, 30 F_1, 90 BC_1, 90 BC_2 and 150 F_2 plants. Data were recorded on these previously mentioned plants for the following characters; the plant height, flowering date, maturity date, number of pods per plant, number of seeds per plant, number of seeds per pod, 100-seed weight and seed yield per plant.

Gene effect estimates were determined using the six parameters model of Gamble (1962). Heterosis was calculated as the percentage increase of the F_1 performance above the mid-parental performance. The inbreeding depression was calculated as the percentage of deviation of the F_2 from F_1 performance. The two estimates of epistatic deviation E_1 and E_2 were calculated as the deviation of the segregating populations; i.e., F_2 and (BC_1 + BC_2) from their non-segregating populations (F_1 and mid parents). E_1 being the epistatic deviation of F_2, and E_2 the epistatic deviation of BC_1 + BC_2 (Mather and Jinks, 1971). The degree of dominance was determined by calculating the potence ratio according to Mather and Jinks (1971). Heritability in both narrow and broad senses were estimated using Warner's method (1952), and the expected gain from selection (G.S), was calculated according to Allard (1960).

$$\text{Potence ratio (P)} = \frac{\overline{F_1} - M.P}{\overline{HP} - M.P}$$

where; $\overline{HP}$ = the high parent mean and M.P = Mid-parent value.

Epistatic deviation:

$$E_1 = \overline{F_2} - \tfrac{1}{2}\overline{F_1} - \tfrac{1}{4}\overline{P_1} - \tfrac{1}{4}\overline{P_2}$$

$$E_2 = \overline{Bc_1} + \overline{Bc_2} - \overline{F_1} - \tfrac{1}{2}\overline{P_1} - \tfrac{1}{2}\overline{P_2}$$

Expected genetic advance (GS) upon selection:

$$GS = (K)\ (\sigma p)\ (h^2 n)$$

where; K = Selection differential (K = 2.06 when selection intensity 5%)

σp = Phenotypic standard deviation of F_2.

$h^2 n$ = heritability in narrow sense.

RESULTS AND DISCUSSION

Yield characters:

Table (1) presents the means and standard errors of the studied traits in the six generations for the two studied crosses. The F_1 means for the yield characters were higher than those for both parents, this was reflected in the appearance of positive highly significant heterosis for the following traits; number of pods per plant, number of seeds per plant, number of seeds per pod, one hundred seed weight and seed yield per plant (Table 2). Table (3) shows potence ratio; i.e., deviation of the F_1 hybrid from the mid-parental value and from the better parent which measure the degree of dominance. Over dominance towards the higher parent was detected for yield and yield components such as number of pods per plant in cross I ($H_2L_{20} \times D_{89\text{-}8940}$), number of seeds per plant, number of seeds per pod, 100-seed weight and seed yield per plant in the two studied crosses. High values of heritability in broad sense were obtained. This parameter measures the proportion of phenotypic variance in a population that is due to genetic differences, the highest values obtained were 92% and 94% for the trait of number of seeds per plant in the two crosses. Moreover, the values of heritability in narrow sense which indicate the proportion of phenotypic variance that results from additive genetic variance, were high in magnitude but were lower than their corresponding broad sense values.

Table 1. Average and standard error values of the parents, F1, F2 and backcrosses for characters studied in the two soybean crosses.

Cross	Population	No. of branches /plant	Plant height (cm)	Flowering date (day)	Maturity date (day)	No. of pods /plant	No. of seeds /plant	No. of seeds /pod	100-seed weight (g)	Seed yield /plant (g)
Cross I H_2L_{20} (P_1) x $D_{89\text{-}8940}$ (P_2)	P_1	4.83±0.14	58.61±0.42	44.67±0.38	122.82±0.22	80.99±1.26	204.85±3.87	2.53±0.03	17.21±0.11	35.20±0.54
	P_2	6.23±0.20	40.88±0.47	63.38±0.38	152.67±0.21	139.98±1.80	237.04±2.36	1.70±0.02	11.06±0.14	26.24±0.39
	F_1	6.20±0.21	45.83±0.28	50.24±0.33	129.00±0.17	163.41±0.84	444.66±2.01	2.72±0.02	19.57±0.16	87.00±0.84
	F_2	5.67±0.16	65.27±0.49	56.68±0.29	131.78±0.16	118.44±1.99	276.39±4.56	2.33±0.04	14.60±0.11	40.09±0.63
	BC_1	7.04±0.18	41.40±0.55	60.73±0.32	138.66±0.18	103.37±2.14	260.92±5.34	2.53±0.04	12.96±0.12	33.73±0.78
	BC_2	5.00±0.19	51.11±0.59	51.39±0.33	124.53±0.18	99.11±2.18	258.65±5.40	2.61±0.05	17.96±0.12	46.42±0.67
Cross II H_1L_{68} (P_1) x $D_{89\text{-}8940}$ (P_2)	P_1	2.53±0.22	75.73±0.48	33.37±0.28	127.68±0.14	59.74±0.92	130.70±1.66	2.19±0.03	14.43±0.12	18.98±0.26
	P_2	7.17±0.15	41.84±0.39	63.00±0.32	154.45±0.14	147.79±1.66	257.74±2.71	1.75±0.02	11.24±0.15	28.87±0.33
	F_1	7.03±0.19	44.76±0.35	53.00±0.18	131.92±0.16	133.58±1.79	317.36±1.99	2.38±0.04	17.68±0.11	56.12±0.77
	F_2	4.57±0.14	50.47±0.48	43.68±0.32	135.37±0.11	82.85±1.95	179.21±3.96	2.16±0.04	13.60±0.10	24.32±0.62
	BC_1	5.67±0.16	67.29±0.59	54.49±0.37	130.76±0.12	76.92±2.02	188.12±4.68	2.45±0.04	16.80±0.13	31.59±0.71
	BC_2	6.87±0.15	44.06±0.56	61.50±0.36	141.00±0.13	122.56±2.20	273.57±4.29	2.23±0.05	12.87±0.11	35.15±0.68

Table 2. The six parameters of gene effect, heterosis percentage, inbreeding depression percentage, F_2 deviation and backcross deviation in the two crosses of soybean.

Character	Cross	Gene effect						Heterosis (%)	Inbreeding depression (%)	F_2 deviation (E_1)	BC deviation (E_2)
		m	a	d	aa	ad	dd				
No. of branches/plant	I	5.97**	2.04**	2.07*	1.40	2.68**	-2.29	12.12**	8.55**	-0.20	0.31
	II	4.57**	1.20**	8.98**	6.80**	-2.24**	-8.12**	44.90**	34.99**	-1.34**	0.66*
Plant height	I	65.27**	-9.71**	-79.98**	-76.06**	-1.69	82.19**	-7.87**	-42.42**	17.48**	-3.07**
	II	50.47**	-23.23**	6.80**	20.82**	-12.57**	-36.43**	-23.86**	-12.75**	-1.30*	7.81**
Flowering date	I	56.68**	9.34**	-6.27**	-2.48	-0.03	-13.23**	-7.01**	-12.82**	4.54**	7.86**
	II	43.68**	7.01**	62.08**	57.26**	-6.61**	-86.87**	9.99**	17.56**	-6.91**	14.81**
Maturity date	I	131.78**	14.13**	-9.49**	-0.74	-1.59**	7.85**	-6.35**	-2.16**	-1.59**	-3.56**
	II	135.37**	10.24**	-7.11**	2.04**	-6.29**	-8.59**	-6.48**	-2.62**	1.12**	-1.23**
No. of pods/plant	I	118.44**	4.26	-15.88	-68.80**	-50.47**	211.63**	47.90**	27.52**	-18.51**	-34.87**
	II	82.85**	45.64**	97.38**	67.56**	3.23	8.17	28.73**	37.97**	-35.82**	-37.87**
No. of seeds/plant	I	276.39**	2.27	157.30**	-66.42**	-27.65	358.49**	101.25**	37.84**	-56.41**	-146.04**
	II	179.21**	85.45**	329.68**	206.54**	43.36**	-106.76**	63.40**	43.53**	-76.58**	-49.69**
No. of seeds/pod	I	2.33**	-0.08	1.57**	0.96**	0.67**	-1.38**	28.60**	14.34**	0.09	0.31**
	II	2.16**	-0.22**	0.50*	0.72**	0.00	-1.38**	20.81**	9.24**	-0.02	0.33**
100-seedweight	I	14.60**	-5.00**	8.88**	3.44**	-3.85**	2.13*	38.45**	25.39**	-2.25**	-2.79**
	II	13.60**	-3.93**	9.79**	4.94**	-4.67**	-3.25**	37.75**	23.08**	-1.66**	-0.86**
seed yield/plant	I	40.09**	-12.69**	56.22**	-0.06	-16.42**	75.20**	183.20**	53.92**	-18.77**	-37.57**
	II	24.32**	3.56**	68.40**	36.20**	-2.77	-9.59*	134.56**	56.66**	-15.70**	-13.31**

Cross I = $H_2L_{20} \times D_{89\text{-}8940}$ Cross II = $H_1L_{68} \times D_{89\text{-}8940}$

* and ** = Significant at 5% and 1% level of probability.

Table 3. Potence ratio, heritability percentage in broad and narrow senses, genetic advance G.S and genetic advance as percentage of the F_2 mean G.S%.

Character	Cross	Potence ratio	Heritability broad sense h^2b %	Heritability narrow sense h^2n %	Genetic advance G.S	Genetic advance G.S/F_2 %
No. of branches/plant	I	0.96	68.24	39.12	1.573	27.74
	II	0.94	66.98	62.93	2.322	50.82
Plant height	I	-0.44	86.70	37.93	4.700	7.21
	II	-0.83	84.94	23.64	2.830	5.61
Flowering date	I	-0.40	67.48	48.38	3.500	6.18
	II	0.33	86.16	40.54	3.270	7.49
Maturity date	I	-0.59	67.47	46.77	1.850	1.41
	II	-0.68	66.32	47.15	1.350	1.00
No. of pods/plant	I	1.79	90.78	59.82	30.160	25.47
	II	0.68	88.12	59.97	29.580	35.70
No. of seeds/plant	I	13.90	92.12	34.01	39.150	14.17
	II	1.94	94.02	45.84	45.780	25.55
No. of seeds/pod	I	1.46	94.06	43.75	0.510	21.88
	II	1.86	89.65	48.28	0.540	25.00
100-seed weight	I	1.77	67.26	52.00	1.420	9.71
	II	3.04	69.70	42.17	1.120	8.23
seed yield/plant	I	12.56	81.21	41.91	6.720	16.79
	II	6.51	86.64	48.55	7.570	31.13

Cross I = H_2L_{20} x $D_{89-8940}$ Cross II = H_1L_{68} x $D_{89-8940}$

The estimated values of the six parameters describing the nature of gene action are also presented in Table (2), the estimated mean effect (m) which reflects the contribution due to the overall mean plus the locus effects and interaction of the fixed loci was highly significant. The additive effect (a) was highly significant in the second cross (H_1L_{68} x $D_{89-8940}$) for the five yield traits, and it was highly significant for 100-seed weight and yield per plant in the first cross, and was insignificant for the three remaining characters. The dominance effect (d) was highly significant for the five yield traits in both crosses, except for the number of pods per plant in cross I which exhibited insignificant value. The interaction between additive x additive (aa) was also highly significant for the yield traits, however, (aa) value for yield per plant in cross I was insignificant. The additive x dominance effect (ad) was highly significant in cross I for all traits, except for the number of seeds per plant, while in the cross II it was significant only for the number of seeds per plant and for 100-seed weight. The dominance x dominance effect (dd) was also highly significant for all yield traits, except for the number of pods per plant in cross II.

Inbreeding depression % was highly significant for all of the studied traits in both crosses. The results of inbreeding depression are in accordance with those of heterosis, and this is expected since the heterosis in F_1 are always followed by F_2 depression.

The estimates of genetic advance from selection 5% superior plants of the F_2 generation reflected high values for the traits of number of pods per plant 30.16, 29.58, number of seeds per plant 39.15, 45.72, low values for number of seeds per pod 0.51, 0.54, 100-seed weight 1.42, 1.12, and intermediate values for seed yield per plant 6.72, 7.57. While the genetic advance as percentage of F_2 mean (G.S/F_2 %) showed high values for the number of pods per plant 25.47, 35.70 and intermediate for the remaining yield characters, the values ranged between 9.71%, 8.23% for 100-seed weight to 21.88%, 25.00% for the number of seeds per pod.

These data strongly reflect the presence of non-allelic gene interaction in the inheritance of these characters in both crosses. Heterosis mainly contributed by dominance components, which were two to many time higher than the additive component. Both heterosis and inbreeding depression are correlated phenomena, therefore, it is logical to predict that heterosis in F_1 will be followed by an appreciable reduction in F_2 performance. These results are in agreement with those reported by Weber *et al.*(1970), Thseng and Tseng (1973), El-Hosary (1981), Bastawisy *et al.*(1997) and El-Hosary *et al.*(2001).

Earliness and some growth attributes:

Table (1) shows that F_1's were intermediate between their parental genotypes for the time required for flowering and maturity, while F_2's were later than their F_1's. While, backcrosses were closer to the backcross parent. The parent $D_{89\text{-}3940}$ was the shortest plant height (about 42 cm) and the highest for the number of branches per plant (7.17 branches).

The data presented in Table (2) indicated that the additive and dominance effect estimates "a, d" for all characters were significant and highly significant in the two crosses studied. Estimates of additive x additive gene effects "aa" were not significant for the number of branches per plant, flowering date and maturity date in cross I. The additive x dominance gene effects "ad" for the plant height and flowering date in cross I were not significant. Dominance x dominance gene effects "dd" were not significant for the number of branches per plant in cross II.

Heterosis for plant height and maturity date in both crosses and flowering date in cross I exhibited highly significant negative value. Minimum value was observed for plant height in cross II (-23.86), the maximum heterosis value was for the number of branches per plant in cross II (44.9).

Significant negative inbreeding depression was observed for plant height and maturity date in the two studied crosses and the flowering date in cross I.

F_2 deviation (E_1) and backcross deviation (E_2) for earliness and plant height were either positive or negative, but both were highly significant, however, the number of branches per plant in cross I was insignificant.

Partial dominance was observed for the number of branches per plant in both crosses and flowering date in cross I, towards higher parent. Moreover, plant height data in both crosses and flowering date in cross I were partially dominant towards lower parent (Table 3). Broad sense heritability estimates for plant height and flowering date in cross II were above 80%. However, broad sense heritability estimates for flowering date in cross I and number of branches per plant and maturity date for the two crosses indicated that these characters were affected by additive and non-additive gene actions. Narrow sense heritability estimates were low for plant height in cross II; i.e., 23.64%.

Genetic advance expressed as a percentage of the F_2 mean for plant height, flowering date and maturity date for both crosses were (7.21-5.61%), (6.18-7.49%) and (1.41-1.0%), respectively, however, for the number of branches per plant were 27.74 and 50.82 for both crosses.

This means that when heritability estimates are high the selection is effective in early generations, therefore, additive gene effects were thought important. The obtained data indicate the predominance of additive gene effects in determining the tested characters. Such results were previously recorded by Mahmoud and Kramer (1951), Caviness (1969), Raut *et al.*(1988), Mansour (1991), Ibrahim *et al.*(1996), Ragaa Eissa *et al.*(1998) and El-Hosary *et al.*(2001).

Thus, it can be recommended that hybridization followed by selection are the most suitable breeding programs to improve soybean for earliness and yield components.

REFERENCES

Allard, R.W.1960. Principles of plant breeding. John Wiley and Sons, Inc. New York, 485 pp.

Bastawisy, M.H., M.S. Eissa, K.A. Ali, S.H. Mansour, and M.S. Ali. 1997. Gene effect and heritability in soybean (*Glycine max* (L.) Merrill). Annals of Agric. Sci., Moshtohor, 35: 15-24.

Brim, C.A. and J.W. Burton. 1979. Recurrent selection in soybean. II. Selection for increased percent protein in seeds. Crop Sci., 19: 494-498.

Caviness, C.E. 1969. Heritability of pod dehiscence and its association with some agronomic characters in soybean. Crop Sci., 9: 207-209.

El-Hosary, A.A. 1981. Genetical studies on field bean (*Vicia faba* L.). Ph.D. Thesis, Fac. Agric. Menoufiya Univ.

El-Hosary, A.A., M.H. Bastawisy, S.H. Mansour, Kh.A. Al-Assily, and M.H. Metawea. 2001. Heterosis, gene effect, heritability and genetic advance in soybean (*Glycine max* (L.) Merrill). Menoufiya J. Agric. Res., 26: 1071-1083.

Fahmi, A.L., R.A. Eissa, A.A. Nawar, M.H. Bastawisy, and E.M. Zayed. 1999. Genetic performance of seed quality characters of five soybean (*Glycine max* (L.) Merrill) varieties and their diallel crosses. Menoufiya J. Agric. Res., 24: 999-1015.

Gamble, E.E. 1962. Gene effects in corn (*Zea mays* L.). 1- Separation and relative importance of gene effects for yield. Canad. J. Plant Sci., 42: 330-348.

Ibrahim, H.M., A.A. Nawar, and S.H. Mansour. 1996. Heterosis, combining ability and components of genetic variance in soybean (*Glycine max* (L.) Merrill). Menoufiya J. Agric. Res., 21: 851-862.

Mahmoud, I. and H.H. Kramer. 1951. Segregations for yield, height and maturity following a soybean cross. Agron. J., 43: 605-609.

Mansour, S.H. 1991. Genetical studies on soybean (*Glycine max* (L.) Merrill). Ph.D. Thesis, Genetic Department, Fac. of Agric., Alex. Univ.

Mather, K. and J.L. Jinks. 1971. Biometrical Genetics. (2nd ed.) Chapman and Hall Ltd., London, 382 pp.

Ragaa Eissa, A., A.L. Fahmi, and M.B. Habeeb. 1998. Genotypic evaluation of four soybean cultivars and their crosses for some important agronomic components. Menoufiya J. Agric. Res., 23: 331-339.

Raut, V.M., G.B. Halwankar, and V.P. Patil. 1988. Heterosis in soybean. Soybean Genetics Newsletter, 15: 57-60.

Tawar, M.L., A.K. Mishra, and S.K. Rao. 1989. Gene action in soybean. Indian J. Heredity, 21: 10-16.

Thseng, F.S. and F.S. Tseng. 1973. Genetic studies on quantitative characters in soybean. VI. Gene number and gene effects for certain agronomic characters. J. of Fac. of Agric., Japan, 57: 193-227.

Warner, J.N. 1952. A method for estimating heritability. Agron. J., 44: 427-430.

Weber, C.R., L.T. Empig, and J.C. Thorne. 1970. Heterotic performance and combining ability of two-way F_1 soybean hybrids. Crop Sci., 10: 159-160.

الملخص العربي

التحليل الوراثي لصفة المحصول ومكوناته والتبكير فى هجن من فول الصويا

سعيد حليم منصور

قسم بحوث المحاصيل البقولية – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية

أجريت هذه الدراسة خلال ثلاثة مواسم هي ١٩٩٩، ٢٠٠٠ ، ٢٠٠١ بمحطة البحوث الزراعية بإيتاى البارود "زرزورة" محافظة البحيرة حيث أجرى خلال الموسم الأول التهجينين التاليين بين ثلاثة آباء من فول الصويا وكان الهجين الأول (H_2L_{20} x $D_{89-8940}$) والهجين الثانى (H_1L_{68} x $D_{89-8940}$). وفى الموسم الثاني تم زراعة الجيل الأول الهجين وأجرى له تهجين رجعى مع كل من أبويه كما تركت بعض نباتات الجيل الأول تتلقح ذاتيا للحصول على بذور الجيل الثانى وفى هذا الموسم أيضا تم التهجين بين الأباء للحصول على بذور الجيل الأول مرة ثانية. وفى الموسم الثالث تم تقييم كل من الأباء والجيل الأول والجيل الثانى والهجينين الرجعيين، وذلك لكل هجين. أوضحت النتائج أن الجيل الأول الهجين أعطى قوة هجين موجبة معنوية عن متوسط الأبوين فى معظم الصفات المدروسة وكانت قوة الهجين سالبة ومعنوية لصفات طول النبات وميعاد النضج لكل من الهجينين وميعاد التزهير للهجين الأول. وأظهرت النتائج أن معامل التربية الداخلية كان معنويا لكل الصفات المدروسة لكل من الهجينين، و كانت قيمته سالبة لصفة طول النبات وميعاد النضج فى الهجينين وكذا ميعاد التزهير للهجين الأول. وقد ظهر انحراف معنوى للجيل الثانى عن متوسط الجيل الأول وقيمة متوسط الأبوين "E_1" لكل الصفات المدروسة عدا صفة عدد البذور فى القرن لكلا الهجينين. وكذا ظهر

انحراف الهجين الرجعي عن الجيل الأول والأبوين الرجعيين معنويا فى كل الصفات المدروسة عدا صفة عدد الفروع للهجين الأول. وأظهرت النتائج الخاصة بطبيعة فعل الجين أن تأثير الجينات المضيفة كان معنويا فى كل الصفات المدروسة للهجين الثانى وكذا الهجين الأول عدا صفات عدد القرون فى النبات وعدد البذور فى النبات وعدد البذور فى القرن التى كانت غير معنوية. وكذا أثر فعل الجين السيادى كان معنويا عدا صفة عدد القرون للنبات فى الهجين الأول. وكان التأثير التفوقى معنويا لمعظم الصفات المدروسة فى كلا الهجينين. وأظهرت درجة السيادة أن هناك سيادة فائقة فى اتجاه الأب الأكبر قيمة لصفات عدد البذور للنبات وعدد البذور للقرن ومحصول النبات بالجرام. وكانت السيادة جزئية فى باقى الصفات. كما أظهرت النتائج أن المكافئ الوراثي بمعناه الواسع كانت قيمته عالية (أكبر من ٨٠%) لمعظم الصفات المدروسة مما يدل على أن هذه الصفات تتأثر تأثرا ضعيفا بالبيئة عدا صفتى عدد الفروع للنبات وميعاد النضج أقل من ٧٠% أى أن هاتين الصفتين يتأثرا أكثر بالظروف البيئية وهذا متوقع. وأظهرت النتائج أيضا أنه أمكن الحصول على تقدم وراثى متوقع من الانتخاب كانت أعلا قيمة له ٥٠,٨٢% لصفة عدد الفروع للنبات فى الهجين الثانى وكانت أقل قيمة له هى ١% لصفة ميعاد النضج فى الهجين الثاني. ويمكن الاستفادة من هذه الهجن فى استنباط سلالات عالية فى المحصول ومبكرة فى النضج وذلك عن طريق الانتخاب في الأجيال التالية.